

Supplemental Information

hUC-MSC-mediated recovery of subacute spinal cord injury through enhancing the pivotal subunits $\beta 3$ and $\gamma 2$ of the GABA_A receptor

Tingting Cao ^{a, 1}, Huan Chen ^{a, 1}, Weiping Huang ^{a, 1}, Sisi Xu ^a, Peilin Liu ^a, Weiwei Zou ^a, Mao Pang ^{b, c, d}, Ying Xu ^{b, c, d}, Xiaochun Bai ^a, Bin Liu ^{b, c, d}, Limin Rong ^{b, c, d}, Zhong-Kai Cui ^{a, *}, Mangmang Li ^{a, *}

a. Department of Cell Biology, School of Basic Medical Sciences, Southern Medical University, Guangzhou, 510515, China.

b. Department of Spine Surgery, The Third Affiliated Hospital of Sun Yat-sen University, Guangzhou, China

c. Guangdong Provincial Center for Engineering and Technology Research of Minimally Invasive Spine Surgery, 510630, China

d. Guangdong Provincial Center for Quality Control of Minimally Invasive Spine Surgery, 510630, China

¹These authors contributed equally to this work.

*To whom correspondence should be addressed. E-mail: zhongkaicui@smu.edu.cn, mangmangli@smu.edu.cn

Supplemental Experimental Procedures

Isolation and expansion of hUC-MSCs

Briefly, umbilical cord tissues collected within 2 h were disinfected with 75% ethanol and washed with 0.9% sodium chloride. Two arteries and one vein within the umbilical cord were dissected with surrounding Wharton's Jelly and mechanically cut into 1-cm³ fragments, then digested in a mixed enzyme solution consisting of 10 mg/ml type I collagenase (Thermo fisher, 17100017) and 1.25 mg/ml hyaluronidase (Sigma, H3506-500mg) for ~3 h. Undigested tissue was removed by filtration and the released cells were washed twice with PBS and cultured in the hUC-MSC growth medium (low-glucose DMEM (Corning, 10-014-CV) containing 10% FBS, 1% glutamine (Corning, 25-005-CI), 1% MEM Nonessential Amino Acids (Thermo fisher, 11140050) and 1x penicillin/streptomycin (Corning, 30-002-CI-100ml)). Once the culture attained 80% confluency, the outgrown cells were passaged three times to remove unwanted cells and obtain the highest purity fraction for further study.

Human cell quantification

The number of survived hUC-MSCs transplanted in rat spinal cord was quantified through amplifying human-specific gene *Xrcc5* in genomic DNA from the rat spinal cord using quantitative real-time PCR (qPCR). Basically, certain amount of spinal cord specimens and/or cells were lysed in the house-made DNA extraction buffer (1 M Tris-HCl (pH 8.0), 0.5 M EDTA, 10% SDS, 5 M NaCl and 10 mg/ml proteinase K in ddH₂O) by agitating at 55°C overnight. DNA was precipitated and dissolved in 10 mM Tris-HCl. DNA concentrations were measured using the NanoDrop-1000 (Thermo Fisher Scientific, Inc., USA). qPCR was performed to quantify the level of *Xrcc5* from 100 ng of genomic DNA in a 10- μ l PCR reaction volume on the StepOnePlus™ system (Applied Biosystems-Thermo Fisher Scientific, USA). Serial dilutions of human

genomic DNA from hUC-MSCs (1000, 100, 10 and 1 cell) mixed with genomic DNA from plain rat spinal cord were used as the standard curve, and the theoretical number of hUC-MSCs in rat spinal cord was calculated accordingly.

Cell-labeling with DiD or DiR and *in vivo* imaging

hUC-MSCs were labeled using lipophilic tracers DiD (aatbio, #22033) or DiR (aatbio, #22070) which are well excited at 633 nm and 750 nm, respectively. Briefly, 1×10^6 cells/ml were incubated with 5 μ M of DiD or DiR working solution for 20 min at 37 °C. The labeled cells were washed twice before resuspending in 40ul of PBS for intrathecal injection using a micro-injection pump (R404, RWD, PRC). 5cm spinal cord tissue (from 1cm rostral to 4 cm caudal from lesion epicenter) was harvested at day 10 (d10) and day 20 (d20) post-transplantation and fluorescent images of spine transplanted with or without labeled MSCs were acquired using In vivo Imaging System FX Pro (Bruker, MIAB1339627).

Principal component analysis (PCA)

The top 1000 DEGs with the most differences (Sort by standard deviation value between samples) were used to perform PCA. Plot3D (v1.3) R package was used to plot the figure.

Axon regeneration of mature cortical neuron *in vitro*

Primary cultures of rat cortical neurons and mature cortical axon scrape assay were performed as described previously [1]. Briefly, brains were removed from E18 Sprague-Dawley rat fetuses and cortical tissues were dissected and minced into small pieces. Chunks of cortex were dissociated in the dissection medium (DMEM (Corning, 10-013) supplemented with the B-27™ Supplement (Thermo Fisher, 17504044), 1 mM sodium pyruvate (Solarbio, sp0100), and 10 μ g/ml gentamicin (Macklin, G810322-25g)) containing 4.2 mg/ml papain (KEH, 9001-73-4) and 0.02 mg/ml DNase I (Roche,

4716728001) for 1 h at 37 °C under gentle shaking. After enzyme digestion, cells were further dispersed by mechanical trituration and filtered through a 70- μ m cell strainer. Cells were resuspended in the Neurobasal (Gibco, 21103-049) supplemented with the B-27, 0.5 mM GultaMAX-I (Thermo Fisher, 35050061), and 10 μ g/ml gentamicin. 1.6×10^5 cells/well were plated in 24-well culture plates coated with 10 μ g/ml poly-D-lysine (Sigma, P6407-5MG). 50% of culture medium was replaced every 7 days. On day 21 *in vitro* (DIV), 24-well cultures were scraped using the tip of a 10- μ l pipette tip. Co-culture with hUC-MSCs was started 12 h post injury. Neurons were co-cultured with 0.8×10^4 hUC-MSCs, plated in the 24-well trans-well upper chamber with a 0.4- μ m filter membrane (Corning, 353095) for 7 days. 50 ng/ml recombinant human BDNF (rhBDNF; Genscript, Z03208) was used as positive control. Cultures were then fixed and immunostained with different primary and secondary antibodies (Table S3). Images were obtained on an Olympus Fluoview FV1000 inverted fluorescence microscope. The immunofluorescence intensity of each protein was determined using the ImageJ software.

Reference

1. Huebner EA, Kim BG, Duffy PJ, Brown RH, Strittmatter SM. A multi-domain fragment of Nogo-A protein is a potent inhibitor of cortical axon regeneration via Nogo receptor 1. *J Biol Chem.* 2011; 286: 18026-36.

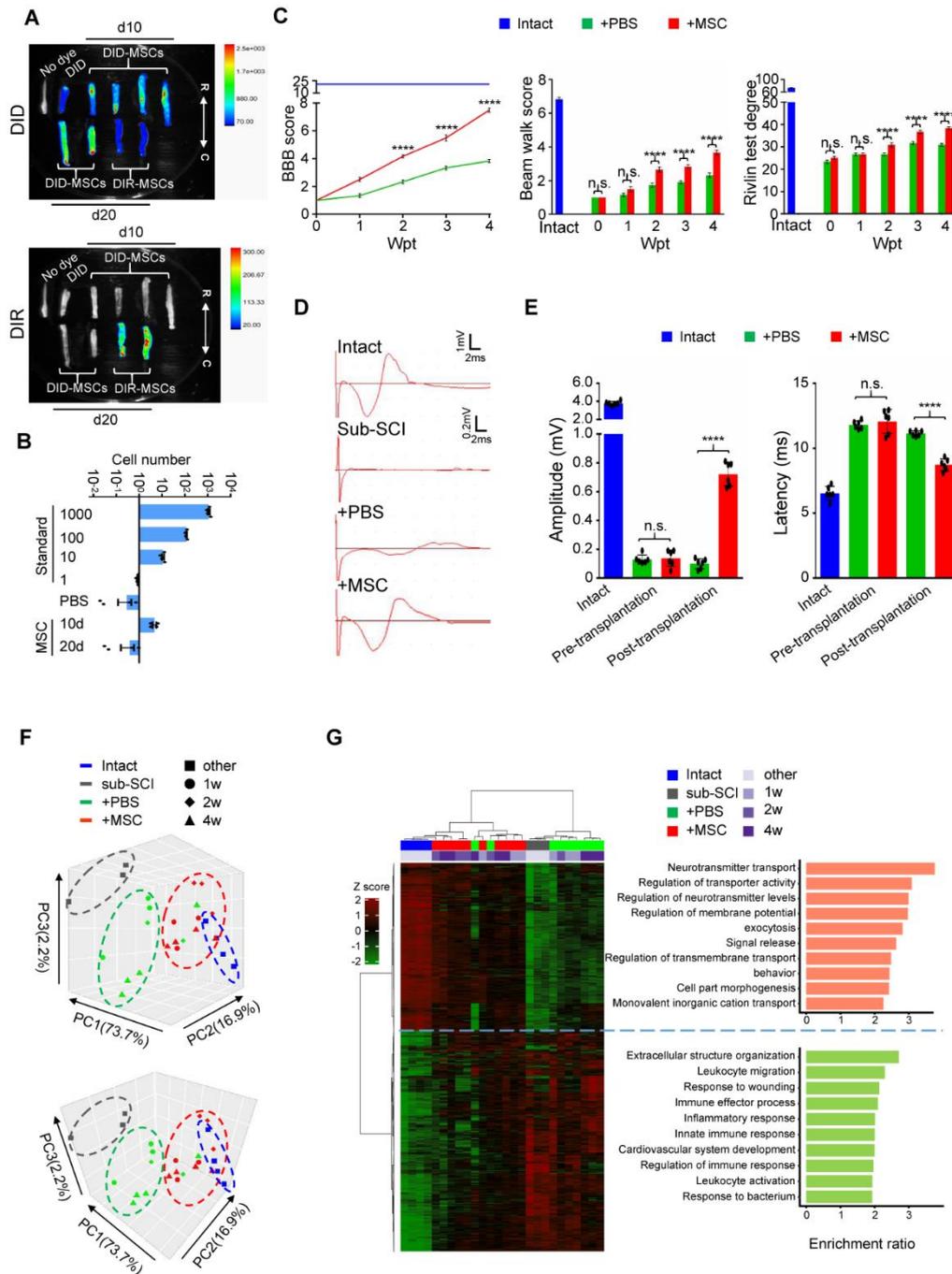


Figure S1 hUC-MSC transplantation exhibits functional recovery in the rat model of subacute SCI. (A) Representative fluorescence images of 5-cm rat spinal cords dissected after intrathecally injected with hUC-MSCs labeled with DiD (top) or DIR (bottom) at day 10 (d10) and day 20 (d20) post-transplantation. The spinal cords injected with PBS or DID working solution were used as negative controls. R, rostral;

C, caudal. (B) Real-time qPCR to quantify the number of survived hUC-MSCs in the rat spinal cords at d10 and d20 post-transplantation (n = 4). Data are presented as mean \pm SEM. (C) A series of behavioral tests to evaluate the effects of hUC-MSCs on the functional recovery after SCI (n = 12/group/time point). The color key is used for C and E. Data are presented as mean \pm SEM. n.s., not significant; **** $p < 0.0001$ by two-way ANOVA. (D) Representative MEP recordings of rats treated with or without hUC-MSCs at 4 wpt (n = 6/group). (E) Quantification and statistical analyses of D. Data are presented as mean \pm SEM. n.s., not significant; **** $p < 0.0001$ by one-way ANOVA. (F) PCA of all samples. (G) Heat map of hierarchical clustering of all 26 samples based on the top 5000 DEGs.

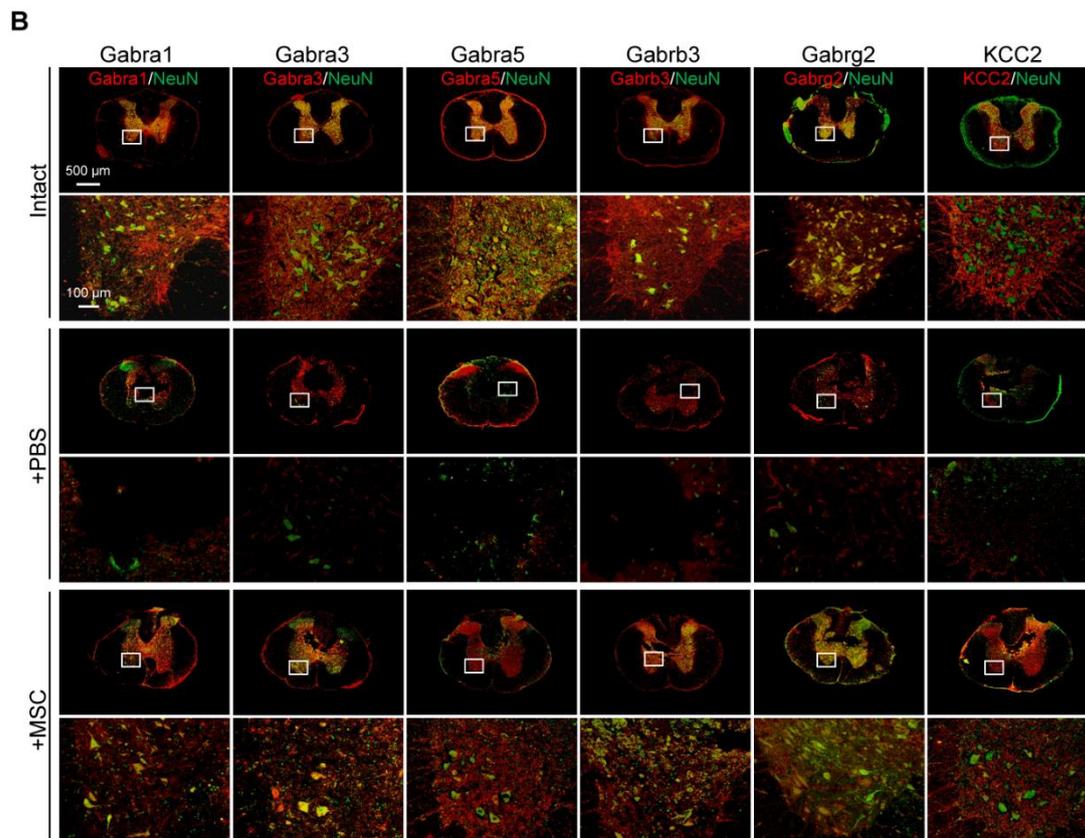
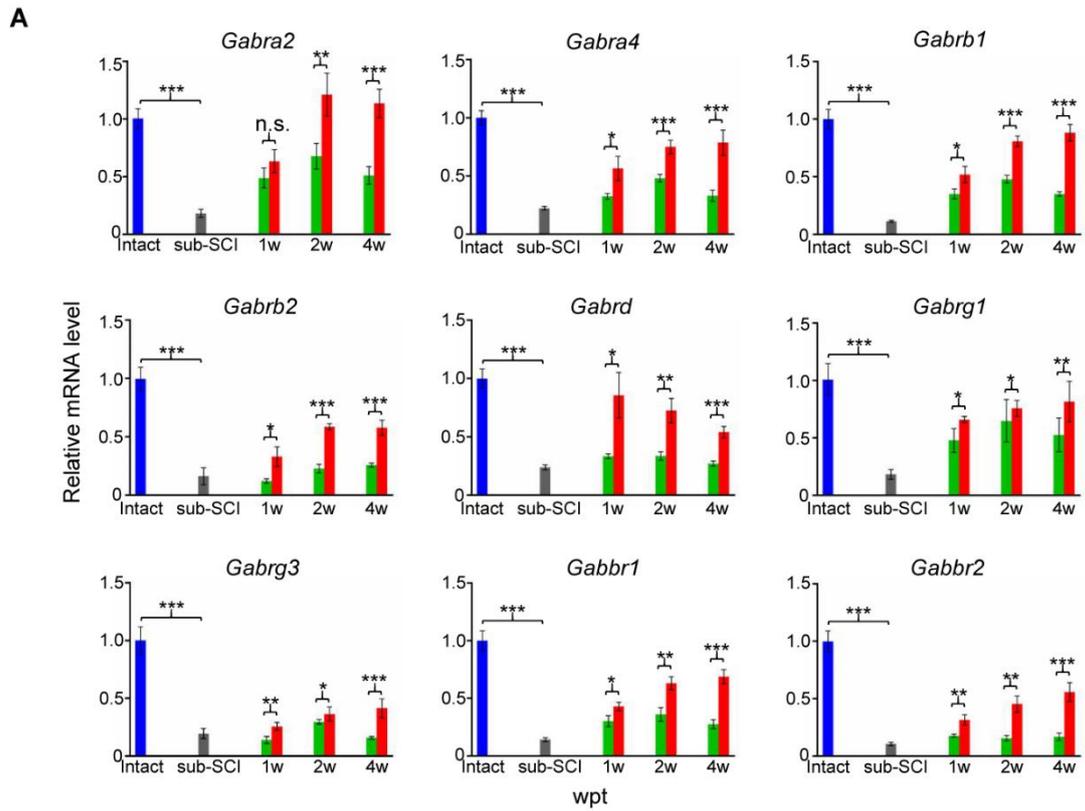


Figure S2 hUC-MSC transplantation increases GABA_ARs in the injured spinal cord. (A) Time course of real-time PCR validation of hUC-MSC-activated GABA

receptor subunits in rat model of subacute SCI treated with or without hUC-MSCs (n = 3). Results are displayed as mean \pm SEM. * p < 0.05; ** p < 0.01; *** p < 0.001 by two-way ANOVA. (B) Representative IF images of transverse spinal cord sections from the Intact, -MSC and +MSC groups at 4 wpt immunostained with Gabra1, Gabra3, Gabra5, Gabrb3, Gabrg2, KCC2 (red) and NeuN (green). Lower panels, higher magnification view of the region indicated by the white rectangle in main panels. Scale bar, 500 μ m (main panels), 100 μ m (lower panels).

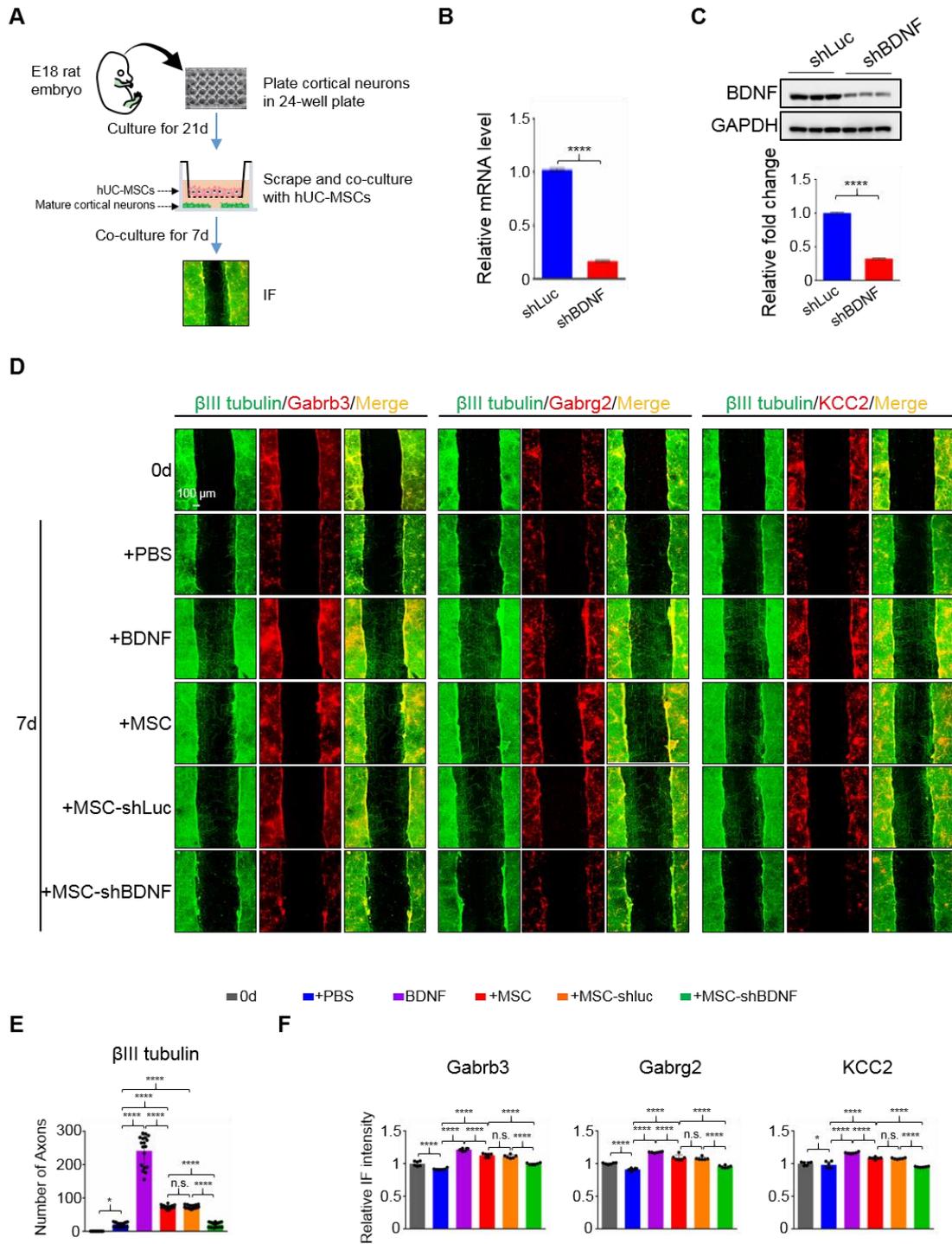


Figure S3 BDNF knockdown abrogates the effects of hUC-MSCs on axonal regeneration and the induction of GABA_ARs in neurons after axonal lesion *in vitro*.

(A) Schematic for hUC-MSC-mediated mature cortical axon regeneration. (B) Real time-PCR to measure BDNF knockdown in hUC-MSCs (n = 3/group). Luc, Luciferase.

(C) Western blot analysis of BDNF in hUC-MSCs transduced with the lentiviral shLuc and shBDNF (n = 3/group). In B and C, data are presented as mean \pm SEM. **** p < 0.0001 by unpaired 2-tailed Student's t test. (D) Representative IF staining of regenerated axons of mature cortical neurons at day 0 and 7 after axotomy with indicated treatments, *i.e.*, 50 ng/ml rhBDNF, without or with hUC-MSCs, shLuc and shBDNF transduced hUC-MSCs. Neurons were co-stained with anti- β III tubulin (green), and anti-Gabrb3 (red), Gabrg2 (red), and KCC2 (red) antibodies. Scratch and non-scratch zones are denoted by the curly braces. Scale bars, 100 μ m. (E) Quantification of β III tubulin-positive regenerating axons in the scratched zone in D (n = 18). (F) Quantification of immunofluorescence intensities for Gabrb3, Gabrg2 and KCC2 in the non-scratched zone in D (n = 6). The color key is used for both E and F. The images were obtained from three independent experiments. The data are presented as mean \pm SEM. n.s., not significant; * p < 0.05, ** p < 0.01, *** p < 0.001, **** p < 0.0001 by one-way ANOVA.

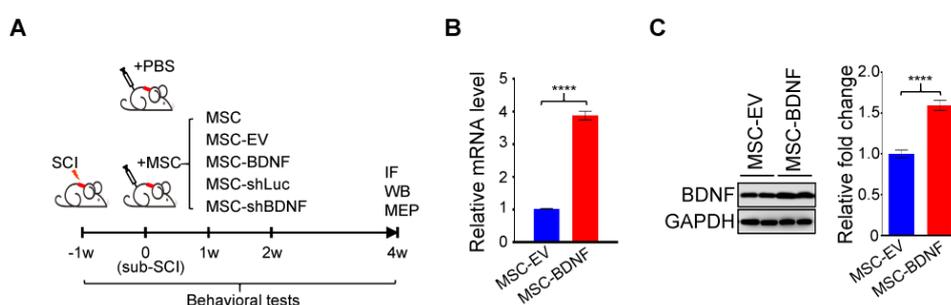


Figure S4 The transplantation of hUC-MSCs with either BDNF overexpression or knockdown into rats with sub-SCI. (A) The experimental scheme for investigating the role of BDNF secreted by hUC-MSCs on SCI repair in the rat models. (B) Real-time qPCR validation of BDNF overexpression in hUC-MSCs (n = 3/group). (C)

Western blotting and quantification analyses of BDNF overexpression in hUC-MSCs (n = 3/group). Results are displayed as mean \pm SEM. **** $p < 0.0001$ by one-way ANOVA.

Table S1. GO and KEGG analyses of hUC-MSC-reversed genes.

