

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

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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-μl 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-µm 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 µg/ml gentamicin. 1.6×10^5 cells/well were plated in 24-well culture plates coated with 10 µg/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-µl 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-µm 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.

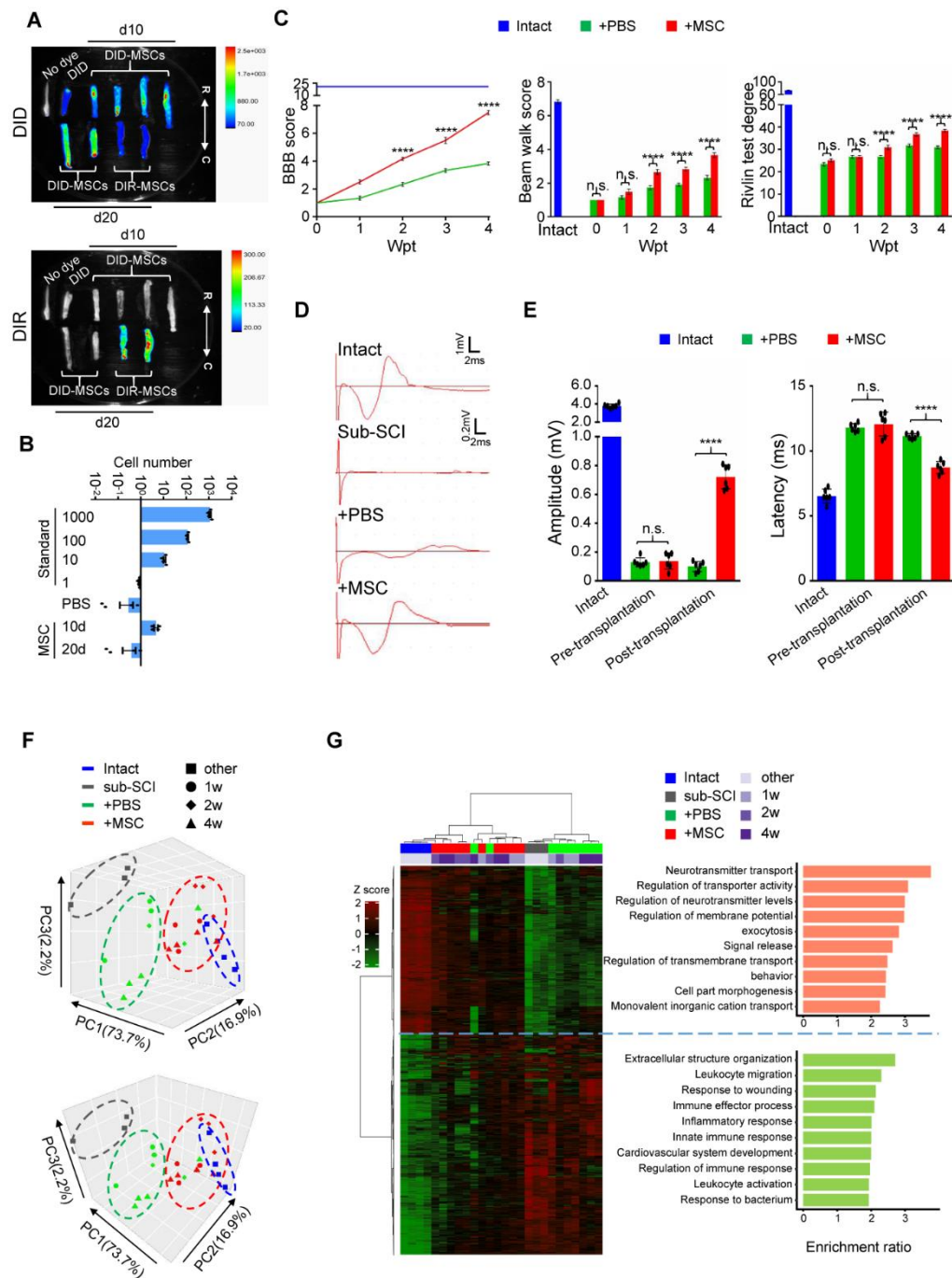


Figure S1 hUC-MSC transplantation exhibits functional recovery in the rat model of subacute SCI. (A) Representative fluorescence images of 5-cm rat spinal cords dissected after intrathecally injected with hUC-MSCs labeled with DiD (top) or DIR (bottom) at day 10 (d10) and day 20 (d20) post-transplantation. 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.

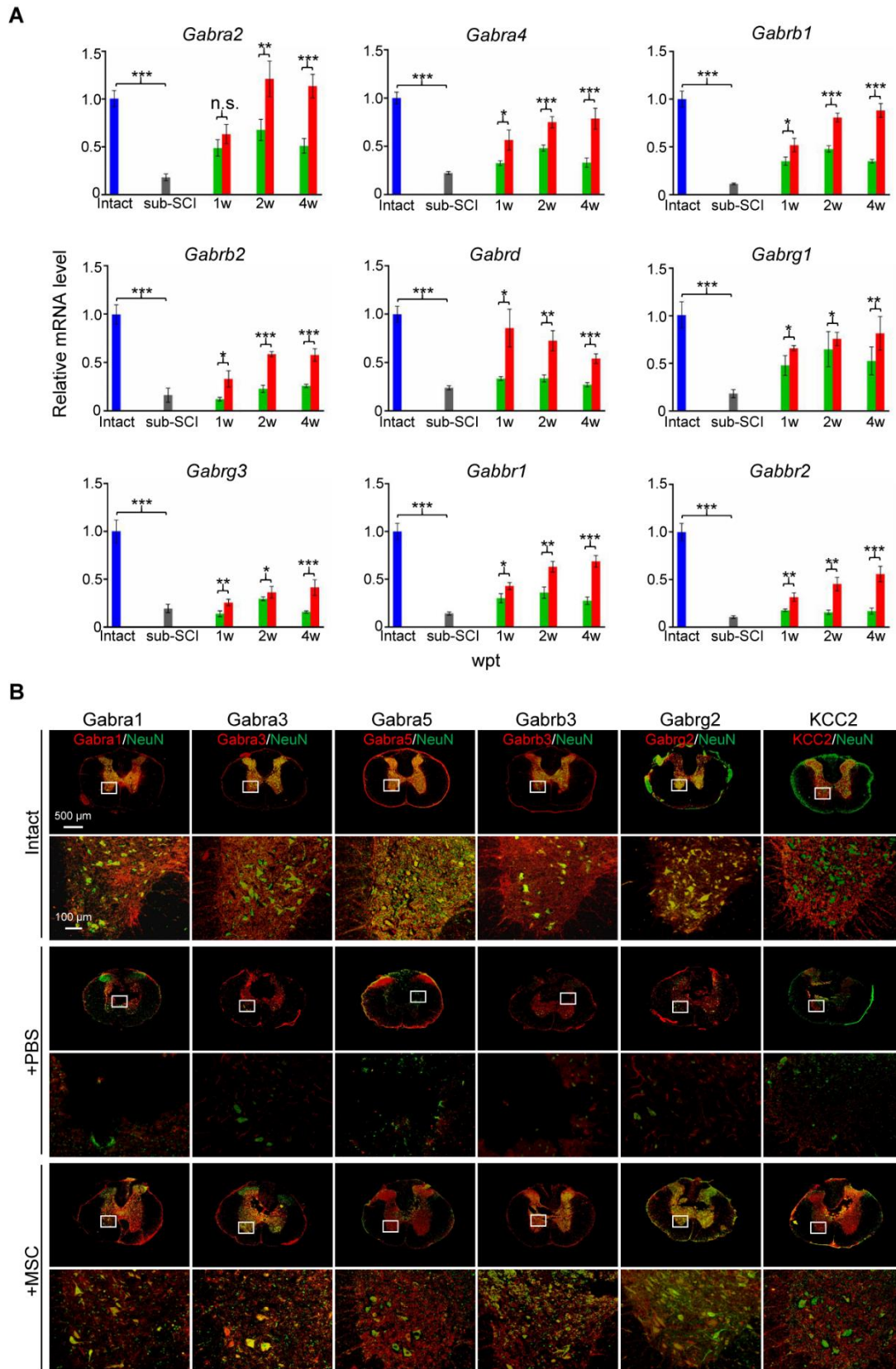


Figure S2 hUC-MSC transplantation increases GABA_ARs in the injured spinal cord. (A) Time course of real-time PCR validation of hUC-MSC-activated GABA

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).

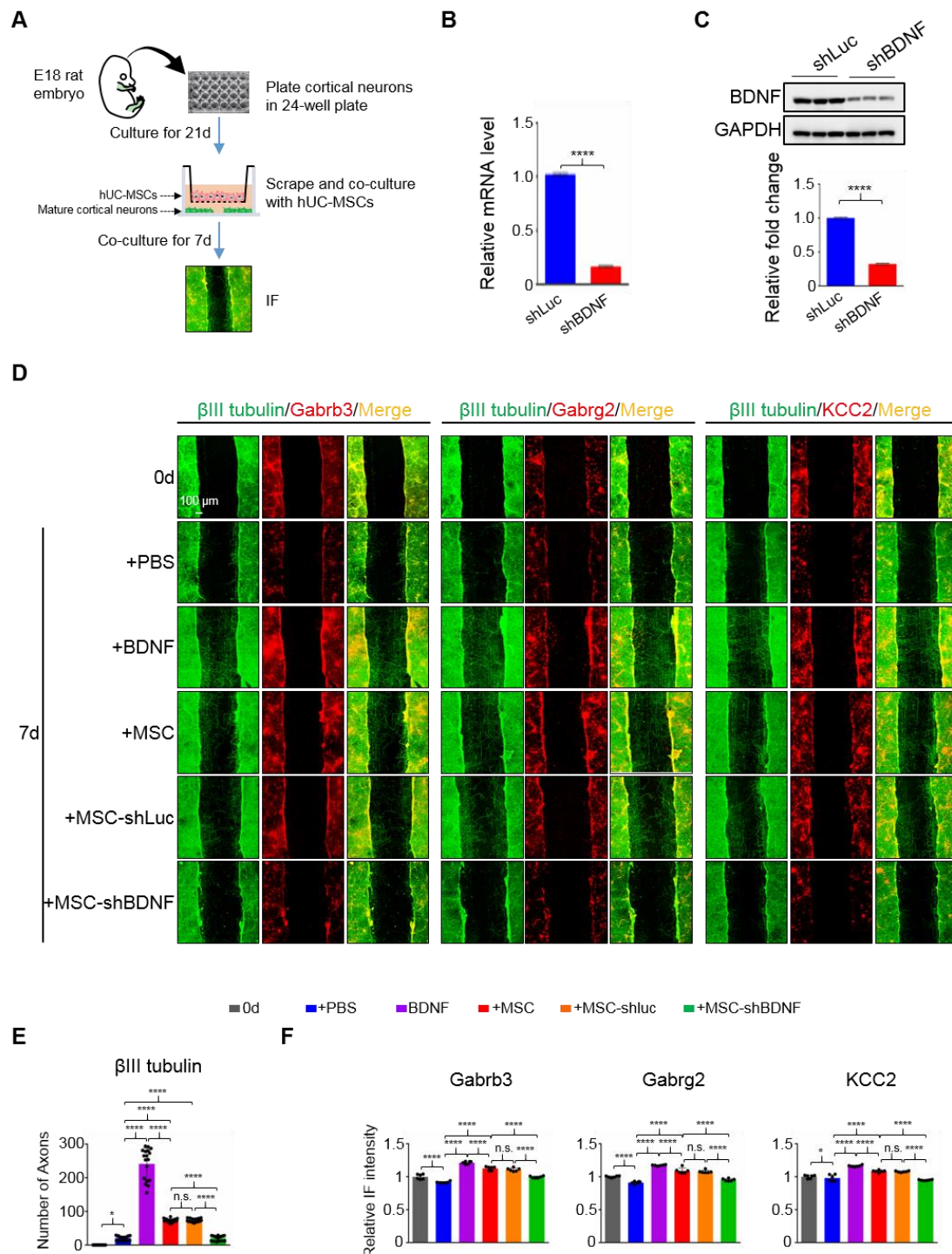


Figure S3 BDNF knockdown abrogates the effects of hUC-MSCs on axonal regeneration and the induction of GABA_ARs in neurons after axonal lesion *in vitro*.

(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.

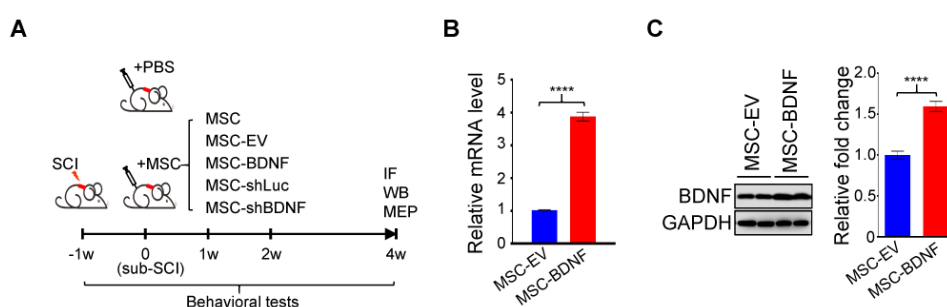


Figure S4 The transplantation of hUC-MSCs with either BDNF overexpression or knockdown into rats with sub-SCI. (A) The experimental scheme for investigating the role of BDNF secreted by hUC-MSCs on SCI repair in the rat models. (B) Real-time qPCR validation of BDNF overexpression in hUC-MSCs (n = 3/group). (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	Count
ONTOLOGY ID Description GeneRatio BgRatio pvalue p.adjust qvalue geneID	
BP GO:0043062 cellular structure organization	23
BP GO:0031589 cell-substrate adhesion	23
BP GO:0030198 extracellular matrix organization	20
BP GO:0097530 granulocyte migration	14
BP GO:0097529 myeloid leukocyte migration	16
BP GO:0010810 regulation of cell-substrate adhesion	16
BP GO:0001425 angiogenesis	24
BP GO:0050707 regulation of cytokine secretion	16
BP GO:0050663 cytokine secretion	17
BP GO:0071295 cellular response to vitamin	8
BP GO:0042060 wound healing	22
BP GO:0007160 cell-matrix adhesion	15
BP GO:0007276 lipid localization	20
BP GO:0008699 lipid transport	19
BP GO:0038063 collagen-activated tyrosine kinase recep	5
BP GO:0050710 negative regulation of cytokine secretion	9
BP GO:0050727 regulation of inflammatory response	19
BP GO:190266 neutrophil migration	11
BP GO:0071621 granulocyte chemotaxis	11
BP GO:0001818 negative regulation of cytokine producti	16
BP GO:0031670 cellular response to nutrient	10
BP GO:1903531 negative regulation of secretion by cell	15
BP GO:0006721 terpenoid metabolic process	9
BP GO:0033273 response to vitamin	13
BP GO:0038065 collagen-activated signaling pathway	5
BP GO:0071560 cellular response to transforming growth	15
BP GO:0071559 response to transforming growth factor	15
BP GO:0016101 diterpenoid metabolic process	8
BP GO:0051048 negative regulation of secretion	15
BP GO:0050900 leukocyte migration	17
BP GO:0019216 regulation of lipid metabolic process	17
BP GO:0031960 response to corticosteroid	16
BP GO:0006720 isoprenoid metabolic process	9
BP GO:0001523 retinoid metabolic process	7
BP GO:0007584 response to nutrient	17
BP GO:0032496 response to lipopolysaccharide	20
BP GO:0007292 negative regulation of peptide secretion	11
BP GO:0001819 positive regulation of cytokine production	19
BP GO:0010811 positive regulation of cell-substrate adhi	10
BP GO:0030595 leukocyte chemotaxis	12
BP GO:1902622 regulation of neutrophil migration	6
BP GO:0051216 cartilage development	21
BP GO:0050709 negative regulation of protein secretion	10
BP GO:1901954 positive regulation of lipid localization	8
BP GO:0044403 symbiont process	16
BP GO:0044419 interspecies interaction between organi	17
BP GO:1905952 regulation of lipid localization	10
BP GO:0030593 neutrophil chemotaxis	8
BP GO:0051384 response to glucocorticoid	14
BP GO:0004585 positive regulation of cell adhesion	17
BP GO:0042542 response to hydrogen peroxide	11
BP GO:0072376 protein activation cascade	7
BP GO:0045765 regulation of angiogenesis	14
BP GO:0071622 regulation of granulocyte chemotaxis	6
BP GO:0072672 neutrophil extravasation	4
BP GO:0031669 cellular response to nutrient levels	13
BP GO:0050673 epithelial cell proliferation	17
BP GO:0098542 defense response to other organism	18
BP GO:0001763 morphogenesis of a branching structure	12
BP GO:0060485 mesenchyme development	13
BP GO:0070663 regulation of leukocyte proliferation	12
BP GO:1901424 positive regulation of neutrophil migrati	5
BP GO:0050866 negative regulation of cell activation	11
BP GO:0062012 regulation of small molecule metabolic	15
BP GO:0002526 acute inflammatory response	9
BP GO:0070162 negative regulation of cell adhesion	13
BP GO:0002685 regulation of leukocyte migration	11
BP GO:0042573 retinoic acid metabolic process	4
BP GO:0031448 connective tissue development	13
BP GO:0090050 positive regulation of cell migration invo	4
BP GO:1901342 regulation of vasculature development	14
BP GO:0061138 morphogenesis of a branching epithelium	11
BP GO:1905521 regulation of macrophage migration	5
BP GO:0034330 cell junction organization	12
BP GO:0060326 cell chemotaxis	13
BP GO:0070664 negative regulation of leukocyte prolifer	7
BP GO:1903672 positive regulation of sprouting angiogen	5
BP GO:0002695 negative regulation of leukocyte activati	10
BP GO:0002062 chondrocyte differentiation	8
BP GO:0051249 regulation of lymphocyte activation	16
BP GO:0050670 regulation of lymphocyte proliferation	11
BP GO:0031668 cellular response to extracellular stimuli	13
BP GO:0032944 regulation of mononuclear cell proliferati	11
BP GO:0050715 positive regulation of cytokine secretion	9
BP GO:0070661 leukocyte proliferation	13
BP GO:0060536 cartilage morphogenesis	8
BP GO:1905523 positive regulation of macrophage migr	4
BP GO:0001503 ossification	15
BP GO:0035987 endodermal cell differentiation	5
BP GO:0036293 response to decreased oxygen levels	16
BP GO:0010565 regulation of cellular ketone metabolic	6
BP GO:0070206 protein trimerization	8
BP GO:1903670 regulation of sprouting angiogenesis	6
BP GO:1904018 positive regulation of vasculature devel	10
BP GO:0042180 cellular ketone metabolic process	10
BP GO:0051224 negative regulation of protein transport	7
BP GO:0048525 negative regulation of viral process	7
BP GO:0007179 transforming growth factor beta recept	9

