# **Supplemental Information**

# hUC-MSC-mediated recovery of subacute spinal cord injury through enhancing the pivotal subunits $\beta$ 3 and $\gamma$ 2 of the GABA<sub>A</sub> 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-cm<sup>3</sup> 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 (lowglucose 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 ddH<sub>2</sub>O) 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<sup>TM</sup>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,  $1\times10^6$  cells/ml were incubated with 5  $\mu$ 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<sup>TM</sup> Supplement (Thermo Fisher, 17504044), 1 mM sodium pyruvate (Solarbio, sp0100), and 10 µg/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- $\mu$ m cell strainer. Cells were resuspended in the Neurobasal (Gibco, 21103-049) supplemented with the B-27, 0.5 mM GultaMAX-I (Thermo Fisher, 35050061), and 10  $\mu$ g/ml gentamicin. 1.6×10<sup>5</sup> cells/well were plated in 24-well culture plates coated with 10  $\mu$ g/ml poly-Dlysine (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- $\mu$ l pipette tip. Co-culture with hUC-MSCs was started 12 h post injury. Neurons were co-cultured with 0.8×10<sup>4</sup> hUC-MSCs, plated in the 24-well trans-well upper chamber with a 0.4- $\mu$ m filter membrane (Corning, 353095) for 7 days. 50 ng/ml recombinant human BDNF (rhBDNF; Genscript, Z03208) was used as positive control. Cultures were then fixed and immunostained with different primary and secondary antibodies (Table S3). Images were obtained on an Olympus Fluoview FV1000 inverted fluorescence microscope. The immunofluorescence intensity of each protein was determined using the ImageJ software.

# Reference

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

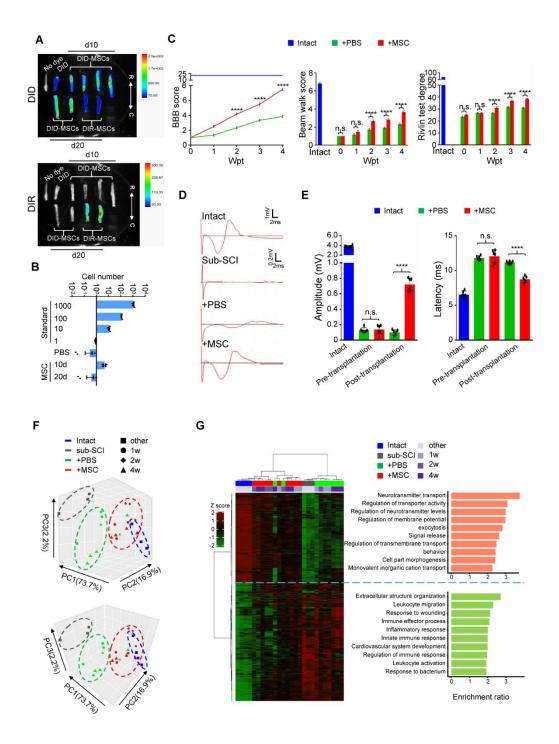
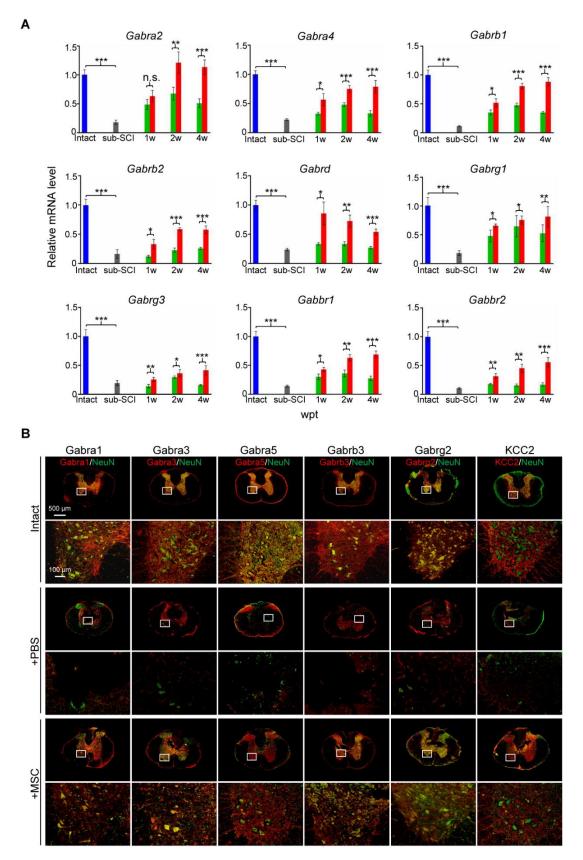
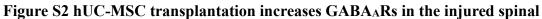


Figure S1 hUC-MSC transplantation exhibits functional recovery in the rat model

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

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





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 µm (main panels), 100 µm (lower panels).

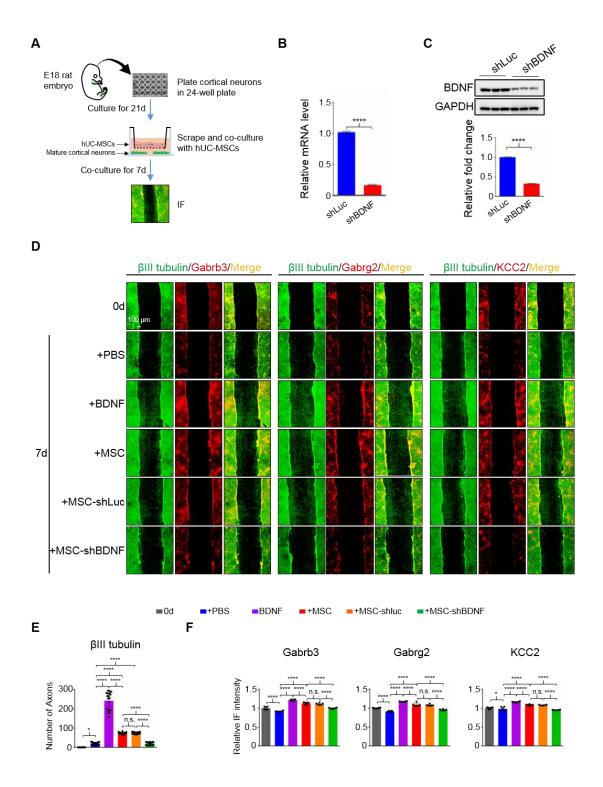


Figure S3 BDNF knockdown abrogates the effects of hUC-MSCs on axonal regeneration and the induction of GABAARs in neurons after axonal lesion *in vitro*.
(A) Schematic for hUC-MSC-mediated mature cortical axon regeneration. (B) Real time-PCR to measure BDNF knockdown in hUC-MSCs (n = 3/group). Luc, Luciferase.

(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- $\beta$ 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 µm. (E) Quantification of  $\beta$ 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.

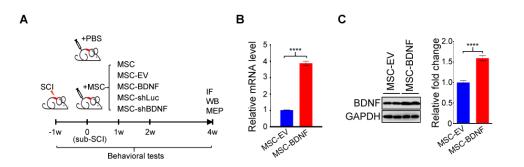


Figure S4 The transplantation of hUC-MSCs with either BDNF overexpression or knockdown into rats with sub-SCI. (A) The experimental scheme for investigating the role of BDNF secreted by hUC-MSCs on SCI repair in the rat models. (B) Real-time qPCR validation of BDNF overexpression in hUC-MSCs (n = 3/group).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

