

Supplementary Table S1. GO enrichment analysis result.

ONTOLOGY	ID	Description	Gene ratio	Bg ratio	P value	P. adjust	q value	geneID	Count
BP	GO:0009306	protein secretion	10/71	368/18870	1.1296470154172e-06	0.000669097880191798	0.000575181191251761	ADCYAP1/VGF/SYTL4/CPLX1/C1QTNF5/PCSK1/VSNL1/CARTPT/SCG2/CBLN4	10
BP	GO:0035592	establishment of protein localization to extracellular region	10/71	369/18870	1.157701375663e-06	0.000669097880191798	0.000575181191251761	ADCYAP1/VGF/SYTL4/CPLX1/C1QTNF5/PCSK1/VSNL1/CARTPT/SCG2/CBLN4	10
BP	GO:0071692	protein localization to extracellular region	10/71	377/18870	1.40468414315983e-06	0.000669097880191798	0.000575181191251761	ADCYAP1/VGF/SYTL4/CPLX1/C1QTNF5/PCSK1/VSNL1/CARTPT/SCG2/CBLN4	10
BP	GO:0023061	signal release	10/71	484/18870	1.27702344543961e-05	0.00338328814326685	0.0029083991478711	ADCYAP1/VGF/SYTL4/SYP/CPLX1/CRH/VSNL1/CARTPT/SV2B/SYT1	10
BP	GO:0050804	modulation of chemical synaptic transmission	10/71	489/18870	1.3957084908231e-05	0.00338328814326685	0.0029083991478711	GFAP/VGF/SYP/CPLX1/SV2B/RGS4/INA/CACNG3/SYT1/CCL2	10
BP	GO:0099177	regulation of trans-synaptic signaling	10/71	490/18870	1.42055485371596e-05	0.00338328814326685	0.0029083991478711	GFAP/VGF/SYP/CPLX1/SV2B/RGS4/INA/CACNG3/SYT1/CCL2	10
BP	GO:0090278	negative regulation of peptide hormone secretion	4/71	45/18870	2.43979234044947e-05	0.00423076964190188	0.00363692547022172	SYTL4/CRH/VSNL1/CARTPT	4
BP	GO:0009914	hormone transport	8/71	319/18870	2.57741561330947e-05	0.00423076964190188	0.00363692547022172	ADCYAP1/CRYM/VGF/SYTL4/CPLX1/CRH/VSNL1/CARTPT	8
BP	GO:002792	negative regulation of peptide secretion	4/71	46/18870	2.66458549874856e-05	0.00423076964190188	0.00363692547022172	SYTL4/CRH/VSNL1/CARTPT	4
BP	GO:0030072	peptide hormone secretion	7/71	241/18870	3.37111361235378e-05	0.00457492590651684	0.00393277487599363	ADCYAP1/VGF/SYTL4/CPLX1/CRH/VSNL1/CARTPT	7
BP	GO:0051588	regulation of neurotransmitter transport	5/71	99/18870	3.553335175602e-05	0.00457492590651684	0.00393277487599363	GFAP/SYP/CPLX1/SV2B/SYT1	5
BP	GO:002790	peptide secretion	7/71	246/18870	3.84178522590638e-05	0.00457492590651684	0.00393277487599363	ADCYAP1/VGF/SYTL4/CPLX1/CRH/VSNL1/CARTPT	7
BP	GO:1904862	inhibitory synapse assembly	3/71	20/18870	5.55778411352879e-05	0.00584340849877582	0.00502320925054059	GABRG2/GABRA1/CBLN4	3
BP	GO:0015833	peptide transport	7/71	262/18870	5.72482288193572e-05	0.00584340849877582	0.00502320925054059	ADCYAP1/VGF/SYTL4/CPLX1/CRH/VSNL1/CARTPT	7
BP	GO:0001505	regulation of neurotransmitter levels	6/71	188/18870	7.55543114668483e-05	0.00715415016432352	0.00614997108155541	SLC6A12/GFAP/SYP/CPLX1/SV2B/SYT1	6
BP	GO:0017157	regulation of exocytosis	6/71	190/18870	8.01024511050919e-05	0.00715415016432352	0.00614997108155541	SYTL4/SYP/CPLX1/VSNL1/SV2B/SYT1	6