BP	GO:0050873	brown fat cell differentiation	5/260	49/19943	0.00043263	0.016659081	0.01406555	Trpv4/Ptgs2/Ar4a/Parres2/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/Serpinb1a/Ar	10
BP	GO:0031299	retina vasculature morphogenesis in car	3/260	12/19943	0.00044171	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/Plscr1/Ifitm6	4
BP	GO:1093557	positive regulation of tumor necrosis fac	7/260	105/19943	0.00045362	0.016659081	0.01406555	Lbp/Adam8/Twist1/Ulra5/P4/Cyp2j4/Sp	7
BP	GO:0006953	acute-phase response	5/260	50/19943	0.00047564	0.017331138	0.01463298	Lbp/Ptgs2/Plscr1/Fn1/Hp	5
BP	GO:0016666	response to hypoxia	15/260	424/19943	0.00047984	0.017348774	0.01464787	Angptl4/Plau/Postn/Hmox1/Adam8/Ifgfb	15
BP	GO:0071496	cellular response to external stimulus	15/260	425/19943	0.0004917	0.017640769	0.0148944	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/Mmp14/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/h	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/Ulra5/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:0010706	endoderm formation	5/260	51/19943	0.00052179	0.017695218	0.01494037	Col7a1/Col4a2/Mmp14/Fn1/Itga5	5
BP	GO:0003032	response to reactive oxygen species	12/260	295/19943	0.00052236	0.017695218	0.01494037	Mapk13/Cdk1/Col1a1/Hmox1/Hk3/Sdc1/f	12
BP	GO:0034329	cell junction assembly	10/260	214/19943	0.00052357	0.017695218	0.01494037	Trpv4/Gjb2/Snai1/Mmp14/Aluab/Cdh5/F	10
BP	GO:0046651	lymphocyte proliferation	12/260	296/19943	0.00053825	0.018020656	0.01521515	Lst1/Bst1/I20rb/Vsig4/Cxcr4/Ahr/Pawr/E	12
BP	GO:0046890	regulation of lipid biosynthetic process	9/260	177/19943	0.00054093	0.018020656	0.01521515	Htr1b/Apoc1/Dab2/lgfbp7/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/Cyp2j	7
BP	GO:0042362	fat-soluble vitamin biosynthetic process	3/260	13/19943	0.0005687	0.018502485	0.01562196	Ptgs2/Snai1/Snai2	3
BP	GO:0032943	mononuclear cell proliferation	12/260	298/19943	0.00057126	0.018502485	0.01562196	Lst1/Bst1/I20rb/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/f	10
BP	GO:0060706	cell differentiation involved in embryoni	4/260	30/19943	0.00059242	0.01866921	0.01576273	Snai1/Krt8/Mdfi/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/Parres2	5
BP	GO:0013835	cytolysis	4/260	31/19943	0.00067327	0.020658819	0.01744259	Ly2z1/lbp/Pglyrp1/P4	4
BP	GO:0010712	regulation of collagen metabolic process	5/260	54/19943	0.00068055	0.020745639	0.0175159	Fap/Emilin1/Ccn2/Cyp2j4/Ltbp1	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/f	8
BP	GO:0048705	skeletal system morphogenesis	11/260	263/19943	0.00070551	0.021229162	0.01792414	Col13a1/Trpv4/Col1a1/Col20a1/Col7a1/h	11
BP	GO:0045766	positive regulation of angiogenesis	9/260	184/19943	0.00071468	0.021295439	0.0179801	Hmox1/Csar1/Ptgs2/Cxcr4/Cdh5/Ama1/f	9
BP	GO:0042268	regulation of cytolysis	3/260	14/19943	0.00071685	0.021295439	0.0179801	Lbp/Pglyrp1/P4	3
BP	GO:0032964	collagen biosynthetic process	5/260	55/19943	0.00074074	0.021731885	0.0183486	Col1a1/Emilin1/Ccn2/Cyp2j4/Ltbp1	5
BP	GO:0034754	cellular hormone metabolic process	7/260	114/19943	0.00074284	0.021731885	0.0183486	Dab2/Snp1/Akr1a1b/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/Ltbf/Vsig4/Tlr6/f	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/Prt	8
BP	GO:0008015	blood circulation	16/260	493/19943	0.00079429	0.022612296	0.01909195	Trpv4/Sic1a5/Postn/Hmox1/Htr2b/Ir3/P	16
BP	GO:0043903	regulation of symbiosis, encompassing r	10/260	226/19943	0.00079809	0.022612296	0.01909195	Hmox1/Hmox1/Lbp/Htm2/Cxcr4/Plscr1/C	10
BP	GO:0032926	response to retinoic acid	8/260	150/19943	0.00080211	0.022612296	0.01909195	Col1a1/Igfbp7/Etna5/Gjb2/Adh1/Igfbp2/F	8
BP	GO:0033280	response to vitamin D	5/260	56/19943	0.00080481	0.022612296	0.01909195	Spp1/Ptgs2/Karh2/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/Plscr1/Ceacam1/Ifit	6
BP	GO:0006775	fat-soluble vitamin metabolic process	4/260	33/19943	0.00085789	0.023536435	0.01987221	Ptgs2/Snai1/Rbp1/Snai2	4
BP	GO:2000778	positive regulation of interleukin-6 secre	4/260	33/19943	0.00085789	0.023536435	0.01987221	Trpv4/Tlr8/Twist1/Ulra5	4
BP	GO:0015850	organic hydroxy compound transport	11/260	270/19943	0.00087478	0.023621422	0.01994397	RGD1305807/Msr1/Ptgs2/Apoc1/Dab2/Slc	11
BP	GO:0031099	regeneration	12/260	313/19943	0.00087739	0.023621422	0.01994397	cdk1/Plau/Postn/Hmox1/Nin1/Spp1/Csa	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/Pglyrp1/Parres2	9
BP	GO:0050792	regulation of viral process	9/260	190/19943	0.00089762	0.023621422	0.01994397	Ifitm1/Hmox1/Ifitm2/Cxcr4/Plscr1/chmp	9
BP	GO:0032945	negative regulation of mononuclear cell	6/260	86/19943	0.00091196	0.023629864	0.0199511	Lst1/I20rb/Vsig4/Pawr/Lrrc32/Ceacam1	6
BP	GO:0050672	negative regulation of lymphocyte prolif	6/260	86/19943	0.00091196	0.023629864	0.0199511	Lst1/I20rb/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/Plscr1/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/Plscr1/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/Fzd7/f	7
BP	GO:0032103	positive regulation of response to exterr	12/260	320/19943	0.00106135	0.026695272	0.02253927	Trpv4/Lbp/Adam8/Csar1/Ptgs2/Cxcr4/Ed	12
BP	GO:0009266	response to temperature stimulus	10/260	235/19943	0.00107386	0.026695272	0.02253927	Trpv4/Hmox1/Htr2b/Igfbp7/Ptgs2/Cxcr4/f	10
BP	GO:0051180	vitamin transport	4/260	35/19943	0.00107556	0.026695272	0.02253927	RGD1305807/Folr2/Stra5/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	Angptl4/Apoc1/Anxa1	3
BP	GO:0006556	complement activation	5/260	60/19943	0.00110514	0.027047568	0.02283672	Col20a1/Clec4e/Cld/Vsig4/C7	5
BP	GO:0060349	bone morphogenesis	7/260	122/19943	0.00110765	0.027047568	0.02283672	Col13a1/Trpv4/Col1a1/Col20a1/Col7a1/h	7
BP	GO:0051250	negative regulation of lymphocyte activ	8/260	158/19943	0.00112313	0.027282808	0.02303534	Lst1/I20rb/Vsig4/Pawr/Pglyrp1/Lrrc32/A	8
BP	GO:0014031	mesenchymal cell development	6/260	90/19943	0.00115666	0.02795154	0.0259996	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/Htm2/Ipoc1/Tlr8/F	11
BP	GO:0032368	regulation of lipid transport	7/260	124/19943	0.00121777	0.02871098	0.02424117	Trpv4/Ptgs2/Apoc1/Dab2/Spp1/Igfbp3/Ch	7
BP	GO:0018217	regulation of fatty acid metabolic proc	6/260	91/19943	0.00122502	0.02871098	0.02424117	Apoc1/Ptgs2/Ctcf/tw1/Twist1/Anxa1/C	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/Igfbp3/Dab2/Csar1/f	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/Cidea/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/Stra5	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/Slc16a3/Srr	8
BP	GO:0045600	positive regulation of fat cell differenti	5/260	63/19943	0.00137551	0.030404698	0.02567121	Ptgs2/Wnt5b/Parres2/Snai2/Zotb7c	5
BP	GO:0042246	tissue regeneration	6/260	94/19943	0.00144875	0.031872559	0.02691055	Plau/Postn/Nin1/Fzd7/Mustn1/Anxa1	6
BP	GO:0035988	chondrocyte proliferation	3/260	18/19943	0.00154523	0.033801113	0.02553886	Mmp14/Ccn2/Mustn1	3
BP	GO:0043900	regulation of multi-organism process	14/260	428/19943	0.00155091	0.033801113	0.02553886	Cdk1/Ifitm1/Plau/Hmox1/Lbp/Ifitm2/C	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/Sik1/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/I20rb/Spp1/Ir3/Tspan6/Kar	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	I20rb/Vsig4/Cxcr4/Pawr/Efnb1/Lrrc32/Ig	9
BP	GO:0046718	viral entry into host cell	5/260	66/19943	0.00169452	0.035125424	0.02965699		