ONTOLC			GeneRatio				qvalue genelD Cou
P	GO:0043062 GO:0031589	extracellular structure organization cell-substrate adhesion	23/260 23/260	313/19943 347/19943	2.4824E-11 1.9514E-10	2.31558E-08 1.13769E-07	1.9551E-08 Col13a1/Col1a1/Fap/Emilin1/Postn/Col4a 9.6057E-08 Col13a1/Bst1/Col1a1/Emilin1/Plau/Postn
sP IP	GO:0031389	extracellular matrix organization	20/260	269/19943	4.2256E-10	2.18978E-07	1.8489E-07 Col13a1/Col1a1/Fap/Emilin1/Postn/Col4a
3P	GO:0097530	granulocyte migration	14/260	143/19943	5.7516E-09	2.68257E-06	2.2649E-06 Trpv4/Bst1/Lbp/Adam8/Trem1/Ccl6/Spp:
3P 3P	GO:0097529 GO:0010810	myeloid leukocyte migration	16/260	203/19943 220/19943	1.0842E-08 3.3824E-08	4.21408E-06 1.1964E-05	3.558E-06 Trpv4/Bst1/Emilin1/Lbp/Adam8/Trem1/C
3P 3P	GO:0010810 GO:0001525	regulation of cell-substrate adhesion angiogenesis	16/260 24/260	494/19943	3.5824E-08 3.5913E-08	1.1964E-05	1.0101E-05 Bst1/Col1a1/Emilin1/Plau/Postn/Ninj1/D; 1.0101E-05 Angptl4/Emilin1/Plau/Hmox1/Col4a1/Ad;
BP	GO:0050707	regulation of cytokine secretion	16/260	225/19943	4.6315E-08	1.39073E-05	1.1742E-05 Trpv4/Postn/Htr2b/Tir8/Srgn/Twist1/Fblr
3P 3P	GO:0050663 GO:0071295	cytokine secretion	17/260	256/19943	4.7709E-08	1.39073E-05	1.1742E-05 Trpv4/Postn/Htr2b/Trem1/Tlr8/Srgn/Twi: 2.0504E-05 Col1a1/Postn/Folr2/Pawr/Kank2/Ltbp1/S
SP SP	GO:0071295 GO:0042060	cellular response to vitamin wound healing	8/260 22/260	44/19943 444/19943	8.8517E-08 9.7164E-08	2.4285E-05 2.51763E-05	2.0504E-05 Col1a1/Postn/Foir2/Pawr/Kank2/Ltbp1/S 2.1257E-05 Col1a1/Plau/Postn/Hmox1/Nini1/Sdc1/C
3P	GO:0007160	cell-matrix adhesion	15/260	209/19943	1.0892E-07	2.67376E-05	2.2575E-05 Col13a1/Bst1/Emilin1/Plau/Postn/Ninj1/P
3P	GO:0010876	lipid localization	20/260	378/19943	1.3305E-07	3.02624E-05	2.5551E-05 Trpv4/Slco2a1/RGD1305807/Msr1/Lbp/P
BP BP	GO:0006869 GO:0038063	lipid transport collagen-activated tyrosine kinase recep	19/260	343/19943 11/19943	1.3626E-07 1.5706E-07	3.02624E-05 3.32971E-05	2.5551E-05 Trpv4/Slco2a1/RGD1305807/Msr1/Lbp/P 2.8113E-05 Col1a1/Col4a1/Col4a2/Col4a5/Col4a6
3P	GO:0050710	negative regulation of cytokine secretion	9/260	68/19943	2.3873E-07	4.84101E-05	4.0873E-05 Tir8/Srgn/Fbin1/Fn1/Lrrc32/Serpinb1a/Ar
3P	GO:0050727	regulation of inflammatory response	19/260	358/19943	2.6385E-07	5.12756E-05	4.3293E-05 Trpv4/Bst1/Enpp3/Lbp/Adam8/II20rb/Vsi
3P 3P	GO:1990266 GO:0071621	neutrophil migration granulocyte chemotaxis	11/260	116/19943 119/19943	3.519E-07 4.5602E-07	6.56502E-05 7 33401E-05	5.543E-05 Bst1/Lbp/Adam8/Trem1/Cd6/Spp1/C5ar: 6.1922E-05 Trpv4/Bst1/Lbp/Trem1/Ccl6/Spp1/C5ar1/
3P	GO:0001818	negative regulation of cytokine producti		267/19943	4.8042E-07	7.46886E-05	6.3061E-05 Hmox1/Lbp/II20rb/Vsig4/Tir8/Srgn/Twist
3P	GO:0031670	cellular response to nutrient	10/260	98/19943	6.1068E-07	8.74974E-05	7.3876E-05 Col1a1/Postn/Hmox1/Folr2/Ptgs2/Pawr/I
3P 3P	GO:1903531		15/260	239/19943	6.1472E-07	8.74974E-05	7.3876E-05 Hmox1/Tir8/Igfbp3/Srgn/Crh/Fbin1/Fn1/I
3P 3P	GO:0006721 GO:0033273	terpenoid metabolic process response to vitamin	9/260 13/260	76/19943 178/19943	6.3029E-07 6.3785E-07	8.74974E-05 8.74974E-05	7.3876E-05 Akr1b10/Adh1/Adh6/Crh/Rbp1/Hrngcs2/i 7.3876E-05 Col1a1/Postn/Folr2/Spp1/Ptgs2/Pawr/Ka
3P	GO:0038065	collagen-activated signaling pathway	5/260	14/19943	6.5911E-07	8.78312E-05	7.4157E-05 Col1a1/Col4a1/Col4a2/Col4a5/Col4a6
P	GO:0071560	cellular response to transforming growth	15/260	246/19943	8.8553E-07	0.000114726	9.6865E-05 Col1a1/Htra3/Emilin1/Ltbp2/Postn/Col4a
SP SP	GO:0071559	response to transforming growth factor		253/19943	1.2593E-06	0.000154566	0.0001305 Col1a1/Htra3/Emilin1/Ltbp2/Postn/Col4a
IP IP	GO:0016101 GO:0051048	diterpenoid metabolic process negative regulation of secretion	8/260 15/260	64/19943 268/19943	1.7653E-06 2.5731E-06	0.000200817 0.000272745	0.00016955 Akr1b10/Adh1/Adh6/Crh/Rbp1/Rarres2/( 0.00023028 Hmox1/Tir8/Igfbp3/Srgn/Crh/FbIn1/Fn1/I
SP SP	GO:0050900	leukocyte migration	17/260	341/19943	2.6731E-06	0.000272745	0.00023392 Trpv4/Bst1/Emilin1/Fut7/Lbp/Adam8/Tre
P	GO:0019216	regulation of lipid metabolic process	17/260	354/19943	4.4092E-06	0.000428423	0.00036172 Angptl4/Apobec1/Htr2b/Apoc1/Dab2/lgf
3P	GO:0031960	response to corticosteroid	16/260	321/19943	5.2951E-06	0.000504003	0.00042554 Col1a1/Sdc1/lgfbp7/Ptgs2/Ahr/Gjb2/Crh/
3P 3P	GO:0006720 GO:0001523	isoprenoid metabolic process retinoid metabolic process	9/260 7/260	98/19943 55/19943	5.4265E-06 7.0258E-06	0.000506184 0.000642519	0.00042738 Akr1b10/Adh1/Adh6/Crh/Rbp1/Hmgcs2/I 0.00054249 Akr1b10/Adh1/Adh6/Rbp1/Rarres2/Cyp2
3P	GO:0007584	response to nutrient	17/260	371/19943	8.1839E-06	0.00073403	0.00061975 Col1a1/Postn/Hmox1/Folr2/Spp1/Ptgs2/F
3P	GO:0032496	response to lipopolysaccharide	20/260	498/19943	9.2923E-06	0.000817726	0.00069042 Plau/Lbp/Mrc1/Cd68/C5ar1/lgfbp3/Ptgs2
3P	GO:0002792	negative regulation of peptide secretion		163/19943	1.0008E-05 1.1215E-05	0.000864357	0.00072979 Tir8/Srgn/Crh/Fbln1/Fn1/Lrrc32/Serpinb1
3P 3P	GO:0001819 GO:0010811	positive regulation of cytokine production positive regulation of cell-substrate adhe		462/19943 135/19943	1.1215E-05 1.1265E-05	0.000938184 0.000938184	0.00079213 Mapk13/Trpv4/Postn/Lbp/Htr2b/Adam8/ 0.00079213 Emilin1/Ninj1/Dab2/Spp1/Abi3bp/Nid1/F
3P	GO:0030595	leukocyte chemotaxis	12/260	208/19943	1.9379E-05	0.001585699	0.00133883 Trpv4/Bst1/Lbp/Adam8/Trem1/Ccl6/Spp:
3P	GO:1902622	regulation of neutrophil migration	6/260	44/19943	2.1596E-05	0.001736632	0.00146627 Bst1/Lbp/Adam8/C5ar1/Pawr/Ednra
SP SP	GO:0051216	cartilage development	12/260	214/19943 149/19943	2.5684E-05	0.002030339 0.00206989	0.00171425 Trpv4/Col1a1/Col20a1/Col7a1/Wnt5b/Sn 0.00174764 Tlr8/Srgn/Fbln1/Fn1/Lrrc32/Serpinb1a/Ar
3P 3P	GO:0050709 GO:1905954	negative regulation of protein secretion positive regulation of lipid localization	8/260	149/19943 92/19943	2.6628E-05 2.7119E-05	0.00206989	0.00174764 Tir8/Srgn/Fbin1/Fn1/Lrrc32/Serpinb1a/Ar 0.00175071 Trov4/Msr1/Pito/Apoc4/Dab2/Spp1/Crh/
3P	GO:0044403	symbiont process	16/260	368/19943	2.8737E-05	0.002161742	0.0018252 lfitm1/Hmox1/Lbp/lfitm2/Siglec1/Trem1/
3P	GO:0044419	interspecies interaction between organi		410/19943	2.9528E-05	0.00218603	0.0018457 lfitm1/Lyz2/Hmox1/Lbp/lfitm2/Siglec1/Tr
3P	GO:1905952	regulation of lipid localization neutrophil chemotaxis	10/260	153/19943	3.3437E-05	0.002436736	0.00205738 Trpv4/Msr1/Pitp/Apoc4/Apoc1/Dab2/Spr
BP BP	GO:0030593 GO:0051384	response to glucocorticoid	8/260 14/260	96/19943 297/19943	3.6942E-05 3.8138E-05	0.002650735 0.002695056	0.00223806 Bst1/Lbp/Trem1/Ccl6/Spp1/C5ar1/Ednra, 0.00227548 Sdc1/lgfbp7/Ptgs2/Ahr/Gjb2/Crh/Fn1/Hp
3P	GO:0045785	positive regulation of cell adhesion	17/260	424/19943	4.4935E-05	0.003082018	0.0026022 Emilin1/Ninj1/Adam8/Dab2/Spp1/Abi3bp
3P	GO:0042542	response to hydrogen peroxide	11/260	194/19943	5.0425E-05	0.003307107	0.00279225 Mapk13/Cdk1/Col1a1/Hmox1/Hk3/Sdc1/
3P 3P	GO:0072376 GO:0045765	protein activation cascade regulation of angiogenesis	7/260 14/260	74/19943 305/19943	5.0484E-05 5.0876E-05	0.003307107	0.00279225 Col20a1/C1qc/Cfd/Vsig4/Fbln1/F5/C7 0.00279225 Emilin1/Hmox1/Stab1/Col4a2/C5ar1/Ptgs
3P 3P	GO:0045765	regulation of anglogenesis regulation of granulocyte chemotaxis	6/260	51/19943	5.08/6E-05 5.1053E-05	0.003307107	0.00279225 Emilin1/Hmox1/Stab1/Col4a2/CSar1/Ptgs 0.00279225 Trpv4/Bst1/Lbp/C5ar1/Ednra/Rarres2
3P	GO:0072672	neutrophil extravasation	4/260	17/19943	5.8779E-05	0.003755398	0.00317075 Adam8/Trem1/Pawr/Prtn3
3P	GO:0031669	cellular response to nutrient levels	13/260	274/19943	6.7501E-05	0.004197681	0.00354417 Col1a1/Postn/Hmox1/Foir2/Cd68/Ptgs2/i
3P 3P	GO:0050673 GO:0098542	epithelial cell proliferation defense response to other organism	17/260 18/260	441/19943 487/19943	7.2917E-05 7.6659E-05	0.004474793 0.004614664	0.00377814 Fap/Plau/Hrnox1/Htr2b/lqgap3/Dab2/C5: 0.00389624 lfitm1/Lyz2/Cd8a/Lbp/lfitm2/Apobec1/St
3P 3P	GO:0001763	morphogenesis of a branching structure		240/19943	7.8133E-05	0.004614664	0.00389624 Col13a1/Col4a1/Cxcr4/Ahr/Mmp14/Ednr.
3P	GO:0060485	mesenchyme development	13/260	278/19943	7.8164E-05	0.004614664	0.00389624 Col1a1/Htr2b/Dab2/Efnb1/Snai1/Twist1/
3P	GO:0070663	regulation of leukocyte proliferation	12/260	242/19943	8.4559E-05	0.004929768	0.00416229 Lst1/Bst1/Enpp3/II20rb/Vsig4/Ahr/Pawr/
3P 3P	GO:1902624 GO:0050866	positive regulation of neutrophil migrati-	5/260 11/260	36/19943 209/19943	9.8174E-05 9.8464E-05	0.005506899	0.00464957 Lbp/Adam8/C5ar1/Pawr/Ednra 0.00464957 Ltt1/Emilio1/Enpo2/Jumov1/J/20cb/J/cir4/
SP SP	GO:0050866 GO:0062012	negative regulation of cell activation regulation of small molecule metabolic p		209/19943 366/19943	9.8464E-05 9.904E-05	0.005506899	0.00464957 Lst1/Emilin1/Enpp3/Hmox1/Il20rb/Vsig4/ 0.00464957 Cdk1/Slc7a7/Apoc1/Dab2/Gcgr/lgfbp3/le
3P	GO:0002526	acute inflammatory response	9/260	141/19943	9.9258E-05	0.005506899	0.00464957 Lbp/Adam8/Trem1/II20rb/Vsig4/Ptgs2/PI
3P	GO:0007162	negative regulation of cell adhesion	13/260	285/19943	0.00010036	0.005506899	0.00464957 Trpv4/Col1a1/Postn/II20rb/Vsig4/Pawr/N
3P 3P	GO:0002685 GO:0042573	regulation of leukocyte migration retinoic acid metabolic process	11/260 4/260	210/19943 20/19943	0.00010273 0.00011603	0.005571268 0.006124583	0.00470392 Trpv4/Bst1/Emilin1/Lbp/Adam8/C5ar1/Pr 0.00517109 Adh1/Adh6/Rbp1/Dhrs9
3P 3P	GO:0042573 GO:0061448	connective tissue development	4/260	20/19943 295/19943	0.00011603	0.006124583	0.00517109 Adn1/Adn6/R0p1/Dnrs9 0.00613902 Trpv4/Col1a1/Col20a1/Col7a1/Wnt5b/Sn
SP .	GO:0090050	positive regulation of cell migration invo	4/260	21/19943	0.00014187	0.007270985	0.00613902 Hmox1/Ptgs2/Anxa1/Rhoj
P	GO:1901342	regulation of vasculature development	14/260	338/19943	0.00015104	0.007656829	0.00646479 Emilin1/Hmox1/Stab1/Col4a2/C5ar1/Ptgs
SP LP	GO:0061138 GO:1905521	morphogenesis of a branching epithelius regulation of macrophage migration	11/260 5/260	221/19943 40/19943	0.00016107 0.00016423	0.008077531	0.00682 Col4a1/Cxcr4/Ahr/Mmp14/Ednra/Tgm2/\ 0.00684648 Trpv4/Emilin1/C5ar1/Mmp14/Rarres2
SP SP	GO:0034330	cell junction or macrophage migration	12/260	260/19943	0.00016423	0.008108897	0.00684648 Trpv4/Gjb2/Snai1/Mmp14/Ajuba/Cdh5/F
SP	GO:0060326	cell chemotaxis	13/260	300/19943	0.00016691	0.008108897	0.00684648 Trpv4/Bst1/Lbp/Adam8/Trem1/Ccl6/Spp:
P	GO:0070664	negative regulation of leukocyte prolifer		90/19943	0.00017565	0.008445787	0.00713092 Lst1/Enpp3/II20rb/Vsig4/Pawr/Lrrc32/Cei
3P 3P	GO:1903672 GO:0002695	positive regulation of sprouting angioger negative regulation of leukocyte activati		41/19943 188/19943	0.00018506 0.0001867	0.008795632	0.0074263 Hmox1/Ptgs2/Anxa1/Rhoj/Itga5 0.0074263 Lst1/Enpp3/Hmox1/Il20rb/Vsie4/Pawr/Ps
3P 3P	GO:0002062	chondrocyte differentiation	8/260	123/19943	0.00021221	0.009850687	0.0083171 Col20a1/Col7a1/Wnt5b/Wnt2b/Ccn2/Mu
P	GO:0051249	regulation of lymphocyte activation	16/260	437/19943	0.00021332	0.009850687	0.0083171 Lst1/Bst1/Lat/Adam8/Il20rb/Vsig4/LOC10
IP	GO:0050670		11/260	230/19943	0.0002278	0.010409443	0.00878887 Lst1/Bst1/II20rb/Vsig4/Ahr/Pawr/Efnb1/L
BP BP	GO:0031668 GO:0032944	cellular response to extracellular stimulu regulation of mononuclear cell proliferat	13/260	310/19943 232/19943	0.00022988 0.00024544	0.010409443 0.010939344	0.00878887 Col1a1/Postn/Hmox1/Folr2/Cd68/Ptgs2/f 0.00923627 Lst1/Bst1/ll20rb/Vsig4/Ahr/Pawr/Efnb1/L
NP NP	GO:0032944 GO:0050715	positive regulation of cytokine secretion		232/19943	0.00024544	0.010939344	0.00923627 Lst1/Bst1/li20rb/vsig4/Anr/Pawr/Ernb1/L 0.00923627 Trpv4/Postn/Htr2b/Tir8/Twist1/Osm/Lilra
P	GO:0070661	leukocyte proliferation	13/260	317/19943	0.00028522	0.012261418	0.01035252 Lst1/Bst1/Enpp3/II20rb/Vsig4/Cxcr4/Ahr/
ΙP	GO:0060536	cartilage morphogenesis	4/260	25/19943	0.00028781	0.012261418	0.01035252 Col20a1/Col7a1/Snai1/Snai2
3P	GO:1905523	positive regulation of macrophage migra		25/19943	0.00028781	0.012261418	0.01035252 Trpv4/C5ar1/Mmp14/Rarres2
3P 3P	GO:0001503 GO:0035987	ossification endodermal cell differentiation	15/260 5/260	404/19943 45/19943	0.00028905	0.012261418 0.012261418	0.01035252 Col13a1/Col1a1/Spp1/lgfbp3/Srgn/Ptgs2, 0.01035252 Col7a1/Col4a2/Mmp14/Fn1/ltga5
3P 3P	GO:0036293	response to decreased oxygen levels	16/260	45/19945	0.00028918	0.012261418	0.01128648 Angpti4/Plau/Postn/Hmox1/Adam8/lgfbr
3P	GO:0010565	regulation of cellular ketone metabolic p	8/260	131/19943	0.00032603	0.01336758	0.01128648 Slc7a7/Apoc1/Dab2/Ptgs2/C1qtnf2/Twist
3P	GO:0070206	protein trimerization	6/260	71/19943	0.00032674	0.01336758	0.01128648 Col1a1/Emilin1/C1qtnf2/Lcn2/Ceacam1/C
3P	GO:1903670	regulation of sprouting angiogenesis	6/260	71/19943	0.00032674	0.01336758	0.01128648 Hmox1/Ptgs2/Anxa1/Ceacam1/Rhoj/Itga
3P 3P	GO:1904018 GO:0042180	positive regulation of vasculature develo cellular ketone metabolic process	10/260	203/19943 204/19943	0.00034571 0.00035944	0.014020864 0.014328543	0.01183805 Hmox1/C5ar1/Ptgs2/Cxcr4/Cdh5/Anxa1/ 0.01209783 Slc7a7/Apoc1/Dab2/Ptgs2/C1qtnf2/Akr1t
3P	GO:0042180 GO:0051224	negative regulation of protein transport		204/19943	0.00035944	0.014328543	0.01209783 Sic/a//Apoci/Dab2/Hgs2/Ciqtin2/Akrit 0.01209783 Tir8/Srgn/Fbln1/Fn1/Lrrc32/Serpinb1a/Ar
3P	GO:0048525	negative regulation of viral process	7/260	102/19943	0.0003804	0.015035413	0.01269466 lfitm1/Hmox1/lfitm2/Plscr1/Fbln1/Ceaca
P	GO:0007179	transforming growth factor beta recepto		169/19943		0.015144579	0.01278683 Htra3/Emilin1/Ltbp2/Dab2/Cdh5/Lrrc32/(