BP	GO:0030073	insulin secretion	6/71	199/18870	0.000103348695263629	0.008219082598396	0.00706542624015921	ADCYAP1/VGF/SYTL4/CPLX1/VSNL1/CARTPT	6
BP	GO:1903532	positive regulation of secretion by cell	7/71	288/18870	0.000103529381925212	0.008219082598396	0.00706542624015921	ADCYAP1/SYTL4/PCSK1/CRH/VSNL1/CARTPT/SYT1	7
BP	GO:0046888	negative regulation of hormone secretion	4/71	67/18870	0.00011792509803309	0.00886920868890978	0.0076242985819732	SYTL4/CRH/VSNL1/CARTPT	4
BP	GO:0006836	neurotransmitter transport	6/71	207/18870	0.000128251031217735	0.00916353618050716	0.00787731333847877	SLC6A12/GFAP/SYP/CPLX1/SV2B/SYT1	6
BP	GO:0048499	synaptic vesicle membrane organization	3/71	28/18870	0.000156301567357929	0.0101407109084232	0.00871732873936862	SYP/CPLX1/SYT1	3
BP	GO:0046879	hormone secretion	7/71	308/18870	0.000156845378951808	0.0101407109084232	0.00871732873936862	ADCYAP1/VGF/SYTL4/CPLX1/CRH/VSNL1/CARTPT	7
BP	GO:0051047	positive regulation of secretion	7/71	310/18870	0.000163216480681409	0.0101407109084232	0.00871732873936862	ADCYAP1/SYTL4/PCSK1/CRH/VSNL1/CARTPT/SYT1	7
BP	GO:0008277	regulation of G protein-coupled receptor signaling pathway	5/71	139/18870	0.000177834614350219	0.010588569329436	0.00910232433976779	RGS7/ADCYAP1/SYP/APLNR/RGS4	5
BP	GO:0001975	response to amphetamine	3/71	31/18870	0.000212733246085009	0.0121598323462191	0.0104530399234192	RGS7/HPRT1/RGS4	3
BP	GO:0046928	regulation of neurotransmitter secretion	4/71	82/18870	0.000257915228578723	0.014175417755346	0.0121857114069381	SYP/CPLX1/SV2B/SYT1	4
BP	GO:0042886	amide transport	7/71	354/18870	0.000365807382586337	0.0193606944339213	0.0166431662954486	ADCYAP1/VGF/SYTL4/CPLX1/CRH/VSNL1/CARTPT	7

BP	GO:0016079	synaptic vesicle exocytosis	4/71	96/18870	0.000470850488262529	0.0240301909902555	0.0206572375865553	SYP/CPLX1/SV2B/SYT1	4
BP	GO:0051952	regulation of amine transport	4/71	97/18870	0.000489716997359178	0.0241312272146988	0.0207440920478461	CRH/CARTPT/RGS4/SYT1	4
BP	GO:2000300	regulation of synaptic vesicle exocytosis	3/71	44/18870	0.000605223775068487	0.0288288258190956	0.0247823208949096	SYP/SV2B/SYT1	3
BP	GO:0015837	amine transport	4/71	108/18870	0.000734289542643867	0.0325226458580569	0.0279576647021122	CRH/CARTPT/RGS4/SYT1	4
BP	GO:0014075	response to amine	3/71	47/18870	0.000735035104099679	0.0325226458580569	0.0279576647021122	RGS7/HPRT1/RGS4	3
BP	GO:0048241	epinephrine transport	2/71	11/18870	0.00075104780497962	0.0325226458580569	0.0279576647021122	CRH/CARTPT	2
BP	GO:0099601	regulation of neurotransmitter receptor activity	3/71	48/18870	0.000781931275615107	0.0328641115545291	0.0282512011963724	CRH/CACNG3/CCL2	3
BP	GO:0090276	regulation of peptide hormone secretion	5/71	195/18870	0.00083897522286987	0.0329426776964059	0.0283187395467612	ADCYAP1/SYTL4/CRH/VSNL1/CARTPT	5