BP	GO:0032623	interleukin-2 production	5/260	69/19943	0.0020647	0.040067088	0.03382933	l120rb/Vsig4/Pawr/Anxa1/Ceacam1	5
BP	GO:0044409	entry into host	5/260	69/19943	0.0020647	0.040067088	0.03382933	lftm1/lftm2/Siglec1/Ceacam1/lftm6	5
BP	GO:0051806	entry into cell of other organism involve	5/260	69/19943	0.0020647	0.040067088	0.03382933	lftm1/lftm2/Siglec1/Ceacam1/lftm6	5
BP	GO:0051828	entry into other organism involved in sy	5/260	69/19943	0.0020647	0.040067088	0.03382933	lftm1/lftm2/Siglec1/Ceacam1/lftm6	5
BP	GO:0051701	interaction with host	7/260	136/19943	0.00207036	0.040067088	0.03382933	lftm1/lftm2/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/Ulras5/PI4/Cyp	8
BP	GO:0042130	negative regulation of T cell proliferator	5/260	70/19943	0.00220026	0.041546568	0.03507848	l20rb/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/l120rb/Vsig4/Pglyrp1/Anxa	7
BP	GO:0019058	viral life cycle	9/260	218/19943	0.00231886	0.04334457	0.03659656	lftm1/Hmx1/lftm2/Siglec1/Lrrc15/Plscr	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/Col68/Plscr1/Plscr2/Lcn2/	11
BP	GO:0032760	positive regulation of tumor necrosis fac	6/260	104/19943	0.00242438	0.04334457	0.03659656	lbp/Twist1/Ulras5/PI4/Cyp2j4/Spn2	6
BP	GO:0010884	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	Angptl4/Apoc1	2
BP	GO:0051304	retinal blood vessel morphogenesis	2/260	6/19943	0.00245347	0.04334457	0.03659656	Col4a1/Lama3	2
BP	GO:0070562	regulation of vitamin D receptor signalin	2/260	6/19943	0.00245347	0.04334457	0.03659656	kank2/Sna2	2
BP	GO:1902219	negative regulation of intrinsic apoptoti	2/260	6/19943	0.00245347	0.04334457	0.03659656	Ptgs2/Ptger2	2
BP	GO:0042742	defense response to bacterium	10/260	264/19943	0.00253429	0.044435811	0.03751791	Ly2/Lbp/Stab1/Trem1/Csar1/Pglyrp1/Lc	10
BP	GO:0035456	response to interferon-beta	4/260	44/19943	0.00254451	0.044447966	0.03752818	lftm1/lftm2/Plscr1/lftm6	4
BP	GO:0042445	hormone metabolic process	9/260	222/19943	0.00261986	0.045593389	0.03849528	Pon3/Dab2/Spp1/Akr1b10/Adh1/Adh6/C	9
BP	GO:0032370	positive regulation of lipid transport	5/260	73/19943	0.00264586	0.045874714	0.0397328	Trpv4/Ptp/Dab2/Spp1/Cch	5
BP	GO:0017015	regulation of transforming growth facto	6/260	106/19943	0.00266763	0.046080812	0.03809682	Htra3/Emilin1/Dab2/Cidea/Ltbp1/Lrg1	6
BP	GO:0060416	response to growth hormone	4/260	45/19943	0.00276454	0.04748597	0.04009321	lgfbp3/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	vitamin biosynthetic process	3/260	22/19943	0.00280805	0.04797337	0.04050473	Ptp/Sna1/Sna2	3
BP	GO:0015711	organic anion transport	14/260	458/19943	0.00288025	0.049027258	0.04139455	Trpv4/Sico2a1/Sic7a7/Sic4a5/RGD13058C	14
BP	GO:0001906	cell killing	9/260	184/19943	0.00292345	0.049135343	0.04148581	Ly2/Trem1/RT1-M2/LC102547056/Colh	8
BP	GO:0048754	branching morphogenesis of an epitheli	8/260	184/19943	0.00292345	0.049135343	0.04148581	Col4a1/Cxcr4/Ahr/Mmp14/Ednra/Wnt2b,	8
BP	GO:0008630	intrinsic apoptotic signaling pathway in	6/260	108/19943	0.00292874	0.049135343	0.04148581	Hmx1/Ier3/Plscr1/Sna1/Uaca/Sna2	6
BP	GO:1903844	regulation of cellular response to transf	6/260	108/19943	0.00292874	0.049135343	0.04148581	Htra3/Emilin1/Dab2/Cidea/Ltbp1/Lrg1	6
BP	GO:0032965	regulation of collagen biosynthetic proc	4/260	46/19943	0.00299726	0.049925791	0.0421532	Emilin1/Ccn2/Cyp2j4/Ltbp1	4
BP	GO:0070207	protein homotrimerization	4/260	46/19943	0.00299726	0.049925791	0.0421532	Emilin1/Lcn2/Ceacam1/Cubn	4
BP	GO:0052408	negative regulation of cell-cell adhesio	8/260	185/19943	0.00302201	0.04999065	0.04220796	Trpv4/ID2b/Vsig4/Pawr/Lrrc32/Anxa1/C	8
BP	GO:0050714	positive regulation of protein secretion	11/260	316/19943	0.00302259	0.04999065	0.04220796	Trpv4/Postn/Htr2b/Tlr8/Twist1/Cch/Ceac	11
CC	GO:0062023	collagen-containing extracellular matrix	28/260	217/19943	6.209E-20	2.858E-16	2.445E-16	Col1a1/Emilin1/Col20a1/Postn/Col4a1/Cc	28
CC	GO:0031012	extracellular matrix	34/260	362/19943	1.5476E-19	3.6090E-16	3.0472E-16	Col13a1/Col1a1/Emilin1/Col20a1/Postn/C	34
CC	GO:0044420	extracellular matrix component	12/260	51/19943	1.8918E-12	2.0582E-09	1.8624E-09	Col1a1/Emilin1/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/Emilin1/Clqc/Col4a1/Cc	12
CC	GO:0000044	basement membrane	14/260	105/19943	9.217E-11	6.14175E-08	5.185E-08	Col4a1/Col1a1/Col4a2/Col15a1/LC10B3	14
CC	GO:0098651	basement membrane collagen trimer	5/260	7/19943	7.4515E-09	3.15944E-06	2.6876E-06	Col4a1/Col4a2/Col18a1/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	Ptp/Apoc4/Apoc1/Lsr	4
CC	GO:1990777	lipoprotein particle	4/260	28/19943	0.00045175	0.016659081	0.01406555	Ptp/Apoc4/Apoc1/Lsr	4
CC	GO:0032594	protein-lipid complex	4/260	30/19943	0.00059242	0.01866921	0.01576273	Ptp/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 parti	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	lgfbp3/igfbp6	2
CC	GO:0036454	growth factor complex	2/260	5/19943	0.00164983	0.03405856	0.02913388	lgfbp3/igfbp6	2
CC	GO:0031091	platelet alpha granule	3/260	19/19943	0.00181856	0.037038325	0.03127109	lgfbp3/PI4/F5	3
CC	GO:0042629	small cell granule	3/260	20/19943	0.00211901	0.040339034	0.03405893	Lat/Srgn/Anxa1	3
CC	GO:0008987	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	Ptp/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/Emilin1/Col4a1/Col4a2/C	14
MF	GO:0005178	integrin binding	11/260	129/19943	1.0261E-06	0.00012934	0.0001092	Fap/Emilin1/Dab2/Spp1/Tspan8/Mmp14/	11
MF	GO:0005520	insulin-like growth factor binding	6/260	28/19943	1.3726E-06	0.000164131	0.00013858	Htra3/lgfbp3/igfbp7/Ccn2/igfbp3/igfbp6	6
MF	GO:0050839	cell adhesion molecule binding	14/260	232/19943	3.268E-06	0.00025838	0.00021815	Fap/Emilin1/Postn/Adam8/Dab2/Spp1/Ts	14
MF	GO:0038024	cargo receptor activity	9/260	89/19943	2.4269E-06	0.000263237	0.00022226	Msr1/Enpp3/Mrc1/Stab1/Scart1/Folr2/Di	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	0.000381053	0.00032257	Col13a1/Ltbp2/Postn/Stab1/Abi3bp/Prelp	13
MF	GO:0008201	heparin binding	10/260	157/19943	4.1884E-05	0.002901711	0.00244996	Col13a1/Ltbp2/Postn/Abi3bp/Prelp/Fn1/I	10
MF	GO:0001968	fibronectin binding	5/260	33/19943	6.3808E-05	0.004021624	0.00339553	Ucnl5/igfbp3/Fn1/Ccn2/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	lgfbp3/igfbp2/igfbp6	3
MF	GO:0031994	insulin-like growth factor I binding	3/260	12/19943	0.00044171	0.016659081	0.01406555	lgfbp3/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	0.020658819	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/Hk3/Clec4a	11
MF	GO:0050840	extracellular matrix binding	5/260	61/19943	0.00118903	0.028439058	0.02401158	Lrrc15/Spp1/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/Prelp/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	lgap3/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	BgRatio	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/Spp1/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/Col8a5		6

Activated genes_GO

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
BP	GO:006836	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	245/19943	1.46E-30	5.78E-28	4.5005E-28	Cplx1/Grm4/Rapgef4/Napb/Syt2/Cadps2/Drd2/Cadps/Ncs1/Sym1	44
BP	GO:007769	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:0001505	regulation of neurotransmitter levels	53/373	402/19943	1.45E-29	3.32E-27	2.5819E-27	Cplx1/Grm4/Rph3a/Trph2/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/Sym1/Rin	39
BP	GO:009903	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 localiz	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/Chrna4	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/Chrna4/Stx1b/Vamp13	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/Chrna4/Stx1b/Vamp13	35
BP	GO:0017158	regulation of calcium ion-dependent exc	32/373	151/19943	1.05E-24	1.06E-22	8.2622E-23	Cplx1/Grm4/Napb/Syt2/Drd2/Cadps/Ncs1/Rims1/Chrna4/Stx1b/V	32
BP	GO:00192803	regulation of synaptic vesicle transport	29/373	118/19943	1.84E-24	1.67E-22	1.2379E-22	Cplx1/Grm4/Napb/Syt2/Drd2/Ncs1/Rims1/Chrna4/Stx1b/Vamp13	29
BP	GO:0051648	vesicle localization	41/373	288/19943	2.61E-24	2.33E-22	1.8091E-22	Cplx1/Gfrd1/Napb/Syt2/Kif5a/Cadps2/Drd2/Cadps/Ncs1/Dync11i	41
BP	GO:0098693	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/Sym1/Rims1/Chrna4	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/Chrna4/Stx1b/Vamp13	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/Dync11i	39
BP	GO:0037157	regulation of exocytosis	37/373	263/19943	7.68E-22	5.77E-20	4.4514E-20	Cplx1/Grm4/Rapgef4/Nsf/Napb/Syt2/Vsm1/Cadps2/Drd2/Cadps/	37
BP	GO:190305	regulation of regulated secretory pathw	24/373	190/19943	1.72E-20	1.25E-18	9.744E-18	Cplx1/Grm4/Napb/Syt2/Drd2/Cadps/Ncs1/Rims1/Chrna4/Stx1b/V	24
BP	GO:0006813	potassium ion transport	33/373	244/19943	4.73E-19	3.27E-17	2.5404E-17	Nsf/Kcnj3/Slc24a2/Drd2/Kcnab3/Kcnab2/Slc12a5/Kcna2/Kc	33
BP	GO:0051656	establishment of organelle localization	45/373	489/19943	8.45E-19	5.75E-17	4.795E-17	Cplx1/Grm4/Napb/Syt2/Kif5a/Cadps2/Drd2/Cadps/Nefh/Ncs1/Dy	45
BP	GO:0060078	regulation of postsynaptic membrane p	26/373	155/19943	1.31E-17	8.54E-16	6.6471E-16	Gabrg2/Gira2/Gabra1/Gabra5/Rims1/Chrna4/Kcnj2/Cacng3/R	26
BP	GO:0071804	cellular potassium ion transport	29/373	212/19943	5.16E-17	3.21E-15	2.5024E-15	Kcnj3/Kcnab3/Kcnj2/Kcnab2/Slc12a5/Kcna2/Kcnj3/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/Kcnj2/Kcnab2/Slc12a5/Kcna2/Kcnj3/Atp1a3/Rgs7	29
BP	GO:0007416	synapse assembly	26/373	184/19943	1E-15	5.9E-14	4.5846E-14	Gabrg2/Gira2/Gabra1/Nptx1/Lrnf5/Drd2/Slitk3/Clstn3/Grin1/Sym	26
BP	GO:0035418	protein localization to synapse	19/373	86/19943	1.62E-15	9.41E-14	7.325E-14	Cplx1/Rapgef4/Arhgap44/Nptx1/Kif5a/Cacng2/Clstn3/Grin1/Cacn	19
BP	GO:1904062	regulation of cation transmembrane tra	34/373	355/19943	5.95E-15	3.32E-13	2.5881E-13	Cabp1/Rph3a/Fgf12/Cacng2/Thy1/Hpca/Drd2/Chrna4/Kcnj2/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/Chrna4/Kcnj2/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:0036534	adult behavior	24/373	190/19943	1.47E-13	7.1E-12	5.5299E-12	Fgf12/Gabrg2/Scn8a/Drd2/Oprd1/Chrna4/Grin1/Chbap/Atp	24
BP	GO:0001508	action potential	21/373	139/19943	1.58E-13	7.55E-12	5.8749E-12	Rapgef4/Fgf12/Scn8a/Gjd2/Chrna4/Gira1/Ryr2/Kcnab2/Scnab/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/Chrna4/Kcnj2/Cacng3/R	27
BP	GO:0050890	cognition	31/373	351/19943	8.64E-13	3.73E-11	2.9014E-11	Grm4/Tafa2/Slc24a2/Drd2/Gabra5/Chrna4/Grin1/Ndrg4/Slc12a5/	31
BP	GO:0050806	positive regulation of synaptic transmissi	29/373	308/19943	9.8E-13	4.15E-11	3.2291E-11	Syt2/Cacng2/Slc24a2/Drd2/Rims1/Clstn3/Grin1/Cacng3/Car7/	29
BP	GO:0104029	exocytic process	17/373	92/19943	1.15E-12	4.81E-11	3.7437E-11	Cplx1/Napb/Syt2/Cadps2/Cadps/Rims1/Rab3c/Dmtn/Stx1b/Vamp	17
BP	GO:0022898	regulation of transmembrane transport	27/373	269/19943	1.23E-12	5.12E-11	3.9877E-11	Cabp1/Rph3a/Fgf12/Cacng2/Hpca/Drd2/Chrna4/Kcnj2/Cacng3/R	27
BP	GO:1903539	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/Stx1b/Grj	14
BP	GO:0097972	regulation of postsynaptic membrane ne	17/373	97/19943	2.83E-12	1.13E-10	8.7951E-11	Cplx1/Rapgef4/Arhgap44/Nptx1/Cacng2/Hpca/Cacng3/Stx1b/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/Chrna4/Kcnj2/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/Stx1b/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/Grin1/Vamp	10
BP	GO:0019226	transmission of nerve impulse	16/373	93/19943	1.67E-11	6.29E-10	4.8395E-10	Rapgef4/Fgf12/Scn8a/Cacng2/Cacng3/Gira1/Kcnab2/Dopp6/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/Clstn3/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/Rab3c/Grin1/Cacng3	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/Kcnab2/Scnab/D	19
BP	GO:003959	regulation of metal ion transport	32/373	433/19943	4.17E-11	1.49E-09	1.1606E-09	Cabp1/Fgf12/Thy1/Hpca/Drd2/Oprd1/Kcnj2/Kcnab2/Grin1/Hecw	32
BP	GO:0019228	neuronal action potential	12/373	48/19943	5.84E-11	2.04E-09	1.5854E-09	Rapgef4/Fgf12/Scn8a/Kcnab2/Dopp6/Scn1a/Kcnj3/Scn2a/Kcnm1/	12
BP	GO:0007626	locomotory behavior	24/373	250/19943	6.28E-11	2.16E-09	1.678E-09	Fgf12/Scn8a/Drd2/Oprd1/Chrna4/Grin1/Glra1/Atp1a3/Se	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/Cacng3	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/Chrna4/Gr	32
BP	GO:009655	chemical synaptic transmission, postsyn	17/373	120/19943	8.61E-11	3.15E-09	2.4502E-09	Gira2/Rims1/Chrna4/Grin1/Gira1/Stx1b/Mapk8ip2/Cbin1/Grp2/R	17
BP	GO:0007613	memory	19/373	156/19943	1.1E-10	3.95E-09	2.795E-09	Tafa2/Slc24a2/Drd2/Grin1/Atp1a3/Slit3/Adcy1/Hrh3/Scn2a/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/Chrna4/Grm1/Glra1/Grm1/St	20
BP	GO:0007612	learning	20/373	178/19943	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/Chrna4/Grm1/Kcnab2/Syt12/Htr2c/Nat8l/Chga/Pcpa/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/Chrna4/Grin1/Gira1/Stx1b/Mapk8ip2/Cbin1/Grp2/R	16
BP	GO:0072511	divalent inorganic cation transport	33/373	497/19943	3.97E-10	1.03E-08	8.054E-09	Cabp1/Cacng2/Thy1/Hpca/Slc24a2/Drd2/Ncs1/Oprd1/Chrna4/Gr	33
BP	GO:0099601	regulation of neurotransmitter receptor	13/373	68/19943	3.45E-10	1.05E-08	8.1833E-09	Rph3a/Nptx1/Lypd6b/Lynx1/Cacng2/Chrna4/Cacng3/Rasgr1/Ch	13
BP	GO:0019932	second-messenger-mediated signaling	31/373	455/19943	6.35E-10	1.86E-08	1.4467E-08	Rapgef4/Lgr5/Vsnl1/Camk1g/Hpca/Drd2/Gpr3/Pexs1/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	Trhr/Thy1/Drd2/Ncs1/Gpr3/Hctr2/Grin1/Hctr1/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/Chrna4/Gr	32
BP	GO:0051952	regulation of amine transport	16/373	123/19943	1.25E-09	3.59E-08	2.792E-08	Syt2/Drd2/Chrna4/Grm1/Kcnab2/Syt12/Htr2c/Nat8l/Chga/Pcpa/H	16
BP	GO:0050432	catecholamine secretion	13/373	78/19943	2.05E-09	5.8E-08	4.5122E-08	Syt2/Drd2/Cadps/Chrna4/Kcnab2/Syt12/Chga/Pcpa/Hrh3/Ht	13
BP	GO:0031503	protein-containing complex localization	22/373	250/19943	2.08E-09	5.85E-08	4.5549E-08	Cplx1/Rapgef4/Arhgap44/Nptx1/Kif5a/Cacng2/Hpca/Cacng3/Stx1	22
BP	GO:0051937	catecholamine transport	14/373	94/19943	2.26E-09	6.32E-08	4.9194E-08	Syt2/Drd2/Cadps/Chrna4/Kcnab2/Syt12/Nat8l/Chga/Pcpa/Hrh3/H	14
BP	GO:0043266	regulation of potassium ion transport	15/373	113/19943	3.11E-09	8.63E-08	6.7213E-08	Drd2/Kcnj2/Kcnab2/Rgs7/Dopp6/Kcnip4/Kcncl1/Kcnab1/Kcnal/Dp	15
BP	GO:0098815	modulation of excitatory postsynaptic p	11/373	53/19943	3.19E-09	8.8E-08	6.8529E-08	Rims1/Chrna4/Grin1/Stx1b/Cbin1/Grp2/Rims2/Grin1/Neto1/C	11
BP	GO:0050803	regulation of synapse structure or activit	23/373	280/19943	3.38E-09	9.26E-08	7.2107E-08	Rapgef4/Arhgap44/Nptx1/Lrnf5/Drd2/Slitk3/Clstn3/Cntnap4/Gr	23
BP	GO:0043270	positive regulation of ion transport	25/373	333/19943	4.4E-09	1.18E-07	9.1267E-07	Fgf12/Cacng2/Thy1/Drd2/Chrna4/Grm1/Cacng3/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/Chrna4/Grm1/Scnab/Scn1a/Scn2a/Scn9a/	13
BP	GO:0050433	regulation of catecholamine secretion	12/373	74/19943	1.19E-08	3.03E-07	2.3578E-07	Syt2/Drd2/Chrna4/Kcnab2/Syt12/Chga/Pcpa/Hrh3/Htr2a/Chma7/C	12
BP	GO:0016358	dendrite development	23/373	201/19943					