Repressed genes_GO	ONTOLGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:0043062	BP	23/260	extracellular structure organization	35/19943	2.4824E-11	2.5295E-06	1.9514E-10	1.13769E-07	Col3a1/Fap/Emilin1/Postn/Col4a	23
GO:0031589	BP	23/260	cell-substrate adhesion	34/19943	1.9514E-10	1.13769E-07	9.6057E-08	Col3a1/Bst1/Col1a1/Emilin1/Plau/Postn	23	
GO:0030198	BP	20/260	extracellular matrix organization	26/9/19943	4.2256E-10	1.18978E-07	1.8498E-07	Col13a1/Col1a1/Fap/Emilin1/Postn/Col4a	20	
GO:0097530	BP	14/260	granulocyte migration	14/3/19943	5.7516E-09	2.68257E-06	2.2649E-06	Trpv4/Bst1/Lbp/Adam8/Trem1/Ccl6/Spp	14	
GO:0097529	BP	16/260	myeloid leukocyte migration	20/3/19943	1.0842E-08	4.21408E-06	3.558E-06	Trpv4/Bst1/Emilin1/Lbp/Adam8/Trem1/C	16	
GO:0010810	BP	16/260	regulation of cell-substrate adhesion	22/0/19943	3.3824E-08	1.1964E-05	1.0101E-05	Bst1/Col1a1/Emilin1/Plau/Postn/Nin1/D	16	
GO:0001525	BP	24/260	angiogenesis	49/4/19943	3.3513E-08	1.1364E-05	1.0101E-05	Angptl4/Emilin1/Plau/Hmox1/Col4a3/Ad	24	
GO:0050707	BP	16/260	regulation of cytokine secretion	22/5/19943	4.6315E-08	1.39073E-05	1.1742E-05	Trpv4/Postn/Htr2b/Tlr8/Srgn/Twist1/Ubr	16	
GO:0050663	BP	17/260	cytokine secretion	25/6/19943	4.7709E-08	1.39073E-05	1.1742E-05	Trpv4/Postn/Htr2b/Trem1/Tlr8/Srgn/Twi	17	
GO:0071295	BP	8/260	cellular response to vitamin	44/1/19943	8.8517E-08	2.4285E-05	2.0504E-05	Col1a1/Postn/Folr2/Pawr/Kank2/Ltpb1/S	8	
GO:0042060	BP	22/260	wound healing	44/4/19943	9.7164E-08	2.51763E-05	2.1257E-05	Col1a1/Plau/Postn/Hmox1/Nin1/Sdc1/C	22	
GO:0007160	BP	15/260	cell-matrix adhesion	20/9/19943	1.0892E-07	2.67376E-05	2.2575E-05	Col13a1/Bst1/Emilin1/Plau/Postn/Nin1/I	15	
GO:0010876	BP	20/260	lipid localization	37/8/19943	1.3305E-07	3.02624E-05	2.5553E-05	Trpv4/Bst1/Lbp/Trem1/Ccl6/Spp1/Csar1	20	
GO:0006899	BP	19/260	lipid transport	34/3/19943	1.3626E-07	3.02624E-05	2.5553E-05	Trpv4/Sca2a1/RG1305807/Msr1/Lbp/P	19	
GO:0038063	BP	5/260	collagen-activated tyrosine kinase recep	11/1/19943	1.5705E-07	3.32971E-05	2.8113E-05	Col1a1/Col4a1/Col4a2/Col4a3/Col4a6	5	
GO:0050710	BP	68/19943	negative regulation of cytokine secretion	2/260	2.3873E-07	4.84101E-05	4.0873E-05	Tlr8/Srgn/Fbln1/Fn1/Lrrc32/Serpinc1a/Ar	9	
GO:0050727	BP	19/260	regulation of inflammatory response	35/8/19943	2.6385E-07	5.12756E-05	4.3293E-05	Trpv4/Bst1/Enpp3/Lbp/Adam8/Il20rb/Vsi	19	
GO:1990266	BP	11/260	neutrophil migration	11/6/19943	3.519E-07	6.56502E-05	5.543E-05	Bst1/Lbp/Adam8/Trem1/Ccl6/Spp1/Csar	11	
GO:0071621	BP	11/260	granulocyte chemotaxis	11/1/19943	4.5602E-07	7.33401E-05	6.1922E-05	Trpv4/Bst1/Lbp/Trem1/Ccl6/Spp1/Csar1	11	
GO:0001819	BP	16/260	negative regulation of cytokine producti	26/7/19943	4.8042E-07	7.46886E-05	6.3061E-05	Hmox1/Lbp/Il20rb/Vsig4/Tlr8/Srgn/Twist	16	
GO:0031670	BP	10/260	cellular response to nutrient	98/19943	6.1068E-07	7.84974E-05	7.3876E-05	Col1a1/Postn/Hmox1/Folr2/Ptgs2/Pawr/I	10	
GO:1993531	BP	15/260	negative regulation of secretion by cell	23/9/19943	6.1472E-07	7.84974E-05	7.3876E-05	Hmox1/Tlr8/Igfbp3/Srgn/Crh/Fbln1/Fn1/I	15	
GO:0067121	BP	9/260	terpenoid metabolic process	76/19943	6.3029E-07	7.84974E-05	7.3876E-05	Akr1b10/Adh1/Adh6/Chr/Rbp1/Hmgcs2/I	9	
GO:0033273	BP	13/260	response to vitamin	17/8/19943	6.3785E-07	7.84974E-05	7.3876E-05	Col1a1/Postn/Folr2/Spp1/Ptgs2/Pawr/Ka	13	
GO:0038065	BP	5/260	collagen-activated signaling pathway	14/1/19943	6.5911E-07	8.78312E-05	7.4157E-05	Col1a1/Col4a1/Col4a2/Col4a3/Col4a6	5	
GO:0031950	BP	15/260	cellular response to transforming growth	24/6/19943	8.9553E-07	0.00021472E	9.6965E-05	Col1a1/Htra3/Emilin1/Ltpb2/Postn/Cola	15	
GO:0071559	BP	15/260	response to transforming growth factor	25/3/19943	1.2593E-06	0.00011546E	0.00011300E	Col1a1/Htra3/Emilin1/Ltpb2/Postn/Cola	15	
GO:0016101	BP	8/260	diterpenoid metabolic process	64/1/19943	1.7653E-06	0.000200817	0.00016955E	Akr1b10/Adh1/Adh6/Chr/Rbp1/Arres2/I	8	
GO:0051048	BP	15/260	negative regulation of secretion	26/8/19943	2.5731E-06	0.00027244E	0.00023028E	Hmox1/Tlr8/Igfbp3/Srgn/Crh/Fbln1/Fn1/I	15	
GO:0050900	BP	17/260	leukocyte migration	34/1/19943	2.6731E-06	0.00027048E	0.00023392E	Trpv4/Bst1/Emilin1/Fun7/Lbp/Adam8/Tre	17	
GO:0019126	BP	17/260	regulation of lipid metabolic process	35/4/19943	4.4092E-06	0.000428423	0.00036172E	Angptl4/Apobec1/Htr2b/Apoc1/Dab2/Igf	17	
GO:0031990	BP	9/260	response to corticosteroid	15/260	4.8042E-07	7.46886E-05	6.3061E-05	Hmox1/Lbp/Il20rb/Vsig4/Tlr8/Srgn/Twist	9	
GO:0006720	BP	10/260	isoprenoid metabolic process	98/19943	5.4265E-06	0.000506184	0.00042738E	Akr1b10/Adh1/Adh6/Chr/Rbp1/Hmgcs2/I	10	
GO:0001523	BP	7/260	retinoid metabolic process	55/1/19943	7.0258E-06	0.000642519	0.00054249E	Akr1b10/Adh1/Adh6/Rbp1/Arres2/Cyp2	7	
GO:0007984	BP	17/260	response to nutrient	37/1/19943	8.1839E-06	0.00073403E	0.00061975E	Col1a1/Postn/Hmox1/Folr2/Spp1/Ptgs2/I	17	
GO:0032496	BP	20/260	response to lipopolysaccharide	49/8/19943	9.2923E-06	0.000817726E	0.00069042E	Plau/Lbp/Mrc1/Cd68/Csar1/Igfbp3/Ptgs2	20	
GO:0002792	BP	11/260	negative regulation of peptide secretion	16/3/19943	1.0008E-05	0.000864357E	0.00072979E	Tlr8/Srgn/Chr/Fbln1/Fn1/Lrrc32/Serpinc1	11	
GO:0031819	BP	19/260	positive regulation of cytokine producti	24/6/19943	8.9553E-07	0.00021472E	9.6965E-05	Col1a1/Htra3/Emilin1/Ltpb2/Postn/Cola	19	
GO:0010811	BP	12/260	positive regulation of cell-substrate adh	13/5/19943	1.1265E-05	0.000938184E	0.00079213E	Emilin1/Nin1/Dab2/Spp1/Alb3b/Nid1/F	12	
GO:0030595	BP	10/260	leukocyte chemotaxis	20/8/19943	1.9379E-05	0.001585699E	0.00133883E	Trpv4/Bst1/Lbp/Adam8/Trem1/Ccl6/Spp	10	
GO:1990222	BP	6/260	regulation of neutrophil migration	44/1/19943	2.1596E-05	0.001736632E	0.00146627E	Bst1/Lbp/Adam8/Csar1/Pawr/Edna	6	
GO:0051216	BP	12/260	cartilage development	21/4/19943	2.5684E-05	0.002030339E	0.00171425E	Trpv4/Col1a1/Col20a1/Col7a1/Wnt5b/Sn	12	
GO:0050709	BP	10/260	negative regulation of protein secretion	14/9/19943	2.6628E-05	0.002069899E	0.00174764E	Tlr8/Srgn/Fbln1/Fn1/Lrrc32/Serpinc1a/Ar	10	
GO:1990554	BP	8/260	positive regulation of lipid localization	92/1/19943	2.7119E-05	0.00207352E	0.00137071E	Trpv4/Nin1/Ptgs2/Apoc1/Dab2/Spp1/Crh/I	8	
GO:0044403	BP	16/260	symbiont process	36/8/19943	2.8737E-05	0.002161742E	0.0018252E	Hmox1/Hmox1/Lbp/Hm2/Siglec1/Trem1/I	16	
GO:0044419	BP	17/260	interspecies interaction between organi	41/0/19943	2.9528E-05	0.002186003E	0.0018457E	Hmox1/Ly2/Hmox1/Lbp/Hm2/Siglec1/T	17	
GO:1990592	BP	10/260	regulation of lipid localization	15/3/19943	3.3437E-05	0.002436736E	0.00205738E	Trpv4/Msr1/Ptgs2/Apoc1/Dab2/Spp	10	
GO:0030593	BP	8/260	neutrophil chemotaxis	96/1/19943	3.6942E-05	0.002650735E	0.00223806E	Bst1/Lbp/Trem1/Ccl6/Spp1/Csar1/Edna	8	
GO:0051384	BP	14/260	response to glucocorticoid	29/7/19943	3.8138E-05	0.002695056E	0.00227548E	Soc1/Igfbp7/Ptgs2/Ahr/Gb2/Crt/Fn1/Hp	14	
GO:0043785	BP	17/260	positive regulation of cell adhesion	42/4/19943	4.4092E-05	0.003082018E	0.0028022E	Emilin1/Nin1/Adam8/Dab2/Spp1/Alb3b	17	
GO:0042542	BP	11/260	response to hydrogen peroxide	19/4/19943	5.0425E-05	0.003307107E	0.00279225E	Maok13/Cdk1/Col1a1/Hmox1/HK3/Sdc1/I	11	
GO:0072736	BP	7/260	protein activation cascade	74/1/19943	5.0484E-05	0.003307107E	0.00279225E	Col20a1/C1qc/Cfd/Vsig4/Fbln1/F5/C7	7	
GO:0045765	BP	14/260	regulation of angiogenesis	30/5/19943	5.0876E-05	0.003307107E	0.00279225E	Emilin1/Hmox1/Stab1/Col4a2/Csar1/Ptgs	14	
GO:0071622	BP	6/260	regulation of granulocyte chemotaxis	51/1/19943	5.1053E-05	0.003307107E	0.00279225E	Trpv4/Bst1/Lbp/Csar1/Edna/Arres2	6	
GO:0072672	BP	4/260	neutrophil extravasation	17/1/19943	5.8779E-05	0.00375398E	0.00317075E	Adam8/Trem1/Pawr/Prtm3	4	
GO:0031669	BP	13/260	cellular response to nutrient levels	27/4/19943	6.7501E-05	0.004197681E	0.00354417E	Col1a1/Postn/Hmox1/Folr2/Ccl6/Ptgs2/I	13	
GO:0050673	BP	17/260	epithelial cell proliferation	44/1/19943	7.2917E-05	0.004474793E	0.00377814E	Fap/Plau/Hmox1/Htr2b/Igfbp3/Dab2/C5	17	
GO:0098542	BP	18/260	defense response to other organism	48/7/19943	7.6659E-05	0.004614664E	0.00389624E	Hmox1/Ly2/Cd8a/Lbp/Hm2/Apobec1/St	18	
GO:0001763	BP	12/260	morphogenesis of a branching structure	24/0/19943	7.8133E-05	0.004614664E	0.00389624E	Col13a1/Col4a1/Cxcr4/Ahr/Mmp14/Edn	12	
GO:0060485	BP	13/260	mesenchyme development	27/8/19943	7.8164E-05	0.004614664E	0.00389624E	Col1a1/Htr2b/Dab2/Edn1/Snai1/Twist1	13	
GO:0070663	BP	12/260	regulation of leukocyte proliferation	24/2/19943	8.4559E-05	0.004929768E	0.00416229E	Lst1/Bst1/Enpp3/Il20rb/Vsig4/Ahr/Pawr/I	12	
GO:1990224	BP	5/260	positive regulation of neutrophil migrati	36/1/19943	9.8174E-05	0.005506899E	0.00464957E	Lbp/Adam8/Csar1/Pawr/Edna	5	
GO:0050866	BP	4/260	negative regulation of cell activation	20/9/19943	9.8464E-05	0.005506899E	0.00464957E	Lst1/Emilin1/Enpp3/Hmox1/Il20rb/Vsig4	4	
GO:0062012	BP	15/260	regulation of small molecule metabolic ;	36/6/19943	9.904E-05	0.005506899E	0.00464957E	Cdk1/Sic7a7/Apoc1/Dab2/Ptgs2/Igfbp3/e	15	
GO:0002526	BP	9/260	acute inflammatory response	14/1/19943	9.9258E-05	0.005506899E	0.00464957E	Lbp/Adam8/Trem1/Il20rb/Vsig4/Ptgs2/P	9	
GO:0007162	BP	13/260	negative regulation of cell adhesion	28/5/19943	0.00010036E	0.005506899E	0.00464957E	Trpv4/Col1a1/Postn/Il20rb/Vsig4/Pawr/I	13	
GO:0002685	BP	11/260	regulation of leukocyte migration	21/0/19943	0.00010273E	0.00551268E	0.00470392E	Trpv4/Bst1/Emilin1/Lbp/Adam8/Csar1/P	11	
GO:0042573	BP	4/260	retinoic acid metabolic process	20/1/19943	0.00011603E	0.005124583E	0.00517109E	Adh1/Adh6/Rbp1/Dhrs9	4	
GO:0051448	BP	13/260	connective tissue development	29/5/19943	0.00014143E	0.007270985E	0.00613902E	Trpv4/Col1a1/Col20a1/Col7a1/Wnt5b/Sn	13	
GO:0090050	BP	4/260	positive regulation of cell migration Invo	21/1/19943	0.00014187E	0.007270985E	0.00613902E	Hmox1/Ptgs2/Anxa1/Rhoj	4	
GO:1991342	BP	14/260	regulation of vasculature development	33/8/19943	0.00015104E	0.007656829E	0.00646479E	Emilin1/Hmox1/Stab1/Col4a2/Csar1/Ptgs	14	
GO:0061138	BP	22/1/19943	morphogenesis of a branching epithelium	22/1/19943	0.00016107E	0.008077531E	0.00682E	Col4a1/Cxcr4/Ahr/Mmp14/Edna/Tgm2/I	4	
GO:1990521	BP	5/260	regulation of macrophage migration	40/1/19943	0.00016423E	0.008108897E	0.00684648E	Trpv4/Emilin1/Csar1/Mmp14/Arres2	5	
GO:0034330	BP	12/260	cell junction organization	26/0/19943	0.00016597E	0.008108897E	0.00684648E	Trpv4/Sgpb/Snai1/Mmp14/Alu/Chd5/I	12	
GO:0006026	BP	13/260	cell chemotaxis	30/0/19943	0.00016691E	0.008108897E	0.00684648E	Trpv4/Bst1/Lbp/Adam8/Trem1/Ccl6/Spp	13	
GO:0070664	BP	7/260	cellular response to extracellular stimuli	90/1/19943	0.00017565E	0.008445787E	0.00713092E	Lst1/Enpp3/Il20rb/Vsig4/Pawr/Lrrc32/Ce	7	
GO:1993672	BP	5/260	positive regulation of sprouting angiogen	41/1/19943	0.00018506E	0.008795632E	0.0074263E	Hmox1/Ptgs2/Anxa1/Rhoj/Igfbp3	5	
GO:0002695	BP	18/19943	negative regulation of leukocyte activati	188/19943	0.0001867E	0.008795632E	0.0074263E	Lst1/Enpp3/Hmox1/Il20rb/Vsig4/Pawr/I	18	
GO:0002062	BP	8/260	chondrocyte differentiation	12/3/19943	0.00021221E	0.009850687E	0.0083171E	Col20a1/Col7a1/Wnt5b/Wnt2/Ccn2/Mu	8	
GO:0051249	BP	16/260	regulation of lymphocyte activation	43/7/19943	0.00021332E	0.00985				