BP		brown fat cell differentiation	5/260	49/19943		0.016659081	0.01406555 Trpv4/Ptgs2/Arl4a/Rarres2/Lrg1
BP	GO:1904950	negative regulation of establishment of		209/19943	0.00043511	0.016659081	0.01406555 Tir8/Srgn/Fbln1/Fn1/Lrrc32/Serpinb1a/Ar
BP	GO:0061299	retina vasculature morphogenesis in car		12/19943	0.00044171	0.016659081	0.01406555 Col4a1/Lama1/Rhoj
BP BP	GO:0035455 GO:1903557	response to interferon-alpha positive regulation of tumor necrosis fac	4/260	28/19943 105/19943	0.00045175 0.00045362	0.016659081 0.016659081	0.01406555 lfitm1/lfitm2/Plscr1/lfitm6 0.01406555 Lbp/Adam8/Twist1/Lilra5/Pf4/Cyp2j4/Spc
BP	GO:1903557 GO:0006953	acute-phase response	5/260	50/19943	0.00045362	0.010059081	0.01406555 Lbp/Adam6/Twist1/Lins5/P14/Cyp2J4/Spt 0.01463298 Lbp/Ptgs2/Piscr1/Fn1/Hp
BP	GO:0001666	response to hypoxia	15/260	424/19943	0.00047984	0.017348774	0.01464787 Angpti4/Plau/Postn/Hmox1/Adam8/lgfbr
BP	GO:0071496		15/260	425/19943	0.0004917	0.017640769	0.0148944 Col1a1/Postn/Hmox1/Foir2/Cd68/Tir8/Pt
BP	GO:0007219	Notch signaling pathway	9/260	175/19943	0.00049823	0.017695218	0.01494037 Postn/Cfd/Snai1/Mmp14/Pear1/Hp/Snai2
BP	GO:0060350	endochondral bone morphogenesis	6/260	77/19943	0.00050688	0.017695218	0.01494037 Col13a1/Trpv4/Col1a1/Col20a1/Col7a1/N
BP BP	GO:0032755 GO:0006929	positive regulation of interleukin-6 prod substrate-dependent cell migration	4/260	107/19943 29/19943	0.00050839 0.0005187	0.017695218	0.01494037 Mapk13/Trpv4/Lbp/Tir8/Twist1/Lilra5/Sp 0.01494037 Adam8/Fbln1/Fn1/Snai2
BP	GO:0008929 GO:0001706	endoderm formation	5/260	29/19943 51/19943	0.00052179	0.017695218	0.01494037 Adams/Fbin1/H1/Shal2 0.01494037 Col7a1/Col4a2/Mmp14/Fn1/itga5
BP	GO:0000302	response to reactive oxygen species	12/260	295/19943	0.00052236	0.017695218	0.01494037 Mapk13/Cdk1/Col1a1/Hmox1/Hk3/Sdc1/
BP	GO:0034329	cell junction assembly	10/260	214/19943	0.00052357	0.017695218	0.01494037 Trpv4/Gjb2/Snai1/Mmp14/Ajuba/Cdh5/F
BP	GO:0046651	lymphocyte proliferation	12/260	296/19943	0.00053825	0.018020656	0.01521515 Lst1/Bst1/II2Orb/Vsig4/Cxcr4/Ahr/Pawr/E
BP	GO:0046890		9/260	177/19943	0.00054093	0.018020656	0.01521515 Htr2b/Apoc1/Dab2/lgfbp7/Ptgs2/Snai1/A
BP BP	GO:0032963 GO:0042362	collagen metabolic process fat-soluble vitamin biosynthetic process	7/260	109/19943 13/19943	0.0005683	0.018502485	0.01562196 Col1a1/Fap/Emilin1/Mmp14/Ccn2/Cyp2j <sup>2</sup> 0.01562196 Pltp/Snai1/Snai2
BP	GO:0042362 GO:0032943	mononuclear cell proliferation	12/260	298/19943	0.00057126	0.018502485	0.01562196 Pttp/snall/snal2 0.01562196 Lst1/Bst1/Il2Orb/Vsig4/Cxcr4/Ahr/Pawr/E
BP	GO:0007492	endoderm development	6/260	79/19943	0.00058153	0.018638887	0.01573713 Col7a1/Col4a2/Dab2/Mmp14/Fn1/Itga5
BP	GO:0048762	mesenchymal cell differentiation	10/260	217/19943	0.00058346	0.018638887	0.01573713 Col1a1/Htr2b/Dab2/Efnb1/Snai1/Twist1/
BP	GO:0060706	cell differentiation involved in embryoni		30/19943	0.00059242	0.01866921	0.01576273 Snai1/Krt8/Mdfi/Krt19
BP 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
BP	GO:1905517 GO:0019835	macrophage migration cytolysis	4/260	53/19943 31/19943	0.0006241	0.020658819	0.01638419 Trpv4/Emilin1/C5ar1/Mmp14/Rarres2 0.01744259 Lyz2/Lbp/Pglyrp1/Pf4
BP	GO:0019833	regulation of collagen metabolic process		54/19943	0.00068055	0.020745639	0.0175159 Fap/Emilin1/Ccn2/Cyp2i4/Ltbp1
BP	GO:0002687	positive regulation of leukocyte migratic		147/19943	0.00070276	0.021229162	0.01792414 Trpv4/Lbp/Adam8/C5ar1/Pawr/Mmp14/E
BP	GO:0048705	skeletal system morphogenesis	11/260	263/19943	0.00070551	0.021229162	0.01792414 Col13a1/Trpv4/Col1a1/Col20a1/Col7a1/N
BP	GO:0045766	positive regulation of angiogenesis	9/260	184/19943	0.00071468	0.021295439	0.0179801 Hmox1/CSar1/Ptgs2/Cxcr4/Cdh5/Anxa1/I
BP	GO:0042268	regulation of cytolysis	3/260	14/19943	0.00071685	0.021295439	0.0179801 Lbp/Pglyrp1/Pf4
BP BP	GO:0032964 GO:0034754	collagen biosynthetic process cellular hormone metabolic process	5/260 7/260	55/19943 114/19943	0.00074074	0.021731885 0.021731885	0.0183486 Colla1/Emilin1/Ccn2/Cyp2J4/Ltbp1 0.0183486 Dab2/Spp1/Akr1b10/Adh1/Adh6/Rbp1/D
BP	GO:0002274	myeloid leukocyte activation	10/260	224/19943	0.00074284	0.021731885	0.0183486 Batf3/Enpp3/Hmox1/Lbp/Lat/Vsig4/Tir8/
BP	GO:0090022	regulation of neutrophil chemotaxis	4/260	32/19943	0.00076164	0.022063811	0.01862885 Bst1/Lbp/C5ar1/Ednra
BP	GO:0045216	cell-cell junction organization	8/260	149/19943	0.00076781	0.022105375	0.01866394 Trpv4/Gjb2/Snai1/Cdh5/Ceacam1/Lsr/Prt
BP	GO:0008015	blood circulation	16/260	493/19943	0.00079429	0.022612296	0.01909195 Trpv4/Slc4a5/Postn/Hmox1/Htr2b/ler3/P
BP BP	GO:0043903 GO:0032526	regulation of symbiosis, encompassing n response to retinoic acid	10/260 8/260	226/19943 150/19943	0.00079809 0.00080211	0.022612296	0.01909195 lfitm1/Hmox1/Lbp/lfitm2/Cxcr4/Plscr1/Cl 0.01909195 Col1a1/lgfbp7/Stra6/Gjb2/Adh1/lgfbp2/P
BP	GO:0032526 GO:0033280	response to retinoic acid response to vitamin D	5/260	150/19943 56/19943	0.00080481	0.022612296	0.01909195 Collai/igrdp//stra0/Gjb2/Adn1/igrdp2/P 0.01909195 Spp1/Ptgs2/Kank2/Ltbp1/Snai2
BP	GO:0014032	neural crest cell development	6/260	85/19943	0.00085754	0.023536435	0.01987221 Htr2b/Efnb1/Twist1/Ednra/Fn1/Snai2
BP	GO:1903901	negative regulation of viral life cycle	6/260	85/19943	0.00085754	0.023536435	0.01987221 lfitm1/Hmox1/lfitm2/Plscr1/Ceacam1/lfit
BP	GO:0006775	fat-soluble vitamin metabolic process	4/260	33/19943	0.00085789	0.023536435	0.01987221 Pltp/Snai1/Rbp1/Snai2
BP	GO:2000778	positive regulation of interleukin-6 secre		33/19943	0.00085789	0.023536435	0.01987221 Trpv4/Tir8/Twist1/Lilra5
BP BP	GO:0015850 GO:0031099	organic hydroxy compound transport regeneration	11/260 12/260	270/19943 313/19943	0.00087478	0.023621422	0.01994397 RGD1305807/Msr1/Pltp/Apoc1/Dab2/Slc 0.01994397 Cdk1/Plau/Postn/Hmox1/Ninj1/Spp1/C5a
BP	GO:0031099 GO:0042953	lipoprotein transport	3/260	15/19943	0.00087759	0.023621422	0.01994397 Cdk1/Pla0/Postr/Hinok1/Ninj1/Spp1/C5a 0.01994397 Msr1/Apobec1/Cubn
BP	GO:0044872	lipoprotein localization	3/260	15/19943	0.00088746	0.023621422	0.01994397 Msr1/Apobec1/Cubn
BP	GO:0047484	regulation of response to osmotic stress	3/260	15/19943	0.00088746	0.023621422	0.01994397 Trpv4/Ptgs2/Ptger2
BP	GO:0006959	humoral immune response	9/260	190/19943	0.00089762	0.023621422	0.01994397 Col20a1/C1qc/Cfd/Vsig4/Pglyrp1/Rarres2
BP BP	GO:0050792 GO:0032945	regulation of viral process	9/260	190/19943	0.00089762	0.023621422	0.01994397 lfitm1/Hmox1/lfitm2/Cxcr4/Plscr1/Chmp
BP	GO:0032945 GO:0050672	negative regulation of mononuclear cell negative regulation of lymphocyte prolif	6/260	86/19943 86/19943	0.00091196	0.023629864	0.0199511 Lst1/ll20rb/Vsig4/Pawr/Lrrc32/Ceacam1
BP	GO:0030872	negative regulation of viral genome repl	5/260	58/19943	0.00091198	0.023325804	0.0199511 Lst1/ll20rb/Vsig4/Pawr/Lrrc32/Ceacam1 0.0205652 lfitm1/lfitm2/Plscr1/Ceacam1/lfitm6
BP	GO:0042572	retinol metabolic process	4/260	34/19943	0.00096241	0.024662951	0.02082335 Akr1b10/Adh1/Adh6/Rbp1
BP	GO:0043901	negative regulation of multi-organism pr	9/260	193/19943	0.00100241	0.025487452	0.02151949 lfitm1/Hmox1/Lbp/lfitm2/Plscr1/Fbln1/C
BP	GO:0001704	formation of primary germ layer	7/260	120/19943	0.00100551	0.025487452	0.02151949 Col7a1/Col4a2/Snai1/Mmp14/Fn1/Fzd7/I
BP	GO:0032103	positive regulation of response to extern	12/260	320/19943	0.00106135	0.026695272	0.02253927 Trpv4/Lbp/Adam8/C5ar1/Ptgs2/Cxcr4/Ed
BP BP	GO:0009266 GO:0051180	response to temperature stimulus vitamin transport	10/260 4/260	235/19943 35/19943	0.00107386	0.026695272 0.026695272	0.02253927 Trpv4/Hmox1/Htr2b/lgfbp7/Ptgs2/Cxcr4/ 0.02253927 RGD1305807/Folr2/Stra6/Cubn
BP	GO:0031180 GO:0043518	negative regulation of DNA damage resp		16/19943	0.00107330	0.026695272	0.02253927 Rdb1303d0770ii2/3tra0/Cdbii 0.02253927 Snai1/Twist1/Snai2
BP	GO:0060192	negative regulation of lipase activity	3/260	16/19943	0.00108178	0.026695272	0.02253927 Angptl4/Apoc1/Anxa1
BP	GO:0006956	complement activation	5/260	60/19943	0.00110314	0.027047568	0.02283672 Col20a1/C1qc/Cfd/Vsig4/C7
BP	GO:0060349	bone morphogenesis	7/260	122/19943	0.00110765	0.027047568	0.02283672 Col13a1/Trpv4/Col1a1/Col20a1/Col7a1/N
BP BP	GO:0051250 GO:0014031	negative regulation of lymphocyte active		158/19943 90/19943	0.00112313 0.00115666	0.027282808 0.02795154	0.02303534 Lst1/Il20rb/Vsig4/Pawr/Pglyrp1/Lrrc32/A 0.02359996 Htr2b/Efnb1/Twist1/Ednra/En1/Snai2
BP	GO:0014031 GO:0010812	mesenchymal cell development negative regulation of cell-substrate adh	6/260 5/260	90/19943 61/19943	0.00115666	0.02795154	0.02359996 Htt2b/Ethb1/Twist1/Ednra/En1/Shai2 0.02401158 Col1a1/Postn/Mmp14/Fbln1/Fzd7
BP	GO:0009615	response to virus	11/260	281/19943	0.00118905	0.028459058	0.02421138 Colla1/Postn/Mmp14/Poin1/P20/ 0.02424117 Batf3/ifitm1/Cd8a/ifitm2/Apobec1/Tir8/F
BP	GO:0032368	regulation of lipid transport	7/260	124/19943	0.00121777	0.02871098	0.02424117 Trpv4/Pitp/Apoc1/Dab2/Spp1/lgfbp3/Crh
BP	GO:0019217	regulation of fatty acid metabolic proces	6/260	91/19943	0.00122502	0.02871098	0.02424117 Apoc1/Ptgs2/C1qtnf2/Twist1/Anxa1/Cear
BP	GO:0048864 GO:0050678	stem cell development regulation of epithelial cell proliferation	6/260	91/19943 371/19943	0.00122502	0.02871098	0.02424117 Htr2b/Efnb1/Twist1/Ednra/Fn1/Snai2
BP	GO:0050678 GO:0014033		13/260	3/1/19943 92/19943	0.0012321	0.028/324/3	0.02425932 Plau/Hmox1/Htr2b/lqgap3/Dab2/C5ar1/1 0.02474958 Htr2b/Ffnb1/Twist1/Ednra/En1/Snai2
BP	GO:0014033 GO:0045833	negative regulation of lipid metabolic pr		92/19943	0.00129643	0.029313139	0.02474958 Apobec1/Apoc1/Snai1/Cidea/Ceacam1/Si
BP	GO:0016114	terpenoid biosynthetic process	3/260	17/19943	0.00130099	0.029313139	0.02474958 Rbp1/Hmgcs2/Dhrs9
BP	GO:0035461	vitamin transmembrane transport	3/260	17/19943	0.00130099	0.029313139	0.02474958 RGD1305807/Folr2/Stra6
BP	GO:0070234	positive regulation of T cell apoptotic pro	3/260	17/19943	0.00130099	0.029313139	0.02474958 Adam8/Siglec1/Ceacam1
BP BP	GO:2000108 GO:0015718	positive regulation of leukocyte apoptot monocarboxylic acid transport	4/260 8/260	37/19943 163/19943	0.0013293 0.00137098	0.02966441	0.02504617 Adam8/Siglec1/Anxa1/Ceacam1 0.02567121 Trpv4/Slco2a1/RGD1305807/Slc16a3/Stra
BP	GO:0015718 GO:0045600	positive regulation of fat cell differentiat		163/19943 63/19943	0.00137098	0.030404698	0.02567121 Ptgs2/Wnt5b/Rarres2/Snai2/Zbtb7c
BP	GO:0042246	tissue regeneration	6/260	94/19943	0.00144875	0.031872559	0.02691055 Plau/Postn/Ninj1/Fzd7/Mustn1/Anxa1
BP	GO:0035988	chondrocyte proliferation	3/260	18/19943	0.00154623	0.033801113	0.02853886 Mmp14/Ccn2/Mustn1
BP	GO:0043900	regulation of multi-organism process	14/260	428/19943	0.00155091	0.033801113	0.02853886 Cdk1/lfitm1/Plau/Hmox1/Lbp/lfitm2/Cxci
BP BP	GO:0016032 GO:0045995	viral process regulation of embryonic development	11/260 7/260	291/19943 130/19943	0.00159535 0.00160025	0.034505856	0.02913388 lfitm1/Hmox1/lfitm2/Siglec1/Lrrc15/Cxcr 0.02913388 Snal1/Lama2/Wnt2b/Fzd7/Lama1/Six1/Pi
BP BP	GO:0045995 GO:0090049	regulation of embryonic development regulation of cell migration involved in s		130/19943 39/19943	0.00160025	0.034505856	0.02913388 Snai1/Lama2/Wht2b/Fzd7/Lama1/Six1/Pi 0.02913388 Hmox1/Ptgs2/Anxa1/Rhoj
BP	GO:0031349	positive regulation of defense response	13/260	383/19943	0.00162211	0.034505856	0.02913388 Trpv4/Lbp/Adam8/Tir8/LOC102547056/P
BP	GO:0032102	negative regulation of response to exter	12/260	337/19943	0.001645	0.034505856	0.02913388 Plau/Enpp3/Il20rb/Spp1/Ier3/Tspan8/Kar
BP	GO:0010957	negative regulation of vitamin D biosynt	2/260	5/19943	0.00164983	0.034505856	0.02913388 Snai1/Snai2
BP	GO:0038044	transforming growth factor-beta secreti	2/260	5/19943	0.00164983	0.034505856	0.02913388 Fbln1/Fn1
BP BP	GO:0042098 GO:0046718	T cell proliferation viral entry into host cell	9/260 5/260	208/19943 66/19943	0.00168545	0.035093381 0.035125424	0.02962994 Il20rb/Vsig4/Cxcr4/Pawr/Efnb1/Lrrc32/Ig 0.02965699 lfitm1/lfitm2/Siglec1/Ceacam1/lfitm6
BP	GO:0046718 GO:2000027	regulation of animal organ morphogene		209/19943	0.00169452	0.035125424	0.03021442 Plau/Dab2/Twist1/Ednra/Wht2b/Ceacam
BP	GO:0001569	branching involved in blood vessel morp	4/260	40/19943	0.0017841	0.036495728	0.03081397 Col4a1/Cxcr4/Ahr/Ednra
BP	GO:1903555	regulation of tumor necrosis factor supe	8/260	171/19943	0.0018561	0.037550363	0.03170441 Lbp/Adam8/Twist1/Cidea/Lilra5/Pf4/Cyp;
BP	GO:0032355	response to estradiol	10/260	253/19943	0.00185981	0.037550363	0.03170441 Col1a1/Postn/Igfbp3/Ptgs2/Ahr/Pawr/Gjł
BP	GO:0071222	cellular response to lipopolysaccharide	11/260	298/19943	0.00192291	0.038657048	0.03263881 Plau/Lbp/Mrc1/Cd68/Plscr1/Plscr2/Lcn2/
BP	GO:0070371	ERK1 and ERK2 cascade positive regulation of fatty acid metabol	12/260	344/19943 41/19943	0.00195205	0.039005489	0.032933 Trpv4/Emilin1/Htr2b/lqgap3/Dab2/Ccl6/C 0.032933 Ptgs2/C1qtnf2/Twist1/Anxa1
BP	GO:0043925 GO:0042129	regulation of T cell proliferation	8/260	173/19943	0.00195696	0.03962079	0.03245251 ll20rb/Vsig4/Pawr/Efnb1/Lrrc32/lgfbp2/A
BP	GO:0030260	entry into host cell	5/260	69/19943	0.0020647	0.040067088	0.03382933 lfitm1/lfitm2/Siglec1/Ceacam1/lfitm6