BP	GO:0031629	synaptic vesicle fusion to presynaptic ac	7/373	23/19943	1.43E-07	3.24E-06	2.5198E-06	Cplx1/Syt2/Rims1/Stx1b/Vamp1/Rab3a/Syt7	7
BP	GO:0019486	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/Sic5a7/Chma4/Sic12a5/Kcna2/Syt12/Htr2c/Nat8l/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/Nat8l/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/Ndrg4/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/Grin1/Dmtn/Ryr2/Gpld1/Chrbp/Syt12/Cj	16
BP	GO:0016081	synaptic vesicle docking	6/373	16/19943	2.81E-07	6.06E-06	4.7208E-06	Rims1/Stx1b/Camk2a/Rims2/Unc13c/Sptbn2	6
BP	GO:0031646	positive regulation of neurological system	11/373	81/19943	3.18E-07	6.83E-06	5.3134E-06	Rapgef4/Rims1/Grin1/Stx1b/Grip2/Rims2/Nrg1/Chma7/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/Grin1/Stx1b/Grip2/Rims2/Chma7/Neto1/Shank1	8
BP	GO:0099173	postsynaptic membrane organization	17/373	205/19943	3.39E-07	7.16E-06	5.5752E-06	Rph3a/Rapgef4/Arhgap44/Nptx1/Grin1/Nefl/Ina2f/Zfp804a/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/Lrrc7	8
BP	GO:0060052	neurofilament cytoskeleton organization	5/373	10/19943	5.2E-07	1.06E-05	8.2418E-06	Nefm/Nefl/Nefm/Ina/Atpsa2	5
BP	GO:0060359	response to ammonium ion	16/373	189/19943	5.69E-07	1.15E-05	8.9317E-06	Gabrg2/Gabra1/Drd2/Nefh/Chma4/Grin1/Chrbp/Chrm2/Tac3/Hrt	16
BP	GO:0140056	organelle localization by membrane tethers	10/373	72/19943	8.88E-07	1.78E-05	1.3824E-05	Nsf/Rims1/Rab3c/Ndrg4/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	Grin1/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/Grin1/Ndrg4/Atp1a3/Grin2b/Chma7/Neto1/C	12
BP	GO:0099633	protein localization to postsynaptic speciality	7/373	30/19943	1.06E-06	2.07E-05	1.6105E-05	Rapgef4/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	Rapgef4/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	Scn5a/Scn4b/Scn1a/Scn2a/Scn9a/Cacna2d1/Cacna1	7
BP	GO:0019722	calcium-mediated signaling	17/373	227/19943	1.41E-06	2.7E-05	2.0999E-05	Vsnl1/Camk1g/Hpca/Grin1/Dmtn/Grm1/Ryr2/Rit2/Tennm2/Necab	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/Grin1/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/Sptbn2	8
BP	GO:0090659	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:0098969	neurotransmitter receptor transport	10/373	22/19943	2.38E-06	4.34E-05	3.3804E-05	Cplx1/Arhgap44/Stx1b/Grip2/Mapk10/Unc7	6
BP	GO:0015893	drug transport	17/373	236/19943	2.4E-06	4.36E-05	3.3975E-05	Syt2/Drd2/Chma4/Sic32a1/Sic17a6/Kcna2/Syt12/Htr2c/Sic6a5/Nz	17
BP	GO:0007721	synaptic transmission, cholinergic	7/373	34/19943	2.63E-06	4.72E-05	3.6782E-05	Lymx1/Sic5a7/Chma4/Htr2c/Camk2b/Chrna7/Chrm2	7
BP	GO:0071248	cellular response to metal ion	17/373	238/19943	2.7E-06	4.81E-05	3.7477E-05	Gira2/Nptx1/Tph2/Syt2/Hpca/Grin1/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/Ndrg4/Stx1b/Rab3a/Camk2a/Rims2/Unc13c/Sp	10
BP	GO:0088877	neurotransmitter receptor transport	10/373	23/19943	3.17E-06	5.55E-05	4.3209E-05	Cplx1/Arhgap44/Stx1b/Grip2/Mapk10/Unc7	6
BP	GO:190340	establishment of protein localization	6/373	23/19943	3.17E-06	5.55E-05	4.3209E-05	Cplx1/Arhgap44/Stx1b/Grip2/Mapk10/Unc7	6
BP	GO:0015580	organic hydroxy compound transport	18/373	270/19943	3.65E-06	6.34E-05	4.9339E-05	Syt2/Drd2/Cadps/Chma4/Kcna2/Syt12/Nat8l/Chga/Pcp4/Hrh3/Al	18
BP	GO:0097164	ammonium ion metabolic process	14/373	172/19943	4.6E-06	7.89E-05	6.1419E-05	Tph2/Drd2/Sic5a7/Asah2/Gpld1/Sncb/Atp2b2/Htr2c/Sppb2/Ddc/C	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/Grin1/Ryr2/Htr2c/Pkch2/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/Grin1/Camk2b/Syng1/Grin2b/Neto1	7
BP	GO:0051590	positive regulation of neurotransmission	18/373	53/19943	5.91E-06	9.4E-05	7.7058E-05	Syt2/Drd2/Rims1/Stx1b/Htr2c/Nat8l/Cacna1b/Syt7	8
BP	GO:0007409	xenogenesis	24/373	465/19943	8.1E-06	0.000134	0.00010454	Nptx1/Kif5a/Cntn4/Thy1/Drd2/Nefh/Sitrk3/Grin1/Nefl/Nefm/Rab	24
BP	GO:0007187	G protein-coupled receptor signaling pathway	16/373	237/19943	1.08E-05	0.000178	0.00013894	Grm4/Lgr5/Drd2/Gpr3/Oprd1/Rit2/Htr2c/Chrm2/Chga/Mrap2/G	16
BP	GO:0032225	regulation of synaptic transmission, dopaminergic	5/373	17/19943	1.15E-05	0.000188	0.00014613	Drd2/Cntnap4/Nat8l/Chma7/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/Chma7/Syt7	5
BP	GO:0007704	positive regulation of cytosolic calcium concentration	20/373	353/19943	1.22E-05	0.000199	0.00015469	Thnr/Thy1/Drd2/Gim1/Gim1/Ryr2/Htr2c/Pkch2/Jph3/Hrh3/Cacna	20
BP	GO:0060401	cytosolic calcium ion transport	14/373	189/19943	1.26E-05	0.000207	0.00016138	Thy1/Drd2/Gim1/Ryr2/Htr2c/Pkch2/Jph3/Akap6/Grin2b/Htr2a/Pri	14
BP	GO:0071242	cellular response to ammonium ion	9/373	77/19943	1.34E-05	0.000216	0.00018808	Gabrg2/Gabra1/Chrna4/Chrbp/Chrm2/Hrh3/Chrna7/Chrm2/Gab	9
BP	GO:0019933	cAMP-mediated signaling	14/373	189/19943	1.36E-05	0.000219	0.00017011	Rapgef4/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	Chma4/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/Lrn5/Sitrk3/Cntn3/Grin1/Syndig1/Cbln1/Lingo4/Sitk1/Chri	11
BP	GO:2001023	regulation of response to drug	11/373	120/19943	1.59E-05	0.00025	0.00019467	Syt2/Drd2/Chma4/Kcna2/Syt12/Htr2c/Nat8l/Pcp4/Htr2a/Chrm2	11
BP	GO:1902476	chloride transmembrane transport	9/373	79/19943	1.65E-05	0.000259	0.00020154	Gabra2/Gira2/Gabra1/Gabra3/Gira1/Sic12a5/Gabra3/Sic12a3/Gal	9
BP	GO:0019935	cyclic nucleotide-mediated signaling	15/373	221/19943	1.91E-05	0.000298	0.00023211	Rapgef4/Lgr5/Drd2/Gpr3/Pex5/Rit2/Gpr61/Htr2c/Chga/Mrap2/G	15
BP	GO:0160227	neuron projection organization	10/373	101/19943	1.97E-05	0.000307	0.00023861	Rph3a/Arhgap44/Grin1/Atp1a3/Pf804a/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:0007773	regulation of dendrite development	11/373	199/19943	2.20E-05	0.000349	0.00027192	Rapgef4/Arhgap44/Grin1/Hecw1/RG073443/Camk2b/Pascin1/I	11
BP	GO:0010807	regulation of synaptic vesicle priming	4/373	10/19943	2.31E-05	0.00035	0.00027249	Nap1/Rims1/Stx1b/Rab3a	4
BP	GO:0061669	spontaneous neurotransmitter secretion	4/373	10/19943	2.31E-05	0.00035	0.00027249	Rph3a/Rims1/Stx1b/Rims2	4
BP	GO:0006821	chloride transport	10/373	103/19943	2.34E-05	0.000353	0.00027464	Gabrg2/Gira2/Gabra1/Gabra5/Car7/Gira1/Sic12a5/Gabra3/Sic12a	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/Kcnq1	8
BP	GO:0045956	positive regulation of calcium ion-dependent processes	3/373	32/19943	2.47E-05	0.00037	0.0002879	Syt2/Cadps/Rims1/Cacna1b/Syt7/Cacna1	3
BP	GO:0019975	positive regulation of neuron projection morphogenesis	20/373	371/19943	2.5E-05	0.000371	0.00028852	Syt2/Serpin1/Rims1/Ndrg4/Nefl/Rit2/Zfp804a/Camk2b/Pascin1/F	20
BP	GO:0097553	calcium ion transmembrane import into cytosol	12/373	151/19943	2.79E-05	0.000411	0.00031025	Thy1/Drd2/Gim1/Ryr2/Htr2c/Pkch2/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/Cadps1/Ncs1/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/Grin1/Hecw1/Mapk8ip2/Camk2b/Camk2a/Cit/Chrna7	13
BP	GO:0050994	sensory perception of mechanical stimulus	16/373	262/19943	3.71E-05	0.000528	0.00041118	Pf124/Scn8a/Gabra5/Rab3a/Atp2b2/Scn1a/Kcna1/Srmr4/Kcnma1	16
BP	GO:0031346	positive regulation of cell projection growth	20/373	478/19943	3.77E-05	0.000535	0.00041649	Syt2/Serpin1/Rims1/Grin1/Ndrg4/Nefl/Rit2/Tennm2/Zfp804a/Cam	20
BP	GO:0010970	transport along microtubule	12/373	156/19943	3.86E-05	0.000544	0.00042342	Kif5a/Nefm/Dync111/Nefl/Nefm/Kif5c/Rasgrp1/Map2/Map1b/Dlg2	12
BP	GO:0007188	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	14/373	208/19943	3.95E-05	0.000554	0.00043151	Grm4/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/Cpne4/Kcnh1/Syt7	9
BP	GO:0099111	microtubule-based transport	12/373	157/19943	4.11E-05	0.000574	0.00044654	Kif5a/Nefm/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/Sic32a1/Htr2c/Sic6a1/Hhm3	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	Grm4/Sic32a1/Htr2c/Sic6a1/Hhm3	5
BP	GO:0060080	inhibitory postsynaptic potential	5/373	22/19943	4.51E-05	0.000617	0.00048009	Rims1/Chma4/Gira1/Rims2/Gabrb3	5
BP	GO:0007622	rhythmic behavior	8/373	70/19943	4.77E-05	0.00065	0.00050587	Drd2/Htr2c/Kcna2/Mapk10/Kcnma1/Opr1/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/Nat8l/Pcp4/Grin2b/Chrm2	7
BP	GO:0001963	synaptic transmission, dopaminergic	6/373	36/19943	4.98E-05	0.000674	0.00052506	Drd2/Cntnap4/Chrbp/Nat8l/Chrna7/Chrm2	6
BP	GO:0097061	dendritic spine organization	9/373	93/19943	6.14E-05	0.000823	0.00060408	Rph3a/Arhgap44/Grin1/Zfp804a/Camk2b/Grin2b/Chrna7/Shank1	9
BP	GO:190532	positive regulation of secretion by cell	23/373	495/19943	6.42E-05	0.000859	0.0006865	Rapgef4/Syt2/Vsnl1/Cadps2/Drd2/Cadps1/Ncs1/Rims1/Chma4/P	23
BP	GO:0045471	response to ethanol	15/373	246/19943	6.57E-05	0.000876	0.00068214	Gira2/Kif5a/Drd2/Gim1/Gira1/Chrbp/Rgs7/Cacna1b/Grin2b/Chrm	15
BP	GO:0006936	muscle contraction	17/373	306/19943	6.98E-05	0.000927	0.00072176	Drd2/Gira1/Ryr2/Atp1a3/Scn4b/Chrm2/Chga/Scn1a/Atp8a2/Grip	17
BP	GO:0095909	regulation of presynaptic cytosolic calcium concentration	5/373	24/19943	7.07E-05	0.000933	0.00072635	Ncs1/Calb2/Atp2b3/Kcnh1/Cacna1b	5
BP	GO:0007200	phospholipase C-activating G protein-coupled receptor signaling pathway	9/373	95/19943	7.25E-05	0.000954	0.00074242	Drd2/Oprd1/Htr2c/Grm1/Htr2c/Hpca/Htr2a/Mlnr/Opr1	9
BP	GO:0098742	cell-cell adhesion via plasma-membrane-associated molecules	14/373	220/19943	7.27E-05	0.000954	0.00074242	Lrn5/Cntn4/Sitrk3/Cntn3/Cdh12/Tennm2/Cdh1/Cbln1/Ptpr/Nrg1	14
BP	GO:0034776								