BP	GO:0050873	brown fat cell differentiation	5/260	49/19943	0.00043263	0.016659081	0.01406555	Trpv4/Ptgs2/Arh4a/Rarres2/Lrg1	5
BP	GO:1904950	negative regulation of establishment of	10/260	209/19943	0.00043511	0.016659081	0.01406555	Trb8/Srgn/Fbn1/Fn1/Lrrc32/Serpin1a/Ar	10
BP	GO:0051299	retina vasculature morphogenesis in car	3/260	12/19943	0.00044771	0.016659081	0.01406555	Col4a1/Lama1/Rhoj	3
BP	GO:0035455	response to interferon-alpha	4/260	28/19943	0.00045175	0.016659081	0.01406555	Ifitm1/Ifitm2/Piscr1/Ifitm6	4
BP	GO:1903557	positive regulation of tumor necrosis fac	7/260	105/19943	0.00045362	0.016659081	0.01406555	Lbp/Adam8/Twist1/Llra5/Pf4/Cyp24/Asp	7
BP	GO:0006953	acute-phase response	5/260	50/19943	0.00047564	0.017331138	0.01463298	Lbp/Ptgs2/Piscr1/Fn1/Hp	5
BP	GO:0001666	response to hypoxia	15/260	424/19943	0.00047984	0.017348774	0.01464787	Angpt4/Plau/Postn/Hmox1/Adam8/igfb	15
BP	GO:0071496	cellular response to external stimulus	15/260	425/19943	0.00049117	0.017640769	0.01494944	Col1a1/Postn/Hmox1/Folr2/Cd68/Tlr8/Pt	15
BP	GO:0007219	Notch signaling pathway	9/260	175/19943	0.00049823	0.017695218	0.01494027	Trpv4/Gjb2/Snai1/Hmox14/Aluab/Cdh5/F	9
BP	GO:0060350	endochondral bone morphogenesis	6/260	77/19943	0.00050688	0.017695218	0.01494037	Col13a1/Trpv4/Col1a1/Col20a1/Col7a1/A	6
BP	GO:0032755	positive regulation of interleukin-6 prod	7/260	107/19943	0.00050839	0.017695218	0.01494037	Mapk13/Trpv4/Lbp/Tlr8/Twist1/Llra5/Sp	7
BP	GO:0006929	substrate-dependent cell migration	4/260	29/19943	0.0005187	0.017695218	0.01494037	Adam8/Fbn1/Fn1/Snai2	4
BP	GO:0001706	endoderm formation	5/260	51/19943	0.00052179	0.017695218	0.01494037	Col7a1/Col4a2/Mmp14/Fn1/Itga5	5
BP	GO:0000302	response to reactive oxygen species	12/260	295/19943	0.00052236	0.017695218	0.01494037	Mapk13/Cdk1/Col1a1/Hmox1/H3/Scd1/C	12
BP	GO:0034329	cell junction assembly	10/260	214/19943	0.00052357	0.017695218	0.01494037	Trpv4/Gjb2/Snai1/Hmox14/Aluab/Cdh5/F	10
BP	GO:0046651	lymphocyte proliferation	12/260	286/19943	0.00053825	0.018020656	0.01521515	Lst1/Bat1/Id2b/Vsig4/Cxcr4/Ahr/Pawr/E	12
BP	GO:0046890	regulation of lipid biosynthetic process	9/260	177/19943	0.00054093	0.018020656	0.01521515	Htr2b/Apoc1/Dab2/igfbp7/Ptgs2/Snai1/A	9
BP	GO:0032963	collagen metabolic process	7/260	109/19943	0.0005683	0.018502485	0.01562196	Col1a1/Fap/Emilin1/Mmp14/Ccn2/Cyp24	7
BP	GO:0042362	fat-soluble vitamin biosynthetic process	3/260	13/19943	0.0005687	0.018502485	0.01562196	Pitp/Snai1/Snai2	3
BP	GO:0032943	mononuclear cell proliferation	12/260	298/19943	0.00057126	0.018502485	0.01562196	Lst1/Bat1/Id2b/Vsig4/Cxcr4/Ahr/Pawr/E	12
BP	GO:0007492	endoderm development	6/260	79/19943	0.00058153	0.018638887	0.01573713	Col7a1/Col4a2/Dab2/Mmp14/Fn1/Itga5	6
BP	GO:0048762	mesenchymal cell differentiation	10/260	217/19943	0.00058346	0.018638887	0.01573713	Col1a1/Htr2b/Dab2/Efnb1/Snai1/Twist1/	10
BP	GO:0060706	cell differentiation involved in embryoni	4/260	30/19943	0.00059242	0.01866921	0.01576273	Snai1/Krt8/Mdf1/Krt19	4
BP	GO:0050729	positive regulation of inflammatory resp	8/260	144/19943	0.00061357	0.019205937	0.0162159	Trpv4/Lbp/Adam8/Ptgs2/Ednra/Tgm2/Os	8
BP	GO:1905517	macrophage migration	5/260	53/19943	0.0006241	0.019405259	0.01638419	Trpv4/Emilin1/Csar1/Mmp14/Rarres2	5
BP	GO:0013835	cytolysis	4/260	31/19943	0.00067327	0.020658819	0.01744259	Lyz2/Lbp/Pgylrp1/Pf4	4
BP	GO:0010712	regulation of collagen metabolic process	5/260	54/19943	0.00068055	0.020745639	0.0173159	Fap/Emilin1/Ccn2/Cyp24/Itgb1	5
BP	GO:0002687	positive regulation of leukocyte migrati	8/260	147/19943	0.00070276	0.021229162	0.01792414	Trpv4/Lbp/Adam8/Csar1/Pawr/Mmp14/I	8
BP	GO:0040875	skeletal system morphogenesis	11/260	263/19943	0.00070551	0.021229162	0.01792414	Col13a1/Trpv4/Col1a1/Col20a1/Col7a1/A	11
BP	GO:0045766	positive regulation of angiogenesis	9/260	184/19943	0.00071468	0.021295439	0.0179801	Hmox1/Csar1/Ptgs2/Cxcr4/Cdh5/Ama1/I	9
BP	GO:0042268	regulation of cytolysis	3/260	14/19943	0.00071685	0.021295439	0.0179801	Lbp/Pgylrp1/Pf4	3
BP	GO:0032964	collagen biosynthetic process	5/260	55/19943	0.00074074	0.021731885	0.0183486	Col1a1/Emilin1/Ccn2/Cyp24/Itgb1	5
BP	GO:0034754	cellular hormone metabolic process	7/260	114/19943	0.00074284	0.021731885	0.0183486	Dab2/Spp1/Akr1a1/Adh1/Adh6/Rbp1/D	7
BP	GO:0002274	myeloid leukocyte activation	10/260	224/19943	0.00074552	0.021731885	0.0183486	Batf3/Enpp3/Hmox1/Lbp/Lat/Vsig4/Tlr6/I	10
BP	GO:0090022	regulation of neutrophil chemotaxis	4/260	32/19943	0.00076164	0.022063811	0.01862885	Bst1/Lbp/Csar1/Ednra	4
BP	GO:0045216	cell-cell junction organization	8/260	149/19943	0.00076781	0.022105375	0.01866394	Trpv4/Gjb2/Snai1/Cdh5/Ceacam1/Lsr/Pt	8
BP	GO:0008015	blood circulation	16/260	493/19943	0.00079429	0.022612296	0.01909195	Trpv4/Sico4a5/Postn/Hmox1/Htr2b/Er3/P	16
BP	GO:0043903	regulation of symbiosis, encompassing r	10/260	226/19943	0.00079809	0.022612296	0.01909195	Hmox1/Hmox1/Lbp/Itfm2/Cxcr4/Piscr1/C	10
BP	GO:0015850	response to retinoic acid	8/260	150/19943	0.00080211	0.022612296	0.01909195	Col1a1/Igfbp7/Stra6/Id2b/Adh1/Igfbp2/F	8
BP	GO:0033280	response to vitamin D	5/260	56/19943	0.00080481	0.022612296	0.01909195	Spp1/Ptgs2/Kank2/Ltbp1/Snai2	5
BP	GO:0014032	neural crest cell development	6/260	85/19943	0.00085754	0.023536435	0.01987221	Htr2b/Efnb1/Twist1/Ednra/Fn1/Snai2	6
BP	GO:1903901	negative regulation of viral life cycle	6/260	85/19943	0.00085754	0.023536435	0.01987221	Ifitm1/Hmox1/Ifitm2/Piscr1/Ceacam1/If	6
BP	GO:0006775	fat-soluble vitamin metabolic process	4/260	33/19943	0.00085789	0.023536435	0.01987221	Pitp/Snai1/Rbp1/Snai2	4
BP	GO:2000778	positive regulation of interleukin-6 secr	4/260	39/19943	0.00085789	0.023536435	0.01987221	Trpv4/Tlr8/Twist1/Llra5	4
BP	GO:0015850	organic hydroxy compound transport	11/260	270/19943	0.00087478	0.023621422	0.01994397	RGD1305807/Msr1/Ptbp/Apoc1/Dab2/Sc	11
BP	GO:0031099	regeneration	12/260	313/19943	0.00087739	0.023621422	0.01994397	Cdk1/Plau/Postn/Hmox1/Nvni1/Spp1/Cs5	12
BP	GO:0042953	lipoprotein transport	3/260	15/19943	0.00088746	0.023621422	0.01994397	Msr1/Apobec1/Cubn	3
BP	GO:0044872	lipoprotein localization	3/260	15/19943	0.00088746	0.023621422	0.01994397	Msr1/Apobec1/Cubn	3
BP	GO:0047484	regulation of response to osmotic stress	3/260	15/19943	0.00088746	0.023621422	0.01994397	Trpv4/Ptgs2/Ptger2	3
BP	GO:0006959	humoral immune response	9/260	190/19943	0.00089762	0.023621422	0.01994397	Col20a1/Clec4e/Cld/Vsig4/Pgylrp1/Rarres2	9
BP	GO:0050792	regulation of viral process	9/260	190/19943	0.00089762	0.023621422	0.01994397	Ifitm1/Hmox1/Ifitm2/Cxcr4/Piscr1/Chmp	9
BP	GO:0032945	negative regulation of mononuclear cell	6/260	86/19943	0.00091196	0.023629864	0.0199511	Lst1/Id2b/Vsig4/Pawr/Lrrc32/Ceacam1	6
BP	GO:0050672	negative regulation of lymphocyte prolif	6/260	86/19943	0.00091196	0.023629864	0.0199511	Lst1/Id2b/Vsig4/Pawr/Lrrc32/Ceacam1	6
BP	GO:0045071	negative regulation of viral genome repl	5/260	58/19943	0.00094525	0.024357205	0.0205652	Ifitm1/Ifitm2/Piscr1/Ceacam1/Ifitm6	5
BP	GO:0042572	retinal metabolic process	4/260	34/19943	0.00096241	0.024662951	0.02082335	Akr1b10/Adh1/Adh6/Rbp1	4
BP	GO:0043901	negative regulation of multi-organism pi	9/260	193/19943	0.00100241	0.025487452	0.02151949	Ifitm1/Hmox1/Lbp/Ifitm2/Piscr1/Fbn1/C	9
BP	GO:0001704	formation of primary germ layer	7/260	120/19943	0.00100551	0.025487452	0.02151949	Col7a1/Col4a2/Snai1/Mmp14/Fn1/Pdzb/I	7
BP	GO:0032102	positive regulation of response to exterr	12/260	320/19943	0.00106135	0.026695272	0.02253927	Trpv4/Lbp/Adam8/Csar1/Ptgs2/Cxcr4/I	12
BP	GO:0009266	response to temperature stimulus	10/260	235/19943	0.00107386	0.026695272	0.02253927	Trpv4/Hmox1/Htr2b/igfbp7/Ptgs2/Cxcr4	10
BP	GO:0051180	vitamin transport	4/260	35/19943	0.00107556	0.026695272	0.02253927	RGD1305807/Folr2/Stra6/Cubn	4
BP	GO:0043518	negative regulation of DNA damage resp	3/260	16/19943	0.00108178	0.026695272	0.02253927	Snai1/Twist1/Snai2	3
BP	GO:0060192	negative regulation of lipase activity	3/260	16/19943	0.00108178	0.026695272	0.02253927	Angpt4/Apoc1/Anxa1	3
BP	GO:0006956	complement activation	5/260	60/19943	0.00110314	0.027047568	0.02283672	Col20a1/Clec4e/Cld/Vsig4/I	5
BP	GO:0035461	bone morphogenesis	7/260	122/19943	0.00110765	0.027047568	0.02283672	Col1a1/Trpv4/Col1a1/Col20a1/Col7a1/A	7
BP	GO:0051250	negative regulation of lymphocyte activ	8/260	158/19943	0.00112313	0.027282808	0.02303534	Lst1/Id2b/Vsig4/Pawr/Pgylrp1/Lrrc32/A	8
BP	GO:0014031	mesenchymal cell development	6/260	90/19943	0.00115666	0.02795154	0.02359966	Htr2b/Efnb1/Twist1/Ednra/Fn1/Snai2	6
BP	GO:0010812	negative regulation of cell-substrate ad	5/260	61/19943	0.00118903	0.028439058	0.02401158	Col1a1/Postn/Mmp14/Fbn1/Fzd7	5
BP	GO:0009615	response to virus	11/260	281/19943	0.0012079	0.02871098	0.02424117	Batf3/Ifitm1/Cd8a/Ifitm2/Apobec1/Tlr8/F	11
BP	GO:0032368	regulation of lipid transport	7/260	124/19943	0.00121777	0.02871098	0.02424117	Trpv4/Ptbp/Apoc1/Dab2/Spp1/igfbp3/Ch	7
BP	GO:0019217	regulation of fatty acid metabolic proc	6/260	91/19943	0.00122502	0.02871098	0.02424117	Apoc1/Ptgs2/Cld/Itfm2/Twist1/Anxa1/Ce	6
BP	GO:0048864	stem cell development	6/260	91/19943	0.00122502	0.02871098	0.02424117	Htr2b/Efnb1/Twist1/Ednra/Fn1/Snai2	6
BP	GO:0050678	regulation of epithelial cell proliferation	13/260	371/19943	0.0012321	0.028732473	0.02425932	Plau/Hmox1/Htr2b/igap3/Dab2/Csar1/I	13
BP	GO:0014033	neural crest cell differentiation	6/260	92/19943	0.00129643	0.029313139	0.02474958	Htr2b/Efnb1/Twist1/Ednra/Fn1/Snai2	6
BP	GO:0045833	negative regulation of lipid metabolic pr	6/260	92/19943	0.00129643	0.029313139	0.02474958	Apobec1/Apoc1/Snai1/Cd8a/Ceacam1/Si	6
BP	GO:0016114	terpenoid biosynthetic process	3/260	17/19943	0.00130099	0.029313139	0.02474958	Rbp1/Hmgcs2/Dnm9	3
BP	GO:0035461	vitamin transmembrane transport	3/260	17/19943	0.00130099	0.029313139	0.02474958	RGD1305807/Folr2/Stra6	3
BP	GO:0070234	positive regulation of T cell apoptotic pr	3/260	17/19943	0.00130099	0.029313139	0.02474958	Adam8/Siglec1/Ceacam1	3
BP	GO:2000108	positive regulation of leukocyte apoptot	4/260	37/19943	0.0013293	0.02966441	0.02504617	Adam8/Siglec1/Anxa1/Ceacam1	4
BP	GO:0015718	monocarboxylic acid transport	8/260	163/19943	0.00137098	0.030404698	0.02567121	Trpv4/Sico2a1/RGD1305807/Sic1e6a3/S	8
BP	GO:0045600	positive regulation of fat cell differentia	5/260	63/19943	0.00137551	0.030404698	0.02567121	Ptgs2/Wnt5b/Rarres2/Snai2/Zbtb7c	5
BP	GO:0042246	tissue regeneration	6/260	94/19943	0.00144875	0.031872559	0.02691055	Plau/Postn/Nvni1/Fzd7/Mustn1/Anxa1	6
BP	GO:0035988	chondrocyte proliferation	3/260	18/19943	0.00154523	0.033801113	0.03265386	Mmp14/Ccn2/Mustn1	3
BP	GO:0043900	regulation of multi-organism process	14/260	428/19943	0.00155091	0.033801113	0.03265386	Cdk1/Ifitm1/Plau/Hmox1/Lbp/Ifitm2/Cxcr	14
BP	GO:0016032	viral process	11/260	291/19943	0.00159535	0.034505856	0.02913388	Ifitm1/Hmox1/Ifitm2/Siglec1/Lrrc15/C	11
BP	GO:0045995	regulation of embryonic development	7/260	130/19943	0.00160025	0.034505856	0.02913388	Snai1/Lama2/Wnt2b/Fzd7/Lama1/Six1/Pi	7
BP	GO:0090049	regulation of cell migration involved in s	4/260	39/19943	0.00162211	0.034505856	0.02913388	Hmox1/Ptgs2/Anxa1/Rhoj	4
BP	GO:0031349	positive regulation of defense response	13/260	383/19943	0.00163579	0.034505856	0.02913388	Trpv4/Lbp/Adam8/Tlr8/LOC102547056/P	13
BP	GO:0032102	negative regulation of response to exte	12/260	337/19943	0.001645	0.034505856	0.02913388	Plau/Enpp3/Id2b/Vsig4/Spp1/Er3/Tspan8/K	12
BP	GO:0010957	negative regulation of vitamin D biosynt	2/260	5/19943	0.00164983	0.034505856	0.02913388	Snai1/Snai2	2
BP	GO:0038044	transforming growth factor-beta secreti	2/260	5/19943	0.00164983	0.034505856	0.02913388	Fbn1/Fn1	2
BP	GO:0042098	T cell proliferation	9/260	208/19943	0.00168545	0.035093381	0.02962994	Id2b/Vsig4/Cxcr4/Pawr/Efnb1/Lrrc32/Ig	9
BP	GO:0046718	viral entry into host cell	5/260	66/19943	0.00169452	0.035125424			

BP	GO:0032623	interleukin-2 production	5/260	69/19943	0.0020647	0.040067088	0.03382933	Il2orb/Vsig4/Pawr/Anxa1/Ceacam1	5
BP	GO:0044409	entry into mitosis	5/260	69/19943	0.0020647	0.040067088	0.03382933	Ittm1/Ittm2/Siglec1/Ceacam1/Ittm6	5
BP	GO:0051806	entry into cell of other organism involved in sy	5/260	69/19943	0.0020647	0.040067088	0.03382933	Ittm1/Ittm2/Siglec1/Ceacam1/Ittm6	5
BP	GO:0051828	entry into other organism involved in sy	5/260	69/19943	0.0020647	0.040067088	0.03382933	Ittm1/Ittm2/Siglec1/Ceacam1/Ittm6	5
BP	GO:0051701	interaction with host	7/260	136/19943	0.00207036	0.040067088	0.03382933	Ittm1/Ittm2/Siglec1/Chmp4c/Fbln1/Ceac	7
BP	GO:0010759	positive regulation of macrophage chem	3/260	20/19943	0.00211901	0.040339034	0.03405893	Trpv4/Csar1/Rarres2	3
BP	GO:0030852	regulation of granulocyte differentiation	3/260	20/19943	0.00211901	0.040339034	0.03405893	Clqc/Rbp1/Ceacam1	3
BP	GO:0071706	tumor necrosis factor superfamily cytok	6/260	175/19943	0.00214478	0.040663572	0.03433295	Lbp/Adam8/Twist1/Cidea/Llra5/Pf4/Cyp	6
BP	GO:0042130	negative regulation of T cell proliferator	5/260	70/19943	0.00220026	0.041546568	0.03507848	Il2orb/Vsig4/Pawr/Lrrc32/Ceacam1	5
BP	GO:0002698	negative regulation of immune effector	7/260	138/19943	0.00224872	0.042290427	0.03570653	Enpp3/Hmx1/Il2orb/Vsig4/Pglyrp1/Anxa	7
BP	GO:0019058	viral life cycle	9/260	218/19943	0.00231886	0.04334457	0.03659656	Ittm1/Hmx1/Ittm2/Siglec1/Lrrc15/Piscr	9
BP	GO:0042304	regulation of fatty acid biosynthetic proc	4/260	43/19943	0.00233681	0.04334457	0.03659656	Apoc1/Ptgs2/Anxa1/Ceacam1	4
BP	GO:0071219	cellular response to molecule of bacteri	11/260	307/19943	0.00242255	0.04334457	0.03659656	Plau/Lbp/Mrc1/Cd68/Piscr1/Piscr2/Lcn2/	11
BP	GO:0032760	positive regulation of tumor necrosis fac	6/260	104/19943	0.00242438	0.04334457	0.03659656	Lbp/Twist1/Llra5/Pf4/Cyp2j4/Spn2	6
BP	GO:0010894	positive regulation of lipid storage	3/260	21/19943	0.00244853	0.04334457	0.03659656	Msr1/Apoc4/Cidea	3
BP	GO:0006069	ethanol oxidation	2/260	6/19943	0.00245347	0.04334457	0.03659656	Adh1/Adh6	2
BP	GO:0033015	tetrapyrrole catabolic process	2/260	6/19943	0.00245347	0.04334457	0.03659656	Hmx1/Cubn	2
BP	GO:0046137	negative regulation of vitamin metabol	2/260	6/19943	0.00245347	0.04334457	0.03659656	Sna1/Sna2	2
BP	GO:0051005	negative regulation of lipoprotein lipase	2/260	6/19943	0.00245347	0.04334457	0.03659656	Angpt4/Apoc1	2
BP	GO:0032370	positive regulation of lipid transport	5/260	184/19943	0.00245347	0.04334457	0.03659656	Angpt4/Apoc1	5
BP	GO:0070562	regulation of vitamin D receptor signal	2/260	6/19943	0.00245347	0.04334457	0.03659656	Kank2/Sna2	2
BP	GO:1902219	negative regulation of intrinsic apoptot	2/260	6/19943	0.00245347	0.04334457	0.03659656	Ptgs2/Ptgs2	2
BP	GO:0042742	defense response to bacterium	10/260	264/19943	0.00253429	0.044435811	0.03751791	Ly2b/Lbp/Stab1/Trem1/Csar1/Pglyrp1/Lc	10
BP	GO:0035456	response to interferon-beta	4/260	44/19943	0.00254451	0.044447966	0.03752818	Ittm1/Ittm2/Piscr1/Ittm6	4
BP	GO:0042445	hormone metabolic process	9/260	222/19943	0.00261986	0.045593389	0.03849528	Pon3/Dab2/Sppl1/Akr1b10/Adh1/Adh6/C	9
BP	GO:0032370	positive regulation of lipid transport	5/260	184/19943	0.00262345	0.049135343	0.04148581	Ly2/Trem1/RT1-M2/LOC102547056/Cdh	5
BP	GO:0017015	regulation of transforming growth facto	6/260	106/19943	0.00265763	0.046800812	0.03890682	Htra3/Emlin1/Dab2/Cidea/Ltbp1/Lrg1	6
BP	GO:0060416	response to growth hormone	4/260	45/19943	0.00276454	0.04748597	0.04009321	Igfbp3/Hp/Hmgcs2/Gdf15	4
BP	GO:0051222	positive regulation of protein transport	14/260	456/19943	0.00276934	0.04748597	0.04009321	Trpv4/Postn/Htr2b/Tlr8/Ptgs2/Twist1/Ce	14
BP	GO:0009110	extracellular matrix component	3/260	22/19943	0.00280805	0.04797337	0.04050473	Ptpr/Sna1/Sna2	3
BP	GO:0015711	organic anion transport	14/260	458/19943	0.00288025	0.049027258	0.04139455	Trpv4/Sico2a1/Sic7a7/Sico4a5/RGD13058C	14
BP	GO:0022408	cell killing	8/260	184/19943	0.00292345	0.049135343	0.04148581	Ly2/Trem1/RT1-M2/LOC102547056/Cdh	8
BP	GO:0048754	branching morphogenesis of an epitheli	8/260	184/19943	0.00292345	0.049135343	0.04148581	Col4a1/Cxcr4/Ahr/Nmnp1A/Ednra/Wnt2b,	8
BP	GO:0008630	intrinsic apoptotic signaling pathway in	6/260	108/19943	0.00292874	0.049135343	0.04148581	Hmx1/Ier3/Piscr1/Sna1/Uaca/Sna2	6
BP	GO:1903844	regulation of cellular response to transk	6/260	108/19943	0.00292874	0.049135343	0.04148581	Htra3/Emlin1/Dab2/Cidea/Ltbp1/Lrg1	6
BP	GO:0032965	regulation of collagen biosynthetic proc	4/260	46/19943	0.00299726	0.049925791	0.0421532	Emlin1/Ccn2/Cyp2j4/Ltbp1	4
BP	GO:0070207	protein homotrimerization	4/260	46/19943	0.00299726	0.049925791	0.0421532	Emlin1/Lcn2/Ceacam1/Cubn	4
BP	GO:0022408	negative regulation of cell-cell adhesi	8/260	185/19943	0.00302201	0.04999065	0.04220796	Trpv4/Il2orb/Vsig4/Pawr/Lrrc32/Anxa1/C	8
BP	GO:0050714	positive regulation of protein secretio	11/260	318/19943	0.00302259	0.04999065	0.04220796	Trpv4/Postn/Htr2b/Tlr8/Twist1/Cx/Ceac	11
CC	GO:0062023	collagen-containing extracellular matrix	28/260	217/19943	6.209E-20	2.85587E-16	2.445E-16	Col1a1/Emlin1/Col20a1/Postn/Col4a1/Cc	28
CC	GO:0031012	extracellular matrix	34/260	362/19943	1.5476E-19	3.60906E-16	3.0472E-16	Col13a1/Col1a1/Emlin1/Col20a1/Postn/C	34
CC	GO:0044420	extracellular matrix component	12/260	51/19943	1.8918E-12	2.20582E-09	1.8624E-09	Col1a1/Emlin1/Col4a1/Col4a2/Col18a1/I	12
CC	GO:0005581	collagen trimer	12/260	68/19943	7.132E-11	5.54397E-08	4.6809E-08	Col13a1/Col1a1/Emlin1/Clqc/Col4a1/Co	12
CC	GO:0005604	basement membrane	14/260	105/19943	9.2179E-11	6.14175E-08	5.1856E-08	Col4a1/Col1a1/Col4a2/Col15a1/LOC1083	14
CC	GO:0009651	basement membrane collagen trimer	5/260	7/19943	7.4515E-09	3.15944E-06	2.6585E-06	Col4a1/Col4a2/Col13a1/Col4a5/Col4a6	5
CC	GO:0005587	collagen type IV trimer	4/260	6/19943	4.1488E-07	6.91068E-05	5.8348E-05	Col4a1/Col4a2/Col4a5/Col4a6	4
CC	GO:0098642	network-forming collagen trimer	4/260	6/19943	4.1488E-07	6.91068E-05	5.8348E-05	Col4a1/Col4a2/Col4a5/Col4a6	4
CC	GO:0098645	collagen network	4/260	6/19943	4.1488E-07	6.91068E-05	5.8348E-05	Col4a1/Col4a2/Col4a5/Col4a6	4
CC	GO:0098644	complex of collagen trimers	5/260	16/19943	1.4076E-06	0.000164131	0.00013858	Col1a1/Col4a1/Col4a2/Col4a5/Col4a6	5
CC	GO:0034358	plasma lipoprotein particle	4/260	28/19943	0.00045175	0.016659081	0.01406555	Ptpr/Apoc4/Apoc1/Lsr	4
CC	GO:1900777	lipoprotein particle	4/260	28/19943	0.00045175	0.016659081	0.01406555	Ptpr/Apoc4/Apoc1/Lsr	4
CC	GO:0032594	protein-lipid complex	4/260	30/19943	0.00059242	0.01866921	0.01576273	Ptpr/Apoc4/Apoc1/Lsr	4
CC	GO:0034361	very-low-density lipoprotein particle	3/260	17/19943	0.00130099	0.029313139	0.02474958	Apoc4/Apoc1/Lsr	3
CC	GO:0034385	triglyceride-rich plasma lipoprotein part	3/260	17/19943	0.00130099	0.029313139	0.02474958	Apoc4/Apoc1/Lsr	3
CC	GO:0016942	insulin-like growth factor binding protei	2/260	5/19943	0.00164983	0.03405856	0.02913388	Igfbp3/Igfbp6	2
CC	GO:0036454	growth factor complex	2/260	5/19943	0.00164983	0.03405856	0.02913388	Igfbp3/Igfbp6	2
CC	GO:0031021	platelet alpha granule	3/260	19/19943	0.00181856	0.03703825	0.03127099	Igfbp3/Pf4/IF	3
CC	GO:0042629	maximal cell granule	3/260	20/19943	0.00211901	0.040339034	0.03405893	Lar/Srgn/Anxa1	3
CC	GO:0009897	external side of plasma membrane	13/260	399/19943	0.00233918	0.04334457	0.03659656	Cd8a/Enpp3/Scart1/Folr2/Tlr8/RT1-M2/S-	13
CC	GO:0034364	high-density lipoprotein particle	3/260	21/19943	0.00244853	0.04334457	0.03659656	Ptpr/Apoc4/Apoc1	3
MF	GO:0005201	extracellular matrix structural constitue	14/260	62/19943	4.8072E-14	7.47359E-11	6.3101E-11	Col13a1/Col1a1/Emlin1/Col4a1/Col4a2/C	14
MF	GO:0005178	integrin binding	11/260	129/19943	1.0261E-06	0.00012934	0.0001092	Fap/Emlin1/Dab2/Sppl1/Tspn8/Mmp14	11
MF	GO:0005220	insulin-like growth factor binding	6/260	28/19943	1.3726E-06	0.000164131	0.00013858	Htra3/Igfbp3/Igfbp7/Ccn2/Igfbp2/Igfbp6	6
MF	GO:0050839	cell adhesion molecule binding	14/260	232/19943	3.2368E-06	0.00025838	0.00021815	Fap/Emlin1/Postn/Adam8/Dab2/Sppl1/Ts	14
MF	GO:0038024	cargo receptor activity	9/260	89/19943	2.4269E-06	0.00026327	0.00022226	Msr1/Enpp3/Mrc1/Stab1/Scart1/Folr2/D-	9
MF	GO:0019838	growth factor binding	11/260	146/19943	3.4733E-06	0.000352162	0.00029734	Col1a1/Htra3/Ltbp2/Col4a1/Igfbp3/Igfbp	11
MF	GO:0005539	glycosaminoglycan binding	13/260	209/19943	3.85E-06	0.000382053	0.00032257	Col13a1/Ltbp2/Postn/Stab1/Abi3bp/Prelj	13
MF	GO:0008201	heparin binding	10/260	157/19943	4.1884E-05	0.002901711	0.00244996	Col13a1/Ltbp2/Postn/Abi3bp/Prelj/Fn1/I	10
MF	GO:0019588	fibronectin binding	5/260	33/19943	6.3808E-05	0.004021624	0.00339553	Lrrc15/Igfbp3/Fn1/Cn2/Igfbp6	5
MF	GO:0004022	alcohol dehydrogenase (NAD) activity	3/260	8/19943	0.00011687	0.006124583	0.00517109	Adh1/Adh6/Dhrs9	3
MF	GO:0031995	insulin-like growth factor II binding	3/260	8/19943	0.00011687	0.006124583	0.00517109	Igfbp3/Igfbp2/Igfbp6	3
MF	GO:0031994	insulin-like growth factor I binding	3/260	12/19943	0.00044171	0.016659081	0.01406555	Igfbp3/Igfbp2/Igfbp6	3
MF	GO:0005044	scavenger receptor activity	5/260	51/19943	0.00052179	0.017695218	0.01494037	Msr1/Enpp3/Stab1/Scart1/Scarf2	5
MF	GO:0016918	retinal binding	3/260	13/19943	0.0005687	0.018502485	0.01562196	Straf6/Akr1b10/Rbp1	3
MF	GO:0005501	retinoid binding	4/260	31/19943	0.00067327	0.020658919	0.01744259	Straf6/Akr1b10/Rbp1/Pgds	4
MF	GO:0030246	carbohydrate binding	11/260	271/19943	0.0009015	0.023621422	0.01994397	Col20a1/Enpp3/Mrc1/Siglec1/Hs3/Clec4a	11
MF	GO:0050840	extracellular matrix binding	5/260	61/19943	0.00118903	0.02849058	0.02401158	Lrrc15/Sppl1/Sdc1/Nid1/Eln	5
MF	GO:0019840	isoprenoid binding	4/260	37/19943	0.0013293	0.02966441	0.02504617	Straf6/Akr1b10/Rbp1/Pgds	4
MF	GO:1901681	sulfur compound binding	10/260	250/19943	0.00170365	0.03515851	0.02968493	Col13a1/Ltbp2/Postn/Abi3bp/Prelj/Fn1/I	10
MF	GO:0004745	retinol dehydrogenase activity	3/260	20/19943	0.00211901	0.040339034	0.03405893	Adh1/Adh6/Dhrs9	3
MF	GO:0004024	alcohol dehydrogenase activity, zinc-dep	2/260	6/19943	0.00245347	0.04334457	0.03659656	Adh1/Adh6	2
MF	GO:0032027	myosin light chain binding	2/260	6/19943	0.00245347	0.04334457	0.03659656	Igkap3/Cxcr4	2
MF	GO:0005518	collagen binding	5/260	72/19943	0.00249067	0.043835759	0.03701128	Lrrc15/Srgn/Abi3bp/Nid1/Ecm2	5