BP	GO:002791	regulation of peptide secretion	5/71	198/18870	0.000898406940367582	0.0329426776964059	0.0283187395467612	ADCYAP1/SYTL4/CRH/VSNL1/CARTPT	5
BP	GO:0031630	regulation of synaptic vesicle fusion to presynaptic active zone membrane	2/71	12/18870	0.000899065381497432	0.0329426776964059	0.0283187395467612	CPLX1/SYT1	2
BP	GO:0033605	positive regulation of catecholamine secretion	2/71	12/18870	0.000899065381497432	0.0329426776964059	0.0283187395467612	CARTPT/SYT1	2
BP	GO:1901632	regulation of synaptic vesicle membrane organization	2/71	12/18870	0.000899065381497432	0.0329426776964059	0.0283187395467612	CPLX1/SYT1	2
BP	GO:0090087	regulation of peptide transport	5/71	200/18870	0.00093973573626281	0.0335720591779889	0.0288597790583868	ADCYAP1/SYTL4/CRH/VSNL1/CARTPT	5
BP	GO:0019933	cAMP-mediated signaling	3/71	53/18870	0.00104491870744014	0.0364192398276089	0.0313073204514159	ADCYAP1/APLNR/CAP2	3
BP	GO:0045744	negative regulation of G protein-coupled receptor signaling pathway	3/71	54/18870	0.00110341502312077	0.0375423825723711	0.0322728153378933	RGS7/APLNR/RGS4	3
BP	GO:0050433	regulation of catecholamine secretion	3/71	56/18870	0.00122652532212431	0.0407605740771079	0.0350392913321682	CRH/CARTPT/SYT1	3
CC	GO:0030133	transport vesicle	12/73	431/19886	5.13520369206654e-08	9.24336664571977e-06	7.40550427171701e-06	SVOP/VGF/SYTL4/SYP/C1QTNF5/PCSK1/SV2B/NCALD/GAD2/MAL2/SYT1/SLC30A3	12
CC	GO:0030658	transport vesicle membrane	9/73	236/19886	2.01169602488157e-07	1.20875300571557e-05	9.6841615077797e-06	SVOP/SYTL4/SYP/SV2B/NCALD/GAD2/MAL2/SYT1/SLC30A3	9
CC	GO:0043025	neuronal cell body	12/73	489/19886	2.01458834285928e-07	1.20875300571557e-05	9.6841615077797e-06	ADCYAP1/STMN2/VGF/CPLX1/RTN1/PCSK1/CRH/ELAVL4/SST/UCHL1/SERPINI1/ENC1	12
CC	GO:0030672	synaptic vesicle membrane	7/73	126/19886	3.99248297757564e-07	1.43729387192723e-05	1.15151614300603e-05	SVOP/SYP/SV2B/GAD2/MAL2/SYT1/SLC30A3	7
CC	GO:0099501	exocytic vesicle membrane	7/73	126/19886	3.99248297757564e-07	1.43729387192723e-05	1.15151614300603e-05	SVOP/SYP/SV2B/GAD2/MAL2/SYT1/SLC30A3	7
CC	GO:0070382	exocytic vesicle	8/73	232/19886	2.129197696308e-06	6.387593088924e-05	5.11754534024906e-05	SVOP/SYTL4/SYP/SV2B/GAD2/MAL2/SYT1/SLC30A3	8
CC	GO:0098982	GABA-ergic synapse	5/73	79/19886	1.05839932009789e-05	0.000272159825168028	0.000218046175719414	GABRG2/GABRA1/GAD2/SST/CBLN4	5
CC	GO:0008021	synaptic vesicle	7/73	213/19886	1.31176653733449e-05	0.000295147470900261	0.00023646317844056	SVOP/SYP/SV2B/GAD2/MAL2/SYT1/SLC30A3	7
CC	GO:0044306	neuron projection terminus	5/73	129/19886	0.000112129415824197	0.00217615628806238	0.00174347024248273	SYP/CPLX1/PCSK1/SYT1/UCHL1	5
CC	GO:0098978	glutamatergic synapse	8/73	407/19886	0.000120897571559021	0.00217615628806238	0.00174347024248273	VGF/CPLX1/NPTX2/ELAVL4/MAL2/CACNG3/SYT1/SLC30A3	8
CC	GO:0043204	perikaryon	5/73	149/19886	0.000220125780740504	0.00360205823029916	0.00288585951784202	ADCYAP1/CPLX1/PCSK1/ELAVL4/SERPINI1	5