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	0.000151	0.016235	0.00736775	Tph2/Drd2/Scn4b/Atp2b2/Htr2c/Ddc/Chrna7	8
BP	GO:0009914	hormone transport	17/373	390/19943	0.001154	0.010244	0.00737494	Cplx2/Rasgef4/Vsn1/Scg5/Drd2/Pex5/Gpld1/Chrbp/Htr2c/Chga/	17
BP	GO:1904375	regulation of protein localization to cell	9/373	139/19943	0.001235	0.010937	0.00851444	Rasgef4/Arhgap44/Cacng2/Grm1/Dup5/Camk2b/Map2/Camk2a,	9
BP	GO:0088887	neurotransmitter receptor transport, en	3/373	12/19943	0.001259	0.011088	0.0086317	Arhgap44/Grip2/Lrrc7	3
BP	GO:0006898	receptor-mediated endocytosis	12/373	228/19943	0.001273	0.011186	0.00870791	Nsf/Napb/Cacng2/Hpc4/Drd2/Cacng3/Pacsin1/Necab2/Scgip1/Nrg	12
BP	GO:0098656	anion transmembrane transport	13/373	260/19943	0.001293	0.011226	0.00876588	Gabrg2/Gira2/Gabra1/Gabra5/Gira1/Slc32a1/Slc17a6/Slc12a5/Slc	13
BP	GO:0021510	spinal cord development	9/373	140/19943	0.001298	0.011226	0.00876588	Rasgef4/Gira2/Nefn/Nefn/Nefm/Acan/Slit1/Lhx4/Novo1	9
BP	GO:0060004	reflex	4/373	26/19943	0.0013	0.011226	0.00876588	Cacng2/Gira1/Kcnm1/Shank1	4
BP	GO:2000311	regulation of AMPA receptor activity	4/373	26/19943	0.0013	0.011226	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 act	5/373	45/19943	0.001473	0.012583	0.00979572	Cabp1/Fg112/Drd2/Kcnab1/Opr1	5
BP	GO:1904063	negative regulation of cation transmem	7/373	90/19943	0.001495	0.012751	0.00991617	Cabp1/Fg112/Drd2/Hecw1/Kcnab1/Prkce/Opr1	7
BP	GO:0097305	response to alcohol	18/373	437/19943	0.001575	0.013377	0.01041345	Gira2/Klf5a/Drd2/Grin1/Gira1/Nefl/Gpld1/Chrbp/Rgs7/Gnas/Cacn	18
BP	GO:0002028	regulation of sodium ion transport	7/373	91/19943	0.001594	0.013517	0.01052241	Fgf12/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/Ctc/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/Grin2b	3
BP	GO:0043954	cellular component maintenance	6/373	68/19943	0.001696	0.01424	0.01108561	Grim1/Rab3a/Zfp804a/Grin2b/Dlg2/Bsn	6
BP	GO:0035235	ionotropic glutamate receptor signaling	4/373	28/19943	0.001728	0.014374	0.0111902	Grim1/Atp1a3/Camk2a/Grin2b	4
BP	GO:0045761	regulation of adenylyate cyclase activity	4/373	28/19943	0.001728	0.014374	0.0111902	Hpc4/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	Kf5a/Nefl/Kf5c/Mao2/Dlg2	5
BP	GO:0030451	sleep	5/373	47/19943	0.001793	0.014858	0.01156693	Drd2/Kcna2/Htr2a/Chrm2/Cacna1	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/Pex5/Epb413/Ryr2/Rit2/Htr2c/Mest/Plch2/Ij	15
BP	GO:0048488	synaptic vesicle endocytosis	6/373	70/19943	0.001969	0.016154	0.01257528	Syt2/Scnb/Pacsin1/Syp/Syt7/Dnm3	6
BP	GO:0140238	presynaptic endocytosis	6/373	70/19943	0.001969	0.016154	0.01257528	Syt2/Scnb/Pacsin1/Syp/Syt7/Dnm3	6
BP	GO:0045104	intermediate filament cytoskeleton orga	5/373	48/19943	0.001972	0.016154	0.01257528	Nefn/Nefl/Nefm/Ina/Atp8a2	5
BP	GO:1902773	positive regulation of long-term synaptic	4/373	29/19943	0.001976	0.016154	0.01257528	Drd2/Adcy1/Grin2b/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/Kcnma1	3
BP	GO:0032252	secretory granule localization	3/373	14/19943	0.002027	0.016326	0.01270915	Klf5a/Rasgr1/Map2	3
BP	GO:0042428	serotonin metabolic process	3/373	14/19943	0.002027	0.016326	0.01270915	Tph2/Atp2b2/Ddc	3
BP	GO:0046879	hormone secretion	16/373	376/19943	0.002036	0.016744	0.01274576	Cplx1/Rasgef4/Vsn1/Scg5/Drd2/Pex5/Gpld1/Chrbp/Htr2c/Chga/	16
BP	GO:0021766	hippocampus development	8/373	123/19943	0.002214	0.017703	0.01378132	Klf5a/Nefn/Nefl/Nefm/Slc32a1/Slc17a6/Kcna1/Grin2b	8
BP	GO:0050795	regulation of behavior	7/373	97/19943	0.002301	0.018331	0.0142702	Drd2/Cntnap4/Hortr2/Kcna2/Scgip1/Opr1/Chrm2	7
BP	GO:0042755	eating behavior	5/373	50/19943	0.002367	0.018752	0.01459826	Oprd1/Atp8a2/Hrh3/Scgip1/Opr1	5
BP	GO:0003912	muscle system process	17/373	418/19943	0.0024	0.018983	0.01477758	Drd2/Gira1/Ryr2/Atp1a3/Scn4b/Chrm2/Chga/Scn1a/Atp8a2/Grip2	17
BP	GO:0048511	rhythmic process	16/373	383/19943	0.002447	0.019321	0.01504091	Tph2/Drd2/Hortr2/Grim1/Kcna2/Chga/Ddc/Adcy1/Mapk10/Kenna	16
BP	GO:0021700	developmental maturation	14/373	314/19943	0.002498	0.019478	0.01516308	Gpr3a/Gira1/Rab3a/Sez62/Camk2b/Grip2/Pax2/Kcnma1/Map	14
BP	GO:0007194	negative regulation of adenylyate 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:0060474	synapse maturation	4/373	31/19943	0.002542	0.019744	0.01537095	Nefl/Sez62/Camk2b/Shank1	4
BP	GO:0009582	detection of abiotic stimulus	8/373	126/19943	0.002573	0.019917	0.01550516	Phf2a/Drd2/Scn1a/Atp8a2/Kcna1/Grin2b/Htr2a	8
BP	GO:0032411	positive regulation of transporter activit	8/373	126/19943	0.002573	0.019917	0.01550516	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	Fgf12/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/Cacna2d1	10
BP	GO:0021761	limbic system development	9/373	155/19943	0.002612	0.020094	0.01564269	Klf5a/Drd2/Nefn/Nefl/Nefm/Slc32a1/Slc17a6/Kcna1/Grin2b	9
BP	GO:0032413	negative regulation of ion transmembran	6/373	74/19943	0.002614	0.020094	0.01564269	Cabp1/Fg112/Drd2/Hecw1/Kcnab1/Opr1	6
BP	GO:0009581	detection of external stimulus	9/373	127/19943	0.002702	0.020698	0.01611287	Phf2a/Atp8a2/Scn1a/Atp8a2/Kcna1/Grin2b/Htr2a	9
BP	GO:0007193	adenylyate cyclase-inhibiting G protein-c	6/373	75/19943	0.002798	0.021391	0.01665252	Grm4/Drd2/Oprd1/Chrm2/Hrh3/Opr1	6
BP	GO:2001222	regulation of neuron migration	5/373	52/19943	0.002816	0.021493	0.01763216	Scrt1/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/Htr2c/Chrm2/Chga/Cacna1b/Akap6/Htr2a/Chrn	12
BP	GO:0098884	postsynaptic neurotransmitter receptor	4/373	32/19943	0.002862	0.021619	0.01683001	Hpc4/Pacsin1/Nrg1/Dnm3	4
BP	GO:0014039	postsynaptic endocytosis	4/373	32/19943	0.002862	0.021619	0.01683001	Hpc4/Pacsin1/Nrg1/Dnm3	4
BP	GO:1902074	response to salt	4/373	32/19943	0.002862	0.021619	0.01683001	Hpc4/Nefn/Nefl	4
BP	GO:0098876	vesicle-mediated transport to the plasm	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	Slitrk3/Cistn3/Syndig1/Cbln1/Lingo4/Cistn2	6
BP	GO:0001967	suckling behavior	3/373	16/19943	0.003033	0.022438	0.01746794	Grim1/Grin2b/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:0098926	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	Kf5a/Klf5c/Dlg2	3
BP	GO:1900271	regulation of long-term synaptic potenti	5/373	53/19943	0.003063	0.022584	0.017581	Drd2/Calb2/Adcy1/Grin2b/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	Grm4/Drd2/Grim1/Htr2c/Hrh3/Grin2b/Opr1/Abcc2	8
BP	GO:0030072	peptide hormone secretion	13/373	288/19943	0.003165	0.023257	0.01810484	Cplx1/Rasgef4/Vsn1/Drd2/Pex5/Gpld1/Chrbp/Htr2c/Chga/Stxbp	13
BP	GO:0021037	metencephalon development	9/373	160/19943	0.00323	0.023656	0.01841552	Grim1/Ctnt1/Sez62/Atp2b2/Slc12a3	9
BP	GO:0045103	intermediate filament-based process	5/373	54/19943	0.003324	0.02413	0.01878472	Nefn/Nefl/Nefm/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/Scgip1/Xkr6/Syt7	7
BP	GO:0010771	negative regulation of cell morphogene	7/373	104/19943	0.003406	0.024336	0.01894504	Thy1/Dmtr/Slit1/Ct1/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	Phf2a/Ano3/Drd2/Ryr2/Acan/Atp2b2/Scn1a/Kcnc1/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/Slitrk3/Cistn3/Cbln1	4
BP	GO:0043268	positive regulation of potassium ion tran	5/373	55/19943	0.003602	0.025399	0.01977238	Rgs7/Dpp6/Kcnc1/Kcna1/Akap6	5
BP	GO:0055064	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/Hpc4/Slc17a6/Atp2b2/Atp2b3/Atp8a2/Pax2/Celf4/Tub/Hen1	10
BP	GO:1901318	neuron projection extension	10/373	195/19943	0.003798	0.026571	0.02068513	Syt2/Rims1/Nrm1/Slit1/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					

BP	GO:0057091	synaptic vesicle clustering	3/373	18/19943	0.004298	0.0295	0.02296492	Syn1/Rab3a/Syndig1	3
BP	GO:008685	modification of postsynaptic actin cytosol	3/373	18/19943	0.004298	0.0295	0.02296492	Cabp1/Pin2/OC100909840	3
BP	GO:0021537	telencephalon development	14/373	334/19943	0.004328	0.029613	0.02303336	Kif5a/Drd2/Nefh/Grin1/Nefl/Nefm/Slc32a1/Slc17a6/Atp1a3/Kcna1	14
BP	GO:0042220	response to cocaine	6/373	82/19943	0.004364	0.029812	0.02320822	Drd2/Nefh/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 activit	6/373	83/19943	0.004632	0.031493	0.02451664	Cabp1/Fg112/Drd2/Hecw1/Kcnab1/Opr1	6
BP	GO:0007018	microtubule-based movement	12/373	267/19943	0.004647	0.031545	0.02455758	Kif5a/Nefh/Dync11/Nefl/Nefm/Kif5c/Rasgrp1/Map2/Map1b/Dlg2	12
BP	GO:0086719	import across plasma membrane	7/373	111/19943	0.004876	0.032778	0.0255171	Kcnj3/Slc12a5/Atp1a3/Slc6a5/Kcnj12/Slc8a3/Slc12a3	7
BP	GO:0045744	negative regulation of G protein-couple	5/373	59/19943	0.004879	0.032778	0.0255171	Drd2/Camk2b/Map2/Necab2/Opr1	5
BP	GO:0051482	positive regulation of cytosolic calcium k	4/373	37/19943	0.004886	0.032778	0.0255171	Drd2/Grm1/Htr2c/Opr1	4
BP	GO:0097366	response to bronchodilator	6/373	84/19943	0.004912	0.032778	0.0255171	Drd2/Grin1/Rasgrf1/Rgs7/Grin2b/Rgs17	6
BP	GO:0007016	cytoskeletal anchoring at plasma membe	2/373	6/19943	0.004979	0.032778	0.0255171	Epb4113/Shank1	2
BP	GO:0006291	acetylcholine metabolic process	2/373	6/19943	0.004979	0.032778	0.0255171	Slc5a7/Chat	2
BP	GO:0031133	regulation of axon diameter	2/373	6/19943	0.004979	0.032778	0.0255171	Nefl/Nefm	2
BP	GO:0042435	indole-containing compound biosynthesi	2/373	6/19943	0.004979	0.032778	0.0255171	Tph2/Ddc	2
BP	GO:0051584	regulation of dopamine uptake involved	2/373	6/19943	0.004979	0.032778	0.0255171	Drd2/Nat8l	2
BP	GO:0051940	regulation of catecholamine uptake invo	2/373	6/19943	0.004979	0.032778	0.0255171	Drd2/Nat8l	2
BP	GO:0098937	anterograde dendritic transport	2/373	6/19943	0.004979	0.032778	0.0255171	Kif5a/Kif5c	2
BP	GO:1900619	acetate ester metabolic process	2/373	6/19943	0.004979	0.032778	0.0255171	Slc5a7/Chat	2
BP	GO:1900408	response to monosodium glutamate	2/373	6/19943	0.004979	0.032778	0.0255171	Hpca/Pec4	2
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	0.033236	0.02587392	Nsf/Hsp90/Nrg1/Map2/Add2/Mao1b/Ogof1/Sptbn2	8
BP	GO:0097306	cellular response to alcohol	9/373	172/19943	0.005185	0.033279	0.02625728	Grn2/Kif5a/Gira1/Gpld1/Gnas/Grin2b/Prkce/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/Dnm1	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	Fg112/Hecw1/Scn4b/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 presynapse organization	4/373	38/19943	0.005382	0.034592	0.02692929	Slrn5/Slitk3/Clistn3/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	0.036844	0.0286828	Thy1/Grin1/Nefl/Nefm/Slit1/Nrg1/Map2/Map1b/Trpc5/L1cam	10
BP	GO:0030900	forebrain development	18/373	495/19943	0.005837	0.037001	0.02880497	Kif5a/Drd2/Nefh/Grin1/Nefl/Nefm/Slc32a1/Slc17a6/Atp1a3/Kcnc	18
BP	GO:0038605	positive regulation of catecholamine sec	3/373	20/19943	0.005841	0.037001	0.02880497	Chd4/Pcpa/Ctrhmb2	3
BP	GO:0050774	negative regulation of dendrite morphoq	3/373	20/19943	0.005841	0.037001	0.02880497	Cit/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:0040511	positive regulation of glutamate recepto	3/373	20/19943	0.005841	0.037001	0.02880497	Cacng2/Cacng3/Necab2	3
BP	GO:0086003	cardiac muscle cell contraction	5/373	62/19943	0.006026	0.038062	0.02963057	Ryr2/Scn4b/Scn1a/Akap6/Cacna2d1	5
BP	GO:0030902	hindbrain development	10/373	209/19943	0.006149	0.038782	0.03019107	Grin1/Cxmt1/Scz82/Atp2b2/Kcnc1/Cbln1/Kihl1/Cend1/Sptbn2/Pt	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	0.00669	0.041964	0.03266815	Cabp1/Fg112/Drd2/Hecw1/Kcnab1/Hrh3/Htr2a/Prkce/Opr1	9
BP	GO:0035584	calcium-mediated signaling using intrac	3/373	21/19943	0.006722	0.041964	0.03266815	Dnmr/Trp2/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	Nefl/Ina/Camk2b	3
BP	GO:0021549	cerebellum development	8/373	148/19943	0.00679	0.041964	0.03266815	Cxmt1/Scz82/Atp2b2/Kcnc1/Cbln1/Kihl1/Cend1/Sptbn2	8
BP	GO:0046083	regulation of hormone secretion	13/373	316/19943	0.00692	0.041964	0.03266815	Vsnl3/Scg5/Drd2/Pex5l/Gpld1/Chrbp/Htr2c/Chga/Gnas/Stxbp5l/N	13
BP	GO:0034764	positive regulation of transmembrane t	11/373	246/19943	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/Cend1	2
BP	GO:0030644	cellular chloride ion homeostasis	2/373	7/19943	0.006885	0.041964	0.03266815	Slc12a5/Abcc2	2
BP	GO:003975	sensory perception of touch	2/373	7/19943	0.006885	0.041964	0.03266815	Rab3a/Kcna1	2
BP	GO:0051582	positive regulation of neurotransmitte	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	Pin2/LOC100909840	2
BP	GO:1903935	response to sodium arsenite	2/373	7/19943	0.006885	0.041964	0.03266815	Nefl/Nefl	2
BP	GO:1900034	calcium ion export across plasma membe	2/373	7/19943	0.006885	0.041964	0.03266815	Atp2b3/Slc8a3	2
BP	GO:1980709	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	180/373	180/19943	0.00693	0.042178	0.03283479	Thy1/Rit2/RGD1307443/Stx1b/Sit1/Cit/Map2/Dnm3/Trpc5	180
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/Prkce/Opr1	4
BP	GO:0006986	dendritic spine development	7/373	122/19943	0.008009	0.048761	0.03739596	Arhgap44/Nsf/Scn8a/Lrnfs/Cacng2/Drd2/Nefh/N	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/Lrnfs/C	80
CC	GO:0099240	intrinsic component of synaptic membra	53/373	254/19943	4.45E-40	9.69E-37	7.5468E-37	Grm4/Gabrg2/Gabra1/Scn8a/Kcnj3/Lrnfs/Cacng2/Drd2/Slitk3/O	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/Lrnfs/Cacng2/Cadp	58
CC	GO:0096999	integral component of synaptic membra	49/373	235/19943	4.67E-37	5.09E-34	3.9647E-34	Grm4/Gabrg2/Gabra1/Scn8a/Kcnj3/Lrnfs/Cacng2/Drd2/Slitk3/O	49
CC	GO:0095972	postsynaptic specialization	62/373	452/19943	1.95E-35	1.18E-32	9.1577E-33	Cabp1/Rapgef4/Gabrg2/Gabra1/Arhgap44/Nsf/Scn8a/Lrnfs/Cacn	62
CC	GO:0042734	presynaptic membrane	45/373	212/19943	1.97E-34	1.43E-31	1.1155E-31	Grm4/Scn8a/Kcnj3/Cadp2/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/PexS	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/PexS	51
CC	GO:1903051	transporter complex	51/373	321/19943	1.86E-32	9E-30	7.0093E-30	Gabrg2/Gira2/Gabra1/Scn8a/Kcnj3/Cacng2/Gabra5/Chrna4/PexS	51
CC	GO:0032279	asymmetric synapse	55/373	421/19943	1.82E-30	6.62E-28	5.1515E-28	Cabp1/Rapgef4/Arhgap44/Nsf/Scn8a/Lrnfs/Cacng2/Drd2/Nefh/N	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/F	35
CC	GO:0098984	neuron to neuron synapse	56/373	445/19943	3.7E-30	1.01E-27	7.8511E-28	Cabp1/Rapgef4/Arhgap44/Nsf/Scn8a/Lrnfs/Cacng2/Drd2/Nefh/N	56
CC	GO:0098936	intrinsic component of postsynaptic mer	39/373	185/19943	8.19E-30	2.1E-27	1.6353E-27	Gabrg2/Gabra1/Scn8a/Lrnfs/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/Rapgef4/Arhgap44/Nsf/Scn8a/Lrnfs/Cacng2/Drd2/Nefh/N	54
CC	GO:0090506	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/Rapgef4/Syt2/Kif5a/Lamp5/Pvalb/Thy1/Drd2/Ncs1/S	52
CC	GO:0090505	integral component of postsynaptic mem	36/373	175/19943	3.44E-27	5.56E-25	4.328E-25	Gabrg2/Gabra1/Scn8a/Lrnfs/Cacng2/Drd2/Slitk3/Opr1/Gabra5	36
CC	GO:0034703	cation channel complex	39/373	221/19943	9.0E-27	1.33E-24	1.0389E-24	Scn8a/Kcnj3/Cacng2/PexS/Kcn2/Kcnab2/Grin1/Cacng3/Dlgap5/I	39
CC	GO:0043679	axon terminus	39/373	222/19943	1.17E-26	1.54E-24	1.202E-24	Cplx1/Grm4/Rapgef4/Syt2/Pvalb/Drd2/Ncs1/Syn1/Opr1/Kcnab2	39
CC	GO:0043006	neuron projection terminus	40/373	245/19943	4.7E-26	5.69E-24	4.4284E-24	Cplx1/Grm4/Rapgef4/Syt2/Pvalb/Drd2/Ncs1/Syn1/Opr1/Kcnab2	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/Lrnfs/Cacng2/Slitk3/Opr1/Gabra5/Clistn	29
CC	GO:0099634	postsynaptic specialization membrane	31/373	139/19943	1.1E-24	1.09E-22	8.4608E-23	Gabrg2/Gabra1/Scn8a/Lrnfs/Cacng2/Slitk3/Opr1/Gabra5/Clistn	31
CC	GO:0090601	integral component of postsynaptic spe	27/373	108/19943	4.95E-23	3.54E-21	2.7545E-21	Gabrg2/Gabra1/Scn8a/Lrnfs/Cacng2/Slitk3/Opr1/Gabra5/Clistn	27
CC	GO:009								