BP	GO:0032623	interleukin-2 production	5/260	69/19943	0.0020647	0.040067088	0.03382933	20rb/Vsig4/Pawr/Anxa1/Ceacam1
BP	GO:0044409	entry into host	5/260	69/19943	0.0020647	0.040067088	0.03382933 H	fitm1/lfitm2/Siglec1/Ceacam1/lfitm6
BP	GO:0051806	entry into cell of other organism involve		69/19943	0.0020647	0.040067088		fitm1/lfitm2/5iglec1/Ceacam1/lfitm6
BP	GO:0051828	entry into other organism involved in sy		69/19943	0.0020647	0.040067088		fitm1/lfitm2/Siglec1/Ceacam1/lfitm6
BP BP	GO:0051701 GO:0010759	interaction with host	7/260	136/19943 20/19943	0.00207036	0.040067088		fitm1/lfitm2/Siglec1/Chmp4c/Fbln1/Cea my4/C5ar1/Barres2
BP	GO:0010759 GO:0030852	positive regulation of macrophage chem regulation of granulocyte differentiation		20/19943 20/19943	0.00211901 0.00211901	0.040339034		rpv4/C5ar1/Rarres2 21qc/Rbp1/Ceacam1
BP	GO:0030832 GO:0071706	tumor necrosis factor superfamily cytok		175/19943	0.00211901	0.040663572		bp/Adam8/Twist1/Cidea/Lilra5/Pf4/Cyp;
BP	GO:0042130	negative regulation of T cell proliferation		70/19943	0.00214478	0.040565572		I20rb/Vsig4/Pawr/Lrrc32/Ceacam1
BP	GO:0002698	negative regulation of immune effector		138/19943	0.00224872	0.042290427		npp3/Hmox1/II20rb/Vsig4/Pglyrp1/Anxe
BP	GO:0019058	viral life cycle	9/260	218/19943	0.00231886	0.04334457	0.03659656	fitm1/Hmox1/lfitm2/Siglec1/Lrrc15/Plscr
BP	GO:0042304	regulation of fatty acid biosynthetic proc	4/260	43/19943	0.00233681	0.04334457		Apoc1/Ptgs2/Anxa1/Ceacam1
BP	GO:0071219	cellular response to molecule of bacteria	11/260	307/19943	0.00242255	0.04334457		Plau/Lbp/Mrc1/Cd68/Plscr1/Plscr2/Lcn2/
BP	GO:0032760	positive regulation of turnor necrosis fac	6/260	104/19943	0.00242438	0.04334457		bp/Twist1/Lilra5/Pf4/Cyp2j4/Spon2
BP	GO:0010884	positive regulation of lipid storage	3/260	21/19943	0.00244853	0.04334457		/lsr1/Apoc4/Cidea
BP	GO:0006069	ethanol oxidation	2/260	6/19943	0.00245347	0.04334457	0.03659656 A	
BP	GO:0033015	tetrapyrrole catabolic process	2/260	6/19943	0.00245347	0.04334457	0.03659656 H	
BP BP	GO:0046137 GO:0051005	negative regulation of vitamin metabolic negative regulation of lipoprotein lipase		6/19943 6/19943	0.00245347 0.00245347	0.04334457 0.04334457	0.03659656 S	
BP	GO:0051005 GO:0061304	retinal blood vessel morphogenesis	2/260	6/19943	0.00245347	0.04334457	0.03659656	
BP	GO:0070562	regulation of vitamin D receptor signalin		6/19943	0.00245347	0.04334457	0.03659656 K	
BP	GO:1902219	negative regulation of intrinsic apoptotic		6/19943	0.00245347	0.04334457	0.03659656 P	
BP	GO:0042742	defense response to bacterium	10/260	264/19943	0.00253429	0.044435811	0.03751791 L	yz2/Lbp/Stab1/Trem1/C5ar1/Pglyrp1/Lc
BP	GO:0035456	response to interferon-beta	4/260	44/19943	0.00254451	0.044447966	0.03752818 H	fitm1/lfitm2/Plscr1/lfitm6
BP	GO:0042445		9/260	222/19943	0.00261986	0.045593389		on3/Dab2/Spp1/Akr1b10/Adh1/Adh6/C
BP	GO:0032370		5/260	73/19943	0.00264586	0.045874714		rpv4/Pltp/Dab2/Spp1/Crh
BP	GO:0017015	regulation of transforming growth factor		106/19943	0.00266763	0.046080812		Hra3/Emilin1/Dab2/Cidea/Ltbp1/Lrg1
BP	GO:0060416	response to growth hormone	4/260	45/19943	0.00276454	0.04748597		gfbp3/Hp/Hmgcs2/Gdf15
BP BP	GO:0051222 GO:0009110	positive regulation of protein transport vitamin biosynthetic process	14/260 3/260	456/19943 22/19943	0.00276934 0.00280805	0.04748597 0.04797337		'rpv4/Postn/Htr2b/Tlr8/Ptgs2/Twist1/Ce Ptp/Snai1/Snai2
BP	GO:0009110 GO:0015711	organic anion transport	3/260	458/19943	0.00280805	0.04797337		rpv4/Slco2a1/Slc7a7/Slc4a5/RGD130580
BP	GO:0015711 GO:0001906	organic anion transport cell killing	14/260 8/260	458/19943 184/19943	0.00288025	0.049027258		yz2/Trem1/RT1-M2/LOC102547056/Cdh
BP	GO:0001750	branching morphogenesis of an epithelia		184/19943	0.00292345	0.049135343		ol4a1/Cxcr4/Ahr/Mmp14/Ednra/Wnt2b,
BP	GO:0008630	intrinsic apoptotic signaling pathway in r		108/19943	0.00292874	0.049135343		Imox1/ler3/Plscr1/Snai1/Uaca/Snai2
BP	GO:1903844	regulation of cellular response to transfo	6/260	108/19943	0.00292874	0.049135343		ltra3/Emilin1/Dab2/Cidea/Ltbp1/Lrg1
BP	GO:0032965	regulation of collagen biosynthetic proce		46/19943	0.00299726	0.049925791		milin1/Ccn2/Cyp2j4/Ltbp1
BP	GO:0070207	protein homotrimerization	4/260	46/19943	0.00299726	0.049925791		milin1/Lcn2/Ceacam1/Cubn
BP	GO:0022408	negative regulation of cell-cell adhesion		185/19943	0.00302201	0.04999065		rpv4/ll20rb/Vsig4/Pawr/Lrrc32/Anxa1/C
BP	GO:0050714	positive regulation of protein secretion		316/19943	0.00302259	0.04999065		rpv4/Postn/Htr2b/Tlr8/Twist1/Crh/Ceac
CC	GO:0062023	collagen-containing extracellular matrix		217/19943	6.209E-20	2.89587E-16		ol1a1/Emilin1/Col20a1/Postn/Col4a1/Co
CC	GO:0031012		34/260	362/19943	1.5476E-19	3.60906E-16		Col13a1/Col1a1/Emilin1/Col20a1/Postn/C
CC CC	GO:0044420 GO:0005581	extracellular matrix component collagen trimer	12/260 12/260	51/19943 68/19943	1.8918E-12 7.132E-11	2.20582E-09 5.54397E-08		col1a1/Emilin1/Col4a1/Col4a2/Col18a1// col13a1/Col1a1/Emilin1/C1gc/Col4a1/Co
CC	GO:0005504	basement membrane	12/260	105/19943	9.2179E-11	6.14175E-08		col4a1/Col7a1/Col4a2/Col15a1/LOC1083
cc	GO:0098651		5/260	7/19943	7.4515E-09	3.15944E-06		col4a1/Col4a2/Col18a1/Col4a5/Col4a6
CC	GO:0005587	collagen type IV trimer	4/260	6/19943	4.1488E-07	6.91068E-05		ol4a1/Col4a2/Col4a5/Col4a6
CC	GO:0098642	network-forming collagen trimer	4/260	6/19943	4.1488E-07	6.91068E-05		ol4a1/Col4a2/Col4a5/Col4a6
CC	GO:0098645	collagen network	4/260	6/19943	4.1488E-07	6.91068E-05	5.8348E-05 C	col4a1/Col4a2/Col4a5/Col4a6
CC	GO:0098644		5/260	16/19943	1.4076E-06	0.000164131		ol1a1/Col4a1/Col4a2/Col4a5/Col4a6
CC	GO:0034358	plasma lipoprotein particle	4/260	28/19943	0.00045175	0.016659081		Ptp/Apoc4/Apoc1/Lsr
CC	GO:1990777	lipoprotein particle	4/260	28/19943	0.00045175	0.016659081		ltp/Apoc4/Apoc1/Lsr
CC	GO:0032994	protein-lipid complex	4/260	30/19943	0.00059242	0.01866921		ltp/Apoc4/Apoc1/Lsr
CC	GO:0034361		3/260	17/19943	0.00130099	0.029313139		Apoc4/Apoc1/Lsr
CC	GO:0034385 GO:0016942	triglyceride-rich plasma lipoprotein parti		17/19943 5/19943	0.00130099	0.029313139 0.034505856	0.02474958 A 0.02913388 Ig	Apoc4/Apoc1/Lsr #Bun3/l#Bun6
CC	GO:0016942 GO:0036454	insulin-like growth factor binding protein growth factor complex	2/260	5/19943	0.00164983	0.034505856	0.02913388 0	
cc	GO:0036454 GO:0031091		3/260	5/19945 19/19943	0.00184985	0.034505856	0.02913388 (	
CC	GO:0042629	mast cell granule	3/260	20/19943	0.00211901	0.040339034		at/Srgn/Anxa1
CC	GO:0009897	external side of plasma membrane	13/260	399/19943	0.00233918	0.04334457		d8a/Enpp3/Scart1/Folr2/Tir8/RT1-M2/S
CC	GO:0034364	high-density lipoprotein particle	3/260	21/19943	0.00244853	0.04334457		htp/Apoc4/Apoc1
MF	GO:0005201	extracellular matrix structural constituer		62/19943	4.8072E-14	7.47359E-11	6.3101E-11 C	col13a1/Col1a1/Emilin1/Col4a1/Col4a2/C
MF	GO:0005178	integrin binding	11/260	129/19943	1.0261E-06	0.00012934		ap/Emilin1/Dab2/Spp1/Tspan8/Mmp14/
MF	GO:0005520	insulin-like growth factor binding	6/260	28/19943	1.3726E-06	0.000164131		ltra3/lgfbp3/lgfbp7/Ccn2/lgfbp2/lgfbp6
MF	GO:0050839	cell adhesion molecule binding	14/260	232/19943	2.3268E-06	0.00025838		ap/Emilin1/Postn/Adam8/Dab2/Spp1/Ts
MF	GO:0038024		9/260	89/19943	2.4269E-06	0.000263237		//sr1/Enpp3/Mrc1/Stab1/Scart1/Folr2/Dz
MF	GO:0019838 GO:0005539	growth factor binding	11/260 13/260	146/19943 209/19943	3.4733E-06 3.85E-06	0.000352162 0.000382053		Col1a1/Htra3/Ltbp2/Col4a1/Igfbp3/Igfbp Col1a1/Ltbp3/Pacts/Stab1/Abi3bp/Pack
MF	GO:0005539 GO:0008201	glycosaminoglycan binding heparin binding	13/260	209/19943	3.85E-06 4.1684E-05	0.000382053		Col13a1/Ltbp2/Postn/Stab1/Abi3bp/Prelp Col13a1/Ltbp2/Postn/Abi3bp/Prelp/Fn1/4
ME	GO:0008201 GO:0001968	fibronectin binding	5/260	33/19943	4.1684E-05 6.3808E-05	0.002901711		rrc15/lgfbp3/Fbln1/Ccn2/lgfbp6
MF	GO:0004022	alcohol dehydrogenase (NAD) activity	3/260	8/19943	0.00011687	0.006124583		Adh1/Adh6/Dhrs9
MF	GO:0031995	insulin-like growth factor II binding	3/260	8/19943	0.00011687	0.006124583		gfbp3/lgfbp2/lgfbp6
MF	GO:0031994	insulin-like growth factor I binding	3/260	12/19943	0.00044171	0.016659081		gfbp3/lgfbp2/lgfbp6
MF	GO:0005044	scavenger receptor activity	5/260	51/19943	0.00052179	0.017695218	0.01494037 N	/lsr1/Enpp3/Stab1/Scart1/Scarf2
MF	GO:0016918	retinal binding	3/260	13/19943	0.0005687	0.018502485	0.01562196 5	tra6/Akr1b10/Rbp1
MF	GO:0005501	retinoid binding	4/260	31/19943	0.00067327	0.020658819		tra6/Akr1b10/Rbp1/Ptgds
MF	GO:0030246	carbohydrate binding	11/260	271/19943	0.0009015	0.023621422		ol20a1/Enpp3/Mrc1/Siglec1/Hk3/Clec4a
MF	GO:0050840 GO:0019840	extracellular matrix binding isoprenoid binding	5/260 4/260	61/19943 37/19943	0.00118903 0.0013293	0.028439058 0.02966441		rrc15/Spp1/Sdc1/Nid1/Eln itra6/Akr1b10/Rbp1/Ptgds
ME	GO:0019840 GO:1901681	isoprenoid binding sulfur compound binding	4/260	37/19943 250/19943	0.0013293	0.02966441 0.03515851		itra6/Akr1b10/Rbp1/Ptgds col13a1/Ltbp2/Postn/Abi3bp/Prelp/Fn1/4
MF	GO:1901681 GO:0004745	sulfur compound binding retinol dehydrogenase activity	3/260	250/19943 20/19943	0.00170365	0.03515851 0.040339034		.ol13a1/Ltbp2/Postn/Abi3bp/Prelp/Fn1/4 Adh1/Adh6/Dhrs9
ME	GO:0004024	alcohol dehydrogenase activity, zinc-dep		6/19943	0.00245347	0.04334457	0.03659656 A	
MF	GO:0032027	myosin light chain binding	2/260	6/19943	0.00245347	0.04334457	0.03659656	
MF	GO:0005518		5/260	72/19943	0.00249067	0.043835759	0.03701128 L	rrc15/Srgn/Abi3bp/Nid1/Ecm2
		-						