CC	GO:0031045	dense core granule	3/73	37/19886	0.000337136951963633	0.0050570542794545	0.00405155810693138	SST/SCG2/SYT1	3
CC	GO:0098685	Schaffer collateral - CA1 synapse	4/73	92/19886	0.000365850556596056	0.00506562309133	0.00405842317843398	SYP/CPLX1/INA/CACNG3	4

CC	GO:0098686	hippocampal mossy fiber to CA3 synapse	3/73	42/19886	0.000491603183885034	0.00632061236423615	0.0050638824204699	MAL2/SYT1/SLC30A3	3
CC	GO:0099571	postsynaptic cytoskeleton	2/73	10/19886	0.00058684301700463	0.00704211620405556	0.00564192935646556	NEFM/INA	2
CC	GO:0060198	clathrin-sculpted vesicle	2/73	12/19886	0.00085661928762074	0.00963696698573332	0.00772084489500272	GAD2/SYT1	2
CC	GO:0060076	excitatory synapse	3/73	63/19886	0.00160929477912288	0.0170395917789481	0.0136516027702684	SYP/CACNG3/SYT1	3
CC	GO:0098984	neuron to neuron synapse	6/73	362/19886	0.00213156776078581	0.0206794127518789	0.0165677166491661	RTN1/MAL2/CACNG3/CAP2/SYT1/SLC30A3	6
CC	GO:1902711	GABA-A receptor complex	2/73	19/19886	0.00218282690158721	0.0206794127518789	0.0165677166491661	GABRG2/GABRA1	2
CC	GO:1902710	GABA receptor complex	2/73	21/19886	0.00266797572254068	0.0240117815028661	0.019237509157267	GABRG2/GABRA1	2
CC	GO:0097060	synaptic membrane	6/73	393/19886	0.00320369268061677	0.0274602229767152	0.0220002956012279	SYP/GABRG2/GABRA1/GAD2/CACNG3/SYT1	6
CC	GO:0150034	distal axon	5/73	276/19886	0.00345906184773907	0.0283014151178651	0.0226742331646054	STMN2/SYP/CPLX1/PCSK1/ELAVL4	5
CC	GO:0098992	neuronal dense core vesicle	2/73	25/19886	0.003775425472347	0.0295468080444548	0.0236720041057913	SST/SCG2	2
MF	GO:0005184	neuropeptide hormone activity	4/70	30/18496	4.78556868962608e-06	0.00056708988972069	0.00048359430968853	ADCYAP1/VGF/CRH/CARTPT	4
MF	GO:0160041	neuropeptide activity	4/70	30/18496	4.78556868962608e-06	0.00056708988972069	0.00048359430968853	ADCYAP1/VGF/CRH/CARTPT	4
MF	GO:0005179	hormone activity	6/70	126/18496	8.13949523962355e-06	0.00064302012393026	0.00054834494245885	ADCYAP1/VGF/CRH/CARTPT/CHGB/SST	6
MF	GO:0001965	G-protein alpha-subunit binding	3/70	29/18496	0.000176762978090697	0.0104732064518738	0.00893118205089837	RGS7/RGS4/RGS1	3
MF	GO:0008503	benzodiazepine receptor activity	2/70	11/18496	0.000759617755319699	0.0328541780128606	0.0280168873127658	GABRG2/GABRA1	2
MF	GO:0005516	calmodulin binding	5/70	204/18496	0.00105186648267145	0.0328541780128606	0.0280168873127658	ITPKB/AEBP1/RGS4/SYT1/RGS1	5
MF	GO:0022851	GABA-gated chloride ion channel activity	2/70	13/18496	0.00107201461607254	0.0328541780128606	0.0280168873127658	GABRG2/GABRA1	2
MF	GO:0015108	chloride transmembrane transporter activity	4/70	120/18496	0.00111056113751604	0.0328541780128606	0.0280168873127658	SLC6A12/GABRG2/GABRA1/ANO3	4