CC	GO:0008021	synaptic vesicle	28/3/73	237/19943	8.37E-15	4.62E-13	3.5965E-13	Rph3a/Syt2/Lamp5/Drd2/Syn1/Oprd1/Slc5a7/Rab3c/Grin1/Slc32a	28
CC	GO:008688	parallel fiber to Purkinje cell synapse	13/3/73	33/19943	1.14E-14	6.2E-13	4.8267E-13	Grm4/Scn8a/Kcnj3/Cadps2/Grin1/Cab2/Atp2b2/Atp2b3/Cbln1/Kc	13
CC	GO:0043204	perikaryon	24/3/73	177/19943	3.34E-14	1.73E-12	1.3506E-12	Rlfos3/Klf5a/Pcsk2/Hpcap4/Hpca/Drd2/Nefn/Serpin1/Slc5a7/Rgs7bp/Gr	24
CC	GO:0043409	neuron spine	26/3/73	217/19943	5.6E-14	2.84E-12	2.2075E-12	Rph3a/Ragef4/Arhgap44/Hpca/Drd2/Oprd1/Grin1/Rgs7bp/Grm1	26
CC	GO:0031256	leading edge membrane	23/3/73	171/19943	1.38E-13	6.76E-12	5.2596E-12	Gabrg2/Gabra1/Arhgap44/Lamp5/Thy1/Hpca/Oprd1/Gabra5/Grin	23
CC	GO:0008076	voltage-gated potassium channel compl	17/3/73	83/19943	1.93E-13	9.16E-12	7.13E-12	Kcnj3/Kcn2/Kcnab2/Kcna2/Kcn2/Dpp6/Kcnip4/Kcncl1/Kcnab1/Kc	17
CC	GO:0030672	synaptic vesicle membrane	20/3/73	127/19943	2.69E-13	1.24E-11	9.6199E-12	Rph3a/Syt2/Lamp5/Drd2/Syn1/O3p1/Rab3c/Slc32a1/Slc17a6/Ga	20
CC	GO:0095901	exocytic vesicle membrane	20/3/73	127/19943	2.69E-13	1.24E-11	9.6199E-12	Rph3a/Syt2/Lamp5/Drd2/Syn1/Oprd1/Rab3c/Slc32a1/Slc17a6/Ga	20
CC	GO:0043197	dendritic spine	25/3/73	214/19943	3.09E-13	1.4E-11	1.0924E-11	Rph3a/Ragef4/Arhgap44/Hpca/Drd2/Oprd1/Grin1/Rgs7bp/Grm1	25
CC	GO:0070382	exocytic vesicle	28/3/73	280/19943	5.6E-13	2.49E-11	1.9389E-11	Rph3a/Syt2/Lamp5/Drd2/Syn1/Oprd1/Slc5a7/Rab3c/Grin1/Slc32a	28
CC	GO:0048786	presynaptic active zone	17/3/73	91/19943	9.52E-13	4.07E-11	1.3651E-11	Grm4/Arhgap44/Scn8a/Syn1/Rims1/Slc32a1/Stx1b/Rab3a/Atp2b2	17
CC	GO:0034705	potassium channel complex	17/3/73	94/19943	1.66E-12	6.75E-11	5.2539E-11	Kcnj3/Kcn2/Kcnab2/Kcna2/Kcn2/Dpp6/Kcnip4/Kcncl1/Kcnab1/Kc	17
CC	GO:0030133	transport vesicle	32/3/73	390/19943	2.66E-12	1.07E-10	8.3664E-11	Rph3a/Npts1/Syt2/Pcsk2/Lamp5/Drd2/Syn1/Oprd1/Slc5a7/Rab3c	32
CC	GO:0032590	dendrite membrane	13/3/73	48/19943	2.97E-12	1.17E-10	9.088E-11	Gabrg2/Gabra1/Lamp5/Thy1/Hpca/Oprd1/Gabra5/Grin1/Slc2a5	13
CC	GO:0031594	neuromuscular junction	16/3/73	99/19943	4.49E-11	1.59E-09	1.2386E-09	Rph3a/Syt2/Slc5a7/Nefn/Nefm/Dlgap3/Scn1b/Vamp1/Kcn2/Syp5	16
CC	GO:0030658	transport vesicle membrane	21/3/73	186/19943	4.87E-11	1.71E-09	1.3337E-09	Rph3a/Syt2/Lamp5/Drd2/Syn1/Oprd1/Rab3c/Slc32a1/Slc17a6/Ga	21
CC	GO:0098685	Schaffer collateral - CA1 synapse	17/3/73	119/19943	8.39E-11	2.79E-09	2.1718E-09	Cplx1/Cacng2/Nefn/Syn1/Cacng3/Nefl/Grm1/Ina/Syp/Camk2a/Ad	17
CC	GO:0030659	cytoplasmic vesicle membrane	29/3/73	397/19943	4.65E-10	1.39E-08	1.0815E-08	Rph3a/Gabrg2/Gabra1/Syt2/Lamp5/Drd2/Cadps/Syn1/Oprd1/Rat	29
CC	GO:0012506	vesicle membrane	29/3/73	423/19943	2.01E-09	5.73E-08	4.46E-08	Rph3a/Gabrg2/Gabra1/Syt2/Lamp5/Drd2/Cadps/Syn1/Oprd1/Rat	29
CC	GO:0030673	axolemma	8/3/73	22/19943	5.53E-09	9.63E-08	7.9492E-08	Thy1/Eps413/Ank1/Kcn2/Kcnl3/Kcnh3/Nrg1/Chna7	8
CC	GO:0043198	dendritic shaft	12/3/73	67/19943	3.65E-09	8.89E-08	7.6977E-08	Grm4/Nst/Rgs7bp/Slc12a5/Syndig1/Zfp804a/Grp1/Cacna1b/Htr2	12
CC	GO:0008328	ionotropic glutamate receptor complex	11/3/73	56/19943	5.93E-09	1.57E-07	1.2192E-07	Cacng2/Grin1/Cacng3/Dlgap3/Olfm3/Nm1/Grin2b/Lrc7/Shank1/I	11
CC	GO:0098881	cholinergic synapse	7/3/73	16/19943	7.49E-09	1.95E-07	1.5216E-07	Rph3a/Chna4/Nefl/Dlgap3/Chrm2/Chrna7	7
CC	GO:0060077	inhibitory synapse	8/3/73	24/19943	7.87E-09	2.04E-07	1.5887E-07	Gabrg2/Rims1/Gira1/Slc32a1/Gad2/Rims2/Bsn/Gabrb3	8
CC	GO:0044224	juxtaparanode region of axon	6/3/73	10/19943	1.58E-06	2.09E-07	1.6276E-07	Kcnab2/Eps413/Kcna2/Kcnab1/Kcna1/Dlg2	6
CC	GO:0098878	neurotransmitter receptor complex	11/3/73	58/19943	8.77E-09	2.25E-07	1.7495E-07	Cacng2/Grin1/Cacng3/Dlgap3/Olfm3/Nm1/Grin2b/Lrc7/Shank1/I	11
CC	GO:0098563	intrinsic component of synaptic vesicle	11/3/73	67/19943	4.26E-08	1.03E-06	7.9801E-07	Syt2/Syn1/Oprd1/Rab3c/Slc32a1/Slc17a6/Vamp1/Rab3a/Syp5/Sv2l	11
CC	GO:0044305	calyx of Held	8/3/73	30/19943	5.68E-08	1.34E-06	1.0408E-06	Cplx1/Ncs1/Gira1/Kcna2/Atp1a3/Kcncl1/Kcna1/Unc13c	8
CC	GO:0043194	axon initial segment	7/3/73	21/19943	7.02E-08	1.65E-06	1.2808E-06	Scn8a/Ank1/Scn1a/Scn2a/Kcn2/Map2/Lrrc7	7
CC	GO:0031252	cell leading edge	26/3/73	414/19943	8.23E-08	1.91E-06	1.4854E-06	Gabrg2/Gabra1/Arhgap44/Lamp5/Thy1/Hpca/Oprd1/Gabra5/Grin	26
CC	GO:0097440	apical dendrite	7/3/73	26/19943	3.66E-07	7.68E-06	5.9772E-06	Klf5a/Rasgr1/Slc7a10/Grin2b/Map2/Map1b/Hcn1	7
CC	GO:0098902	plasma membrane receptor complex	16/3/73	185/19943	4.26E-07	8.83E-06	6.8747E-06	Cacng2/Chna4/Grin1/Cacng3/Grm1/Dlgap3/Olfm3/Nm1/Gabrb2	16
CC	GO:0031045	dense core granule	7/3/73	27/19943	4.87E-07	1E-05	7.7903E-06	Syt2/Cadps/Ncs1/Oprd1/Cchp/Svbp5/Syt7	7
CC	GO:0030426	growth cone	17/3/73	219/19943	8.58E-07	1.72E-05	1.3418E-05	Ragef4/Klf5a/Lamp5/Thy1/Nefl/Rasgr1/Nrsn1/Sncb/Tenm2/Zfpi	17
CC	GO:0095969	presynaptic cytoskeleton	5/3/73	11/19943	9.38E-07	1.86E-05	1.4472E-05	Rims1/Nefl/Nefm/Rims2/Bsn	5
CC	GO:0030427	site of polarized growth	17/3/73	222/19943	1.04E-06	2.04E-05	1.5849E-05	Ragef4/Klf5a/Lamp5/Thy1/Nefl/Rasgr1/Nrsn1/Sncb/Tenm2/Zfpi	17
CC	GO:0005883	neurofilament	5/3/73	12/19943	1.58E-06	3.01E-05	2.3468E-05	Nefn/Nefl/Nefm/Ina/Pcp4	5
CC	GO:1902710	GABA receptor complex	6/3/73	21/19943	1.76E-06	3.29E-05	2.5621E-05	Gabra1/Gabra5/Gabra3/Gabrb2/Gabrb3	6
CC	GO:0043235	receptor complex	23/3/73	399/19943	2.04E-06	3.78E-05	2.9396E-05	Gabrg2/Gabra1/Cacng2/Gabra5/Chna4/Pcs1/Grin1/Cacng3/Gmr	23
CC	GO:0030285	integral component of synaptic vesicle	8/3/73	47/19943	2.31E-06	4.25E-05	3.3072E-05	Syt2/Oprd1/Slc32a1/Slc17a6/Vamp1/Syp5/Sv2b/Sv2c	8
CC	GO:0032809	neuronal cell body membrane	7/3/73	35/19943	3.24E-06	5.65E-05	4.3976E-05	Thy1/Hpca/Gabra5/Kcna2/Kcn2/Atp2b2/Kcncl1	7
CC	GO:0001518	voltage-gated sodium channel complex	5/3/73	14/19943	3.88E-06	6.71E-05	5.2268E-05	Scn8a/Scn4b/Scn1a/Scn2a/Scn9a	5
CC	GO:0044298	cell body membrane	7/3/73	37/19943	4.8E-06	8.21E-05	6.3918E-05	Thy1/Hpca/Gabra5/Kcna2/Kcn2/Atp2b2/Kcncl1	7
CC	GO:0120111	neuron projection cytoplasm	10/3/73	90/19943	7.03E-06	0.000117	9.1423E-05	Klf5a/Dync111/Nefl/Kcnab1/Camk2a/Klf5/Map2/Dlg2/Bsn	10
CC	GO:0031225	anchored component of membrane	12/3/73	132/19943	7.15E-06	0.000119	9.2591E-05	Cntn4/Cntn3/Thy1/Syn1/Rab3c/Rgs7bp/Gad2/Rab3a/Nm1/Cntn5	12
CC	GO:0034707	chloride channel complex	7/3/73	42/19943	1.16E-05	0.00019	0.00014761	Gabrg2/Gira2/Gabra1/Gabra5/Gira1/Gabra3/Gabrb3	7
CC	GO:0034704	calcium channel complex	8/3/73	60/19943	1.52E-05	0.000242	0.00018836	Cacng2/Ryr2/Cacna1b/Akap6/Cacna2d2/Trpc5/Cacna2d1/Cacna1	8
CC	GO:1902711	GABA-A receptor complex	5/3/73	19/19943	2.09E-05	0.00032	0.00024894	Gabrg2/Gabra1/Gabra5/Gabra3/Gabrb3	5
CC	GO:0042383	sarcolemma	13/3/73	171/19943	2.09E-05	0.00032	0.00024894	Kcnj3/Rtn2/Ryr2/Ank1/Atp1a3/Scn1a/Gnas/Kcnj12/Akap6/Scn2a/	13
CC	GO:0048787	presynaptic active zone membrane	7/3/73	47/19943	2.5E-05	0.000371	0.00028052	Grm4/Scn8a/Slx1b/Atp2b2/Kcnma1/Nrg1/Cacna2d1	7
CC	GO:0043083	synaptic cleft	5/3/73	20/19943	2.74E-05	0.000405	0.0003152	Nptx1/Grin1/Cbln1/Grin2b/Dnm3	5
CC	GO:0098945	intrinsic component of presynaptic active	6/3/73	33/19943	2.97E-05	0.000436	0.0003937	Gmr4/Scn8a/Atp2b2/Kcnma1/Nrg1/Cacna2d1	6
CC	GO:0098686	hippocampal mossy fiber to CA3 synaps	7/3/73	49/19943	3.31E-05	0.00048	0.00037384	Ragef4/Cacng2/Grin1/Adcy1/Grin2b/Syt7/Bsn	7
CC	GO:0098831	presynaptic active zone cytoplasmic con	5/3/73	21/19943	3.54E-05	0.000511	0.00039761	Rims1/Rims2/Erc2/Bsn/Unc13c	5
CC	GO:0095971	postsynaptic cytoskeleton	5/3/73	21/19943	3.54E-05	0.000511	0.00039761	Nefn/Nefl/Nefm/Ina/Sptbn2	5
CC	GO:0032839	dendrite cytoplasm	8/3/73	24/19943	3.55E-05	0.000511	0.00039761	Klf5a/Kcna1/Kcnab1/Camk2a/Klf5c/Map2	8
CC	GO:0030315	T-tubule	8/3/73	69/19943	4.3E-05	0.000594	0.00046362	Kcnj3/Rtn2/Scn1a/Kcnj12/Akap6/Scn2a/Prkce/Cacna2d1	8
CC	GO:0017146	NMDA selective glutamate receptor com	4/3/73	12/19943	5.29E-05	0.000714	0.0005593	Grin1/Dlgap3/Grin2b/Shank1	4
CC	GO:0034706	sodium channel complex	5/3/73	24/19943	7.07E-05	0.000933	0.00072635	Scn8a/Scn4b/Scn1a/Scn2a/Scn9a	5
CC	GO:0098690	glycinergic synapse	4/3/73	13/19943	7.53E-05	0.000977	0.00076057	Gira2/Gira1/Slc6a5/Chrna7	4
CC	GO:0016528	sarcomere	8/3/73	78/19943	0.000104	0.0013	0.0010119	Rtn2/Ryr2/Ank1/Camk2b/jph3/Akap6/Slc8a3/Cacna2d1	8
CC	GO:0048788	cytoskeleton of presynaptic active zone	3/3/73	6/19943	0.000124	0.001512	0.00117741	Rims1/Rims2/Bsn	3
CC	GO:0098959	integral component of presynaptic active	5/3/73	28/19943	0.000154	0.001825	0.00142083	Kcnj3/Rtn2/Scn1a/Kcnj12/Akap6/Scn2a/Prkce/Cacna2d1	5
CC	GO:0044327	dendritic spine head	4/3/73	16/19943	0.000183	0.002154	0.00167707	Hpca/Rgs7bp/Atp1a3/Dnm3	4
CC	GO:0046658	anchored component of plasma membr	7/3/73	65/19943	0.000207	0.002397	0.00186633	Cntn3/Thy1/Rgs7bp/Nm1/Cntn5/Dlg2/Cacna2d1	7
CC	GO:0014731	spectrin-associated cytoskeleton	3/3/73	7/19943	0.000215	0.002437	0.00189682	Dmtm1/Ank1/Sptbn2	3
CC	GO:0032281	AMPA glutamate receptor complex	5/3/73	30/19943	0.000216	0.002437	0.00189682	Cacng2/Cacng3/Olfm3/Nm1/Vwc12	5
CC	GO:0032688	node of Ranvier	4/3/73	18/19943	0.000289	0.003278	0.00255172	Scn8a/Scn1a/Scn2a/Kcn2	4
CC	GO:0030141	secretory granule	18/3/73	382/19943	0.000336	0.003614	0.00231313	Rph3a/Syt2/Pcsk2/Scg5/Drd2/Cadps/Ncs1/Serpin1/Oprd1/Ica1/Ic	18
CC	GO:0099144	anchored component of synaptic memb	4/3/73	19/19943	0.000374	0.003933	0.00306165	Rgs7bp/Cntn5/Dlg2/Cacna2d1	4
CC	GO:0044292	dendrite terminus	4/3/73	20/19943	0.00046	0.004763	0.00370821	Slc32a1/Rgs7/Map2/L1cam	4
CC	GO:1904115	axon cytoplasm	6/3/73	55/19943	0.00055	0.005551	0.00432169	Klf5a/Dync111/Nefl/Klf5c/Dlg2/Bsn	6
CC	GO:0030863	cortical cytoskeleton	9/3/73	128/19943	0.000687	0.006757	0.00526022	Pvalb/Rims1/Dmtm1/Calb2/Ank1/Cap2/Rims2/Bsn/Sptbn2	9
CC	GO:0099025	anchored component of postsynaptic m	3/3/73	10/19943	0.000706	0.00684	0.00532521	Rgs7bp/Dlg2/Cacna2d1	3
CC	GO:0031300	intrinsic component of organelle membr	13/3/73	245/19943	0.000752	0.007218	0.0061898	Syt2/Gdps1/Syn1/Oprd1/Rab3c/Slc32a1/Slc17a6/Vamp1/Rab3a/S	13
CC	GO:0005891	voltage-gated calcium channel complex	5/3/73	39/19943	0.00076	0.007284	0.00567022	Cacng2/Cacna1b/Cacna2d2/Cacna2d1/Cacna1	5
CC	GO:0098992	neuronal dense core vesicle	3/3/73	12/19943	0.001259	0.011088	0.0086317	Cadps/Oprd1/Stxbp51	3
CC	GO:0099233	presynaptic cytosol	4/3/73	26/19943	0.0013	0.01126	0.00876588	Ncs1/Sncb/Camk2a/Prkce	4
CC	GO:0045121	membrane raft	17/3/73	396/19943	0.00136	0.011759	0.00915441	Thy1/Oprd1/Slc5a7/Asah2/Rit2/Rgs7/Atp2b2/Atp2b3/Gnas/Akap	17
CC	GO:0098857	membrane microdomain	17/3/73	397/19943	0.001397	0.012057	0.00938584	Thy1/Oprd1/Slc5a7/Asah2/Rit2/Rgs7/Atp2b2/Atp2b3/Gnas/Akap	17
CC	GO:0016529	saroplasmic reticulum	6/3/73	66/19943	0.001452	0.012484	0.00971848	Rtn2/Ryr2/Ank1/Camk2b/Akap6/Cacna2d1	6
CC	GO:0099026	anchored component of presynaptic me	3/3/73	13/19943	0.001615	0.013584	0.01057497	Rgs7bp/Cntn5/Cacna2d1	3
CC	GO:0098589	membrane region	17/3/73	411/19943	0.002014	0.016326	0.01270915	Thy1/Oprd1/Slc5a7/Asah2/Rit2/Rgs7/Atp2b2/Atp2b3/Gnas/Akap	17
CC	GO:0044448	cell cortex part	11/3/73	212/19943	0.002239	0.01787	0.01391128	Pvalb/Rims1/Dmtm1/Calb2/Ank1/Cap2/Rims2/Erc2/Bsn/Unc13c/Sp	11
CC	GO:0032588	trans-Golgi network membrane	4/3/73	31/19943	0.002542	0.019744	0.01537005	Lgr5/Cabp7/Caln1/Gnas	4
CC	GO:0044853	plasma membrane raft	8/3/73	127/19943	0.002702	0.020698	0.01611287	Slc5a7/Asah2/Akap6/Kcnma1/Htr2a/Chrna7/Add2/Chrm2	8
CC	GO:0005892	acetylcholine-gated channel complex	3/3/73	16/19943	0.003033	0.022438	0.01746794	Drd2/Chrna4/Chrm2	3
CC	GO:0098691	dopaminergic synapse	3/3/73	16/19943	0.003033	0.022438	0.01746794	Drd2/Chrna4/Chrm2	3
CC	GO:0044307	dendritic branch							