Repressed	genes_KEGG							
ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	genelD	Count
rno04512	ECM-receptor interaction	9/92	74/6610	6.93784E-07	7.3541E-05		Col1a1/Col4a1/Col4a2/Spp1/Sdc1/Lama2/Fn1/Col	
rno04974	Protein digestion and absorption	8/92	78/6610	1.09418E-05	0.00057992	0.00052981	Col1a1/Sic7a7/Col4a1/Col4a2/Col15a1/Col18a1/C	1
rno04610	Complement and coagulation cascades	6/92	69/6610	0.000365571	0.01121097	0.0102424	Plau/C1qc/Cfd/C5ar1/F5/C7	
rno05146	Amoebiasis	7/92	99/6610	0.000423055	0.01121097	0.0102424	Col1a1/Col4a1/Col4a2/Lama2/Fn1/Serpinb1a/Col-	4
rno05222	Small cell lung cancer	6/92	84/6610	0.001049059	0.02224005	0.02031862	Col4a1/Col4a2/Ptgs2/Lama2/Fn1/Col4a5	

NTOLOGY	ID	Description	GeneRatio		pvalue	p.adjust 9.47E-30	qvalue genelD
P		neurotransmitter transport synaptic vesicle cycle	51/373 44/373	322/19943 243/19943	2.17E-32 1.46E-30	9.47E-30 5.78E-28	7.3752E-30 Cpix1/Grm4/Rph3a/Nsf/Napb/Syt2/Cadps2/Drd2/Cadps/Ncs1/Syr 4.5005E-28 Cpix1/Grm4/Rapgef4/Napb/Syt2/Cadps2/Drd2/Cadps/Ncs1/Syn1/
-		neurotransmitter secretion	41/373	204/19943	2.02E-30	6.77E-28	5.2716E-28 Cpix1/Grm4/Rph3a/Nsf/Napb/Syt2/Cadps2/Drd2/Cadps/Ncs1/Syr
,	GO:0099643	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
•		regulation of neurotransmitter levels	53/373	402/19943	1.45E-29	3.32E-27	2.5819E-27 Cplx1/Grm4/Rph3a/Tph2/Nsf/Napb/Syt2/Cadps2/Drd2/Cadps/Nc
•	GO:0042391	regulation of membrane potential	56/373	464/19943	3.31E-29	7.21E-27	5.6151E-27 Rapgef4/Fgf12/Gabrg2/Glra2/Gabra1/Scn8a/Cacng2/Gjd2/Oprd1/
,		synaptic vesicle localization	39/373	201/19943	2.31E-28	4.46E-26	3.4711E-26 Cplx1/Grm4/Napb/Syt2/Kif5a/Cadps2/Drd2/Cadps/Ncs1/Syn1/Rin
		vesicle-mediated transport in synapse	43/373 54/373	262/19943	4.77E-28	8.66E-26	6.7395E-26 Cplx1/Grm4/Napb/Syt2/Kif5a/Hpca/Cadps2/Drd2/Cadps/Ncs1/Rir
,		synapse organization synaptic vesicle transport	54/3/3 37/373	470/19943 190/19943	4.2E-27 5.18E-27	6.53E-25 7.52E-25	5.0866E-25 Cabp1/Rph3a/Rapgef4/Gabrg2/Gira2/Gabra1/Arhgap44/Nptx1/Lr 5.8526E-25 Cplx1/Grm4/Napb/Syt2/Kif5a/Cadps2/Drd2/Cadps/Ncs1/Rims1/C
		establishment of synaptic vesicle localiza		190/19943	5.18E-27	7.52E-25 7.52E-25	5.8526E-25 Cpix1/Grm4/Napb/Syt2/Kif5a/Cadps2/Drd2/Cadps/Ncs1/Rims1/Ci 5.8526E-25 Cpix1/Grm4/Napb/Syt2/Kif5a/Cadps2/Drd2/Cadps/Ncs1/Rims1/Ci
		synaptic vesicle exocytosis	34/373	153/19943	6.4E-27	8.99E-25	7.0017E-25 Cplx1/Grm4/Napb/Svt2/Cadps2/Drd2/Cadps/Ncs1/Rims1/Chrna4,
,		regulation of neurotransmitter secretion		148/19943	3.29E-26	4.1E-24	3.1936E-24 Cplx1/Grm4/Napb/Syt2/Drd2/Ncs1/Rims1/Chrna4/Stx1b/Vamp1/
Þ		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:
2	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
,	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:
3		regulation of neurotransmitter transport		190/19943	9.61E-25	9.97E-23	7.7646E-23 Cpix1/Grm4/Napb/Syt2/Drd2/Ncs1/Rims1/Chrna4/Stx1b/Vamp1/
		regulation of calcium ion-dependent exc		151/19943 118/19943	1.05E-24 1.84E-24	1.06E-22 1.67E-22	8.2622E-23 Cplx1/Grm4/Napb/Syt2/Drd2/Cadps/Ncs1/Rims1/Chrna4/Stx1b/V
2	GO:1902805	regulation of synaptic vesicle transport vesicle localization	41/373	288/19943	2.61E-24	2.32E-22	1.2979E-22 Cplx1/Grm4/Napb/Syt2/Drd2/Ncs1/Rims1/Chrna4/Stx1b/Vamp1/ 1.8091E-22 Cplx1/Grm4/Napb/Syt2/Kif5a/Cadps2/Drd2/Cadps/Ncs1/Dync1i1/
		regulation of synaptic vesicle cycle	32/373	157/19943	3.81E-24	3.32E-22	2.586E-22 Cplx1/Grm4/Rapgef4/Napb/Syt2/Drd2/Ncs1/Syn1/Rims1/Chrna4/
		regulation of synaptic vesicle exocytosis		114/19943	1.19E-23	1.02E-21	7.94E-22 Cplx1/Grm4/Napb/Syt2/Drd2/Ncs1/Rims1/Chrna4/Stx1b/Vamp1/
1	GO:0006887	exocytosis	46/373	391/19943	1.35E-23	1.13E-21	8.7801E-22 Cplx1/Grm4/Rapgef4/Arhgap44/Nsf/Napb/Syt2/Vsnl1/Cadps2/Dri
		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/Dync1i1/
,	GO:0017157	regulation of exocytosis	37/373	263/19943	7.68E-22	5.77E-20	4.4914E-20 Cplx1/Grm4/Rapgef4/Nsf/Napb/Syt2/Vsnl1/Cadps2/Drd2/Cadps/f
1		regulation of regulated secretory pathwa	32/373	204/19943	1.72E-20	1.25E-18	9.744E-19 Cplx1/Grm4/Napb/Syt2/Drd2/Cadps/Ncs1/Rims1/Chrna4/Stx1b/V
		potassium ion transport	33/373 45/373	244/19943 489/19943	4.73E-19 8.45E-19	3.27E-17 5.75E-17	2.5484E-17 Nsf/Kcnj3/Slc24a2/Drd2/Kcnab3/Kcns2/Kcnab2/Slc12a5/Kcna2/Kc 4.42655.17 Calut (Cart & Nach (Sub2) (Kiffs (Cadad 2) Drd2) (Cadad (Nach
1	GO-0060070	establishment of organelle localization regulation of postsynaptic membrane po		489/19943	8.45E-19 1.31E-17	5.75E-17 8.54E-16	4.4795E-17 Cplx1/Grm4/Napb/Syt2/Kif5a/Cadps2/Drd2/Cadps/Nefh/Ncs1/Dy 6.6471E-16 Gabrg2/Glra2/Gabra1/Gabra5/Rims1/Chrna4/Grin1/Rgs7bp/Glra1
,		cellular potassium ion transport	29/373	212/19943	5.16E-17	3.21E-15	2.5024E-15 Kcnj3/Kcnab3/Kcns2/Kcnab2/Slc12a5/Kcna2/Kcnc3/Atp1a3/Rgs7/
		potassium ion transmembrane transport		212/19943	5.16E-17	3.21E-15	2.5024E-15 Kcnj3/Kcnab3/Kcns2/Kcnab2/Sic12a5/Kcna2/Kcnc3/Atp1a3/Rgs7/
P	GO:0007416	synapse assembly	26/373	184/19943	1E-15	5.9E-14	4.5944E-14 Gabrg2/Glra2/Gabra1/Nptx1/Lrfn5/Drd2/Slitrk3/Clstn3/Grin1/Syn
,	GO:0035418	protein localization to synapse	19/373	86/19943	1.62E-15	9.41E-14	7.329E-14 Cplx1/Rapgef4/Arhgap44/Nptx1/Kif5a/Cacng2/Clstn3/Grin1/Cacn
	GO:1904062	regulation of cation transmembrane tran	34/373	355/19943	5.95E-15	3.32E-13	2.5881E-13 Cabp1/Rph3a/Fgf12/Cacng2/Thy1/Hpca/Drd2/Chrna4/Kcns2/Kcna
		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/
		regulation of cation channel activity	24/373 21/373	175/19943 134/19943	2.58E-14 7.47E-14	1.37E-12 3.72E-12	1.0686E-12 Cabp1/Rph3a/Fgf12/Cacng2/Hpca/Drd2/Chrna4/Kcns2/Cacng3/R: 2.894E-12 Fgf12/Rbfox1/Scn8a/Drd2/Kcnab2/Grin1/Gira1/Nefl/Atp2b2/Cam
2	GO:0050905	neuromuscular process adult behavior	21/3/3 24/373	134/19943	1.47E-14	3.72E-12 7.1E-12	2.894E-12 Fgf12/Rbfox1/Scn8a/Drd2/Kcnab2/Grin1/Gira1/Nefl/Atp2b2/Cam 5.5298E-12 Fgf12/Gabrg2/Scn8a/Drd2/Oprd1/Chrna4/Grin1/Gira1/Crhbp/Atp
-		action potential	24/5/5 21/373	139/19943	1.47E-13 1.58E-13	7.55E-12	5.8749E-12 Rapgef4/Fgf12/Scn8a/Gjd2/Chrna4/Gira1/Ryr2/Kcna2/Scn4b/Dpp
-		regulation of ion transmembrane transp		260/19943	5.97E-13	2.63E-11	2.0473E-11 Cabp1/Rph3a/Fgf12/Cacne2/Hpca/Drd2/Chrna4/Kcns2/Cacne3/Re
,	GO:0050890		31/373	351/19943	8.64E-13	3.73E-11	2.9014E-11 Grm4/Tafa2/Slc24a2/Drd2/Gabra5/Chrna4/Grin1/Ndrg4/Slc12a5/
,	GO:0050806	positive regulation of synaptic transmiss	29/373	308/19943	9.8E-13	4.15E-11	3.2291E-11 Syt2/Cacng2/Slc24a2/Drd2/Rims1/Clstn3/Grin1/Cacng3/Car7/Call
<b>b</b>		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
,		regulation of transmembrane transporte		268/19943	1.23E-12	5.12E-11	3.9877E-11 Cabp1/Rph3a/Fgf12/Cacng2/Hpca/Drd2/Chrna4/Kcns2/Cacng3/Ra
		protein localization to postsynaptic men		56/19943	1.43E-12	5.89E-11	4.5869E-11 Cplx1/Rapgef4/Arhgap44/Nptx1/Cacng2/Grin1/Cacng3/Stx1b/Grij
P	GO:0099072	regulation of postsynaptic membrane ne	17/373	97/19943 278/19943	2.83E-12 2.94E-12	1.13E-10	8.7951E-11 Cplx1/Rapgef4/Arhgap44/Nptx1/Cacng2/Hpca/Cacng3/Stx1b/Pac
, ,	GO:0032409	regulation of transporter activity receptor localization to synapse	15/373	278/19943 71/19943	2.94E-12 3.2E-12	1.1/E-10 1.25E-10	9.0822E-11 Cabp1/Rph3a/Fgf12/Cacng2/Hpca/Drd2/Chrna4/Kcns2/Cacng3/R; 9.7045E-11 Colx1/Rapgef4/Arhgap44/Nptx1/Kif5a/Cacng2/Cacng3/Stx1b/Grip