Repressed genes, KEGG

ID	Description	GeneRatio	RgRatio	pvalue	p.adjust	qvalue	geneID	Count
rno04512	ECM-receptor interaction	9/92	74/6610	6.93784E-07	7.3541E-05	6.7187E-05	Col1a1/Col4a1/Col4a2/Sppl1/Sdc1/Lama2/Fn1/Col	9
rno04974	Protein digestion and absorption	8/92	78/6610	1.09418E-05	0.00057992	0.00052981	Col1a1/Sic7a7/Col4a1/Col4a2/Col15a1/Col18a1/C	8
rno04610	Complement and coagulation cascades	6/92	69/6610	0.000365571	0.01121097	0.0102424	Plau/C1qc/Cfd/C5ar1/F5/C7	6
rno05146	Amoebiasis	7/92	99/6610	0.000423055	0.01121097	0.0102424	Col1a1/Col4a1/Col4a2/Lama2/Fn1/Serpinb1a/Col	7
rno05222	Small cell lung cancer	6/92	84/6610	0.001049059	0.02224005	0.02031862	Col4a1/Col4a2/Ptgs2/Lama2/Fn1/Col4a5	6

Activated genes_GO

ONTOLOGY ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:0006356	neurotransmitter transport	51/373	322/19943	2.17E-32	9.47E-30	7.3752E-30	Cplx1/Grm4/Rph3a/Nsf/Napb/Syt2/Cadps2/Drd2/Cadps/Ncs1/Syr	51
BP	GO:009504 synaptic vesicle cycle	44/373	243/19943	1.46E-30	5.78E-28	4.5005E-28	Cplx1/Grm4/Rapgef4/Napb/Syt2/Cadps2/Drd2/Cadps/Ncs1/Syr	44
BP	GO:007269 neurotransmitter secretion	41/373	204/19943	2.02E-30	6.77E-28	5.2716E-28	Cplx1/Grm4/Rph3a/Nsf/Napb/Syt2/Cadps2/Drd2/Cadps/Ncs1/Syr	41
BP	GO:009643 signal release from synapse	41/373	205/19943	2.48E-30	7.73E-28	6.0185E-28	Cplx1/Grm4/Rph3a/Nsf/Napb/Syt2/Cadps2/Drd2/Cadps/Ncs1/Syr	41
BP	GO:0015905 regulation of neurotransmitter levels	53/373	402/19943	1.45E-29	3.32E-27	2.5819E-27	Cplx1/Grm4/Rph3a/Trh2/Nsf/Napb/Syt2/Cadps2/Drd2/Cadps/Nc	53
BP	GO:0042391 regulation of membrane potential	56/373	464/19943	3.31E-29	7.21E-27	5.6151E-27	Rapgef4/Fgf12/Gabrg2/Gira2/Gabra1/Scn8a/Cacng2/Gjd2/Oprd1	56
BP	GO:0097479 synaptic vesicle localization	39/373	201/19943	2.31E-28	4.46E-26	3.4711E-26	Cplx1/Grm4/Napb/Syt2/Kif5a/Cadps2/Drd2/Cadps/Ncs1/Syn1/Rin	39
BP	GO:009003 vesicle-mediated transport in synapse	43/373	262/19943	4.77E-28	8.65E-26	6.7395E-26	Cplx1/Grm4/Napb/Syt2/Kif5a/Hpca/Cadps2/Drd2/Cadps/Ncs1/Rin	43
BP	GO:0050808 synapse organization	54/373	470/19943	4.2E-27	6.53E-25	5.0886E-25	Cabp1/Rph3a/Rapgef4/Gabrg2/Gira2/Gabra1/Arhgap44/Nptx1/Lr	54
BP	GO:0048489 synaptic vesicle transport	37/373	190/19943	5.18E-27	7.52E-25	5.8526E-25	Cplx1/Grm4/Napb/Syt2/Kif5a/Cadps2/Drd2/Cadps/Ncs1/Rims1/C	37
BP	GO:0097480 establishment of synaptic vesicle localiza	37/373	190/19943	5.18E-27	7.52E-25	5.8526E-25	Cplx1/Grm4/Napb/Syt2/Kif5a/Cadps2/Drd2/Cadps/Ncs1/Rims1/C	37
BP	GO:0016079 synaptic vesicle exocytosis	34/373	153/19943	6.4E-27	8.89E-25	7.0017E-25	Cplx1/Grm4/Napb/Syt2/Cadps2/Drd2/Cadps/Ncs1/Rims1/Chrn4	34
BP	GO:0046928 regulation of neurotransmitter secretion	33/373	148/19943	5.29E-26	4.1E-24	3.1936E-24	Cplx1/Grm4/Napb/Syt2/Drd2/Ncs1/Rims1/Chrn4/Stx1b/Vamp1/	33
BP	GO:0017155 calcium ion regulated exocytosis	36/373	190/19943	7.18E-26	8.24E-24	6.4137E-24	Cplx1/Grm4/Rapgef4/Napb/Syt2/Cadps2/Drd2/Cadps/Ncs1/Rims	36
BP	GO:0034765 regulation of ion transmembrane transp	53/373	483/19943	1.22E-25	1.37E-23	1.0639E-23	Cabp1/Rph3a/Fgf12/Scn8a/Kcnj3/Cacng2/Thy1/Hpca/Drd2/Kcnab	53
BP	GO:0045055 regulated exocytosis	41/373	276/19943	4.85E-25	5.29E-23	4.1173E-23	Cplx1/Grm4/Rapgef4/Napb/Syt2/Cadps2/Drd2/Cadps/Ncs1/Rims	41
BP	GO:0051588 regulation of neurotransmitter transport	35/373	190/19943	9.61E-25	9.97E-23	7.7646E-23	Cplx1/Grm4/Napb/Syt2/Drd2/Ncs1/Rims1/Chrn4/Stx1b/Vamp1/	35
BP	GO:0017158 regulation of calcium ion-dependent exc	32/373	151/19943	1.05E-24	1.06E-22	8.2622E-22	Cplx1/Grm4/Napb/Syt2/Drd2/Cadps/Ncs1/Rims1/Chrn4/Stx1b/V	32
BP	GO:1902803 regulation of synaptic vesicle transport	29/373	118/19943	1.84E-24	1.67E-22	1.2979E-22	Cplx1/Grm4/Napb/Syt2/Drd2/Ncs1/Rims1/Chrn4/Stx1b/Vamp1/	29
BP	GO:0051648 vesicle localization	41/373	288/19943	2.61E-24	2.32E-22	1.8091E-22	Cplx1/Grf1/Napb/Syt2/Kif5a/Cadps2/Drd2/Cadps/Ncs1/Dyn111	41
BP	GO:0098593 regulation of synaptic vesicle cycle	32/373	157/19943	3.81E-24	3.32E-22	2.586E-22	Cplx1/Grm4/Rapgef4/Napb/Syt2/Drd2/Ncs1/Syn1/Rims1/Chrn4	32
BP	GO:2000300 regulation of synaptic vesicle exocytosis	28/373	114/19943	1.19E-23	1.02E-21	7.94E-22	Cplx1/Grm4/Napb/Syt2/Drd2/Ncs1/Rims1/Chrn4/Stx1b/Vamp1/	28
BP	GO:0006887 exocytosis	46/373	391/19943	1.35E-23	1.13E-21	8.7801E-22	Cplx1/Grm4/Rapgef4/Arhgap44/Nsf/Napb/Syt2/Vsm1/Cadps2/Dr	46
BP	GO:0051650 establishment of vesicle localization	39/373	269/19943	1.84E-23	1.51E-21	1.1776E-21	Cplx1/Grm4/Napb/Syt2/Kif5a/Cadps2/Drd2/Cadps/Ncs1/Dyn111	39
BP	GO:0017157 regulation of exocytosis	37/373	263/19943	7.68E-22	5.77E-20	4.4941E-20	Cplx1/Grm4/Rapgef4/Nsf/Napb/Syt2/Vsm1/Cadps2/Drd2/Cadps1/	37
BP	GO:0019035 regulation of regulated secretory pathw	32/373	204/19943	1.72E-22	1.25E-18	9.7484E-18	Cplx1/Grm4/Napb/Syt2/Drd2/Cadps/Ncs1/Rims1/Chrn4/Stx1b/V	32
BP	GO:0006813 potassium ion transport	33/373	244/19943	4.73E-19	3.27E-17	2.5484E-17	Nsf/Kcnj3/Slc24a2/Drd2/Kcnab3/Kcnk2/Kcnab2/Kcnab3/Rgs7/	33
BP	GO:0051656 establishment of organelle localization	45/373	489/19943	4.85E-19	5.75E-17	4.4795E-17	Cplx1/Grm4/Napb/Syt2/Kif5a/Cadps2/Drd2/Cadps/Nsf/Ncs1/Dy	45
BP	GO:0060078 regulation of postsynaptic membrane pe	26/373	155/19943	1.31E-17	8.54E-16	6.6471E-16	Gabrg2/Gira2/Gabra1/Nptx1/Lrfs5/Drd2/Sitrik3/Cln3/Grin1/Sym	26
BP	GO:0071804 cellular potassium ion transport	29/373	212/19943	5.16E-17	3.21E-15	2.5024E-15	Kcnj3/Kcnab3/Kcnk2/Kcnab2/Slc12a5/Kcnk2/Kcnab3/Atp1a3/Rgs7/	29
BP	GO:0071805 potassium ion transmembrane transport	29/373	212/19943	5.16E-17	3.21E-15	2.5024E-15	Kcnj3/Kcnab3/Kcnk2/Kcnab2/Slc12a5/Kcnk2/Kcnab3/Atp1a3/Rgs7/	29
BP	GO:0007416 synapse assembly	26/373	184/19943	1E-15	5.9E-14	4.5948E-14	Gabrg2/Gira2/Gabra1/Nptx1/Lrfs5/Drd2/Sitrik3/Cln3/Grin1/Sym	26
BP	GO:0035418 protein localization to synapse	19/373	86/19943	1.62E-15	9.41E-14	7.329E-14	Cplx1/Rapgef4/Arhgap44/Nptx1/Kif5a/Cacng2/Cln3/Grin1/Cacn	19
BP	GO:1904062 regulation of cation transmembrane tra	34/373	355/19943	5.9E-15	3.32E-13	2.5881E-13	Cabp1/Rph3a/Fgf12/Cacng2/Thy1/Hpca/Drd2/Chrn4/Kcnk2/Kcn	34
BP	GO:0032386 regulation of intracellular transport	38/373	464/19943	2.24E-14	1.21E-12	9.3852E-13	Cplx1/Grm4/Cabp1/Arhgap44/Napb/Syt2/Hpca/Drd2/Nefh/Ncs1/	38
BP	GO:2001257 regulation of cation channel activity	24/373	175/19943	2.58E-14	1.37E-12	1.0686E-12	Cabp1/Rph3a/Fgf12/Cacng2/Hpca/Drd2/Chrn4/Cacng2/Cacng3/R	24
BP	GO:0050905 neuromuscular process	21/373	134/19943	7.47E-14	3.72E-12	2.894E-12	Fgf12/Rbfox1/Scn8a/Drd2/Kcnab2/Grin1/Gira1/Nefl/Atp2b2/Cam	21
BP	GO:003594 adult behavior	24/373	189/19943	1.47E-13	7.1E-12	5.5298E-12	Cabp1/Rph3a/Fgf12/Cacng2/Hpca/Drd2/Chrn4/Cacng2/Cacng3/R	24
BP	GO:0001508 action potential	21/373	139/19943	1.59E-13	7.55E-12	5.8749E-12	Rapgef4/Fgf12/Scn8a/Cj2/Chrn4/Gira1/Ryr2/Kcnk2/Scn4b/Op	21
BP	GO:0032412 regulation of ion transmembrane transp	27/373	260/19943	5.97E-13	2.63E-11	2.0473E-11	Cabp1/Rph3a/Fgf12/Cacng2/Hpca/Drd2/Chrn4/Kcnk2/Cacng3/R	27
BP	GO:0050890 cognition	31/373	351/19943	6.64E-13	3.73E-11	2.9014E-11	Grm4/Tafa2/Slc24a2/Drd2/Gabra5/Chrn4/Grin1/Ndrg4/Slc12a5/	31
BP	GO:0050806 positive regulation of synaptic transmiss	29/373	308/19943	9.8E-13	4.15E-11	3.2291E-11	Syt2/Cacng2/Slc24a2/Drd2/Rims1/Cln3/Grin1/Cacng3/Car7/Ca	29
BP	GO:0140029 exocytic process	17/373	92/19943	1.15E-12	4.81E-11	3.7437E-11	Cplx1/Napb/Syt2/Cadps2/Cadps/Rims1/Rab3e/Dmtn/Stx1b/Vamp	17
BP	GO:0022098 regulation of transmembrane transport	27/373	269/19943	1.23E-12	5.12E-11	3.9077E-11	Cabp1/Rph3a/Fgf12/Cacng2/Hpca/Drd2/Chrn4/Kcnk2/Cacng3/R	27
BP	GO:1905539 protein localization to postsynaptic mem	14/373	56/19943	1.43E-12	5.89E-11	4.5869E-11	Cplx1/Rapgef4/Arhgap44/Nptx1/Cacng2/Grin1/Cacng3/Sitx1b/Gri	14
BP	GO:0090742 regulation of postsynaptic membrane n	17/373	97/19943	2.83E-12	1.13E-10	8.7951E-11	Cplx1/Rapgef4/Arhgap44/Nptx1/Cacng2/Hpca/Cacng3/Sitx1b/Pac	17
BP	GO:0032409 regulation of transporter activity	27/373	278/19943	2.94E-12	1.17E-10	9.0822E-11	Cabp1/Rph3a/Fgf12/Cacng2/Hpca/Drd2/Chrn4/Cacng2/Cacng3/R	27
BP	GO:0097120 receptor localization to synapse	15/373	71/19943	3.2E-12	1.25E-10	9.7045E-11	Cplx1/Rapgef4/Arhgap44/Nptx1/Kif5a/Cacng2/Cacng3/Sitx1b/Grp	15
BP	GO:0007611 learning or memory	28/373	314/19943	9.1E-12	3.48E-10	2.7068E-10	Grm4/Tafa2/Slc24a2/Drd2/Gabra5/Grin1/Ndrg4/Slc12a5/Atp1a3/	28
BP	GO:0016082 synaptic vesicle priming	10/373	25/19943	1.18E-11	4.46E-10	3.4903E-10	Napb/Cadps2/Cadps/Rims1/Stx1b/Vsm1/Rab3a/Rims2/Gr12/Uvx	10
BP	GO:0019926 transmission of nerve impulse	16/373	93/19943	1.67E-11	6.29E-10	4.8985E-10	Rapgef4/Fgf12/Scn8a/Cacng2/Cacng3/Gira1/Kcnab2/Dpp6/Scn1a	16
BP	GO:0048167 regulation of synaptic plasticity	28/373	327/19943	2.39E-11	8.9E-10	6.9284E-10	Cabp1/Slc24a2/Drd2/Rims1/Grin1/Rasgr1/Calb2/Syt12/Rab3a/At	28
BP	GO:0051932 synaptic transmission, GABAergic	13/373	56/19943	2.54E-11	9.4E-10	7.3162E-10	Phf2/Grm4/Gabrg2/Gabra1/Drd2/Gabra5/Cln3/Cntnap4/Car7	13
BP	GO:1909778 protein localization to cell periphery	29/373	356/19943	3.5E-11	1.27E-09	9.8841E-10	Cplx1/Rapgef4/Arhgap44/Nptx1/Nsf/Cacng2/Rab3e/Cacng2/Chrn	29
BP	GO:0035637 multicellular organismal signaling	19/373	147/19943	3.87E-11	1.39E-09	1.0843E-09	Rapgef4/Fgf12/Scn8a/Cacng2/Cacng3/Gira1/Ryr2/Kcnk2/Scn4b	19
BP	GO:0010959 regulation of metal ion transport	32/373	433/19943	4.17E-11	1.49E-09	1.1606E-09	Cabp1/Fgf12/Thy1/Hpca/Drd2/Oprd1/Kcnk2/Kcnab2/Grin1/Heaw	32
BP	GO:0019228 neuronal action potential	12/373	48/19943	5.84E-11	2.04E-09	1.5285E-09	Rapgef4/Fgf12/Scn8a/Cacng2/Cacng3/Gira1/Kcnab2/Dpp6/Scn1a	12
BP	GO:0007626 locomotory behavior	24/373	250/19943	6.28E-11	2.16E-09	1.678E-09	Fgf12/Scn8a/Drd2/Oprd1/Chrn4/Grin1/Gira1/Atp1a3/Seit	24
BP	GO:0051668 localization within membrane	21/373	189/19943	6.61E-11	2.25E-09	1.7515E-09	Cplx1/Rapgef4/Arhgap44/Nptx1/Kif5a/Cacng2/Thy1/Hpca/Cacng	21
BP	GO:0007215 glutamate receptor signaling pathway	16/373	103/19943	8.33E-11	2.79E-09	2.1718E-09	Grm4/Rph3a/Cacng2/Grin1/Cacng3/Rasgr1/Grm1/Chrbp/Atp1a3	16
BP	GO:0006816 calcium ion transport	32/373	446/19943	8.94E-11	2.95E-09	2.2968E-09	Cabp1/Cacng2/Thy1/Hpca/Slc24a2/Drd2/Ncs1/Oprd1/Chrn4/Gr	32
BP	GO:009665 chemical synaptic transmission, postsyn	17/373	120/19943	9.61E-11	3.15E-09	2.4502E-09	Gira2/Rims1/Chrn4/Grin1/Gira1/Stx1b/Mapk8ip2/Cbin1/Grip2/R	17
BP	GO:0007613 memory	19/373	156/19943	1.1E-10	3.89E-09	2.995E-09	Rapgef4/Fgf12/Scn8a/Cacng2/Cacng3/Gira1/Atp1a3/Htr2c/Htr3a/Gr	19
BP	GO:0031644 regulation of neurological system proces	20/373	177/19943	1.4E-10	4.51E-09	3.5129E-09	Rapgef4/Fgf12/Nptx1/Oprd1/Rims1/Chrn4/Grin1/Gira1/Grm1/S	20
BP	GO:0007612 learning	20/373	177/19943	1.71E-10	5.45E-09	4.2433E-09	Grm4/Tafa2/Slc24a2/Drd2/Gabra5/Grin1/Ndrg4/Slc12a5/Atp1a3/	20
BP	GO:0015837 amine transport	17/373	127/19943	2.39E-10	7.56E-09	5.8872E-09	Syt2/Drd2/Chrn4/Grm1/Kcnk2/Syt12/Htr2c/Nat8/Chga/Pcp4/D	17
BP	GO:0070588 calcium ion transmembrane transport	26/373	314/19943	2.62E-10	8.23E-09	6.4042E-09	Cabp1/Cacng2/Thy1/Hpca/Slc24a2/Drd2/Ncs1/Grin1/Cacng3/Ryr	26
BP	GO:0060079 excitatory postsynaptic potential	16/373	111/19943	2.64E-10	8.23E-09	6.4042E-09	Gira2/Rims1/Chrn4/Grin1/Stx1b/Mapk8ip2/Cbin1/Grip2/R	16
BP	GO:0072511 divalent inorganic cation transport	33/373	497/19943	3.37E-10	1.03E-08	8.054E-09	Cabp1/Cacng2/Thy1/Hpca/Slc24a2/Drd2/Ncs1/Oprd1/Chrn4/Gr	33
BP	GO:0096501 regulation of neurotransmitter receptor	13/373	68/19943	3.45E-10	1.05E-08	8.1833E-08	Rph3a/Nptx1/Lyph6b/Lyxn1/Cacng2/Chrn4/Cacng3/Rasgr1/Chl	13
BP	GO:0019932 second-messenger-mediated signaling	31/373	455/19943	6.35E-10	1.86E-08	1.4467E-08	Rapgef4/Lgr5/Vsn1/Camk1g/Hpca/Drd2/Gpr3/Pex5/Grin1/Dmtn	31
BP	GO:0051480 regulation of cytosolic calcium ion conc	29/373	406/19943	7.84E-10	2.28E-08	1.7723E-08	Thr/Thy1/Drd2/Ncs1/Grp3/Htr2c/Grin1/Hctr1/Grm1/Calb2/Ryr	29
BP	GO:0070838 divalent metal ion transport	32/373	494/19943	1.17E-09	3.37E-08	2.6232E-08	Cabp1/Cacng2/Thy1/Hpca/Slc24a2/Drd2/Ncs1/Oprd1/Chrn4/Gr	32
BP	GO:0051952 regulation of amine transport	16/373	123/19943	1.25E-09	3.59E-08	2.792E-08	Syt2/Drd2/Chrn4/Grm1/Kcnk2/Syt12/Htr2c/Nat8/Chga/Pcp4/H	16
BP	GO:0034270 positive regulation of ion transport	25/373	333/19943	4.4E-09	1.18E-07	9.1261E-07	Fgf12/Cacng2/Thy1/Drd2/Chrn4/Grin1/Cacng2/Ryr2/Rgs7/Scn	25
BP	GO:0051899 membrane depolarization	13/373	83/19943	4.52E-09	1.2E-07	9.3428E-08	Fgf12/Scn8a/Cacng2/Chrn4/Grm1/Cacng3/Scn1a/Scn2a/Scn9a/C	13
BP	GO:0050433 regulation of catecholamine secretion	12/373	74/19943	1.19E-08	3.03E-07	2.3578E-07	Syt2/Drd2/Chrn4/Kcnk2/Syt12/Chga/Pcp4/Htr3a/Htr2a/Chrn7/C	12
BP	GO:0016398 dendrite development	23/373	301/19943	1.33E-08	3.38E-07	2.6288E-07	Rapgef4/Mcf2/Arhgap44/Grin1/Hecw1/Slc12a5/RG1307443/Ma	23
BP	GO:1901379 regulation of potassium ion transmembr	13/373	91/19943	1.43E-08	3.59E-07	2.7913E-07	Kcnk2/Kcnab2/Rgs7/Dpp6/Kcnip4/Kcnk1/Kcnab1/Kcnk1/Dpp10/At	13
BP	GO:0008344 adult locomotory behavior	14/373	108/19943	1.43E-08	3.59E-07	2.7913E-07	Fgf12/Scn8a/Drd2/Oprd1/Grin1/Gira1/Atp1a3	