CC	GO:009522	region of cytosol	4/373	42/19943	0.007698	0.046466	0.03617298	Nes1/Sncb/Camk2a/Ppkce	4
CC	GO:0031301	integral component of organelle memb	10/373	218/19943	0.008175	0.04921	0.03830922	Syt2/Gdapl/Oprd1/Sic32a1/Sic17a6/Vamp1/Syp/Sv2b/Sv2c/Chrn	10
MF	GO:0022839	ion gated channel activity	48/373	326/19943	5.05E-29	1.05E-26	8.1634E-27	Gabrg2/Glra2/Gabra1/Scn8a/Kcnj3/Cacng2/Kcnab3/Ncs1/Gabra5	48
MF	GO:0022836	gated channel activity	48/373	337/19943	2.95E-28	4.46E-26	3.4711E-26	Gabrg2/Glra2/Gabra1/Scn8a/Kcnj3/Cacng2/Kcnab3/Ncs1/Gabra5	48
MF	GO:0005216	ion channel activity	50/373	406/19943	1.6E-26	2.05E-24	1.5898E-24	Gabrg2/Glra2/Gabra1/Scn8a/Kcnj3/Cacng2/Sic24a2/Kcnab3/Ncs1	50
MF	GO:0022838	substrate-specific channel activity	50/373	417/19943	5.56E-26	6.55E-24	5.0978E-24	Gabrg2/Glra2/Gabra1/Scn8a/Kcnj3/Cacng2/Sic24a2/Kcnab3/Ncs1	50
MF	GO:0005261	cation channel activity	43/373	317/19943	1.35E-24	1.26E-22	9.8249E-23	Scn8a/Kcnj3/Cacng2/Sic24a2/Kcnab3/Ncs1/Chrna4/Pex5/Kcnk2/H	43
MF	GO:0015267	channel activity	50/373	447/19943	1.36E-24	1.26E-22	9.8249E-23	Gabrg2/Glra2/Gabra1/Scn8a/Kcnj3/Cacng2/Sic24a2/Kcnab3/Ncs1	50
MF	GO:0022803	passive transmembrane transporter act	50/373	447/19943	1.36E-24	1.26E-22	9.8249E-23	Gabrg2/Glra2/Gabra1/Scn8a/Kcnj3/Cacng2/Sic24a2/Kcnab3/Ncs1	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/Ncs1/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/Ncs1/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/Sic24a2/Kcnab3/Ncs1/Sic5a7/Kcnk2/Kcnab2/H	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/Ncs1/Kcnk2/Kcnab2/Grin1/Cacng3/Kcnab3/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/Rargr1/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/Sic24a2/Kcnab3/Kcnk2/Kcnab2/Sic12a5/Kcnk2/Kcnk3/Atp1	24
MF	GO:0015077	monovalent inorganic cation transmembr	34/373	375/19943	2.99E-14	1.57E-12	1.2242E-12	Scn8a/Kcnj3/Sic24a2/Kcnab3/Sic5a7/Kcnk2/Kcnab2/Sic32a1/Sic12	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/Kcnab1/Kcnk1/I	18
MF	GO:0030594	neurotransmitter receptor activity	20/373	119/19943	7.51E-14	3.72E-12	2.894E-12	Gabrg2/Glra2/Gabra1/Drd2/Gabra5/Chrna4/Grin1/Glra1/Grm1/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/Kcnab3/I	20
MF	GO:0015276	ligand-gated ion channel activity	20/373	131/19943	4.92E-13	2.21E-11	1.7218E-11	Gabrg2/Glra2/Gabra1/Kcnj3/Gabra5/Chrna4/Pex5/Grin1/Grin1/R	20
MF	GO:0022834	ligand-gated channel activity	20/373	134/19943	7.63E-13	3.32E-11	2.5876E-11	Gabrg2/Glra2/Gabra1/Kcnj3/Gabra5/Chrna4/Pex5/Grin1/Grin1/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/Itna/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/Glra2/Gabra1/Gabra5/Chrna4/Grin1/Grin1/Glra1/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	Glra2/Sic5a7/Chrna4/Grin1/Grin1/Crhbp/Htr2c/Sic6a11/Grin2b/H	13
MF	GO:1904915	transmitter-gated ion channel activity	12/373	52/19943	1.62E-10	5.13E-09	4.0056E-09	Gabra2/Gabra1/Gabra5/Chrna4/Grin1/Grin1/Glra1/Gabra3/Grin2	12
MF	GO:0095929	neurotransmitter receptor activity invol	12/373	55/19943	3.27E-10	1.01E-08	7.8677E-09	Gabrg2/Glra2/Gabra1/Gabra5/Chrna4/Grin1/Grin1/Glra1/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/Glra2/Gabra1/Gabra5/Chrna4/Grin1/Grin1/Glra1/Gabra3/Grin2	12
MF	GO:0022835	transmitter-gated channel activity	12/373	58/19943	6.32E-10	1.86E-08	1.4467E-08	Gabrg2/Glra2/Gabra1/Gabra5/Chrna4/Grin1/Grin1/Glra1/Gabra3/Grin2	12
MF	GO:0015085	calcium ion transmembrane transporter	16/373	134/19943	4.44E-09	1.19E-07	9.2805E-08	Cacng2/Sic24a2/Ncs1/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	1.2594E-07	Gabra2/Glra2/Gabra1/Gabra5/Chrna4/Grin1/Grin1/Glra1/Gabra3/Grin2	12
MF	GO:0095095	ligand-gated anion channel activity	7/373	20/19943	4.76E-08	1.14E-06	8.8687E-07	Gabrg2/Glra2/Gabra1/Gabra5/Glra1/Gabra3/Gabra3	7
MF	GO:0070405	ammonium ion binding	11/373	79/19943	2.45E-07	5.36E-06	4.17E-06	Drd2/Sic5a7/Chrna4/Htr2c/Gpr12/Rasgrp1/Htr2a/Chrna7/Pcy11b	11
MF	GO:0095094	ligand-gated cation channel activity	12/373	99/19943	3.29E-07	7.03E-06	5.4728E-06	Kcnj3/Chrna4/Pex5/Grin1/Ryr2/Iph3/Kcnj12/Kcnh7/Grin2b/Chrn	12
MF	GO:0005262	cation channel activity	13/373	119/19943	3.64E-07	7.66E-06	5.9603E-06	Cacng2/Sic24a2/Ncs1/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	Fg12/Lymx1/Cacng2/Kcnab2/Cacng3/Gpld1/Scn4b/Dpp6/Kcnip4/I	14
MF	GO:0005237	inhibitory extracellular ligand-gated ion	6/373	17/19943	4.28E-07	8.83E-06	6.8747E-06	Gabra2/Glra2/Gabra1/Gabra5/Glra1/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/Kcnh1/Kcnq2/Kcnq1	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:0095186	structural constituent of postsynapse	6/373	20/19943	1.28E-06	2.46E-05	1.9168E-05	Nefn/Nefn/Itna/Camk2b/Dlg2/Dnm3	6
MF	GO:0095008	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 activi	5/373	19/19943	2.53E-06	4.58E-05	3.565E-05	Gabra2/Gabra1/Gabra5/Gabra3/Gabrb3	5
MF	GO:0015081	sodium ion transmembrane transporter	13/373	141/19943	2.54E-06	4.58E-05	3.565E-05	Scn8a/Sic24a2/Sic5a7/Atp1a3/Scn4b/Sic6a5/Scn1a/Sic6a11/Scn2a	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/Cxox4/Atp2b3/Cit/Kcnj12/Erc2	12
MF	GO:0043425	ion channel binding	13/373	143/19943	2.98E-06	5.27E-05	4.1063E-05	Cabp1/Fg12/Rims1/Kcnab2/Ank1/Scn4b/Kcnk1/Kcnab1/Dpp10/K	13
MF	GO:0088882	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	5.59E-06	9.49E-05	7.3857E-05	Rph3a/Arhgap44/Syt2/Thy1/Cadps/Syt12/Pla2g4e/Pascin1/Cpne4	23
MF	GO:0095181	structural constituent of presynapse	4/373	8/19943	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	0.00028852	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 cation 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	Glra2/Chrna4/Glra1/Grin2b/Chrna7/Chrm2	6
MF	GO:0015464	acetylcholine receptor activity	5/373	22/19943	5.41E-05	0.000617	0.00048009	Chrm4/Glra2/Gabra1/Gabra5/Grin1/Gabra3/Gabrb3	5
MF	GO:0000149	SNARE binding	10/373	115/19943	5.06E-05	0.000816	0.00053494	Cplk1/Nsf/Napb/Syt2/Stxb3/Syt12/Syp/Stxbp5/Syt7/Unc13c	10
MF	GO:0031402	sodium ion binding	4/373	13/19943	7.53E-05	0.000977	0.00076057	Scn8a/Sic1a/Scn2a/Scn9a	4
MF	GO:0005272	sodium 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 act	9/373	97/19943	8.54E-05	0.001094	0.00085203	Gabrg2/Glra2/Gabra1/Gabra5/Glra1/Sic12a5/Gabra3/Sic12a3/Gal	9
MF	GO:0005200	structural constituent of cytoskeleton	7/373	58/19943	0.0001	0.001265	0.00085059	Nefn/Nefn/Itna/Tuba8/Camk2b/Ado2/Sptbn2	7
MF	GO:0019965	synthetin binding	6/373	79/19943	0.000114	0.001419	0.00110466	Cplk1/Nsf/Napb/Syt2/Syp/Stxbp5/Syt7/Unc13c	6
MF	GO:0004683	calmodulin-dependent protein kinase ac	5/373	27/19943	0.000128	0.001551	0.00120764	Camk1g/Camk2b/Camk1d/Camk1d/Camk4	5
MF	GO:0008022	protein C-terminus binding	14/373	234/19943	0.00014	0.001683	0.00131033	Rfxo1/Nsf/Nef/Rargr1/Rab3a/Atp2b2/Grp2/Cacna1b/Sgtb/Lrrc	14
MF	GO:0016594	glycine binding	4/373	16/19943	0.000183	0.002154	0.00167707	Grin2/Grin1/Glra1/Grin2b	4
MF	GO:1902945	phosphatidylinositol biphosphate bindi	9/373	108/19943	0.000195	0.002275	0.0017711	Rph3a/Cadps/Kcnh1/Clv1/Pfn2/LOC100909840/Amer3/Syt7/Hcn	9
MF	GO:0095106	ion channel regulator activity	9/373	115/19943	0.000313	0.003386	0.00263607	Lymx1/Cacng2/Kcnab2/Dpp6/Kcnip4/Kcnab1/Dpp10/Cacna2d2/Nr	9
MF	GO:0005254	chloride channel activity	7/373	70/19943	0.00033	0.003357	0.00276887	Gabra2/Glra2/Gabra1/Gabra5/Grin1/Gabra3/Gabrb3	7
MF	GO:0005544	calcium-dependent phospholipid binding	6/373	52/19943	0.000405	0.004233	0.00329545	Rph3a/Syt1/Syt12/Pla2g4e/Conea4/Syt7	6
MF	GO:0005326	neurotransmitter transporter activity	6/373	53/19943	0.00045	0.004677	0.0036409	Cplk1/Sic5a7/Sic32a1/Sic17a6/Sic6a5/Sic6a11	6
MF	GO:1907663	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/Dlgap3/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/Syt7/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	Map4b2/Grp2/Kar2/Shank1	4
MF	GO:0006509	anion transmembrane transporter activ	15/373	311/19943	0.000815	0.007724	0.00601319	Gabrg2/Glra2/Gabra1/Gabra5/Glra1/Sic32a1/Sic17a6/Sic12a5/Sic	15
MF	GO:0005253	anion channel activity	7/373	83/19943	0.000928	0.008665	0.00674519	Gabrg2/Glra2/Gabra1/Gabra5/Glra1/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:0095959	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	Glra2/Grin1/Glra1/Ryr2/Gad2/Acan/Hapln1/Hapln4/Ddc/Grin2b/C	12
MF	GO:0015103	inorganic anion transmembrane transpo	9/373	136/19943	0.001059	0.009584	0.00746894	Gabrg2/Glra2/Gabra1/Gabra5/Glra1/Sic12a5/Gabra3/Sic12a3/Gal	9
MF	GO:0035256	G protein-coupled glutamate receptor b	3/373	12/19943	0.001259	0.011088	0.0086317	Cabp1/Necab2/Dnm3	3
MF	GO:0009604	ligand-gated calcium channel activity	4/373	26/19943	0.0013	0.01126	0.00876588	Nsf/Atp2a3/Gnas/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:0006065	glutamate receptor activity	4/373	28/19943	0.001728	0.014374	0.0111802	Grm4/Grin1/Grm1/Grin2b	4
MF	GO:0015643	toxic substance binding	3/373	14/19943	0.002027	0.016326	0.01270915	Nefn/Nefn/Chrna7	3
MF	GO:0016595	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/Atp2a3/Gnas	3
MF	GO:0016597	amino acid binding	6/373	71/19943	0.002				