, ,		learning or memory	28/373	314/19943	9.1E-12	3.48E-10	2.7045c-11 Cpix1/Rapgel4/Arngap44/Npix1/Kii5a/Cachg2/Cachg5/Stx10/Grip 2.7068E-10 Grm4/Tafa2/Sic24a2/Drd2/Gabra5/Grin1/Ndrg4/Sic12a5/Ato1a3/
P		synaptic vesicle priming	10/373	25/19943	1.18E-11	4.48E-10	3.4903E-10 Napb/Cadps2/Cadps/Rims1/Stx1b/Vamp1/Rab3a/Rims2/Erc2/Unc
Р		transmission of nerve impulse	16/373	93/19943	1.67E-11	6.29E-10	4.8985E-10 Rapgef4/Fgf12/Scn8a/Cacng2/Cacng3/Gira1/Kcna2/Dpp6/Scn1a/k
Р	GO:0048167	regulation of synaptic plasticity	28/373	327/19943	2.39E-11	8.9E-10	6.9284E-10 Cabp1/Slc24a2/Drd2/Rims1/Grin1/Rasgrf1/Calb2/Syt12/Rab3a/At
Р		synaptic transmission, GABAergic	13/373	56/19943	2.54E-11	9.4E-10	7.3162E-10 Phf24/Grm4/Gabrg2/Gabra1/Drd2/Gabra5/Clstn3/Cntnap4/Car7/
P	GO:1990778	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
P P	GO:0035637	multicellular organismal signaling	19/373 32/373	147/19943 433/19943	3.87E-11 4.17E-11	1.39E-09 1.49E-09	1.0843E-09 Rapgef4/Fgf12/Scn8a/Cacng2/Cacng3/Gira1/Ryr2/Kcna2/Scn4b/D
P		regulation of metal ion transport neuronal action potential	12/373	433/19943	4.1/E-11 5.84E-11	2.04E-09	1.1606E-09 Cabp1/Fgf12/Thy1/Hpca/Drd2/Oprd1/Kcns2/Kcnab2/Grin1/Hecw: 1.5854E-09 Rapgef4/Fgf12/Scn8a/Kcna2/Dpp6/Scn1a/Kcna1/Scn2a/Kcnma1/S
P		locomotory behavior	24/373	250/19943	6.28E-11	2.04E-09 2.16E-09	<ol> <li>1.5054E-09 Rapger4/FgT12/Schoa/Rcha2/Dpp0/Sch1a/Rcha1/Sch2a/Rchma1/S 1.678E-09 Fgf12/Sch8a/Drd2/Oprd1/Chrna4/Grin1/Glra1/Grm1/Atp1a3/Sez6</li> </ol>
		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
>			16/373	103/19943	8.33E-11	2.79E-09	2.1718E-09 Grm4/Rph3a/Cacng2/Grin1/Cacng3/Rasgrf1/Grm1/Crhbp/Atp1a3
P	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/Gri
P	GO:0099565	chemical synaptic transmission, postsyn		120/19943	9.61E-11	3.15E+09	2.4502E-09 Glra2/Rims1/Chrna4/Grin1/Glra1/Stx1b/Mapk8ip2/Cbln1/Grip2/R
Р	GO:0007613		19/373	156/19943	1.1E-10	3.59E-09	2.795E-09 Tafa2/Slc24a2/Drd2/Grin1/Atp1a3/Jph3/Adcy1/Hrh3/Scn2a/Grin2
Р	GO:0031644	regulation of neurological system proces		177/19943	1.4E-10	4.51E-09	3.5129E-09 Rapgef4/Fgf12/Nptx1/Oprd1/Rims1/Chrna4/Grin1/Glra1/Grm1/St
P	GO:0007612		20/373	179/19943	1.71E-10	5.45E-09	4.2433E-09 Grm4/Tafa2/Slc24a2/Drd2/Gabra5/Grin1/Ndrg4/Slc12a5/Atp1a3/
P		amine transport	17/373	127/19943	2.39E-10	7.56E-09	5.8872E-09 Syt2/Drd2/Chrna4/Grm1/Kcna2/Syt12/Htr2c/Nat8l/Chga/Pcp4/Dc
P P		calcium ion transmembrane transport	26/373 16/373	314/19943 111/19943	2.62E-10 2.64E-10	8.23E-09 8.23E-09	6.4042E-09 Cabp1/Cacng2/Thv1/Hpca/Slc24a2/Drd2/Ncs1/Grin1/Cacng3/Ryri 6.4042E-09 Glra2/Rims1/Chrna4/Grin1/Glra1/Stx1b/Mapk8ip2/Cbln1/Grip2/R
P		excitatory postsynaptic potential divalent inorganic cation transport	16/3/3 33/373	497/19943	2.64E-10 3.37E-10	8.23E-09 1.03E-08	6.4042E-09 Gira2/Rims1/Chrna4/Grin1/Gira1/Stx1b/Mapk8ip2/Cbin1/Grip2/R 8.054E-09 Cabp1/Cacng2/Thy1/Hpca/Slc24a2/Drd2/Ncs1/Oprd1/Chrna4/Gri
P			13/373	68/19943	3.45E-10	1.05E-08	8.1833E-09 Rph3a/Nptx1/Lypd6b/Lynx1/Cacng2/Chrna4/Cacng3/Rasgrf1/Crhi
	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/Pex5I/Grin1/Dmtn.
Р	GO:0051480	regulation of cytosolic calcium ion conce	29/373	406/19943	7.84E-10	2.28E-08	1.7723E-08 Trhr/Thy1/Drd2/Ncs1/Gpr3/Hcrtr2/Grin1/Hcrtr1/Grm1/Calb2/Ryr
P	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/Gri
Р		regulation of amine transport	16/373	123/19943	1.25E-09	3.59E-08	2.792E-08 Syt2/Drd2/Chrna4/Grm1/Kcna2/Syt12/Htr2c/Nat8i/Chga/Pcp4/Hr
P		catecholamine secretion	13/373	78/19943	2.05E-09	5.8E-08	4.5122E-08 Syt2/Drd2/Cadps/Chrna4/Kcna2/Syt12/Chga/Pcp4/Hrh3/Htr2a/Ch
P P			22/373 14/373	250/19943 94/19943	2.08E-09 2.26E-09	5.85E-08 6.32E-08	4.5549E-08 Cplx1/Rapgef4/Arhgap44/Nptx1/Kif5a/Cacng2/Hpca/Cacng3/Stx1 4.9194E-08 Svt2/Drd2/Cadps/Chrna4/Kcna2/Svt12/Nat8I/Chga/Pcp4/Hrh3/Ht
P		catecholamine transport regulation of potassium ion transport	14/373 15/373	94/19943 113/19943	2.26E-09 3.11E-09	6.32E-08 8.63E-08	4.9194E-08 Syt2/Drd2/Cadps/Chrna4/Kcna2/Syt12/Nat8i/Chga/Pcp4/Hrh3/Ht 6.7213E-08 Drd2/Kcns2/Kcnab2/Rgs7/Dpp6/Kcnip4/Kcnc1/Kcnab1/Kcna1/Dpp
P		regulation of potassium ion transport modulation of excitatory postsynaptic po		53/19943	3.11E-09 3.19E-09	8.8E-08	6.8529E-08 Rims1/Chrna4/Grin1/Stx1b/Cbln1/Grip2/Rims2/Chrna7/Neto1/Ce
>	GO:0050803	regulation of synapse structure or activit	23/373	280/19943	3.38E-09	9.26E-08	7.2107E-08 Rapgef4/Arhgap44/Nptx1/Lrfn5/Drd2/Slitrk3/Clstn3/Cntnap4/Grir
,	GO:0043270	positive regulation of ion transport	25/373	333/19943	4.4E-09	1.18E-07	9.2167E-08 Fgf12/Cacng2/Thy1/Drd2/Chrna4/Grin1/Cacng3/Ryr2/Rgs7/Scn4b
Þ	GO:0051899	membrane depolarization	13/373	83/19943	4.52E-09	1.2E-07	9.3428E-08 Fgf12/Scn8a/Cacng2/Chrna4/Grm1/Scn4b/Scn1a/Scn2a/Scn9a/Ch
•	GO:0050433	regulation of catecholamine secretion	12/373	74/19943	1.19E-08	3.03E-07	2.3578E-07 Syt2/Drd2/Chrna4/Kcna2/Syt12/Chga/Pcp4/Hrh3/Htr2a/Chrna7/C
	GO:0016358	dendrite development	23/373	301/19943	1.33E-08	3.38E-07	2.6288E-07 Rapgef4/Mcf2/Arhgap44/Grin1/Hecw1/Slc12a5/RGD1307443/Ma
1		regulation of potassium ion transmembr		91/19943	1.43E-08	3.59E-07	2.7913E-07 Kcns2/Kcnab2/Rgs7/Dpp6/Kcnip4/Kcnc1/Kcnab1/Kcna1/Dpp10/Al
	GO:0008344	adult locomotory behavior	14/373 14/373	108/19943 110/19943	1.43E-08 1.82E-08	3.59E-07 4.53E-07	2.7913E-07 Fgf12/Scn8a/Drd2/Oprd1/Grin1/Gira1/Atp1a3/Sez6i2/Scn1a/Kcnn 2.57255.07 Sut3 (Drd2/Codes (/hrss2/Krn23/Sut32/kl)t2) (/htp2/kl)
2	GO:0015844	monoamine transport		110/19943 78/19943	1.82E-08 2.2E-08	4.53E-07 5.45E-07	3.5275E-07 Syt2/Drd2/Cadps/Chrna4/Kcna2/Syt12/Nat8l/Chga/Pcp4/Hrh3/Ht 4.32945.07 Drd2/Pimc1/Crin1/Pacert1/Pab2a/Camk2b/Syn/Camk2a/Inb3/Cri
2	60:0007214	regulation of neuronal synaptic plasticity gamma-aminobutyric acid signaling path	2/373	/8/19943 27/19943	2.2E-08 2.26E-08	5.45E-07 5.57E-07	4.2394E-07 Drd2/Rims1/Grin1/Rasgrf1/Rab3a/Camk2b/Syp/Camk2a/Jph3/Gri 4.3338E-07 Phf24/Gabrg2/Gabra1/Gabra5/Gabra3/Gabbr2/Htr4/Gabrb3
P	GO:0019233	sensory perception of pain	16/373	27/19945	3.33E-08	5.57E-07 8.16E-07	6.3554E-07 Phf24/Oprd1/Chrna4/Grin1/Grm1/Kcna2/Htr2c/Scn1a/Kcna1/Cac
-		regulation of synaptic vesicle fusion to p		12/19943	3.46E-08	8.41E-07	6.5498E-07 Cplx1/Syt2/Rims1/Vamp1/Rab3a/Syt7
-	GO:0050807	regulation of synapse organization	21/373	270/19943	4.25E-08	1.03E-06	7.9801E-07 Rapgef4/Arhgap44/Nptx1/Lrfn5/Drd2/Slitrk3/Clstn3/Cntnap4/Grir
•	GO:0099632	protein transport within plasma membra		30/19943	5.68E-08	1.34E-06	1.0408E-06 Cplx1/Arhgap44/Cacng2/Cacng3/Stx1b/Grip2/Mapk10/Lrrc7
	GO:0099637	neurotransmitter receptor transport	8/373	30/19943	5.68E-08	1.34E-06	1.0408E-06 Cplx1/Arhgap44/Cacng2/Cacng3/Stx1b/Grip2/Mapk10/Lrrc7
Р		sodium ion transport	18/373	208/19943	8E-08	1.86E-06	1.4509E-06 Fgf12/Scn8a/Slc24a2/Drd2/Slc5a7/Hecw1/Slc17a6/Atp1a3/Scn4b/
P				57/19943	9.18E-08	2.12E-06	1.6472E-06 Rph3a/Cacng2/Cacng3/Rasgrf1/Crhbp/Mapk8ip2/Necab2/Neto1/
P	GO:1900449	regulation of glutamate receptor signaling	10/3/3				1.04722-00 hphos/cacigo/hasbit/cacigo/hasbit/hacabi/hacabi/
P	GO:1900449 GO:0035249	regulation of glutamate receptor signalir synaptic transmission, glutamatergic feeding behavior	10/3/3 13/373 14/373	107/19943 128/19943	1.03E-07 1.27E-07	2.37E-06 2.9E-06	1.8432E-06 Grm4/Napb/Cacng2/Drd2/Clstn3/Grin1/Cacng3/Grm1/Slc17a6/M 2.2575E-06 Drd2/Oprd1/Hctr2//rin1/Hctr2/Atp8a2/Mrap2/Hrh3/Sgi