BP	GO:0031629	synaptic vesicle fusion to presynaptic act	7/373	23/19943	1.43E-07	3.24E-06	2.5198E-06	Cplx1/Syt2/Rims1/Stx1b/Vamp1/Rab3a/Syt7	7
BP	GO:0014046	dopamine secretion	9/373	46/19943	1.52E-07	3.4E-06	2.6469E-06	Syt2/Drd2/Chma4/Kcna2/Syt12/Pcp4/Htr2a/Chrm2/Syt7	9
BP	GO:0014059	regulation of dopamine secretion	9/373	46/19943	1.52E-07	3.4E-06	2.6469E-06	Syt2/Drd2/Chma4/Kcna2/Syt12/Pcp4/Htr2a/Chrm2/Syt7	9
BP	GO:0015696	ammonium transport	14/373	131/19943	1.7E-07	3.78E-06	2.9436E-06	Syt2/Drd2/Slc5a7/Chma4/Slc12a5/Kcna2/Syt12/Htr2c/Nat8/Pcp4	14
BP	GO:0015872	dopamine transport	10/373	61/19943	1.79E-07	3.97E-06	3.0879E-06	Syt2/Drd2/Chma4/Kcna2/Syt12/Nat8/Pcp4/Htr2a/Chrm2/Syt7	10
BP	GO:0095900	vesicle fusion to plasma membrane	7/373	24/19943	1.99E-07	4.38E-06	3.4121E-06	Cplx1/Syt2/Rims1/Stx1b/Vamp1/Rab3a/Syt7	7
BP	GO:0048278	vesicle docking	10/373	63/19943	2.46E-07	5.36E-06	4.17E-06	Nsf/Rims1/Rab3c/Ndr4/Stx1b/Rab3a/Camk2a/Rims2/Unc13c/Sp	10
BP	GO:0051592	response to calcium ion	16/373	178/19943	2.52E-07	5.46E-06	4.2539E-06	Tph2/Syt2/Cacng2/Hpca/Grim1/Dmtn/Ryr2/Gpld1/Chrbp/Syt12/Ci	16
BP	GO:0031601	synaptic vesicle docking	6/373	16/19943	2.81E-07	6.06E-06	4.7208E-06	Rims1/Stx1b/Camk2a/Rims2/Unc13c/Spbn2	6
BP	GO:0031646	positive regulation of neurological system	11/373	81/19943	3.18E-07	6.83E-06	5.1314E-06	Ragef4/Rims1/Grim1/Stx1b/Grip2/Rims2/Nrg1/Chrna7/Neto1/Oc	11
BP	GO:2000463	positive regulation of excitatory postsynaptic transmission	8/373	37/19943	3.34E-07	7.1E-06	5.5261E-06	Rims1/Grim1/Stx1b/Grip2/Rims2/Chrna7/Neto1/Shank1	8
BP	GO:0051973	postsynaptic organization	17/373	205/19943	3.39E-07	7.16E-06	5.5752E-06	Rph3a/Ragef4/Arhgap44/Nptx1/Grim1/Nefl/Ina2/Zp804a/Camk2l	17
BP	GO:0032594	protein transport within lipid bilayer	8/373	39/19943	5.15E-07	1.05E-05	8.2031E-06	Cplx1/Arhgap44/Cacng2/Cacng3/Stx1b/Grip2/Mapk10/Lrcc7	8
BP	GO:0060052	neurofilament cytoskeleton organization	5/373	10/19943	5.2E-07	1.06E-05	8.2416E-06	Nefl/Nefl/Nefm/Ina/Atps2	5
BP	GO:0060359	response to ammonium ion	16/373	189/19943	5.69E-07	1.15E-05	8.9317E-06	Gabra2/Gabra1/Drd2/Nefh/Chma4/Grim1/Chrbp/Chrm2/Tac3/Ht	16
BP	GO:00140056	organelle localization by membrane tethers	10/373	72/19943	8.88E-07	1.78E-05	1.3824E-05	Nsf/Rims1/Rab3c/Ndr4/Stx1b/Rab3a/Camk2a/Rims2/Unc13c/Sp	10
BP	GO:0095905	regulation of presynaptic membrane potential	5/373	11/19943	9.38E-07	1.86E-05	1.4472E-05	Grim1/Kcncl1/Kcna1/Scn2a/Kcnma1	5
BP	GO:0008306	associative learning	12/373	109/19943	9.43E-07	1.86E-05	1.4483E-05	Tafa2/Drd2/Gabra5/Grim1/Ndr4/Atp1a3/Grin2b/Chrna7/Neto1/C	12
BP	GO:0099633	protein localization to postsynaptic specializations	7/373	30/19943	1.06E-06	2.07E-05	1.6105E-05	Ragef4/Nptx1/Cacng2/Cacng3/Camk2a/Dlg2/Adam22	7
BP	GO:0099645	neurotransmitter receptor localization	7/373	30/19943	1.06E-06	2.07E-05	1.6105E-05	Ragef4/Nptx1/Cacng2/Cacng3/Camk2a/Dlg2/Adam22	7
BP	GO:0086010	membrane depolarization during action potential	7/373	31/19943	1.35E-06	2.59E-05	2.0199E-05	Scn8a/Scn4a/Scn1a/Scn2a/Scn9a/Cacna2d1/Cacna1	7
BP	GO:0011922	calcium-mediated signaling	17/373	227/19943	1.41E-06	2.7E-05	2.0999E-05	Vsnl1/Camk1g/Hpca/Grim1/Dmtn/Grm1/Ryr2/Rit2/Tenm2/Necab1	17
BP	GO:0007628	adult walking behavior	8/373	45/19943	1.64E-06	3.1E-05	2.4134E-05	Scn8a/Drd2/Gira1/Scn1a/Kcnma1/Chat/Khlh1/Cend1	8
BP	GO:0001964	startle response	7/373	32/19943	1.7E-06	3.21E-05	2.5001E-05	Drd2/Grim1/Gira1/Kcna1/Kcnh1/Grin2b/Nrg1	7
BP	GO:0006904	vesicle docking involved in exocytosis	8/373	46/19943	1.95E-06	3.63E-05	2.8251E-05	Rims1/Rab3c/Stx1b/Rab3a/Camk2a/Rims2/Unc13c/Spbn2	8
BP	GO:0096599	walking behavior	8/373	47/19943	2.31E-06	4.25E-05	3.3072E-05	Scn8a/Drd2/Gira1/Scn1a/Kcnma1/Chat/Khlh1/Cend1	8
BP	GO:0058963	neurotransmitter receptor transport	6/373	22/19943	2.38E-06	4.34E-05	3.3040E-05	Cplx1/Arhgap44/Stx1b/Grip2/Mapk10/Lrcc7	6
BP	GO:0015893	drug transport	17/373	236/19943	2.4E-06	4.3E-05	3.3975E-05	Syt2/Drd2/Chma4/Slc32a1/Slc17a6/Kcna2/Syt12/Htr2c/Slc6a5/Ne	17
BP	GO:0007721	synaptic transmission, cholinergic	7/373	34/19943	2.63E-06	4.72E-05	3.6782E-05	Lyrx1/Slc5a7/Chrna4/Htr2c/Camk2b/Chrna7/Chrm2	7
BP	GO:0007128	cellular response to metal ion	17/373	238/19943	2.7E-06	4.81E-05	3.7477E-05	Gira2/Nptx1/Tph2/Syt2/Hpca/Grim1/Dmtn/Gira1/Gpld1/Chrbp/Sy	17
BP	GO:0022406	membrane docking	10/373	82/19943	3E-06	5.3E-05	4.1242E-05	Nsf/Rims1/Rab3c/Ndr4/Stx1b/Rab3a/Camk2a/Rims2/Unc13c/Sp	10
BP	GO:0088877	neurotransmitter receptor transport	6/373	23/19943	3.17E-06	5.55E-05	4.3209E-05	Cplx1/Arhgap44/Stx1b/Grip2/Mapk10/Lrcc7	6
BP	GO:1903540	establishment of protein localization	6/373	23/19943	3.17E-06	5.55E-05	4.3209E-05	Cplx1/Arhgap44/Stx1b/Grip2/Mapk10/Lrcc7	6
BP	GO:0015850	organic hydroxy compound transport	17/373	270/19943	3.65E-06	6.34E-05	4.9339E-05	Syt2/Drd2/Cadps/Chrna4/Kcna2/Syt12/Nat8/Chga/Pcp4/Htr3/At	17
BP	GO:0097164	ammonium ion metabolic process	14/373	172/19943	4.6E-06	7.89E-05	6.1419E-05	Tph2/Drd2/Slc5a7/Asah2/Gpld1/Sncb/Atp2b2/Htr2c/Spp2/Ddc/	14
BP	GO:0050885	neuromuscular process controlling balance	9/373	69/19943	5.36E-06	9.12E-05	7.102E-05	Rbfox1/Nefl/Atp2b2/Camk2b/jph3/Kcnma1/Camta1/Shank1/Pou	9
BP	GO:0060402	calcium ion transport into cytosol	14/373	175/19943	5.62E-06	9.5E-05	7.3938E-05	Thy1/Drd2/Grim1/Ryr2/Htr2c/jph3/Akap6/Grin2b/Htr2a/Pri	14
BP	GO:0048169	regulation of long-term neuronal synapse	7/373	38/19943	5.8E-06	9.75E-05	7.5911E-05	Drd2/Rims1/Grim1/Camk2b/Syng1/Grin2b/Neto1	7
BP	GO:0051590	positive regulation of neurotransmission	9/373	53/19943	5.91E-06	9.9E-05	7.7058E-05	Syt2/Drd2/Rims1/Slc1b/Htr2c/Nat8/Cacna1b/Chrbp	9
BP	GO:0007409	xenogenesis	24/373	465/19943	8.1E-06	0.000134	0.00010454	Nptx1/Kif5a/Cnta4/Thy1/Drd2/Nefl/Sit3r3/Grim1/Nefl/Nefm/Rab	24
BP	GO:0007187	G-protein-coupled receptor signaling pathway	16/373	237/19943	1.08E-05	0.000178	0.0001384	Grm4/Lgr5/Drd2/Gpr3/Oprd1/Rit2/Htr2c/Chrm2/Chga/Mrap2/Gn	16
BP	GO:0032225	regulation of synaptic transmission, dopaminergic	5/373	17/19943	1.15E-05	0.000188	0.00014613	Drd2/Cntna4/Nat8/Chrna7/Chrm2	5
BP	GO:1902805	positive regulation of synaptic vesicle trafficking	5/373	17/19943	1.15E-05	0.000188	0.00014613	Syt2/Rims1/Cacna1b/Map2/Syt7	5
BP	GO:0007204	positive regulation of cytosolic calcium concentration	20/373	353/19943	1.22E-05	0.000199	0.00015469	Thyr1/Thy1/Drd2/Grim1/Gm1/Ryr2/Htr2c/jph3/Hh3/Cacna	20
BP	GO:0064001	cytosolic calcium ion transport	14/373	180/19943	1.25E-05	0.000207	0.00015138	Thy1/Drd2/Grim1/Ryr2/Htr2c/jph3/Akap6/Grin2b/Htr2a/Pri	14
BP	GO:0007142	cellular response to ammonium ion	9/373	77/19943	1.34E-05	0.000216	0.00018808	Gabra2/Gabra1/Chrna4/Chrbp/Chrm2/Hh3/Chrna7/Chrm2/Gab	9
BP	GO:0019933	cAMP-mediated signaling	14/373	189/19943	1.36E-05	0.000219	0.00017011	Ragef4/Lgr5/Drd2/Gpr3/Pex5/Rit2/Gpr61/Chga/Mrap2/Gnas/At	14
BP	GO:0035095	behavioral response to nicotine	4/373	9/19943	1.41E-05	0.000225	0.00017506	Chrna4/Htr2c/Chrna7/Chrm2	4
BP	GO:0048791	calcium ion-regulated exocytosis of neurotransmitter	5/373	18/19943	1.56E-05	0.000248	0.00019271	Syt2/Rims1/Stx1b/Rims2/Syt7	5
BP	GO:0051963	regulation of synapse assembly	11/373	120/19943	1.59E-05	0.00025	0.00019467	Nptx1/Lrnf5/Sit3r3/Cntn3/Grim1/Syndig1/Cbln1/Lingo4/Sit1/Chri	11
BP	GO:2001023	regulation of response to drug	11/373	120/19943	1.59E-05	0.00025	0.00019467	Syt2/Drd2/Chrna4/Kcna2/Syt12/Htr2c/Nat8/Pcp4/Htr2a/Chrm2	11
BP	GO:1902476	chloride transmembrane transport	9/373	79/19943	1.65E-05	0.000259	0.00020154	Gabra2/Gabra1/Gabra3/Gira1/Slc12a5/Gabra3/Slc12a3/Gal	9
BP	GO:0019935	cyclic nucleotide-mediated signaling	15/373	221/19943	1.91E-05	0.000298	0.0002311	Ragef4/Lgr5/Drd2/Gpr3/Pex5/Rit2/Gpr61/Htr2c/Chga/Mrap2/G	15
BP	GO:0016027	neuron projection organization	10/373	101/19943	1.97E-05	0.000307	0.00023861	Rph3a/Arhgap44/Grim1/Atp1a3/Zp804a/Camk2b/Grin2b/Chrna7	10
BP	GO:0001956	positive regulation of neurotransmission	6/373	31/19943	2.04E-05	0.000316	0.0002461	Syt2/Rims1/Stx1b/Htr2c/Cacna1b/Syt7	6
BP	GO:0060081	membrane hyperpolarization	5/373	19/19943	2.09E-05	0.00032	0.00024894	Cacng2/Kcnma1/Kcnq2/Tpvc5/Hcn1	5
BP	GO:0050773	regulation of dendrite development	14/373	199/19943	2.20E-05	0.000349	0.00027199	Ragef4/Arhgap44/Grim1/Hecw1/RGD1307443/Camk2b/Pascin1/	14
BP	GO:0010807	regulation of synaptic vesicle priming	4/373	10/19943	2.31E-05	0.00035	0.00027409	Naptx1/Rims1/Stx1b/Rab3a	4
BP	GO:0061669	spontaneous neurotransmitter secretion	4/373	10/19943	2.31E-05	0.00035	0.00027409	Rph3a/Rims1/Stx1b/Rims2	4
BP	GO:0006821	chloride transport	10/373	103/19943	2.34E-05	0.000353	0.00027464	Gabra2/Gira2/Gabra1/Gabra5/Car7/Gira1/Slc12a5/Gabra3/Slc12a	10
BP	GO:1901016	regulation of potassium ion transmembrane transport	8/373	64/19943	2.47E-05	0.00037	0.0002879	Kcns2/Kcncl1/Kcnab1/Kcna1/Akap6/Neto1/Neto2/Kcng1	8
BP	GO:0045956	positive regulation of calcium ion-dependent synaptic transmission	6/373	32/19943	2.47E-05	0.00037	0.0002879	Syt2/Cadps/Rims1/Cacna1b/Syt7/Cacna1i	6
BP	GO:0010975	positive regulation of neuron projection morphogenesis	20/373	371/19943	2.5E-05	0.000371	0.00028852	Syt2/Serpini1/Rims1/Ndr4/Nefl/Rit2/Zp804a/Camk2b/Pascin1/F	20
BP	GO:0097553	calcium ion transmembrane transport	12/373	151/19943	2.79E-05	0.000411	0.0003025	Thy1/Drd2/Grim1/Ryr2/Htr2c/jph3/Akap6/Grin2b/Htr2a/Pri	12
BP	GO:0045921	positive regulation of exocytosis	10/373	106/19943	3.01E-05	0.00044	0.00034224	Syt2/Vsnl1/Cadps2/Cadps/Ncsl1/Rims1/Rab3a/Cacna1b/Syt7/Cac	10
BP	GO:0072659	protein localization to plasma membrane	17/373	288/19943	3.28E-05	0.000478	0.0003721	Arhgap44/Nsf/Rab3c/Grm1/Epb413/Ank1/Rab3a/Dpp6/Kenip4/C	17
BP	GO:0048813	dendrite morphogenesis	13/373	180/19943	3.59E-05	0.000513	0.00039917	Arhgap44/Grim1/Hecw1/Mapk8ip2/Camk2b/Camk2a/Cit/Chrna7/	13
BP	GO:0050994	sensory perception of mechanical stimulus	16/373	262/19943	3.71E-05	0.000528	0.00041138	Phf24/Scn8a/Gabra5/Rab3a/Atp2b2/Scn1a/Kcna1/Srm4/Kcnma1	16
BP	GO:0031346	positive regulation of cell projection organization	20/373	478/19943	3.77E-05	0.000535	0.00041649	Syt2/Serpini1/Rims1/Grim1/Ndr4/Nefl/Rit2/Tenm2/Zp804a/Cam	20
BP	GO:0010970	transport along microtubule	12/373	156/19943	3.86E-05	0.000544	0.00042342	Kif5a/Nefl/Dync111/Nefl/Nefm/Kif5c/Rasgrp1/Map2/Map1b/Dlg2	12
BP	GO:0007188	adenylylate cyclase-modulating G-protein signaling	14/373	208/19943	3.95E-05	0.000554	0.00043151	Grim4/Lgr5/Drd2/Gpr3/Oprd1/Rit2/Chrm2/Chga/Mrap2/Gnas/Adi	14
BP	GO:0071277	cellular response to calcium ion	9/373	88/19943	3.96E-05	0.000554	0.00043151	Syt2/Hpca/Dmtn/Gpld1/Chrbp/Syt12/Ccne4/Kcnh1/Syt7	9
BP	GO:0098911	microtubule-based transport	12/373	157/19943	4.11E-05	0.000574	0.00044654	Kif5a/Nefl/Dync111/Nefl/Nefm/Kif5c/Rasgrp1/Map2/Map1b/Dlg2	12
BP	GO:0031338	regulation of vesicle fusion	6/373	35/19943	4.22E-05	0.000586	0.00045582	Cplx1/Syt2/Rims1/Vamp1/Rab3a/Syt7	6
BP	GO:0015812	gamma-aminobutyric acid transport	5/373	22/19943	4.51E-05	0.000617	0.00048009	Grm4/Slc32a1/Htr2c/Slc6a11/Hmh3	5
BP	GO:0050966	detection of mechanical stimulus involved in sensory perception of touch	5/373	22/19943	4.51E-05	0.000617	0.00048009	Rims1/Chrna4/Gira1/Rims2/Gabrb3	5
BP	GO:0060080	inhibitory postsynaptic potential	5/373	22/19943	4.51E-05	0.000617	0.00048009	Rims1/Chrna4/Gira1/Rims2/Gabrb3	5
BP	GO:0007622	rhythmic behavior	8/373	70/19943	4.77E-05	0.00065	0.00050587	Drd2/Hert2/Kcna2/Mapk10/Kcnma1/Oprl1/Chrm2/Chat	8
BP	GO:0051954	positive regulation of amine transport	7/373	52/19943	4.91E-05	0.000666	0.00051859	Drd2/Chrna4/Htr2c/Nat8/Pcp4/Grin2b/Chrm2	7
BP	GO:0001963	synaptic transmission, dopaminergic	6/373	36/19943	4.98E-05	0.000674	0.00052506	Drd2/Cntna4/Chrbp/Nat8/Chrna7/Chrm2	6
BP	GO:0097061	dendritic spine organization	9/373	99/19943	6.14E-05	0.000823	0.00064048	Rph3a/Arhgap4	

BP	GO:009175	regulation of postsynapse organization	10/373	125/19943	0.000122	0.001506	0.0011727	Rapgef4/Arhgap44/Nptx1/Grin1/Zfp804a/Camk2b/Cbln1/Grip2/G	10
BP	GO:0021631	optic nerve morphogenesis	3/373	6/19943	0.000124	0.001512	0.00117741	Kcna2/Pax2/Chrm2	3
BP	GO:0031632	positive regulation of synaptic vesicle fu	3/373	6/19943	0.000124	0.001512	0.00117741	Syt2/Rims1/Syt7	3
BP	GO:1902630	regulation of membrane hyperpolarizati	3/373	6/19943	0.000124	0.001512	0.00117741	Kcnma1/Trip5/Hcn1	3
BP	GO:0058005	negative regulation of synaptic transmi	8/373	80/19943	0.000125	0.001512	0.00117741	Grrm4/Rapgef4/Slc24a2/Drd2/Cbln1/Htr2a/Celf4/Grtd2ip	8
BP	GO:0034665	synaptic vesicle recycling	8/373	81/19943	0.000136	0.001642	0.00127834	Syt2/Snch/Stx1b/Rab3a/Pacsin1/Syp/Syt7/Dnm3	8
BP	GO:0051705	multi-organism behavior	8/373	82/19943	0.000148	0.001781	0.00138612	Grin1/Chrbp/Mapk8ip2/Grin2b/Shank1/Chrm2/Nrxn3/Pou4f1	8
BP	GO:0085500	acetylcholine receptor signaling pathwa	5/373	28/19943	0.000154	0.001825	0.00142082	Chrna4/Chrm2/Hrh3/Chrna7/Chrm2	5
BP	GO:1903951	signal transduction involved in cellular r	4/373	28/19943	0.000154	0.001825	0.00142082	Chrna4/Chrm2/Hrh3/Chrna7/Chrm2	5
BP	GO:0050982	detection of mechanical stimulus	7/373	62/19943	0.000154	0.001825	0.00142082	Phf24/Ano3/Atp2b2/Scn1a/Kcna1/Grin2b/Htr2a	7
BP	GO:0031623	receptor internalization	10/373	129/19943	0.000159	0.001881	0.00146435	Nefl/Napb/Cacng2/Hpca/Drd2/Cacng3/Pacsin1/Necab2/Nrg1/Dnm	10
BP	GO:2000302	positive regulation of synaptic vesicle ex	4/373	16/19943	0.000183	0.002154	0.00167707	Syt2/Rims1/Cacna1b/Syt7	4
BP	GO:1901019	regulation of calcium ion transmembran	8/373	85/19943	0.000191	0.002235	0.00173978	Cabp1/Hpca/Drd2/Ryr2/Phh3/Akap6/Opr1/Cacna2d1	8
BP	GO:0008277	regulation of G protein-coupled receptor	10/373	132/19943	0.000192	0.002242	0.00174504	Phf24/Drd2/Rgs7/Camk2b/Chga/Syp/Map2/Necab2/Opr1/Tub	10
BP	GO:0007189	adenylate cyclase-activating G protein-c	10/373	133/19943	0.000204	0.002372	0.00184623	Lgfs5/Drd2/Gpr3/R12/Chga/Map2/Gnas/Adcy1/Opr1/Htr4	10
BP	GO:0045849	regulation of cAMP-mediated signaling	7/373	65/19943	0.000207	0.002397	0.00186633	Gpr3/Peax1/Gpr61/Chga/Map2/Gnas/Opr1	7
BP	GO:0032226	positive regulation of synaptic transmi	3/373	7/19943	0.000215	0.002437	0.00189682	Drd2/Nat8/Chrm2	3
BP	GO:0045110	intermediate filament bundle assembly	3/373	7/19943	0.000215	0.002437	0.00189682	Nefl/Nefm/Nefm	3
BP	GO:0060012	synaptic transmission, glycinergic	3/373	7/19943	0.000215	0.002437	0.00189682	Gira2/Gira1/Slc6a5	3
BP	GO:0060024	rhythmic synaptic transmission	3/373	7/19943	0.000215	0.002437	0.00189682	Scn9a/Cacna2d2/Chat	3
BP	GO:0007214	neuromuscular synaptic transmission	5/373	30/19943	0.000216	0.002437	0.00189682	Chrna4/Chrm2/Hrh3/Chrna7/Chrm2	5
BP	GO:1905144	response to acetylcholine	5/373	30/19943	0.000216	0.002437	0.00189682	Chrna4/Chrm2/Hrh3/Chrna7/Chrm2	5
BP	GO:1905145	cellular response to acetylcholine	5/373	30/19943	0.000216	0.002437	0.00189682	Chrna4/Chrm2/Hrh3/Chrna7/Chrm2	5
BP	GO:0031345	negative regulation of cell projection org	13/373	215/19943	0.000217	0.002437	0.00189682	Thy1/R12/RGD1307443/Stx1b/Cit/Grin2b/Map2/Pfn2/LOC11	13
BP	GO:0072347	response to anesthetic	10/373	134/19943	0.000217	0.002437	0.00189682	Hpca/Drd2/Nefh/Grin1/Chrbp/Tac3/Grin2b/Htr2a/Pkce/Chrm2	10
BP	GO:0001504	neurotransmitter uptake	6/373	47/19943	0.000221	0.002589	0.00201524	Drd2/Slc17a6/Slc6a5/Nat8/Slc6a11/Sv2b	6
BP	GO:0031280	negative regulation of cyclase activity	4/373	17/19943	0.000235	0.00264	0.00203558	Hpca/Drd2/Hrh3/Akap6	4
BP	GO:0048259	regulation of receptor-mediated endocy	9/373	111/19943	0.00024	0.002677	0.00208397	Nefl/Napb/Hpca/Drd2/Pacsin1/Necab2/Sgip1/Nrg1/Aak1	9
BP	GO:0050974	detection of mechanical stimulus involv	6/373	48/19943	0.00026	0.00289	0.00224991	Phf24/Atp2b2/Scn1a/Kcna1/Grin2b/Htr2a	6
BP	GO:0048512	circadian behavior	7/373	68/19943	0.000275	0.003053	0.00237647	Drd2/Htr2r2/Kcna2/Mapk10/Kcnma1/Opr1/Chrm2	7
BP	GO:0032535	regulation of cellular component size	19/373	410/19943	0.000285	0.003152	0.00254512	Nefl/Nefm/Spire2/Slc12a5/Atp2b2/Slit1/Cit/Kcnma1/Nrg1/Map2/	19
BP	GO:0089054	presynapse assembly	6/373	49/19943	0.000292	0.003217	0.00250476	Lrnfs/Sltnc3/Ctstn3/Cbln1/Cnns5/Bsn	6
BP	GO:0007214	neuromuscular synaptic transmission	5/373	32/19943	0.000296	0.003258	0.00233663	Slc5a7/Chrm4/Rab3a/Chrm2/Chat	5
BP	GO:0050584	neuromuscular process controlling post	4/373	18/19943	0.000299	0.003278	0.00255172	Gira1/Scn1a/Atp8a2/Pou4f1	4
BP	GO:0008542	visual learning	7/373	69/19943	0.000302	0.003285	0.00255737	Tafa2/Drd2/Grin1/Ndr4g4/Atp1a3/Neto1/Chrm2	7
BP	GO:1903307	positive regulation of regulated secretor	7/373	69/19943	0.000302	0.003285	0.00255737	Syt2/Cadps/Rims1/Rab3a/Cacna1b/Syt7/Cacna1i	7
BP	GO:0006906	vesicle fusion	8/373	91/19943	0.000306	0.003317	0.00252818	Cplx1/Nsf/Syt2/Rims1/Stx1b/Vamp1/Rab3a/Syt7	8
BP	GO:0051924	regulation of calcium ion transport	15/373	283/19943	0.000306	0.003317	0.00252818	Cabp1/Thy1/Hpca/Drd2/Opr1/Grin1/Ryr2/Atp2b2/Camk2a/Jph3	15
BP	GO:0046958	nonassociative learning	3/373	8/19943	0.000339	0.003638	0.00283232	Mapk8ip2/Grin2b/Shank1	3
BP	GO:0021680	cerebellar Purkinje cell layer developm	5/373	33/19943	0.000344	0.003679	0.0028642	Sei2b/Atp2b2/Kln1/Cend1/Sgptb2	5
BP	GO:0010769	regulation of cell morphogenesis involv	17/373	350/19943	0.000345	0.003687	0.00287066	Arhgap44/Thy1/Grin1/Dmtr/Nefl/Nefm/Hecw1/Camk2b/Slit1/Cit	17
BP	GO:0002090	regulation of receptor internalization	7/373	71/19943	0.00036	0.003836	0.00298616	Nefl/Napb/Hpca/Drd2/Pacsin1/Necab2/Nrg1	7
BP	GO:0060291	long-term synaptic potentiation	12/373	198/19943	0.000368	0.003911	0.00304488	Slc24a2/Drd2/Rims1/Calb2/Syt12/Camk2b/Adcy1/Grin2b/Chrna7	12
BP	GO:1904064	positive regulation of cation transmembr	11/373	170/19943	0.000369	0.003911	0.00304488	Cacng2/Thy1/Cacng3/Rgs7/Rgs7/Dpp6/Kcnc1/Kcna1/Akap6/Cacn	11
BP	GO:0051350	negative regulation of lyase activity	4/373	19/19943	0.000374	0.003933	0.00306165	Hpca/Drd2/Hrh3/Akap6	4
BP	GO:1902259	regulation of delayed rectifier potassium	4/373	19/19943	0.000374	0.003933	0.00306165	Kcnc2/Kcnab1/Akap6/Kcnc1	4
BP	GO:0007632	visual behavior	7/373	72/19943	0.000392	0.004121	0.00320836	Tafa2/Drd2/Grin1/Ndr4g4/Atp1a3/Neto1/Chrm2	7
BP	GO:0017085	response to insecticide	5/373	34/19943	0.000397	0.004156	0.00323544	Kif5a/Nefl/Nefm/Ddc/Map1b	5
BP	GO:0090174	organelle membrane fusion	8/373	96/19943	0.00044	0.004588	0.00357166	Cplx1/Nsf/Syt2/Rims1/Stx1b/Vamp1/Rab3a/Syt7	8
BP	GO:0048284	organelle fusion	9/373	121/19943	0.000456	0.004733	0.00368483	Cplx1/Nsf/Syt2/Gdap1/Rims1/Stx1b/Vamp1/Rab3a/Syt7	9
BP	GO:0001975	response to amphetamine	6/373	54/19943	0.000498	0.005141	0.00400233	Drd2/Grin1/Rasgef1/Rgs7/Grin2b/Rgs17	6
BP	GO:0095964	anterograde axonal protein transport	3/373	9/19943	0.000501	0.005141	0.00400233	Kif5a/Kif5c/Dlg2	3
BP	GO:1905383	protein localization to presynapse	9/373	9/19943	0.000501	0.005141	0.00400233	Kif5a/Kif5c/Dlg2	9
BP	GO:0032228	regulation of synaptic transmission, GAB	5/373	36/19943	0.000521	0.005296	0.00412253	Phf24/Drd2/Cntnap4/Car7/Pkce	5
BP	GO:0043950	positive regulation of cAMP-mediated si	5/373	36/19943	0.000521	0.005296	0.00412253	Gpr3/Gpr61/Chga/Map2/Gnas	5
BP	GO:0089563	modification of synaptic structure	5/373	36/19943	0.000521	0.005296	0.00412253	Cabp1/Arhgap44/Dlgap3/Pfn2/LOC10090840	5
BP	GO:0007218	neuropeptide signaling pathway	8/373	99/19943	0.000541	0.005466	0.00427093	Gira2/Scg5/Opr1/Htr2/Gira1/Htr1/Tac3/Opr1	8
BP	GO:0008090	retrograde axonal transport	4/373	21/19943	0.00055	0.005611	0.0044683	Kif5a/Nefm/Bsn	4
BP	GO:0030100	regulation of endocytosis	15/373	300/19943	0.000564	0.005637	0.00438844	Nefl/Napb/Hpca/Drd2/R12/Stx1b/Pacsin1/Necab2/Sgip1/Nrg1/Mc	15
BP	GO:0014075	response to amine	7/373	77/19943	0.000592	0.0059	0.00459309	Drd2/Grin1/Rasgef1/Rgs7/Kcnc1/Grin2b/Rgs17	7
BP	GO:0008088	axo-dendritic transport	7/373	78/19943	0.00064	0.006365	0.00495492	Kif5a/Nefl/Nefm/Kif5c/Map2/Dlg2/Bsn	7
BP	GO:0006594	catecholamine metabolic process	6/373	57/19943	0.000668	0.006597	0.00519801	Drd2/Snch/Htr2c/Ddc/Chrna7/Chrm2	6
BP	GO:0006912	catechol-containing compound metabo	6/373	57/19943	0.000668	0.006597	0.00519801	Drd2/Snch/Htr2c/Ddc/Chrna7/Chrm2	6
BP	GO:0099172	postsynapse organization	6/373	57/19943	0.000668	0.006597	0.00519801	Lrnfs/Nefm/Ctstn3/Cbln1/Cnns5/Bsn	6
BP	GO:0007156	homophilic cell adhesion via plasma mer	9/373	128/19943	0.000687	0.006757	0.00520622	Cntna4/Ctstn3/Cdh12/Cdh7/Ptprt/Ctstn2/Podha4/Celr3/L1cam	9
BP	GO:0006865	amino acid transport	10/373	155/19943	0.000691	0.006783	0.00528044	Grrm4/Grm1/Slc32a1/Slc17a6/Htr2c/Slc6a5/Slc6a11/Slc7a10/Hrh3	10
BP	GO:0071420	cellular response to histamine	3/373	10/19943	0.000706	0.00684	0.00532521	Gabrg2/Gabra1/Gabrb3	3
BP	GO:0098700	neurotransmitter loading into synaptic v	3/373	10/19943	0.000706	0.00684	0.00532521	Slc32a1/Slc17a6/Ddc	3
BP	GO:0089553	receptor diffusion trapping	3/373	10/19943	0.000706	0.00684	0.00532521	Cacng2/Cacng3/Camk2a	3
BP	GO:0089970	postsynaptic neurotransmitter receptor	3/373	10/19943	0.000706	0.00684	0.00532521	Cacng2/Cacng3/Camk2a	3
BP	GO:0095928	neurotransmitter receptor diffusion trap	3/373	10/19943	0.000706	0.00684	0.00532521	Cacng2/Cacng3/Camk2a	3
BP	GO:0043279	response to alkaloid	11/373	184/19943	0.000717	0.006931	0.00539577	Drd2/Nefh/Grin1/Ryr2/Chrbp/Tac3/Ddc/Grin2b/Htr2a/Pkce/Chrr	11
BP	GO:0007528	neuromuscular junction development	6/373	58/19943	0.000733	0.007068	0.00550245	Cacng2/Ky/Cacna2d2/Shank1/Chat/Unc13c	6
BP	GO:0072384	organelle transport along microtubule	7/373	80/19943	0.000745	0.007168	0.00558028	Kif5a/Nefm/Dync111/Nefl/Rasgrp1/Map2/Map1b	7
BP	GO:0060047	heart contraction	12/373	215/19943	0.000767	0.007326	0.00570293	Drd2/Ryr2/Atp1a3/Scn4b/Chrm2/Chga/Scn1a/Cacna1b/Akap6/Ch	12
BP	GO:0034767	positive regulation of ion transmembran	11/373	180/19943	0.000784	0.007479	0.00582221	Cacng2/Thy1/Cacng3/Rgs7/Rgs7/Dpp6/Kcnc1/Kcna1/Akap6/Cacn	11
BP	GO:0048639	positive regulation of developmental gr	12/373	216/19943	0.000798	0.007596	0.00591321	Syt2/Drd2/Rims1/Atp8a2/Rim2/Akap6/Sgip1/Nrg1/Cacna2d2/Ni	12
BP	GO:0089830	axonal transport	6/373	59/19943	0.000803	0.007628	0.00593836	Kif5a/Nefl/Kif5c/Map2/Dlg2/Bsn	6
BP	GO:0089864	G protein-coupled serotonin receptor sig	5/373	40/19943	0.000855	0.008045	0.00626309	Htr2c/Chrm2/Hrh3/Htr2a/Htr4	5
BP	GO:1901385	regulation of voltage-gated calcium cha	5/373	40/19943	0.000855	0.008045	0.00626309	Cabp1/Hpca/Drd2/Opr1/Cacna2d1	5
BP	GO:1905773	potassium ion import across plasma mem	5/373	40/19943	0.000855	0.008045	0.00626309	Kcnc3/Slc12a5/Atp1a3/Kcnj12/Slc12a3	5
BP	GO:0051209	release of sequestered calcium ion into	9/373	132/19943	0.000857	0.008045	0.00626309	Thy1/Drd2/Ryr2/Htr2c/Pkch2/Jph3/Akap6/Htr2a/Pkce	9
BP	GO:2001259	positive regulation of cation channel act	7/373	82/19943	0.000864	0.008096	0.00630226	Cacng2/Cacng3/Kcnc1/Kcna1/Akap6/Cacna2d1/Hcn1	7
BP	GO:0015698	inorganic anion transport	10/373	161/19943	0.000926	0.008661	0.00674237	Gabrg2/Gabra1/Gabra5/Gabra3/Slc12a	10
BP	GO:0089810	neurotransmitter reuptake	4/373	24/19943	0.000				