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 chi	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/Civ1s/Pfn2/LOC100909840/Amer3/Syt7/Hcn	9
MF	GO:0030507	spectrin binding	4/373	34/19943	0.003585	0.025388	0.0197643	Dync1l1/Dmtn/Ank1/Add2	4
MF	GO:0043492	ATPase activity, coupled to movement o	8/373	133/19943	0.003589	0.025388	0.0197643	Atp1a3/Atp8b3/Atp2b2/Atp2b3/Atp8a2/Abca5/Abcg4/Abcc2	8
MF	GO:0003779	actin binding	16/373	406/19943	0.004312	0.029548	0.02300241	Hpcal/Synn1/Dmtn/Typh411b/Spire1/Cap2/Kcnma1/Coro2a/Nap2/Pl	16
MF	GO:0042277	peptide binding	13/373	302/19943	0.004713	0.031942	0.02486603	Cabp1/Oprd1/Pex5l/Hcrt2/Grin1/Hcrt1/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/Kcnma1	2
MF	GO:0031489	myosin V binding	3/373	19/19943	0.005034	0.032843	0.02556785	Rab6b/Rab3c/Rab3a	3
MF	GO:0005242	inward rectifier potassium channel activ	3/373	20/19943	0.005841	0.037001	0.02380497	Kcnj8/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/Trhr/Drd2/Oprd1		27
rno04020	Calcium signaling pathway	20/98	186/6610	1.76863E-12	9.1969E-11	7.35379E-11	Trhr/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	4.50497E-05	0.001197292	0.000957349	Gjd2/Drd2/Grm1/Htr2c/Tuba8/Gnas/Adcy1/Ht		8
rno04972	Pancreatic secretion	8/98	104/6610	0.000139958	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/Rasgrt1/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/Kcnma1		6
rno04260	Cardiac muscle contraction	6/98	84/6610	0.001457718	0.016844736	0.013468969	Cacng2/Cacng3/Ryr2/Atp1a3/Cacna2d2/Cacna		6
rno05014	Amyotrophic lateral sclerosis (ALS)	5/98	66/6610	0.002627798	0.029409096	0.02351537	Nefm/Grin1/Nefl/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	Arrhythmogenic right ventricular cardiomyopathy	5/98	72/6610	0.00412902	0.035784842	0.028613386	Cacng2/Cacng3/Ryr2/Cacna2d2/Cacna1		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/Pex51/Kcns2/Kcnab2/Grin1/Cacng3/Gira1/Dlgap3/Ryr2/Olfm3/Kcna2/Kcnc3/Scn4b/Dpp6/Kcnip4/Nrn1/Scn1a/Kcnc1/Gabra3/Kcnab1/Kcna1/Dpp10/Kcnh1/Cacna1b/Akap6/Scn2a/Kcnma1/Scn9a/Grin2b/Chrna7/Kcnq2/Lrrc7/Cacna2d2/Shank1/Chrn2/Dlg2/Trpc5/Vwc2l/Cacna2d1/Kcng1/Hcn1/Cacna1i/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/Prkce/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^{-4}	<i>Gabrg2/Gabra1/Gabra5/Gabra3/Gabrb3</i>
chloride transport	3.53×10^{-4}	<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>

Table S3. Antibodies.

Antibody	company	cat#	Application
Purified anti-GABRA1 Antibody (m)	Biogenied	832301	WB, IF
Anti-GABA A Receptor alpha 3/GABRA3 antibody (R)	Abcam	ab972446	WB, IF
Anti-GABA A Receptor alpha 5/GABRA5 antibody (R)	Abcam	ab110098	WB, IF
Anti-GABA A Receptor beta 3/GABRB3 antibody [N87/25] (m)	Abcam	ab89686	WB, IF
GABRG2 Antibody (R)	Proteintech	14104-1AP	WB, IF
KCC2 Monoclonal Antibody (S1-12) (m)	Invitrogen	MAS-27610	WB, IF
Anti-K+Cl- Cotransporter (KCC2) Antibody (R)	millipore	07-432	WB, IF
Monoclonal Anti-Ha- clone Ha-7, produced in mouse, ascites fluid (m)	signa	H9558-200UL	WB, IF
HA tag Rabbit Polyclonal Antibody (R)	Proteintech	S10664-2AP-100ul	WB, IF
Anti-FLAG* Antibody produced in rabbit (R)	Sigma	F7425-2MG	WB
Flag tag Antibody (m)	Proteintech	20543-1-AP	IF
Anti-NeuN Antibody, clone A60 (m)	millipore	MA8377	WB, IF
Recombinant Anti-NeuN antibody [EPRI2763] - Neuronal Marker (R)	Abcam	ab17487-40ul	WB, IF
Anti-MAP2 antibody (chicken)	Abcam	ab5352	WB, IF
BDNF Monoclonal Antibody (m)	Proteintech	66292-1lg	WB
GADPH Mouse Monoclonal Antibody	Beijing Ray antibody Biotech	RM2002	WB
Goat anti-Rabbit IgG (H+L) Cross-Adsorbed Secondary Antibody, Alexa Fluor 488	Thermo	A-11008	IF
Goat anti-mouse IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor Plus 488	Thermo	A32723	IF
Goat anti-Rabbit IgG (H+L) Cross-Adsorbed Secondary Antibody, Alexa Fluor 594	Thermo	A21207	IF
Goat anti-mouse IgG (H+L) Cross-Adsorbed Secondary Antibody, Alexa Fluor 594	Thermo	A-11005	IF
Goat anti-Chicken IgG (H+L) Cross-Adsorbed Secondary Antibody, Alexa Fluor 568	Thermo	A11041	IF
IGG(H+L)Peroxidase AffiniPure Goat Anti-Rabbit	Jackson	111-035-003	WB
IGG(H+L)Peroxidase AffiniPure Goat Anti-Mouse	Jackson	115-035-003	WB
CD105 (Endoglin) Monoclonal Antibody (3G6), PE, eBioscience™	invitrogen	12-1057-41	Flow
CD90 (Thy-1) Monoclonal Antibody (eBioSE10 [SE10]), PE-Cyanine7, eBioscience™	invitrogen	25-0909-41	Flow
CD166 (ALCAM) Monoclonal Antibody (3A6), PE, eBioscience™	invitrogen	12-1668-41	Flow
CD11b Monoclonal Antibody (ICRF44), PE-Cyanine5, eBioscience™	invitrogen	15-0118-41	Flow
CD45 Monoclonal Antibody (H304), APC-eFluor 780, eBioscience™	invitrogen	47-0459-41	Flow
CD73 Monoclonal Antibody (AD2), APC, eBioscience™	invitrogen	Cat # 17-0739-41	Flow
HLA-DR Monoclonal Antibody [LN3], FITC, eBioscience™	invitrogen	Cat # 11-3956-41	Flow
CD34 Monoclonal Antibody (4H11), APC, eBioscience™	Invitrogen	Cat # 17-0349-41	Flow

Table S4. Primers.

Primer Name	Sequence
Fwd Gabrg2(r) RT01	CTCCAGTATGGTTATCCT
Rev Gabrg2(r) RT01	TCCATGACCTTGTTGTCTC
Fwd Gabra3(r) RT01	TGCTTTACAACCTGGGAAG
Rev Gabra3(r) RT01	ATTGAGCGTGTACCACA
Fwd Gabrb3(r) RT01	TTCTCAATGTTGGAGCAC
Rev Gabrb3(r) RT01	CCGAAACTCATAGAGAG
Fwd Slc12a5(r) RT01	GGAGACAGACCAGCAAGAAG
Rev Slc12a5(r) RT01	TTCATCCCTCCGAGGAGA
Fwd Gabra4(r) RT01	ACCATAGAACCAGAGAA
Rev Gabra4(r) RT01	CCTGTTAAAGGTTTTCT
Fwd Gabra3(r) RT01	ACTGTCACTGTGCACAAGT
Rev Gabra3(r) RT01	TGACACCAAAGACTGTGC
Fwd Gabra4(r) RT01	ATCAAGTCTCGGCATCTT
Rev Gabra4(r) RT01	TATGAACCAATCAATGCG
Fwd Gabrb4(r) RT01	AGCAAACAGACACAGAT
Rev Gabrb4(r) RT01	AACCTG6AATTTGTCTA
Fwd Gabrb2(r) RT01	TGTAAGAAGCAATTGACAT
Rev Gabrb2(r) RT01	AAGAAGATGTAGTTGCCAA
Fwd Gabrg3(r) RT01	TAACCATGACCAACACTCAGC
Rev Gabrg3(r) RT01	GTFGACATGAGACACCCGA
Fwd Gabrd(R) RT01	GCCTCAGAGCAATCAATGAC
Rev Gabrd(R) RT01	CGCTAGCCCTCATTAGTCC
Fwd Gad1(R) RT01	GATGGTTTTGATGT
Rev Gad1(R) RT01	CCATGGTTGTTCTCTA
Fwd Gabbr1(R) RT01	CTCTCGGGCTGGATGGTTAC
Rev-Gabbr1(R) RT01	GGCTCTTAGGGTTCTTCCCTCA
Fwd Gabra2(R) RT01	CAGSAGAGACTCCAGGAGT
Rev-Gabra2(R) RT01	AGSGCTACCATGSGAATCTG
Fwd Gabra2(R) RT01	CGTATGGTTTCCGCTGCTTG
Rev Gabra2(R) RT01	GTAATGCTGTCTCCAGTCTC
Fwd Gad2(R) RT02	AATTATGCACTTCTCAACCAACA
Rev Gad2(R) RT02	AAGATCGAGAGTGGGCTTTT
Fwd Gabra3(R) RT03	TCTGTTTATCGGGTTTG
Rev Gabrg1(R) RT03	CGAAGTGATTAATTATGGACT
Fwd slc6a1(r) RT01	TGTGATGGCAATCTACCAGC
Rev slc6a1(r) RT01	AGCAGGTAGATGCTCTCAG
Fwd Slc12a2(r) RT02	CTCTGTCTCATCTAAGTGAGC
Rev Slc12a2(r) RT02	CGAAACACACAGCTTCTA
Fwd Slc32a1(r) RT02	TGCCACGCTCTCTCCACTT
Rev Slc32a1(r) RT02	AGATGCGCCGATGACGAA
Fwd 28rRNA(m) RT01	GTGACGGCGATCAATGGA
Rev 28rRNA(m) RT01	TGTTGTTTCTGGTGATAGTAGT
ddDNA: 3XFLAG-MCS-3XHA	CATTTGGCCCACTGGACTCAAGGACCATGACGGAGACTCAAGGACCATGACATGACTCAAGGACGACGATCAAGGAATTCCTC GAGATCTGTATAGAGCGCCCGGGATCCGATACCATACGATGTCTTCTGACTATCGGGCTATCCCTATGACGTCCCAGGACTATGAGGAT TGACTCTTCATAGGCTTCCAGATTAACGTGGTCTTAAAGATCT
Flag-HA F	GAGCGCTGATCGAAGAAGTACCATAATCTGTGGCCACATGGTACATCAAGGACCATGAG
Flag-HA R	AGAGGTCGATTATCGATAAGCTTTAGGACCCAGGATGATATCTGGAAG
Gabra1 F	GGACGACGATGACAAGGAATTCatataaacacacaactatg
Gabra1 R	AACATCGTAGGGTACGGATCTcatagtagtcttttgaaggttttatg
Gabra3 F	GGACGACGATGACAAGGAATTCatataaacacacaactatg
Gabra3 R	AACATCGTAGGGTACGGATCTcatagtagtcttttgaaggttttatg
rGABRA5-F	GGACGACGATGACAAGGAATTCatataaacacacaactatg
rGABRA5-R	GACATCTGTATGGTATCGGATCTcttgaaagagtatttcct
RKCC2-F	GGACGACGATGACAAGGAATTCatataaacacacaactatg
RKCC2-R	GAACTATCGTAGGGTACGGATCTcaaatgatatttatgtaact
Fwd Gabrb3(III) EcoRI one step cloning02	GACGACGATGACAAGGAATTCATGTGGGCTTTGCGGGAGG
Rev Gabrb3(III) BamHI one step cloning	ACATCGTATGSGGTACGATCTCCASTTAAACATAGTACAGCAC
Fwd Gabrg2(II) EcoRI one step cloning02	GACGACGATGACAAGGAATTCATGTGGGCTTTGCGGGAGG
Rev Gabrg2(II) BamHI one step cloning	ACATCTATGSGGTACGATCTCCASTTAAACATAGTACAGCAC
Fwd Kon1_3XFLAG-2	GAGCGCGATGACAAGGAATTCACCATGGGAATCTCCGAGGATGTC
Rev HindIII_3XFLAG	AGGTTGATTATGCAATGAAGTTTcatCTGCTCATGCTGCTCTTGT
Fwd Kon1_3XHA	GAGCGCGATGACAAGGAATTCACCATGGGAATCTCCGAGGATGTC
Rev-3XFLAG-KCC2(r)-KonHl	GAGCGCGATGACAAGGAATTCatataaacacacaactatg
Rev-3XHA-KCC2(r)-KonRl	CTTGTAGTCCCATGGGGATCCaaatgatatttatgtaact
Rev Bdnf(r) EcoRI one step cloning	AGAACTAGTCTGGAAGAAGTACCTGCTGAGGATGATGATGATG
Rev Bdnf(r)NotI one step cloning	GACGACGATGACAAGGAATTCatataaacacacaactatg
	AGAGGGCGGGGCTGTCGCGCGCGCTcatctcccccttttaagg