BP BP BP								
	GO:0031629	synaptic vesicle fusion to presynaptic act	7/373	23/19943	1.43E-07	3.24E-06	2.5198E-06	Cplx1/Syt2/Rims1/Stx1b/Vamp1/Rab3a/Syt7
	GO:0014046		9/373	46/19943	1.52E-07	3.4E-06	2.6469E-06	Syt2/Drd2/Chrna4/Kcna2/Syt12/Pcp4/Htr2a/Chrnb2/Syt7
			9/373	46/19943	1.52E-07	3.4E-06	2.6469E-06	Syt2/Drd2/Chrna4/Kcna2/Syt12/Pcp4/Htr2a/Chrnb2/Syt7
BP	GO:0015696		14/373	131/19943	1.7E-07	3.78E-06	2.9436E-06	Syt2/Drd2/Slc5a7/Chrna4/Slc12a5/Kena2/Syt12/Htr2c/Nat8l/Pep4
BP	GO:0015872		10/373	61/19943	1.79E-07	3.97E-06	3.0879E-06	Syt2/Drd2/Chrna4/Kcna2/Syt12/Nat8I/Pcp4/Htr2a/Chrnb2/Syt7
BP			7/373	24/19943	1.99E-07	4.38E-06	3.4121E-06	Cplx1/Syt2/Rims1/Stx1b/Vamp1/Rab3a/Syt7
BP BP			10/373 16/373	63/19943 178/19943	2.46E-07 2.52E-07	5.36E-06 5.46E-06	4.175-06	Nsf/Rims1/Rab3c/Ndrg4/Stx1b/Rab3a/Camk2a/Rims2/Unc13c/Sp
BP			6/373	16/19943	2.32E-07 2.81E-07	6.06E-06	4.23592-00	Tph2/Syt2/Cacng2/Hpca/Grin1/Dmtn/Ryr2/Gpld1/Crhbp/Syt12/Cl Rims1/Stx1b/Camk2a/Rims2/Unc13c/Sptbn2
BP		positive regulation of neurological system		81/19943	3.18E-07	6.83E-06		Rapgef4/Rims1/Grin1/Stx1b/Grip2/Rims2/Nrg1/Chrna7/Neto1/Op
BP		positive regulation of excitatory postsyn		37/19943	3.34E-07	7.1E-06	5.5261E-06	Rims1/Grin1/Stx1b/Grip2/Rims2/Chrna7/Neto1/Shank1
BP	GO:0099173	postsynapse organization	17/373	205/19943	3.39E-07	7.16E-06	5.5752E-06	Rph3a/Rapgef4/Arhgap44/Nptx1/Grin1/Nefl/Ina/Zfp804a/Camk2ł
BP			8/373	39/19943	5.15E-07	1.05E-05		Cplx1/Arhgap44/Cacng2/Cacng3/Stx1b/Grip2/Mapk10/Lrrc7
BP		neurofilament cytoskeleton organization		10/19943	5.2E-07	1.06E-05	8.2416E-06	Nefh/Nefl/Nefm/Ina/Atp8a2
BP	GO:0060359	response to ammonium ion	16/373	189/19943	5.69E-07	1.15E-05	8.9817E-06	Gabrg2/Gabra1/Drd2/Nefh/Chrna4/Grin1/Crhbp/Chrm2/Tac3/Hrł
BP	GO:0140056	organelle localization by membrane teth	10/373	72/19943	8.88E-07	1.78E-05	1.3824E-05	Nsf/Rims1/Rab3c/Ndrg4/Stx1b/Rab3a/Camk2a/Rims2/Unc13c/Sp
BP	GO:0099505	regulation of presynaptic membrane pot	5/373	11/19943	9.38E-07	1.86E-05	1.4472E-05	Grin1/Kenc1/Kena1/SenZa/Kenma1
BP	GO:0008306	i associative learning	12/373	109/19943	9.43E-07	1.86E-05		Tafa2/Drd2/Gabra5/Grin1/Ndrg4/Atp1a3/Grin2b/Chrna7/Neto1/C
BP		protein localization to postsynaptic spec		30/19943	1.06E-06	2.07E-05		Rapgef4/Nptx1/Cacng2/Cacng3/Camk2a/Dig2/Adam22
BP		neurotransmitter receptor localization to		30/19943	1.06E-06	2.07E-05		Rapgef4/Nptx1/Cacng2/Cacng3/Camk2a/Dlg2/Adam22
BP BP		membrane depolarization during action	17/373	31/19943 227/19943	1.35E-06 1.41E-06	2.59E-05 2.7E-05		Scn8a/Scn4b/Scn1a/Scn2a/Scn9a/Cacna2d1/Cacna1i
BP			8/373	45/19943	1.41E-06 1.64E-06	2.7E-05 3.1E-05		Vsnl1/Camk1g/Hpca/Grin1/Dmtn/Grm1/Ryr2/Rit2/Tenm2/Necab; Scn8a/Drd2/Gira1/Scn1a/Kcnma1/Chat/Kihl1/Cend1
BP			7/373	43/19943 32/19943	1.7E-06	3.21E-05		Drd2/Grin1/Glra1/Kcna1/Kcnh1/Grin2b/Nrg1
BP			8/373	46/19943	1.95E-06	3.63E-05	2.30010-03	Rims1/Rab3c/Stx1b/Rab3a/Camk2a/Rims2/Unc13c/Sptbn2
BP	GO:0090659	walking behavior	8/373	47/19943	2.31E-06	4.25E-05	3.3072E-05	Scn8a/Drd2/Gira1/Scn1a/Kcnma1/Chat/Kihl1/Cend1
BP	GO:0098969	neurotransmitter receptor transport to p	6/373	22/19943	2.38E-06	4.34E-05	3.3804E-05	Cplx1/Arhgap44/Stx1b/Grip2/Mapk10/Lrrc7
BP			17/373	236/19943	2.4E-06	4.36E-05		Syt2/Drd2/Chrna4/Slc32a1/Slc17a6/Kcna2/Syt12/Htr2c/Slc6a5/Na
BP			7/373	34/19943	2.63E-06	4.72E-05		Lynx1/Slc5a7/Chrna4/Htr2c/Camk2b/Chrna7/Chrnb2
BP	GO:0071248		17/373	238/19943	2.7E-06	4.81E-05	3.7477E-05	Glra2/Nptx1/Tph2/Syt2/Hpca/Grin1/Dmtn/Glra1/Gpld1/Crhbp/Sy
BP		i membrane docking	10/373	82/19943	3E-06	5.3E-05		Nsf/Rims1/Rab3c/Ndrg4/Stx1b/Rab3a/Camk2a/Rims2/Unc13c/Sp
BP	GO:0098877	neurotransmitter receptor transport to p	6/373	23/19943	3.17E-06	5.55E-05	4.3209E-05	Cplx1/Arhgap44/Stx1b/Grip2/Mapk10/Lrrc7
BP	GO:1903540	l establishment of protein localization to p	6/373	23/19943	3.17E-06	5.55E-05	4.3209E-05	Cplx1/Arhgap44/Stx1b/Grip2/Mapk10/Lrrc7
BP	GO:0015850		18/373	270/19943	3.65E-06	6.34E-05	4.9339E-05	Syt2/Drd2/Cadps/Chrna4/Kcna2/Syt12/Nat8l/Chga/Pcp4/Hrh3/At
BP			14/373	172/19943	4.6E-06	7.89E-05 9 12E-05	6.1419E-05	Tph2/Drd2/Slc5a7/Asah2/Gpld1/Sncb/Atp2b2/Htr2c/Sgpp2/Ddc/C
BP	GO:0050885	neuromuscular process controlling balan	9/3/3 14/373	69/19943	5.36E-06	9.12E-05 9.5E-05	7.102E-05	Rbfox1/Nefl/Atp2b2/Camk2b/Jph3/Kcnma1/Camta1/Shank1/Pou
BP				175/19943 38/19943	5.62E-06	9.5E-05 9.75E-05		Thy1/Drd2/Grin1/Ryr2/Htr2c/Plch2/Jph3/Akap6/Grin2b/Htr2a/Prl
BP	GO:0048165	I regulation of long-term neuronal synapti I positive regulation of neurotransmitter t	0/272	53/19943 53/19943	5.8E-06	9.75E-05 9.9E-05		Drd2/Rims1/Grin1/Camk2b/Syp/Grin2b/Neto1 Syt2/Drd2/Rims1/Stx1b/Htr2c/Nat8I/Cacna1b/Syt7
BP			24/373	465/19943		0.000134		Nptx1/Kif5a/Cntn4/Thv1/Drd2/Nefh/Slitrk3/Grin1/Nefl/Nefm/Rab
BP		G protein-coupled receptor signaling pat	16/373	237/19943				Grm4/Lgr5/Drd2/Gpr3/Oprd1/Rit2/Htr2c/Chrm2/Chga/Mrap2/Gn
BP	GO:0032225	regulation of synaptic transmission, dop	5/373	17/19943				Drd2/Cntnap4/Nat8i/Chrna7/Chrnb2
BP		positive regulation of synaptic vesicle tra		17/19943		0.000188	0.00014613	Syt2/Rims1/Cacna1b/Map2/Syt7
BP	GO:0007204	positive regulation of cytosolic calcium ic	20/373	353/19943		0.000199	0.00015469	Trhr/Thy1/Drd2/Grin1/Grm1/Ryr2/Htr2c/Pich2/Jph3/Hrh3/Cacna1
BP	GO:0060401	cytosolic calcium ion transport	14/373	188/19943		0.000207	0.00016138	Thy1/Drd2/Grin1/Ryr2/Htr2c/Plch2/Jph3/Akap6/Grin2b/Htr2a/Prl
BP	GO:0071242		9/373	77/19943	1.34E-05	0.000216	0.00016808	Gabrg2/Gabra1/Chrna4/Crhbp/Chrm2/Hrh3/Chrna7/Chrnb2/Gabr
BP	GO:0019933	CAMP-mediated signaling	14/373	189/19943	1.36E-05	0.000219	0.00017011	Rapgef4/Lgr5/Drd2/Gpr3/Pex5I/Rit2/Gpr61/Chga/Mrap2/Gnas/Ac
BP			4/373	9/19943				Chrna4/Htr2c/Chrna7/Chrnb2
BP		. calcium ion-regulated exocytosis of neur		18/19943				Syt2/Rims1/Stx1b/Rims2/Syt7
BP			11/373		1.59E-05			Nptx1/Lrfn5/Slitrk3/Clstn3/Grin1/Syndig1/Cbln1/Lingo4/Slit1/Chrr
BP BP			11/373	120/19943 79/19943	1.59E-05 1.65E-05			Syt2/Drd2/Chrna4/Kcna2/Syt12/Htr2c/Nat8l/Pcp4/Htr2a/Chrnb2/
BP			9/373 15/373	/9/19943 221/19943			0.00020154	Gabrg2/Gira2/Gabra1/Gabra5/Gira1/Sic12a5/Gabra3/Sic12a3/Gal
BP	GO:0019935		10/373				0.00023211	Rapgef4/Lgr5/Drd2/Gpr3/Pex5l/Rit2/Gpr61/Htr2c/Chga/Mrap2/G Rph3a/Arhgap44/Grin1/Atp1a3/Zfp804a/Camk2b/Grin2b/Chrna7/
BP	60:0106027	i positive regulation of neurotransmitter s		31/19943		0.000316	0.00023861	Syt2/Rims1/Stx1b/Htr2c/Cacna1b/Syt7
BP			5/373	19/19943	2.04E-05		0.0002401	Cacng2/Kenma1/Kenq2/Trpc5/Hen1
BP	GO:0050773	regulation of dendrite development	14/373	198/19943		0.000349	0.00027192	Rapgef4/Arhgap44/Grin1/Hecw1/RGD1307443/Camk2b/Pacsin1/
BP			4/373	10/19943	2.31E-05			Napb/Rims1/Stx1b/Rab3a
BP	GO:0061669	spontaneous neurotransmitter secretion	4/373	10/19943	2.31E-05			Rph3a/Rims1/Stx1b/Rims2
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
BP		regulation of potassium ion transmembr		64/19943	2.47E-05	0.00037		Kcns2/Kcnc1/Kcnab1/Kcna1/Akap6/Neto1/Neto2/Kcng1
			6/373	32/19943	2.47E-05	0.00037		Syt2/Cadps/Rims1/Cacna1b/Syt7/Cacna1i
BP	GO:0045956	positive regulation of calcium ion-depen		371/19943	2.5E-05	0.000371	0.00028852	
BP BP	GO:0010976	positive regulation of neuron projection	20/373			0.0000778	0.00020052	Syt2/Serpini1/Rims1/Ndrg4/Nefl/Rit2/Zfp804a/Camk2b/Pacsin1/P
BP BP BP	GO:0010976 GO:0097553	i positive regulation of neuron projection calcium ion transmembrane import into	20/373 12/373	151/19943	2.79E-05	0.000411	0.00032025	Thy1/Drd2/Grin1/Ryr2/Htr2c/Plch2/Jph3/Akap6/Grin2b/Htr2a/Pri
BP BP BP BP	GO:0010976 GO:0097553 GO:0045921	i positive regulation of neuron projection calcium ion transmembrane import into positive regulation of exocytosis	20/373 12/373 10/373	151/19943 106/19943	3.01E-05	0.000411 0.00044	0.00032025 0.00034224	Thy1/Drd2/Grin1/Ryr2/Htr2c/Plch2/Jph3/Akap6/Grin2b/Htr2a/Prl Syt2/Vsnl1/Cadps2/Cadps/Ncs1/Rims1/Rab3a/Cacna1b/Syt7/Cacr