BP	GO:0021695 cerebellar cortex development	6/373	63/19943	0.001138	0.010143	0.00789627	Sez62/Atp2b2/Cbln1/Kihl1/Cend1/Sptbn2	6
BP	GO:0018958 phenol-containing compound metabolic	8/373	111/19943	0.001151	0.010235	0.00796775	Tph2/Drd2/Sncb/Atp2b2/Htr2c/Ddc/Chrna7/Chrm2	8
BP	GO:0009914 hormone transport	17/373	390/19943	0.001154	0.010244	0.00797494	Cplx1/Rargge4/Van1/Scg5/Drd2/Hecw1/Kcnab1/Chrbp/Htr2c/Chga/	17
BP	GO:1904375 regulation of protein localization to cell	9/373	159/19943	0.001235	0.010937	0.00851444	Rargge4/Arhgap44/Cacng2/Grm1/Dup6/Camk2b/Map2/Camk2a,	9
BP	GO:0098887 neurotransmitter receptor transport, en	3/373	12/19943	0.001259	0.011088	0.00863117	Arhgap44/Grip2/Lrrc7	3
BP	GO:0006898 receptor-mediated endocytosis	12/373	228/19943	0.001273	0.011186	0.00870791	Nsf/Nabp/Cacng2/Hpca/Drd2/Cacng3/Pacsin1/Necab2/Sgip1/Nrg	12
BP	GO:0098656 anion transmembrane transport	13/373	260/19943	0.001293	0.01126	0.00876588	Gabrg2/Gira2/Gabra1/Gabrac5/Gira1/Slc32a1/Slc17a6/Slc12a5/Sic	13
BP	GO:0021510 spinal cord development	9/373	140/19943	0.001298	0.01126	0.00876588	Rargge4/Gira2/Nefn/Nefn/Nefn/Acan/Sit1/Lhx4/Novo1	9
BP	GO:0060004 reflex	4/373	26/19943	0.0013	0.01126	0.00876588	Cacng2/Gira1/Kcnm1/Shank1	4
BP	GO:2000311 regulation of AMPA receptor activity	4/373	26/19943	0.0013	0.01126	0.00876588	Cacng2/Cacng3/Mapk8ip2/Shank1	4
BP	GO:0021675 nerve development	7/373	89/19943	0.001401	0.012065	0.00999238	Nptx1/Gabra5/Kcna2/Pax2/Chrm2/Gabrb3/Pou4f1	7
BP	GO:0010107 potassium ion import	5/373	45/19943	0.001473	0.012583	0.00979572	Kcnj3/Slc12a5/Atp1a3/Kcnj12/Slc12a3	5
BP	GO:1901381 positive regulation of potassium ion tran	5/373	45/19943	0.001473	0.012583	0.00979572	Rgs7/Dpp6/Kcnc1/Kcna1/Akap6	5
BP	GO:2001258 negative regulation of cation channel ac	5/373	45/19943	0.001473	0.012583	0.00979572	Cabp1/Fg12/Drd2/Kcnab1/Opr1	5
BP	GO:1904063 negative regulation of cation transmem	7/373	90/19943	0.001495	0.012751	0.00991617	Cabp1/Fg12/Drd2/Hecw1/Kcnab1/Prkce/Opr1	7
BP	GO:0097305 response to alcohol	18/373	437/19943	0.001575	0.013377	0.01041345	Fg12/Kif5a/Drd2/Grin1/Gira1/Nefn/Gpld1/Chrbp/Rgs7/Gnas/Cacn	18
BP	GO:0002028 regulation of sodium ion transport	7/373	91/19943	0.001594	0.013517	0.01052241	Fg12/Drd2/Hecw1/Scn4b/Gnas/Neto1/Neto2	7
BP	GO:0048814 regulation of dendrite morphogenesis	8/373	117/19943	0.001614	0.013584	0.01057497	Arhgap44/Grin1/Hecw1/Camk2b/Ct/Chrm2/Dnm3/Trpc5	8
BP	GO:0099639 neurotransmitter receptor transport, en	3/373	13/19943	0.001615	0.013584	0.01057497	Arhgap44/Grip2/Lrrc7	3
BP	GO:1902390 regulation of dendritic spine maintenanc	3/373	13/19943	0.001615	0.013584	0.01057497	Grim1/Zfp804a/Grim2b	3
BP	GO:0043954 cellular component maintenance	6/373	68/19943	0.001696	0.01424	0.01103861	Grin1/Rab3a/Zfp804a/Grim2b/Dlg2/Bsn	6
BP	GO:0035235 ionotropic glutamate receptor signaling	4/373	28/19943	0.001728	0.014374	0.0111902	Grim1/Atp1a3/Camk2a/Grim2b	4
BP	GO:0045761 regulation of adenylylase cyclase activity	4/373	28/19943	0.001728	0.014374	0.0111902	Hpca/Drd2/Hrh3/Akap6	4
BP	GO:0060384 innervation	4/373	28/19943	0.001728	0.014374	0.0111902	Nptx1/Gabra5/Gabrb3/Pou4f1	4
BP	GO:0099010 modification of postsynaptic structure	4/373	28/19943	0.001728	0.014374	0.0111902	Cabp1/Arhgap44/Pfn2/LOC100909840	4
BP	GO:0008089 anterograde axonal transport	5/373	47/19943	0.001793	0.014858	0.01156693	Kif5a/Nefn/Kif5c/Mao2/Dlg2	5
BP	GO:0030451 sleep	5/373	47/19943	0.001793	0.014858	0.01156693	Kif5a/Nefn/Kif5c/Mao2/Dlg2	5
BP	GO:0032414 positive regulation of ion transmembran	8/373	119/19943	0.001798	0.014865	0.01157197	Cacng2/Cacng3/Ryr2/Kcnc1/Kcna1/Akap6/Cacna2d1/Hcn1	8
BP	GO:0051235 maintenance of location	15/373	339/19943	0.001914	0.015796	0.01229718	Vstm2a/Thy1/Drd2/Pex5l/Epb413/Ryr2/Rit2/Htr2c/Mest/Pich2/U	15
BP	GO:0048488 synaptic vesicle endocytosis	6/373	70/19943	0.001969	0.016154	0.01257528	Syt2/Sncb/Pacsin1/Syp/Syt7/Dnm3	6
BP	GO:140238 presynaptic endocytosis	6/373	70/19943	0.001969	0.016154	0.01257528	Syt2/Sncb/Pacsin1/Syp/Syt7/Dnm3	6
BP	GO:0045104 intermediate filament cytoskeleton orga	5/373	48/19943	0.001972	0.016154	0.01257528	Nefn/Nefn/Nefn/Ina/Atp8a2	5
BP	GO:1902073 positive regulation of long-term synaptic	4/373	29/19943	0.001976	0.016154	0.01257528	Drd2/Acty1/Grim2b/Chrna7	4
BP	GO:2000310 regulation of NMDA receptor activity	4/373	29/19943	0.001976	0.016154	0.01257528	Rph3a/Rasgr1/Chrbp/Mapk8ip2	4
BP	GO:0021554 optic nerve development	3/373	14/19943	0.002027	0.016326	0.01270915	Kcna2/Pax2/Chrm2	3
BP	GO:0030007 cellular potassium ion homeostasis	3/373	14/19943	0.002027	0.016326	0.01270915	Drd2/Atp1a3/Kcnm1	3
BP	GO:0032252 secretory granule localization	3/373	14/19943	0.002027	0.016326	0.01270915	Kif5a/Rasgr1/Map2	3
BP	GO:0042438 serotonin metabolic process	3/373	14/19943	0.002027	0.016326	0.01270915	Tph2/Atp2b2/Ddc	3
BP	GO:0060074 hormone secretion	16/373	376/19943	0.002036	0.016373	0.01274576	Cplx1/Rargge4/Van1/Scg5/Drd2/Pex5l/Gpld1/Chrbp/Htr2c/Chga/	16
BP	GO:0021766 hippocampus development	8/373	123/19943	0.002214	0.017703	0.01378133	Kif5a/Nefn/Nefn/Nefn/Slc32a1/Slc17a6/Kcna1/Grim2b	8
BP	GO:0050795 regulation of behavior	7/373	97/19943	0.002301	0.018331	0.0142702	Drd2/Cntnaap4/Hortr2/Kcna2/Sgip1/Opr1/Chrm2	7
BP	GO:0042755 eating behavior	5/373	50/19943	0.002367	0.018752	0.01459826	Oprd1/Atp8a2/Hrh3/Sgip1/Opr1	5
BP	GO:0003012 muscle system process	17/373	418/19943	0.0024	0.018983	0.01477358	Drd2/Gira1/Ryr2/Atp1a3/Scn4b/Chrm2/Chga/Scn1a/Atp8a2/Grip/	17
BP	GO:0048511 rhythmic process	16/373	383/19943	0.002447	0.019321	0.01504091	Tph2/Drd2/Hortr2/Grim1/Kcna2/Chga/Ddc/Acty1/Mapk10/Kcnm1	16
BP	GO:0021700 developmental maturation	14/373	314/19943	0.002458	0.019478	0.01516308	Spr3/Gira1/Nefn/Rab3a/Sez62/Camk2b/Grip2/Kcnm1/Map	14
BP	GO:0007194 negative regulation of adenylylase cyclase	3/373	15/19943	0.002498	0.019478	0.01516308	Drd2/Hrh3/Akap6	3
BP	GO:0031340 positive regulation of vesicle fusion	3/373	15/19943	0.002498	0.019478	0.01516308	Syt2/Rims1/Syt7	3
BP	GO:1901160 primary amino compound metabolic pro	3/373	15/19943	0.002498	0.019478	0.01516308	Tph2/Atp2b2/Ddc	3
BP	GO:1901386 negative regulation of voltage-gated cal	3/373	15/19943	0.002498	0.019478	0.01516308	Cabp1/Drd2/Opr1	3
BP	GO:1903818 positive regulation of voltage-gated poti	3/373	15/19943	0.002498	0.019478	0.01516308	Kcnc1/Kcna1/Akap6	3
BP	GO:0060074 synaptic maturation	4/373	31/19943	0.002542	0.019744	0.01537005	Nefn/Sez62/Camk2b/Shank1	4
BP	GO:0009582 detection of abiotic stimulus	8/373	126/19943	0.002573	0.019917	0.01550518	Rh2/Ano3/Atp2b2/Scn1a/Atp8a2/Kcna1/Grim2b/Htr2a	8
BP	GO:0032411 positive regulation of transporter activit	8/373	126/19943	0.002573	0.019917	0.01550518	Cacng2/Cacng3/Ryr2/Kcnc1/Kcna1/Akap6/Cacna2d1/Hcn1	8
BP	GO:2000649 regulation of sodium ion transmembran	5/373	51/19943	0.002584	0.019969	0.01554528	Fg12/Hecw1/Scn4b/Neto1/Neto2	5
BP	GO:0008016 regulation of heart contraction	10/373	185/19943	0.002607	0.020094	0.01564269	Drd2/Ryr2/Scn4b/Chrm2/Chga/Cacna1b/Akap6/Chrna7/Cacna2d	10
BP	GO:0021761 limbic system development	9/373	155/19943	0.002612	0.020094	0.01564269	Kif5a/Drd2/Nefn/Nefn/Nefn/Slc32a1/Slc17a6/Kcna1/Grim2b	9
BP	GO:0052413 negative regulation of ion transmembran	6/373	74/19943	0.002614	0.020094	0.01564269	Cabp1/Fg12/Drd2/Hecw1/Kcnab1/Opr1	6
BP	GO:0009591 detection of external stimulus	8/373	127/19943	0.002702	0.020698	0.01611287	Hpca/Rab3a/Sez62/Camk2b/Grip2/Kcnm1/Map	8
BP	GO:0007193 adenylylase cyclase-inhibiting G prot	6/373	75/19943	0.002798	0.021391	0.01665252	Grim4/Drd2/Oprd1/Chrm2/Hrh3/Opr1	6
BP	GO:2001222 regulation of neuron migration	5/373	52/19943	0.002816	0.021493	0.01673216	Scri1/Camk2b/Camk2a/Nrg1/Nexmif	5
BP	GO:1903522 regulation of blood circulation	12/373	251/19943	0.002835	0.021575	0.01679596	Drd2/Ryr2/Scn4b/Chrm2/Chga/Cacna1b/Akap6/Htr2a/Chrn	12
BP	GO:0098884 postsynaptic neurotransmitter receptor	4/373	32/19943	0.002862	0.021619	0.01688001	Hpca/Pacsin1/Nrg1/Dnm3	4
BP	GO:0140239 postsynaptic endocytosis	4/373	32/19943	0.002862	0.021619	0.01688001	Hpca/Pacsin1/Nrg1/Dnm3	4
BP	GO:1903074 response to salt	4/373	32/19943	0.002862	0.021619	0.01688001	Hpca/Nefn/Nefn/Pou4	4
BP	GO:0098876 vesicle-mediated transport to the plas	7/373	101/19943	0.002892	0.021803	0.01697295	Cplx1/Arhgap44/Nsf/Stx1b/Grip2/Mapk10/Lrrc7	7
BP	GO:0051965 positive regulation of synapse assembly	6/373	76/19943	0.002991	0.022438	0.01746794	Sittrk3/Cistn3/Syndig1/Cbln1/Lingo4/Cistn2	6
BP	GO:0001967 suckling behavior	3/373	16/19943	0.003033	0.022438	0.01746794	Grim1/Grim2b/Pou4f1	3
BP	GO:0035865 cellular response to potassium ion	3/373	16/19943	0.003033	0.022438	0.01746794	Nptx1/Chrbp/Dlg2	3
BP	GO:0098925 postsynaptic signal transduction	3/373	16/19943	0.003033	0.022438	0.01746794	Cabp1/Nrg1/Camk4	3
BP	GO:0099527 postsynapse to nucleus signaling pathw	3/373	16/19943	0.003033	0.022438	0.01746794	Cabp1/Nrg1/Camk4	3
BP	GO:0099640 axo-dendritic protein transport	3/373	16/19943	0.003033	0.022438	0.01746794	Kif5a/Kif5c/Dlg2	3
BP	GO:1900271 regulation of long-term synaptic potenti	5/373	53/19943	0.003063	0.022584	0.017581	Drd2/Calb2/Adcy1/Grim2b/Chrna7	5
BP	GO:1904645 response to amyloid-beta	5/373	53/19943	0.003063	0.022584	0.017581	Atp1a3/Syp/Cacna1b/Chrna7/Cacna2d1	5
BP	GO:0046717 acid secretion	8/373	130/19943	0.003121	0.022976	0.01788637	Grim4/Drd2/Grim1/Htr2c/Hrh3/Grim2b/Opr1/Abcc2	8
BP	GO:0030072 peptide hormone secretion	13/373	288/19943	0.003165	0.023257	0.01810484	Cplx1/Rargge4/Van1/Drd2/Pex5l/Gpld1/Chrbp/Htr2c/Chga/Stxbp	13
BP	GO:0022037 metencephalon development	9/373	160/19943	0.003203	0.023656	0.01841552	Grim1/Cmt1/Sez62/Atp2b2/Kcnc1/Cbln1/Kihl1/Cend1/Sptbn2	9
BP	GO:0045103 intermediate filament-based process	5/373	54/19943	0.003324	0.02413	0.01878472	Nefn/Nefn/Nefn/Ina/Atp8a2	5
BP	GO:0010513 positive regulation of phosphatidylinosit	2/373	5/19943	0.003361	0.02413	0.01878472	Htr2c/Htr2a	2
BP	GO:0099502 calcium-dependent activation of synapt	2/373	5/19943	0.003361	0.02413	0.01878472	Syt2/Syt7	2
BP	GO:1902952 positive regulation of dendritic spine ma	2/373	5/19943	0.003361	0.02413	0.01878472	Grim1/Zfp804a	2
BP	GO:0007009 plasma membrane organization	7/373	104/19943	0.003406	0.024336	0.01894504	Ano3/Epb413/Rab3a/Pacsin1/Sgip1/Xkr6/Syt7	7
BP	GO:0010771 negative regulation of cell morphogene	7/373	104/19943	0.003406	0.024336	0.01894504	Thy1/Dmtr/Sit1/Cil/Map2/Dnm3/Trpc5	7
BP	GO:0003407 neural retina development	6/373	78/19943	0.003406	0.024336	0.01894504	Thy1/Slc17a6/Atp2b2/Atp2b3/Atp8a2/Hcn1	6
BP	GO:0009612 response to mechanical stimulus	14/373	326/19943	0.003497	0.024942	0.01941662	Phf2/Ano3/Drd2/Ryr2/Acan/Atp2b2/Scn1a/Kcncl/Atp8a2/Pax2/	14
BP	GO:0042749 regulation of circadian sleep/wake cycle	4/373	34/19943	0.003585	0.025388	0.0197643	Drd2/Hortr2/Kcna2/Chrm2	4
BP	GO:1905606 regulation of presynapse assembly	4/373	34/19943	0.003585	0.025388	0.0197643	Lrfn5/Sittrk3/Cistn3/Cbln1	4
BP	GO:0043268 positive regulation of potassium ion tran	5/373	55/19943	0.003602	0.025399	0.01977288	Rgs7/Dpp6/Kcnc1/Kcna1/Akap6	5
BP	GO:0053064 chloride ion homeostasis	3/373	17/19943	0.003632	0.025487	0.01984144	Slc12a5/Abcc2/Slc12a3	3
BP	GO:0099638 endosome to plasma membrane protein	3/373	17/19943	0.003632	0.025487	0.01984144	Arhgap44/Grip2/Lrrc7	3
BP	GO:0060041 retina development in camera-type eye	10/373	194/19943	0.003663	0.025663	0.01997851	Thy1/Hpca/Slc17a6/Atp2b2/Atp2b3/Atp8a2/Pax2/CeH4/Tub/Hcn1	10
BP	GO:1909138 neuron projection extension	10/373	195/19943	0.003798	0.026571	0.02068513	Syt2/Rims1/Nrg1/Sit1/Rims2/Nrg1/Map2/Map1b/Trpc5/L1cam	10
BP	GO:0098659 inorganic cation import across plasma m	6/373	80/19943	0.003863	0.026939	0.02097142	Kcnj3/Slc12a5/Atp1a3/Kcnj12/Slc8a3/Slc12a3	6
BP	GO:0099587 inorganic ion import across plasma mem	6/373	80/19943	0.003863	0.026939	0.02097142	Kcnj3/Slc12a5/Atp1a3/Kcnj12/Slc8a3/Slc12a3	6
BP	GO:0061025 membrane fusion	8/373	135/19943	0.003929	0.027354	0.02128466	Cplx1/Nsf/Syt2/Rims1/Stx1b/Vamp1/Rab3a/Syt7	8
BP	GO:0034766 negative regulation of ion transmembra	7/373	107/19943	0.003988	0.027679	0.02154746	Cabp1/Fg12/Drd2/Hecw1/Kcnab1/Prkce/Opr1	7
BP	GO:0045745 positive regulation of G protein-coupled	4/373	35/19943	0.003989	0.027679	0.02154746	Drd2/Chga/Map2/Necab2	4
BP	GO:0031102 neuron projection regeneration	6/373	81/19943	0.004108	0.028457	0.02215356	Thy1/Nefn/Nefn/Nefn/Nrg1/Map1b	6
BP	GO:0009410 response to xenobiotic stimulus	16/373	40					