MF	GO:0005237	inhibitory extracellular ligand-gated monoatomic ion channel activity	2/70	14/18496	0.0012476270131466	0.0328541780128606	0.0280168873127658	GABRG2/GABRA1	2
MF	GO:0008509	monoatomic anion transmembrane transporter activity	4/70	141/18496	0.0020098992030018	0.0457401160304653	0.0390055619713495	SLC6A12/GABRG2/GABRA1/ANO3	4
MF	GO:0004890	GABA-A receptor activity	2/70	19/18496	0.00231595524204888	0.0457401160304653	0.0390055619713495	GABRG2/GABRA1	2
MF	GO:0099095	ligand-gated monoatomic anion channel activity	2/70	19/18496	0.00231595524204888	0.0457401160304653	0.0390055619713495	GABRG2/GABRA1	2
MF	GO:0015103	inorganic anion transmembrane transporter activity	4/70	153/18496	0.00270276123483031	0.0492734163580602	0.0420186362014105	SLC6A12/GABRG2/GABRA1/ANO3	4

**Supplementary Table S2.** KEGG enrichment analysis result.

category	subcategory	ID	Description	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
Organismal Systems	Nervous system	hsa04727	GABAergic synapse	89/8538	1.27522276480515e-05	0.00110944380538048	0.00100675481431986	SLC6A12/GABRG2/GABRA1/GAD2/GNG2	5
Environmental Information Processing	Signaling molecules and interaction	hsa04080	Neuroactive ligand-receptor interaction	370/8538	0.000232396519949048	0.0101092486177836	0.00917354684009402	ADCYAP1/VGF/CRH/GABRG2/GABRA1/APLNR/SST	7
Organismal Systems	Nervous system	hsa04721	Synaptic vesicle cycle	79/8538	0.00258595185616931	0.07499260382891	0.0680513646360345	SLC6A12/CPLX1/SYT1	3
Human Diseases	Substance dependence	hsa05032	Morphine addiction	91/8538	0.00386165764637984	0.0839910538087616	0.0762169272311811	GABRG2/GABRA1/GNG2	3
Human Diseases	Substance dependence	hsa05033	Nicotine addiction	41/8538	0.00898928505704227	0.156413559992535	0.141936079848036	GABRG2/GABRA1	2
Environmental Information Processing	Signal transduction	hsa04371	Apelin signaling pathway	140/8538	0.0126761039477189	0.160592764115613	0.145728461084949	KLF2/APLNR/GNG2	3
Human Diseases	Cardiovascular disease	hsa05418	Fluid shear stress and atherosclerosis	141/8538	0.0129212568828655	0.160592764115613	0.145728461084949	DUSP1/KLF2/CCL2	3
Organismal Systems	Nervous system	hsa04723	Retrograde endocannabinoid signaling	149/8538	0.0149810702584114	0.162919139060224	0.14783950912906	GABRG2/GABRA1/GNG2	3
Organismal Systems	Digestive system	hsa04971	Gastric acid secretion	76/8538	0.0289626568288974	0.279972349346008	0.254058393235942	EZR/SST	2
Environmental Information Processing	Signal transduction	hsa04024	cAMP signaling pathway	226/8538	0.0439570673880667	0.348868571948489	0.316577651495906	ADCYAP1/CRH/SST	3
Organismal Systems	Environmental adaptation	hsa04713	Circadian entrainment	97/8538	0.0452239423785886	0.348868571948489	0.316577651495906	ADCYAP1/GNG2	2
Metabolism	Glycan biosynthesis and metabolism	hsa00533	Glycosaminoglycan biosynthesis - keratan sulfate	14/8538	0.0481198030273777	0.348868571948489	0.316577651495906	CHST6	1