BP	GO:0057091	synaptic vesicle clustering	3/373	18/19943	0.004298	0.0295	0.02296492	Syn1/Rab3a/Syndig1	3
BP	GO:0058885	modification of postsynaptic actin cytosol	3/373	18/19943	0.004298	0.0295	0.02296492	Cabp1/Pim2/OC100908840	3
BP	GO:0021537	telencephalon development	14/373	334/19943	0.004328	0.029613	0.02303336	Kif5a/Drd2/Neft/Grin1/Neft/Neftm/Slc32a1/Slc17a6/Atp1a3/Kcna	14
BP	GO:0042220	response to cocaine	6/373	82/19943	0.004364	0.029812	0.02320822	Drd2/Neft/Chrbp/Grin2b/Htr2a/Chrm2	6
BP	GO:2000171	negative regulation of dendrite develop	4/373	36/19943	0.004422	0.030158	0.02347764	RGD1307443/Cit/Dnm3/Trpc5	4
BP	GO:0006941	striated muscle contraction	9/373	169/19943	0.004628	0.031493	0.02451664	Ryr2/Atp1a3/Scn4b/Chga/Scn1a/Atp8a2/Akap6/Slc8a3/Cacna2d1	9
BP	GO:0032410	negative regulation of transporter activi	6/373	83/19943	0.004632	0.031493	0.02451664	Cabp1/Fgf12/Drd2/Hecwl1/Kenab1/Opr1	6
BP	GO:0007018	microtubule-based movement	12/373	267/19943	0.004647	0.031545	0.02455758	Kif5a/Neftm/Dync11/Neft/Neftm/Kif5c/Rasgrp1/Map2/Map1b/Dlg2	12
BP	GO:0098739	import across plasma membrane	7/373	111/19943	0.004876	0.032778	0.02355171	Kcnj3/Slc12a5/Atp1a3/Slc6a5/Kcnj12/Slc8a3/Slc12a3	7
BP	GO:0054744	negative regulation of G protein-couple	5/373	59/19943	0.004879	0.032778	0.02355171	Drd2/Camk2b/Map2/Necab2/Opr1	5
BP	GO:0051482	positive regulation of cytosolic calcium k	4/373	37/19943	0.004886	0.032778	0.02355171	Drd2/Grm1/Htr2c/Opr1	4
BP	GO:0097366	response to bronchodilator	6/373	84/19943	0.004912	0.032778	0.02355171	Drd2/Grin1/Rasgrf1/Rgs7/Grin2b/Rgs17	6
BP	GO:0007016	cytoskeletal anchoring at plasma membe	2/373	6/19943	0.004979	0.032778	0.02355171	Epb41i3/Shank1	2
BP	GO:0006291	acetylcholine metabolic process	2/373	6/19943	0.004979	0.032778	0.02355171	Slc6a7/Chat	2
BP	GO:0031133	regulation of axon diameter	2/373	6/19943	0.004979	0.032778	0.02355171	Neft/Neftw	2
BP	GO:0042435	indole-containing compound biosynthet	2/373	6/19943	0.004979	0.032778	0.02355171	Tph2/Ddc	2
BP	GO:0051584	regulation of dopamine uptake involved	2/373	6/19943	0.004979	0.032778	0.02355171	Drd2/Nat8l	2
BP	GO:0051940	regulation of catecholamine uptake invo	2/373	6/19943	0.004979	0.032778	0.02355171	Drd2/Nat8l	2
BP	GO:0098937	anterograde dendritic transport	2/373	6/19943	0.004979	0.032778	0.02355171	Kif5a/Kif5c	2
BP	GO:1900619	acetate ester metabolic process	2/373	6/19943	0.004979	0.032778	0.02355171	Slc6a7/Chat	2
BP	GO:0043624	cellular protein complex disassembly	8/373	141/19943	0.005102	0.033266	0.02387392	Nefl/Hpa3/Nrg1/Map2/Add2/Mao1b/Ogof1/Sptbn2	8
BP	GO:0021692	cerebellar Purkinje cell layer morphogen	3/373	19/19943	0.005034	0.032843	0.02556785	Atp2b2/Cend1/Sptbn2	3
BP	GO:0070886	positive regulation of calcineurin-NFAT s	3/373	19/19943	0.005034	0.032843	0.02556785	Akap6/Nrg1/Camta1	3
BP	GO:0098840	protein transport along microtubule	3/373	19/19943	0.005034	0.032843	0.02556785	Kif5a/Kif5c/Dlg2	3
BP	GO:0099118	microtubule-based protein transport	3/373	19/19943	0.005034	0.032843	0.02556785	Kif5a/Kif5c/Dlg2	3
BP	GO:0106058	positive regulation of calcineurin-mediat	3/373	19/19943	0.005034	0.032843	0.02556785	Akap6/Nrg1/Camta1	3
BP	GO:0043624	cellular protein complex disassembly	8/373	141/19943	0.005102	0.033266	0.02387392	Nefl/Hpa3/Nrg1/Map2/Add2/Mao1b/Ogof1/Sptbn2	8
BP	GO:0097306	cellular response to alcohol	9/373	172/19943	0.005185	0.033729	0.02625728	Grd2/Kif5a/Gr1a1/Gpld1/Gnas/Grin2b/Pknox/Sptbn2/L1cam	9
BP	GO:0043112	receptor metabolic process	10/373	204/19943	0.005207	0.033816	0.02632552	Nsf/Napb/Cacng2/Hpca/Drd2/Cacng3/Pacsin1/Necab2/Nrg1/Dnm	10
BP	GO:0035176	social behavior	5/373	60/19943	0.005242	0.033846	0.02634842	Grin1/Mapk8ip2/Shank1/Chrm2/Nrxn3	5
BP	GO:0051703	intraspecies interaction between organi	5/373	60/19943	0.005242	0.033846	0.02634842	Grin1/Mapk8ip2/Shank1/Chrm2/Nrxn3	5
BP	GO:0090102	cochlea development	5/373	60/19943	0.005242	0.033846	0.02634842	Pvalb/Gabra5/Atp2b2/Pax2/Gabrb3	5
BP	GO:1902305	regulation of sodium ion transmembran	5/373	60/19943	0.005242	0.033846	0.02634842	Fgf12/Hesw1/Scn8a/Neto1/Neto2	5
BP	GO:0022410	circadian sleep/wake cycle process	4/373	38/19943	0.005382	0.034592	0.02692929	Drd2/Htr2c/Kcna2/Chrm2	4
BP	GO:0099174	regulation of presynaptic organization	4/373	38/19943	0.005382	0.034592	0.02692929	Lfrn5/Slitk3/Ctstn3/Cbln1	4
BP	GO:1903076	regulation of protein localization to plas	7/373	114/19943	0.005635	0.036168	0.0281564	Arhgap44/Grm1/Dpp6/Camk2b/Map2/Camk2a/Dpp10	7
BP	GO:0050770	regulation of axonogenesis	10/373	207/19943	0.005757	0.036644	0.0286828	Thy1/Grin1/Neft/Neftm/Sit1/Nrg1/Map2/Map1b/Trpcs/L1cam	10
BP	GO:0039300	forebrain development	18/373	495/19943	0.005837	0.037001	0.02880497	Kif5a/Drd2/Neft/Grin1/Neft/Neftm/Slc32a1/Slc17a6/Atp1a3/Kcnc	18
BP	GO:0033605	positive regulation of catecholamine see	3/373	20/19943	0.005841	0.037001	0.02880497	Chrbp/Pknox/Chrm2	3
BP	GO:0050774	negative regulation of dendrite morpho	3/373	20/19943	0.005841	0.037001	0.02880497	Chrbp/Dnm3/Trpc5	3
BP	GO:0097107	postsynaptic density assembly	3/373	20/19943	0.005841	0.037001	0.02880497	Nptx1/Cbln1/Shank1	3
BP	GO:1900451	positive regulation of glutamate recepto	3/373	20/19943	0.005841	0.037001	0.02880497	Cacng2/Cacng3/Necab2	3
BP	GO:0086003	cardiac muscle contraction	5/373	62/19943	0.006026	0.038062	0.02963057	Ryr2/Scn4b/Scn1a/Akap6/Cacna2d1	5
BP	GO:0039302	hindbrain development	10/373	209/19943	0.006149	0.038782	0.03019107	Grin1/Cmt1/Scn8a2/Atp2b2/Kcnc1/Cbln1/Kihl1/Cend1/Sptbn2/Pr	10
BP	GO:0031279	regulation of cyclase activity	4/373	40/19943	0.006471	0.040755	0.03172681	Hpca/Drd2/Hrh3/Akap6	4
BP	GO:0043271	negative regulation of ion transport	9/373	179/19943	0.006659	0.041964	0.03266815	Cabp1/Fgf12/Drd2/Hecwl1/Hrh3/Htr2a/Pknox/Opr1	9
BP	GO:0035584	calcium-mediated signaling using intrac	3/373	21/19943	0.006722	0.041964	0.03266815	Dmtr/Ryr2/Tenm2	3
BP	GO:0045475	locomotor rhythm	3/373	21/19943	0.006722	0.041964	0.03266815	Mapk10/Kcnma1/Opr1	3
BP	GO:0099188	postsynaptic cytoskeleton organization	3/373	21/19943	0.006722	0.041964	0.03266815	Neft/Ina/Camk2b	3
BP	GO:0021549	cerebellum development	8/373	148/19943	0.006729	0.041964	0.03266815	Ckmt1/Scn6l2/Atp2b2/Kcnc1/Cbln1/Kihl1/Cend1/Sptbn2	8
BP	GO:0046053	regulation of hormone secretion	13/373	316/19943	0.006922	0.041964	0.03266815	Vsn1/Scg5/Drd2/Pex51/Gpld1/Chrbp/Htr2c/Chga/Gnas/Shxbp5/N	13
BP	GO:0034764	positive regulation of transmembrane t	11/373	249/19943	0.006836	0.041964	0.03266815	Cacng2/Thy1/Cacng3/Ryr2/Rgs7/Dpp6/Kcnc1/Kcna1/Akap6/Cacn	11
BP	GO:0001661	conditioned taste aversion	2/373	7/19943	0.006885	0.041964	0.03266815	Grin1/Chrm2	2
BP	GO:0010511	regulation of phosphatidylinositol biosy	2/373	7/19943	0.006885	0.041964	0.03266815	Htr2c/Htr2a	2
BP	GO:0021578	hindbrain maturation	2/373	7/19943	0.006885	0.041964	0.03266815	Grin1/Cand1	2
BP	GO:0030644	cellular chloride ion homeostasis	2/373	7/19943	0.006885	0.041964	0.03266815	Slc12a5/Abcc2	2
BP	GO:009075	sensory perception of touch	2/373	7/19943	0.006885	0.041964	0.03266815	Rab3a/Kcna1	2
BP	GO:0051582	positive regulation of neurotransmitter	2/373	7/19943	0.006885	0.041964	0.03266815	Drd2/Nat8l	2
BP	GO:0098943	neurotransmitter receptor transport, po	2/373	7/19943	0.006885	0.041964	0.03266815	Cacng2/Cacng3	2
BP	GO:1900028	negative regulation of ruffle assembly	2/373	7/19943	0.006885	0.041964	0.03266815	Pfn2/LOC100909840	2
BP	GO:1903935	response to sodium arsenite	2/373	7/19943	0.006885	0.041964	0.03266815	Neft/Neftw	2
BP	GO:1990334	calcium ion export across plasma membe	2/373	7/19943	0.006885	0.041964	0.03266815	Atp2b2/Slc8a3	2
BP	GO:1990709	presynaptic active zone organization	2/373	7/19943	0.006885	0.041964	0.03266815	Rab3a/Bsn	2
BP	GO:0010977	negative regulation of neuron projectio	9/373	180/19943	0.006929	0.042178	0.03384479	Thy1/Prkcd1/RGD1307443/Slc1b1/Sit1/Cit/Map2/Dnm3/Trpc5	9
BP	GO:0021696	cerebellar cortex morphogenesis	4/373	41/19943	0.007067	0.042955	0.03343982	Atp2b2/Cbln1/Cend1/Sptbn2	4
BP	GO:0097062	dendritic spine maintenance	3/373	22/19943	0.007676	0.046466	0.03617298	Grin1/Zfp804a/Grin2b	3
BP	GO:0099558	maintenance of synapse structure	3/373	22/19943	0.007676	0.046466	0.03617298	Rab3a/Dlg2/Bsn	3
BP	GO:0042745	circadian sleep/wake cycle	4/373	42/19943	0.007698	0.046466	0.03617298	Drd2/Htr2c/Kcna2/Chrm2	4
BP	GO:1903170	negative regulation of calcium ion trans	4/373	42/19943	0.007698	0.046466	0.03617298	Cabp1/Drd2/Pknox/Opr1	4
BP	GO:0060996	dendritic spine development	7/373	122/19943	0.008009	0.048761	0.03739506	Arhgap44/Slc12a5/Camk2b/Camk2a/Nrg1/Shank1/Dnm3	7
CC	GO:0097060	synaptic membrane	80/373	493/19943	6.57E-52	2.86E-48	2.2283E-48	Grm4/Rph3a/Magee1/Gabrg2/Gira2/Gabra1/Scn8a/Kcnj3/Lfrn5/C	80
CC	GO:0025440	intrinsic component of synaptic membra	53/373	254/19943	4.45E-40	9.69E-37	7.5468E-37	Grrm4/Gabra2/Gabra1/Scn8a/Kcnj3/Lfrn5/Cacng2/Drd2/Slitk3/Ot	53
CC	GO:0045211	postsynaptic membrane	58/373	354/19943	1.17E-37	1.7E-34	1.3214E-34	Rph3a/Magee1/Gabrg2/Gira2/Gabra1/Scn8a/Lfrn5/Cacng2/Cadp	58
CC	GO:0098969	integral component of synaptic membra	49/373	235/19943	4.67E-37	5.09E-34	3.9647E-34	Grm4/Gabrg2/Gabra1/Scn8a/Kcnj3/Lfrn5/Cacng2/Drd2/Slitk3/Ot	49
CC	GO:0099572	postsynaptic specialization	62/373	452/19943	1.95E-35	1.18E-32	9.1577E-33	Cabp1/Ragef4/Gabrg2/Gabra1/Arhgap44/Neft/Scn8a/Lfrn5/Cacng	62
CC	GO:0042734	presynaptic membrane	45/373	212/19943	1.97E-34	1.43E-31	1.1115E-31	Grm4/Scn8a/Kcnj3/Cadps2/Drd2/Opr1/Gabra5/Rims1/Chrna4/C	45
CC	GO:0034702	ion channel complex	50/373	294/19943	2.71E-33	1.69E-30	1.3134E-30	Gabrg2/Gira2/Gabra1/Scn8a/Kcnj3/Cacng2/Gabra5/Chrna4/Pex51	50
CC	GO:1902495	transmembrane transporter complex	51/373	314/19943	6.13E-33	3.34E-30	2.5978E-30	Gabrg2/Gira2/Gabra1/Scn8a/Kcnj3/Cacng2/Gabra5/Chrna4/Pex51	51
CC	GO:1903351	transporter complex	51/373	321/19943	1.86E-32	9E-30	7.0093E-30	Gabrg2/Gira2/Gabra1/Scn8a/Kcnj3/Cacng2/Gabra5/Chrna4/Pex51	51
CC	GO:0032279	asymmetric synapse	55/373	421/19943	1.82E-30	6.62E-28	5.1515E-28	Cabp1/Ragef4/Arhgap44/Neft/Scn8a/Lfrn5/Cacng2/Drd2/Neft/Nv	55
CC	GO:0098889	intrinsic component of presynaptic mem	33/373	135/19943	3.44E-30	9.99E-28	7.773E-28	Grm4/Scn8a/Kcnj3/Drd2/Opr1/Gabra5/Chrna4/Cntnap4/Grin1/LF	33
CC	GO:0098984	neuron to neuron synapse	56/373	445/19943	3.7E-30	1.01E-27	7.8511E-27	Cabp1/Ragef4/Arhgap44/Neft/Scn8a/Lfrn5/Cacng2/Drd2/Neft/Nv	56
CC	GO:0098936	intrinsic component of postsynaptic mem	39/373	185/19943	8.19E-30	2.1E-27	1.6335E-27	Gabrg2/Gabra1/Scn8a/Lfrn5/Cacng2/Drd2/Slitk3/Opr1/Gabra5	39
CC	GO:0014069	postsynaptic density	54/373	417/19943	1.01E-29	2.45E-27	1.9101E-27	Cabp1/Ragef4/Arhgap44/Neft/Scn8a/Lfrn5/Cacng2/Drd2/Neft/Nv	54
CC	GO:0099056	integral component of presynaptic mem	32/373	122/19943	7.32E-28	1.28E-25	9.9358E-26	Grm4/Scn8a/Kcnj3/Drd2/Opr1/Gabra5/Chrna4/Cntnap4/Grin1/C	32
CC	GO:0150034	distal axon	52/373	423/19943	1.58E-27	2.65E-25	2.0618E-25	Cplx1/Grm4/Ragef4/Syt2/Kif5a/Lamp5/Thy1/Drd2/Ncs1/S	52
CC	GO:0099035	integral component of postsynaptic mem	36/373	175/19943	3.44E-27	5.56E-25	4.328E-25	Gabrg2/Gabra1/Scn8a/Lfrn5/Cacng2/Drd2/Slitk3/Opr1/Gabra5	36
CC	GO:0034703	cation channel complex	39/373	221/19943	9.0E-27	1.33E-24	1.0385E-24	Scn8a/Kcnj3/Cacng2/Pex51/Cacng2/Kcna2/Grin1/Cacng3/Dlgap5/Pf	39
CC	GO:0043679	axon terminus	39/373	222/19943	1.17E-26	1.54E-24	1.202E-24	Cplx1/Grm4/Ragef4/Syt2/Pvalb/Drd2/Ncs1/Syn1/Opr1/Kcna2	39
CC	GO:0044306	neuron projection terminus	40/373	245/19943	4.7E-26	5.69E-24	4.4284E-24	Cplx1/Grm4/Ragef4/Syt2/Pvalb/Drd2/Ncs1/Syn1/Opr1/Kcna2	40
CC	GO:0098948	intrinsic component of postsynaptic spe	29/373	114/19943	6.25E-25	6.64E-23	5.1742E-23	Gabrg2/Gabra1/Scn8a/Lfrn5/Cacng2/Slitk3/Opr1/Gabra5/Clstn	29
CC	GO:0099634	postsynaptic specialization membrane	31/373	139/19943	1.1E-24	1.09E-22	8.4608E-22	Gabrg2/Gabra1/Scn8a/Lfrn5/Cacng2/Slitk3/Opr1/Gabra5/Clstn	31
CC	GO:0099060	integral component of postsynaptic spe	27/373	108/19943	4.95E-23	3.54E-21	2.7		

CC	GO:009522	region of cytosol	4/373	42/19943	0.007698	0.046466	0.03617298	Nes1/Snch/Camk2a/Pfkce	4
CC	GO:0031301	integral component of organelle memb	10/373	218/19943	0.008175	0.04921	0.03892092	Syt2/Gdap1/Oprc1/Slc32a1/Slc17a6/Vamp1/Syp/Sv2b/Sv2c/Chrn	10
MF	GO:0022839	ion gated channel activity	48/373	326/19943	0.05629	1.05E-26	8.1634E-27	Gabrg2/Gira2/Gabra1/Scn8a/Kcnj3/Cacng2/Kcnab3/Nes1/Gabra5	48
MF	GO:0022836	gated channel activity	48/373	337/19943	2.95E-28	4.46E-26	3.471E-26	Gabrg2/Gira2/Gabra1/Scn8a/Kcnj3/Cacng2/Kcnab3/Nes1/Gabra5	48
MF	GO:0005216	ion channel activity	50/373	406/19943	1.6E-26	2.05E-24	1.5898E-24	Gabrg2/Gira2/Gabra1/Scn8a/Kcnj3/Cacng2/Slc24a2/Kcnab3/Nes1	50
MF	GO:0022838	substrate-specific channel activity	50/373	417/19943	5.56E-26	6.59E-24	5.0976E-24	Gabrg2/Gira2/Gabra1/Scn8a/Kcnj3/Cacng2/Slc24a2/Kcnab3/Nes1	50
MF	GO:0005261	cation channel activity	43/373	317/19943	1.35E-24	1.26E-22	9.8249E-23	Scn8a/Kcnj3/Cacng2/Slc24a2/Kcnab3/Nes1/Chna4/Pex5/Kcnk2/H	43
MF	GO:0015267	channel activity	50/373	447/19943	1.36E-24	1.26E-22	9.8249E-23	Gabrg2/Gira2/Gabra1/Scn8a/Kcnj3/Cacng2/Slc24a2/Kcnab3/Nes1	50
MF	GO:0022803	passive transmembrane transporter act	50/373	447/19943	1.36E-24	1.26E-22	9.8249E-23	Gabrg2/Gira2/Gabra1/Scn8a/Kcnj3/Cacng2/Slc24a2/Kcnab3/Nes1	50
MF	GO:0005244	voltage-gated ion channel activity	34/373	195/19943	3E-23	2.38E-21	1.852E-21	Scn8a/Kcnj3/Cacng2/Kcnab3/Nes1/Kcnk2/Kcnab2/Grin1/Cacng3/H	34
MF	GO:0022832	voltage-gated channel activity	34/373	195/19943	3E-23	2.38E-21	1.852E-21	Scn8a/Kcnj3/Cacng2/Kcnab3/Nes1/Kcnk2/Kcnab2/Grin1/Cacng3/H	34
MF	GO:0046873	metal ion transmembrane transporter a	47/373	430/19943	1.01E-22	7.72E-21	6.01E-21	Scn8a/Kcnj3/Cacng2/Slc24a2/Kcnab3/Nes1/Slc5a7/Kcnab2/Kcnab2	47
MF	GO:0022843	voltage-gated cation channel activity	27/373	146/19943	2.2E-19	1.57E-17	1.2255E-17	Kcnj3/Cacng2/Kcnab3/Nes1/Kcnk2/Kcnab2/Grin1/Cacng3/Kcnab2/H	27
MF	GO:0035254	glutamate receptor binding	19/373	67/19943	9.9E-18	6.54E-16	5.0902E-16	Cabp1/Nsf/Cacng2/Drd2/Grin1/Cacng3/Rasgr1/Atp2b2/Syndig1/I	19
MF	GO:0015079	potassium ion transmembrane transpor	24/373	161/19943	8.81E-15	2.15E-13	1.6775E-13	Kcnj3/Slc24a2/Kcnab3/Kcnk2/Kcnab2/Slc12a5/Kcnk2/Kcnk3/Atp1	24
MF	GO:0015077	monovalent inorganic cation transmem	34/373	375/19943	2.99E-14	1.57E-12	1.2242E-12	Scn8a/Kcnj3/Slc24a2/Kcnab3/Slc5a7/Kcnk2/Kcnab2/Kcnk3/Slc32a1/Slc12	34
MF	GO:0005249	voltage-gated potassium channel activi	18/373	88/19943	3.83E-14	1.96E-12	1.5278E-12	Kcnj3/Kcnab3/Kcnk2/Kcnab2/Kcnk2/Kcnk3/Kcnk1/Kcnk1/Gria1/Krnl1/I	18
MF	GO:0030594	neurotransmitter receptor activity	20/373	119/19943	7.51E-14	3.72E-12	2.894E-12	Gabrg2/Gira2/Gabra1/Drd2/Gabra5/Chrna4/Grin1/Gria1/Gm1/H	20
MF	GO:0005267	potassium channel activity	20/373	127/19943	2.69E-13	1.24E-11	9.6199E-12	Kcnj3/Kcnab3/Kcnk2/Kcnab2/Kcnk2/Kcnk3/Kcnk4/Kcnk1/Kcnab1	20
MF	GO:0035276	ligand-gated ion channel activity	20/373	131/19943	4.92E-13	2.21E-11	1.7218E-11	Gabrg2/Gira2/Gabra1/Kcnj3/Gabra5/Chrna4/Pex5/Grin1/Gria1/R	20
MF	GO:0022834	ligand-gated channel activity	20/373	134/19943	7.63E-13	3.32E-11	2.5876E-11	Gabrg2/Gira2/Gabra1/Kcnj3/Gabra5/Chrna4/Pex5/Grin1/Gria1/R	20
MF	GO:0089818	structural constituent of synapse	11/373	30/19943	3.36E-12	1.3E-10	1.0094E-10	Nefn/Rims1/Nefn/Ina/Camk2b/Rims2/Erc2/Dlg2/Dnm3/Bsn/Sptbn	11
MF	GO:0089860	postsynaptic neurotransmitter receptor	13/373	57/19943	3.24E-11	1.19E-09	9.2409E-10	Gabrg2/Gira2/Gabra1/Gabra5/Chrna4/Grin1/Gria1/Gm1/Gabra3	13
MF	GO:0005516	calmodulin binding	20/373	169/19943	6.01E-11	2.08E-09	1.6187E-09	Grm4/Camk1g/Grin1/Ryr2/Rit2/Atp2b2/Camk2b/Atp2b3/Pepp4/Ca	20
MF	GO:0042165	neurotransmitter binding	13/373	61/19943	8.13E-11	2.75E-09	2.137E-09	Gira2/Slc5a7/Chrna4/Grin1/Gria1/Crbp/Htr2c/Slc6a11/Grin2b/H	13
MF	GO:1904915	transmitter-gated ion channel activity	12/373	52/19943	1.62E-09	5.18E-09	4.0056E-09	Gabra2/Gira2/Gabra1/Gabra5/Chrna4/Grin1/Gria1/Gabra3/Grin2	12
MF	GO:0095929	neurotransmitter receptor activity invol	12/373	55/19943	3.27E-10	1.01E-08	7.8677E-09	Gabrg2/Gira2/Gabra1/Gabra5/Chrna4/Grin1/Gria1/Gabra3/Grin2	12
MF	GO:0035255	ionotropic glutamate receptor binding	11/373	44/19943	3.73E-10	1.13E-08	8.7957E-09	Nsf/Cacng2/Drd2/Cacng3/Gnas/Grin2b/Lrrc7/Neto1/Neto2/Shank	11
MF	GO:0022824	transmitter-gated ion channel activity	12/373	58/19943	6.32E-10	1.86E-08	1.4467E-08	Gabrg2/Gira2/Gabra1/Gabra5/Chrna4/Grin1/Gria1/Gabra3/Grin2	12
MF	GO:0022835	transmitter-gated channel activity	12/373	58/19943	6.32E-10	1.86E-08	1.4467E-08	Gabrg2/Gira2/Gabra1/Gabra5/Chrna4/Grin1/Gria1/Gabra3/Grin2	12
MF	GO:0015085	calcium ion transmembrane transporter	16/373	134/19943	4.46E-09	1.19E-07	9.2805E-08	Cacng2/Slc24a2/Nes1/Grin1/Cacng3/Ryr2/Atp2b2/Atp2b3/Iph3/C	16
MF	GO:0005240	extracellular ligand-gated ion channel ac	12/373	70/19943	6.16E-09	1.61E-07	1.2584E-07	Gabrg2/Gira2/Gabra1/Gabra5/Chrna4/Grin1/Gria1/Gabra3/Grin2	12
MF	GO:0095905	ligand-gated anion channel activity	7/373	20/19943	4.76E-08	1.14E-06	8.8687E-07	Gabrg2/Gira2/Gabra1/Gabra5/Gira1/Gabra3/Gabra3	7
MF	GO:0070405	ammonium ion binding	11/373	79/19943	2.45E-07	5.36E-06	4.17E-06	Drd2/Slc5a7/Chrna4/Htr2c/Gpr12/Rasgr1/Htr2a/Chrna7/Pcy1b/I	11
MF	GO:0095904	ligand-gated cation channel activity	12/373	99/19943	3.29E-07	7.03E-06	5.4728E-06	Kcnj3/Chna4/Pex5/Grin1/Ryr2/Iph3/Kcnj12/Kcnj7/Grin2b/Chrn	12
MF	GO:0005262	calcium channel activity	13/373	119/19943	3.64E-07	7.66E-06	5.9603E-06	Cacng2/Slc24a2/Nes1/Grin1/Cacng3/Ryr2/Iph3/Cacna1b/Grin2b/I	13
MF	GO:0016247	channel regulator activity	14/373	141/19943	4.24E-07	8.83E-06	6.8747E-06	Fgl12/Lymx1/Cacng2/Kcnab2/Cacng3/Gpld1/Scn4b/Dpp6/Kcnip4/I	14
MF	GO:0022821	GABA-gated chloride ion channel activ	6/373	17/19943	4.28E-07	8.83E-06	6.8747E-06	Gabra2/Gira2/Gabra1/Gabra5/Gira1/Gabra3	6
MF	GO:0005251	delayed rectifier potassium channel act	7/373	29/19943	8.28E-07	1.67E-05	1.3012E-05	Kcnk2/Kcnk3/Kcnk1/Kcnk1/Kcnh1/Kcnk2/Kcnk1	7
MF	GO:0005248	voltage-gated sodium channel activity	6/373	20/19943	1.28E-06	2.46E-05	1.9168E-05	Scn8a/Scn4b/Scn1a/Scn2a/Scn9a/Hcn1	6
MF	GO:0095918	structural constituent of postsynapse	6/373	20/19943	1.28E-06	2.46E-05	1.9168E-05	Nefn/Nefn/Ina/Camk2b/Dlg2/Dnm3	6
MF	GO:0095908	voltage-gated ion channel activity invol	4/373	6/19943	1.75E-06	3.29E-05	2.5621E-05	Kcnk1/Kcnk1/Kcnh1/Scn2a	4
MF	GO:0016917	GABA receptor activity	6/373	22/19943	2.38E-06	4.34E-05	3.3804E-05	Gabrg2/Gabra1/Gabra5/Gabra3/Gabrb2/Gabrb3	6
MF	GO:0022851	GABA-gated chloride ion channel activ	5/373	19/19943	4.51E-05	0.000617	0.00048009	Chrna4/Chrm2/Hrh3/Chrm7/Chrm2	5
MF	GO:0015081	sodium ion transmembrane transporter	13/373	141/19943	2.54E-06	4.58E-05	3.565E-05	Scn8a/Slc24a2/Slc5a7/Atp1a3/Scn4b/Slc6a5/Scn1a/Slc6a11/Scn2	13
MF	GO:0030165	PDZ domain binding	12/373	121/19943	2.88E-06	5.13E-05	3.9913E-05	Nsf/Cacng3/Dlgap3/Lin7b/Atp2b2/Cox6a4/Atp2b3/Cit/Kcnj12/Erc2	12
MF	GO:0044325	ion channel binding	13/373	143/19943	2.98E-06	5.27E-05	4.1063E-05	Cabp1/Fgl12/Rims1/Kcnab2/Ank1/Scn4b/Kcncl1/Kcnab1/Dpp10/K	13
MF	GO:0089882	structural constituent of presynaptic act	4/373	7/19943	4.03E-06	6.94E-05	5.4058E-05	Rims1/Rims2/Erc2/Bsn	4
MF	GO:0005543	phospholipid binding	23/373	424/19943	5.99E-06	9.49E-05	7.3857E-05	Rph3a/Arhgap4/Syrt2/Thy1/Cadps/Syrt12/Pla2g4e/Pacsin1/Cpne4	23
MF	GO:0095981	structural constituent of synapse	4/373	9/19943	1.41E-05	0.000225	0.00017506	Rims1/Rims2/Erc2/Bsn	4
MF	GO:0004890	GABA-A receptor activity	5/373	19/19943	2.09E-05	0.00032	0.00024894	Gabrg2/Gabra1/Gabra5/Gabra3/Gabrb3	5
MF	GO:0095928	G protein-coupled neurotransmitter rec	7/373	47/19943	2.5E-05	0.000371	0.00028582	Grm1/Htr2c/Chrm2/Hrh3/Gabrb2/Htr2a/Htr4	7
MF	GO:0008503	benzodiazepine receptor activity	4/373	11/19943	3.58E-05	0.000513	0.00039917	Gabrg2/Gabra1/Gabra5/Gabra3	4
MF	GO:0005245	voltage-gated calcium channel activity	7/373	50/19943	3.78E-05	0.000535	0.00041667	Cacng2/Ncs1/Cacng3/Cacna1b/Cacna2d2/Cacna2d1/Cacna1	7
MF	GO:0005231	excitatory extracellular ligand-gated ion	6/373	35/19943	4.22E-05	0.000586	0.00045582	Gira2/Chrna4/Gira1/Grin2b/Chrna7/Chrm2	6
MF	GO:0015494	acetylcholine receptor activity	5/373	22/19943	4.51E-05	0.000617	0.00048009	Chrna4/Chrm2/Hrh3/Chrm7/Chrm2	5
MF	GO:0000149	SNARE binding	10/373	115/19943	6.06E-05	0.000816	0.00059348	Cplk1/Nsf/Napb/Syrt2/Stx3b/Syrt12/Sytp5/Sytp5/Sy7/Unc13c	10
MF	GO:0031402	sodium ion binding	4/373	13/19943	7.53E-05	0.000977	0.00076057	Scn8a/Scn1a/Scn2a/Scn9a	4
MF	GO:0005272	structural channel activity	6/373	39/19943	7.96E-05	0.001027	0.00079919	Scn8a/Scn4b/Scn1a/Scn2a/Scn9a/Hcn1	6
MF	GO:0015108	chloride transmembrane transporter ac	9/373	97/19943	8.54E-05	0.001094	0.00085203	Gabrg2/Gira2/Gabra1/Gabra5/Slc12a5/Gabra3/Slc12a3/Gal	9
MF	GO:0005200	structural constituent of cytoskeleton	7/373	58/19943	0.0001	0.001265	0.00098509	Nefn/Nefn/Ina/Tubab/Camk2b/Ado2/Sptbn2	7
MF	GO:001995	synxin binding	6/373	79/19943	0.000114	0.001419	0.00110466	Cplk1/Nsf/Napb/Syrt2/Sytp5/Sytp5/Sy7/Unc13c	6
MF	GO:0004683	calmodulin-dependent protein kinase ac	5/373	27/19943	0.000128	0.001551	0.00120764	Camk1/Camk2b/Camk2a/Camk1d/Camk4	5
MF	GO:0008022	protein C-terminus binding	14/373	234/19943	0.00014	0.001683	0.00130133	Rbfox1/Nsf/Nef/Rasgr1/Rab3a/Atp2b2/Grip2/Cacna1b/Sgtsb/Lrrc	14
MF	GO:0016594	glycine binding	4/373	16/19943	0.000183	0.002154	0.00167707	Gira2/Grin1/Gria1/Grin2b	4
MF	GO:1902935	phosphatidylinositol biphosphate bindi	9/373	108/19943	0.000195	0.002275	0.0017711	Rph3a/Cadps/Kcnh1/Cv1s1/Pfn2/LOC100909840/Amer3/Sy7/Hcn	9
MF	GO:0089106	ion channel regulator activity	9/373	115/19943	0.000313	0.003386	0.00236007	Lymx1/Cacng2/Kcnab2/Dpp6/Kcnip4/Kcnab1/Dpp10/Cacna2d2/Nr	9
MF	GO:0005254	calcium channel activity	7/373	70/19943	0.00033	0.003557	0.00276807	Gabra2/Gira2/Gabra1/Gabra5/Gabra3/Gabrb3	7
MF	GO:0005544	calcium-dependent phospholipid binding	6/373	52/19943	0.000405	0.004233	0.00329545	Rph3a/Syrt2/Syrt12/Pla2g4e/Cox6a4/Syrt	6
MF	GO:0005326	neurotransmitter transporter activity	6/373	53/19943	0.00045	0.004677	0.0036409	Cplk1/Slc5a7/Slc32a1/Slc17a6/Slc6a5/Slc6a11	6
MF	GO:1990763	arrestin family protein binding	3/373	9/19943	0.000501	0.005141	0.00400232	Gpr61/Chrm2/Gpr135	3
MF	GO:0097110	scaffold protein binding	7/373	75/19943	0.000504	0.005157	0.00401467	Kif5a/Digap3/Ryr2/Cit/Grin2b/Chrna7/Shank1	7
MF	GO:0005546	phosphatidylinositol-4,5-bisphosphate b	7/373	76/19943	0.000546	0.005526	0.00430161	Rph3a/Cadps/Pfn2/LOC100909840/Amer3/Sy7/Hcn1	7
MF	GO:0031420	alkali metal ion binding	4/373	21/19943	0.00056	0.005611	0.0043683	Scn8a/Scn1a/Scn2a/Scn9a	4
MF	GO:0032947	protein-containing complex scaffold act	4/373	21/19943	0.00056	0.005611	0.0043683	Napab/Syrt2/Grip2/Koz1/Shank1	4
MF	GO:0008509	anion transmembrane transporter act	15/373	311/19943	0.000815	0.007724	0.00601319	Gabra2/Gira2/Gabra1/Gabra5/Gira1/Slc32a1/Slc17a6/Slc12a5/Sic	15
MF	GO:0005253	anion channel activity	7/373	83/19943	0.000928	0.008665	0.00674519	Gabrg2/Gira2/Gabra1/Gabra5/Gira1/Gabra3/Gabrb3	7
MF	GO:0004993	G protein-coupled serotonin receptor ac	5/373	41/19943	0.00096	0.008771	0.00682815	Htr2c/Chrm2/Hrh3/Htr2a/Htr4	5
MF	GO:0095989	serotonin receptor activity	5/373	41/19943	0.00096	0.008771	0.00682815	Htr2c/Chrm2/Hrh3/Htr2a/Htr4	5
MF	GO:0043177	organic acid binding	12/373	223/19943	0.001053	0.009578	0.00745634	Gira2/Grin1/Gria1/Ryr2/Gad2/Acan/Hapln1/Hapln4/Ddc/Grin2b/C	12
MF	GO:0015103	inorganic anion transmembrane transp	9/373	130/19943	0.001059	0.009594	0.00748694	Gabrg2/Gira2/Gabra1/Gabra5/Gira1/Slc12a5/Gabra3/Slc12a3/Gal	9
MF	GO:0035256	G protein-coupled glutamate receptor bi	3/373	12/19943	0.001259	0.011088	0.0086317	Cabp1/Necab2/Dnm3	3
MF	GO:0050780	dopamine receptor binding	4/373	26/19943	0.0013	0.01126	0.00876588	Nsf/Atp1a3/Gnas/Grin2b	4
MF	GO:0099604	ligand-gated calcium channel activity	4/373	26/19943	0.0013	0.01126	0.00876588	Grin1/Ryr2/Iph3/Grin2b	4
MF	GO:0017075	synxin-1 binding	4/373	27/19943	0.001503	0.012796	0.00996183	Cplk1/Nsf/Syp/Unc13c	4
MF	GO:0008065	glutamate receptor activity	4/373	28/19943	0.001728	0.014374	0.0113602	Grm4/Grin1/Gm1/Grin2b	4
MF	GO:0015643	toxic substance binding	3/373	14/19943	0.002027	0.016326	0.01270915	Nefn/Nefn/Chna7	3
MF	GO:0016995	glutamate binding	3/373	14/19943	0.002027	0.016326	0.01270915	Grin1/Gad2/Grin2b	3
MF	GO:0031748	D1 dopamine receptor binding	3/373	14/19943	0.002027	0.016326	0.01270915	Nsf/Atp1a3/Gnas	3
MF	GO:0016597	amino acid binding							

MF	GO:0016933	extracellularly glycine-gated ion channel	2/373	5/19943	0.003361	0.02413	0.01878472	Gira2/Gira1	2
MF	GO:0016934	extracellularly glycine-gated chloride ch	2/373	5/19943	0.003361	0.02413	0.01878472	Gira2/Gira1	2
MF	GO:0022849	glutamate-gated calcium ion channel act	2/373	5/19943	0.003361	0.02413	0.01878472	Grin1/Grin2b	2
MF	GO:0098973	structural constituent of postsynaptic ac	2/373	5/19943	0.003361	0.02413	0.01878472	Ina/Camk2b	2
MF	GO:1901981	phosphatidylinositol phosphate binding	9/373	162/19943	0.003507	0.024973	0.01944111	Rph3a/Cadps/Kcnh1/Civ1/Pfn2/LOC100909840/Amer3/Syt7/Hcn	4
MF	GO:0030507	spectrin binding	4/373	34/19943	0.003585	0.025388	0.0197643	Dync1i1/Dmtn/Ank1/Add2	4
MF	GO:0043492	ATPase activity, coupled to movement o	8/373	133/19943	0.003589	0.025388	0.0197643	Atp1a3/Atp8b5/Atp2b2/Atp2b3/Atp8a2/Abca5/Abcg4/Abcc2	8
MF	GO:0003779	actin binding	16/373	406/19943	0.004312	0.025948	0.02300241	Hcca/Sytn1/Dmtn/Esp11b/Spire2/Cap2/Kcma1/Coro2a/Mas2/P	16
MF	GO:0042277	peptide binding	13/373	302/19943	0.004713	0.031942	0.02486603	Cabp1/Oprd1/Pex5l/Hcrr2/Grin1/Hcrr1/Dlgap3/Crhbp/Atp1a3/C	13
MF	GO:0031802	type 5 metabotropic glutamate receptor	2/373	6/19943	0.004979	0.032778	0.0255171	Necab2/Dnm3	2
MF	GO:0033265	choline binding	2/373	6/19943	0.004979	0.032778	0.0255171	Slc5a7/Chat	2
MF	GO:0099507	ligand-gated ion channel activity involve	2/373	6/19943	0.004979	0.032778	0.0255171	Grin1/Kcma1	2
MF	GO:0031489	myosin V binding	3/373	19/19943	0.005034	0.032843	0.02556785	Rabb5/Rabb3c/Rabb3a	3
MF	GO:0005242	inward rectifier potassium channel activ	3/373	20/19943	0.005841	0.037001	0.02380497	Kcnj3/Kcnj12/Kcnh7	3
MF	GO:0005540	hyaluronic acid binding	3/373	21/19943	0.006722	0.041964	0.03266815	Acan/Hapln1/Hapln4	3
MF	GO:0004972	NMDA glutamate receptor activity	2/373	7/19943	0.006885	0.041964	0.03266815	Grin1/Grin2b	2
MF	GO:0004985	opioid receptor activity	2/373	7/19943	0.006885	0.041964	0.03266815	Oprd1/Oprl1	2
MF	GO:0016907	G protein-coupled acetylcholine recepto	2/373	7/19943	0.006885	0.041964	0.03266815	Chrm2/Hrh3	2
MF	GO:0019992	diacylglycerol binding	2/373	7/19943	0.006885	0.041964	0.03266815	Rasgrp1/Unc13c	2

Activated genes, KEGG

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
rno04080	Neuroactive ligand-receptor interaction	27/98	284/6610	2.41849E-15	2.51523E-13	2.01116E-13	Grm4/Gabrg2/Gira2/Gabra1/Ttrhr/Drd2/Oprd1	27
rno04020	Calcium signaling pathway	20/98	186/6610	1.76863E-12	9.1969E-11	7.35379E-11	Ttrhr/Grin1/Grm1/Ryr2/Atp2b2/Htr2c/Chrm2/C	20
rno04720	Long-term potentiation	8/98	69/6610	6.95357E-06	0.000241057	0.000192748	Rps6ka6/Grin1/Grm1/Camk2b/Camk2a/Adcy1	8
rno04540	Gap junction	8/98	89/6610	4.60497E-05	0.001197292	0.000957349	Gj2/Drd2/Grm1/Htr2c/Tuba8/Gnas/Adcy1/Ht	8
rno04972	Pancreatic secretion	8/98	104/6610	0.000139558	0.002632948	0.002105292	Ryr2/Atp1a3/Pia2g4/Atp2b2/Atp2b3/Gnas/Ac	8
rno04010	MAPK signaling pathway	13/98	269/6610	0.000151901	0.002632948	0.002105292	Fgf12/Rps6ka6/Cacng2/Cacng3/Rasgrf1/Pia2g4	13
rno05414	Dilated cardiomyopathy	7/98	88/6610	0.000302343	0.00491952	0.003591743	Cacng2/Cacng3/Ryr2/Gnas/Adcy1/Cacna2d2/C	7
rno04970	Salivary secretion	6/98	78/6610	0.000989171	0.012859224	0.010282173	Atp1a3/Atp2b2/Atp2b3/Gnas/Adcy1/Kcma1	6
rno04260	Cardiac muscle contraction	6/98	84/6610	0.001457718	0.016844736	0.013469869	Cacng2/Cacng3/Ryr2/Atp1a3/Cacna2d2/Cacna1	6
rno05014	Amyotrophic lateral sclerosis (ALS)	5/98	66/6610	0.002627798	0.029409096	0.02351537	Nefh/Grin1/Nefh/Nefm/Grm2b	5
rno04912	GnRH signaling pathway	6/98	99/6610	0.003363685	0.031802111	0.025438813	Pia2g4/Camk2b/Camk2a/Gnas/Adcy1/Mapk1	6
rno05412	Arrhythmic right ventricular cardiomyopathy	5/98	72/6610	0.00412902	0.035784842	0.028613386	Cacng2/Cacng3/Ryr2/Cacna2d2/Cacna1d1	5
rno04971	Gastric acid secretion	5/98	74/6610	0.004644749	0.037157991	0.029711349	Atp1a3/Camk2b/Camk2a/Gnas/Adcy1	5
rno05410	Hypertrophic cardiomyopathy (HCM)	5/98	80/6610	0.006465856	0.048032075	0.038406214	Cacng2/Cacng3/Ryr2/Cacna2d2/Cacna2d1	5

Table S2. Representative GO terms containing GABAARs in hUC-MSC-activated genes.

GO term	p.adjust	gene
ion channel complex	1.69×10^{-30}	<i>Gabrg2/Gira2/Gabra1/Scn8a/Kcnj3/Cacng2/Gabra5/Chrna4/Pex5l/Kcns2/Kcnab2/Grin1/Cacng3/Gira1/Dlgap3/Ryr2/Olfm3/Kcna2/Kcnc3/Scn4b/Dpp6/Kcnp4/Nrn1/Scn1a/Kcnc1/Gabra3/Kcnab1/Kcna1/Dpp10/Kcnh1/Cacna1b/Akap6/Scn2a/Kcma1/Scn9a/Grin2b/Chrna7/Kcnq2/Lrrc7/Cacna2d2/Shank1/Chrn2/Dlg2/Trpc5/Vwv2/Cacna2d1/Kcng1/Hcn1/Cacna1/Gabrb3</i>
GABA-ergic synapse	6.68×10^{-19}	<i>Gabrg2/Gabra1/Lrfn5/Drd2/Slitrk3/Gabra5/Rims1/Clstn3/Cntnap4/Slc32a1/Acan/Atp2b2/Gabra3/Atp2b3/Slc6a11/Rims2/Cntn5/Gabbr2/Nrg1/Erc2/Camk4/Syt7/Bsn/Nrxn3/Gabrb3</i>
synaptic transmission, GABAergic	9.40×10^{-10}	<i>Phf24/Grm4/Gabrg2/Gabra1/Drd2/Gabra5/Clstn3/Cntnap4/Car7/Grm1/Gabra3/Pkce/Gabrb3</i>
GABA receptor complex	3.29×10^{-5}	<i>Gabrg2/Gabra1/Gabra5/Gabra3/Gabbr2/Gabrb3</i>
GABA-gated chloride ion channel activity	4.58×10^{-5}	<i>Gabrg2/Gabra1/Gabra5/Gabra3/Gabrb3</i>
GABA-A receptor complex	3.20×10^{-1}	<i>Gabrg2/Gabra1/Gabra5/Gabra3/Gabrb3</i>
chloride transport	3.53×10^{-1}	<i>Gabrg2/Gira2/Gabra1/Gabra5/Car7/Gira1/Slc12a5/Gabra3/Slc12a3/Gabrb3</i>
chloride transmembrane transporter activity	1.09×10^{-3}	<i>Gabrg2/Gira2/Gabra1/Gabra5/Gira1/Slc12a5/Gabra3/Slc12a3/Gabrb3</i>