BP BP BP BP BP	GO:0010976 GO:0097553 GO:0045921 GO:0072659	i positive regulation of neuron projection calcium ion transmembrane import into positive regulation of exocytosis protein localization to plasma membrane	20/373 12/373 10/373 17/373	151/19943 106/19943 288/19943	3.01E-05 3.28E-05	0.000411 0.00044 0.000478	0.00032025 0.00034224 0.0003721	Thy1/Drd2/Grin1/Ryr2/Htr2c/Plch2/Jph3/Akap6/Grin2b/Htr2a/Prl Syt2/Vsnl1/Cadps2/Cadps/Ncs1/Rims1/Rab3a/Cacna1b/Syt7/Cacr Arhgap44/Nsf/Rab3c/Grm1/Epb4113/Ank1/Rab3a/Dpp6/Kcnip4/C
BP BP BP BP BP	GO:0010976 GO:0097553 GO:0045921 GO:0072655 GO:0048813	<ul> <li>positive regulation of neuron projection</li> <li>calcium ion transmembrane import into</li> <li>positive regulation of exocytosis</li> <li>protein localization to plasma membrane</li> <li>dendrite morphogenesis</li> </ul>	20/373 12/373 10/373 17/373 13/373	151/19943 106/19943 288/19943 180/19943	3.01E-05 3.28E-05 3.59E-05	0.000411 0.00044 0.000478 0.000513	0.00032025 0.00034224 0.0003721 0.00039917	Thy1/Drd2/Grin1/Ryr2/Htr2c/Pich2/Jph3/Akap6/Grin2b/Htr2a/Pri Syt2/Vsn1/Cadps2/Cadps/Ws1/Rim51/Rab3a/Cacna1b/Syt7/Cacr Arhgap44/Ws1/Rab3c/Grm1/Epb4113/Ank1/Rab3a/Dpp6/Kcnip4/C Arhgap44/Grin1/Hecw1/Mapk8ip2/Camk2b/Camk2a/Cit/Chrma7/i
ВР ВР ВР ВР ВР ВР	GO:0010976 GO:0097553 GO:0045921 GO:0072655 GO:0048813 GO:0050954	<ul> <li>positive regulation of neuron projection calcium ion transmembrane import into positive regulation of exocytosis</li> <li>protein localization to plasma membrane i dendrite morphogenesis</li> <li>sensory perception of mechanical stimul</li> </ul>	20/373 12/373 10/373 17/373 13/373 16/373	151/19943 106/19943 288/19943 180/19943 262/19943	3.01E-05 3.28E-05 3.59E-05 3.71E-05	0.000411 0.00044 0.000478 0.000513 0.000528	0.00032025 0.00034224 0.0003721 0.00039917 0.00041118	Thy J/DrdJ/GrinL/RryZ/HtrZc/PlchZ/Jph3/Akap6/GrinZb/HtrZa/Pri yct2/vn1/LGdap2/Cdao5/Ncs/JRmsJ/Rb3/Cacan2b/syT/Cacr Arhgap44/Nst/Rab3c/Grm1/Epb4113/Ank1/Rab3a/Dpp6/Kcnip4/C Arhgap44/Grin1/Hecw1/Mapk8ip2/CamkZb/CamkZa/Cit/Chrna7/I Pft2/5/cn83/Gabra/Shab3Actp2D2/Scn13/Kcna1/Strm4/Krmn1
BP BP BP BP BP BP BP BP	GO:0010976 GO:0097553 GO:0045921 GO:0072659 GO:0048813 GO:0050954 GO:0050954	positive regulation of neuron projection calcium ion transmembrane import into positive regulation of excorptosis protein localization to plasma membrane dendrite morphogenesis sensory perception of mechanical stimul positive regulation of cell projection orge	20/373 12/373 10/373 17/373 13/373 16/373 23/373	151/19943 106/19943 288/19943 180/19943 262/19943 478/19943	3.01E-05 3.28E-05 3.59E-05 3.71E-05 3.77E-05	0.000411 0.00044 0.000478 0.000513 0.000528 0.000535	0.00032025 0.00034224 0.0003721 0.00039917 0.00041118 0.00041649	ThruJLDraJLGriniLJRvr2/Htr2/PibcJ2/hpi3/Akap6/Grin2b/Htr2/Pir Svt2/Vsn11/Cadps2/Cadps/Ncs1/Rims1/Rab3a/Cacna1b/Svt7/Cacr Arhgpa4/Mt/Sta5/Crm1LjPab113/Ant1/Rab33/Dpb/Kcnip4/C Arhgpa4/dvfin1/Heew.J/MapsKbp2/Camk2b/Cark2a/CitVChrm37/ Phf24/Scn8a/Gabra5/Rab3a/Atp2b2/Scn1a/Kcna1/Srm4/Kcnma1 Svt2/Serpin1/Rims1/Gin1/Mtdg4/HevR(ht2/Temm2/ZpB04a/Cam
ВР ВР ВР ВР ВР ВР	GO:0010976 GO:0097553 GO:0045921 GO:0072659 GO:0048813 GO:0050954 GO:0050954 GO:0010970	positive regulation of neuron projection calcium ion transmembrane import into positive regulation of excorptosis protein localization to plasma membrane dendrite morphogenesis sensory perception of mechanical stimul positive regulation of cell projection orge	20/373 12/373 10/373 17/373 13/373 16/373 23/373 12/373	151/19943 106/19943 288/19943 180/19943 262/19943	3.01E-05 3.28E-05 3.59E-05 3.71E-05 3.77E-05 3.86E-05	0.000411 0.00044 0.000478 0.000513 0.000528 0.000535	0.00032025 0.00034224 0.0003721 0.00039917 0.00041118 0.00041649 0.00042342	Thy J/DrdJ/GrinL/RryZ/HtrZc/PlchZ/Jph3/Akap6/GrinZb/HtrZa/Pri yct2/vn1/LGdap2/Cdao5/Ncs/JRmsJ/Rb3/Cacan2b/syT/Cacr Arhgap44/Nst/Rab3c/Grm1/Epb4113/Ank1/Rab3a/Dpp6/Kcnip4/C Arhgap44/Grin1/Hecw1/Mapk8ip2/CamkZb/CamkZa/Cit/Chrna7/I Pft2/5/cn83/Gabra/Shab3Actp2D2/Scn13/Kcna1/Strm4/Krmn1
8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P	G0:0010976 G0:0097553 G0:0045921 G0:00726555 G0:0048813 G0:0050954 G0:0031346 G0:0010970 G0:0007188	positive regulation of neuron projection calcium ion transmembrane import into positive regulation of exocytoation positive regulation of exocytoation dendrite morphogenesis sensory perception of mechanical stimuli positive regulation of cell projection orgis transport along microtubule adenylate cyclase-modulating G protein- cellular response to calcium ion	20/373 12/373 10/373 17/373 13/373 16/373 23/373 12/373 12/373 14/373 9/373	151/19943 106/19943 288/19943 180/19943 262/19943 478/19943 156/19943 208/19943 88/19943	3.01E-05 3.28E-05 3.59E-05 3.71E-05 3.77E-05 3.86E-05 3.95E-05 3.96E-05	0.000411 0.00044 0.000513 0.000528 0.000528 0.000554 0.000554 0.000554	0.00032025 0.00034224 0.0003721 0.00039917 0.00041118 0.00041649 0.00042342 0.00043151 0.00043151	ThryL/Draf2/Grin1/Ryr2/Hrt2/Pibc2/Jp32/Akap6/Grin2b/Hrt2a/Pri Syt2/vniL/Gadgx/CadgyNcst/Bitms/Ab334/Canabl/Syt7/Car Arhgap44/Nst/Rab32/Grm1/EbA113/An1/Rab33/Dp65/Kcin4/C Arhgap44/Scin1/HeevJ/Mapk8ip2/Caml2b/Caml2a/Ct/Chm7/i Pf12/Scn8di Gabra3/Rab34/At2p23/Scn1a/Kcna1/Srm14/Kcima1 Syt2/Sepin1/Rim14/Grin1/Mdrg4/Net/Nit2/Tem72/2b804a/Cam Kifs/Netf/Upcr11/Net1/ef1/KcfKSagsp1/Map2/Map1b/01g2 Grm4/Lgf5/Drd2/Gar3/Opr14/Rit2/Chm72/Cpa8/Mrap2/Gna3/Adi Syt2/Pap2/Dm1/Syt2/Cpae4/Kcn15/Syt7
8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P	G0:0010976 G0:0097553 G0:0045921 G0:0072659 G0:0048813 G0:0050954 G0:0031348 G0:0010977 G0:0007188 G0:007188 G0:0071277 G0:0099111	positive regulation of neuron projection cialcuim ion transmembrane import into positive regulation of exocytosis protain localization to plasma membran- dentitre morphogenesis sensory perception of mechanical stimul positive regulation of call projection org transport along microtubule adenylate cyclase-modulating 6 protein- cellular response to calcium ion microtubule-based transport	20/373 12/373 10/373 17/373 13/373 16/373 23/373 12/373 14/373 9/373 12/373	151/19943 106/19943 288/19943 180/19943 262/19943 156/19943 208/19943 208/19943 157/19943	3.01E-05 3.28E-05 3.59E-05 3.71E-05 3.77E-05 3.86E-05 3.95E-05 3.96E-05 4.11E-05	0.000411 0.00044 0.000513 0.000528 0.000535 0.000544 0.000554 0.000554 0.000554	0.00032025 0.00034224 0.0003721 0.00039917 0.00041118 0.00041649 0.00042342 0.00043151 0.00043151	Thy L/Draf2/Grin1/Rry2/Hrt2/Pib2/Jp37A/kap6/Grin2/Hrt2/Pi 572/Sn1/LG92/Cdap5/Nc15/Hrt2/Ld92/Cdap5/Nc15/Hrt2/ Arhgap4/4/In1/Rab32/Com1/Epb113/An1/JRab33/Dop5/Kc104/C Arhgap4/4/In1/Hev1/Map8k9/ZC12mt2/Cant2/2C17L92/CV12/Hrt2/ Pit/25/Csta9/Gb12/Sn23/At222/2Sn13/Kcna1/Strm4/Kcnm1 Klf5a/Neft/Dync11/Neft/Neft/NC12Tom12/ZB043/Can Klf5a/Neft/Dync11/Neft/Neft/NC12Tom12/Cst04/Can Klf5a/Neft/Dync11/Neft/Neft/NC12Tom12/Cst04/Ac
8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P	G0:0010976 G0:0097553 G0:0045921 G0:0072655 G0:0048813 G0:0050954 G0:0013146 G0:0010970 G0:0007187 G0:0007187 G0:0099111 G0:0031338	positive regulation of neuron projection ciclium ion transmembrane import into positive regulation of exocytosis protein localization to plasma membran- dendrite morphogenesis sensory perception of mechanical stimul positive regulation of cell projection orgi transport along microtubule adenylate cyclase-modulating & protein- cellular response to calcium ion microtubule-based transport regulation of vesicle fusion	20/373 12/373 10/373 17/373 13/373 16/373 23/373 12/373 12/373 14/373 9/373 12/373 12/373	151/19943 106/19943 288/19943 262/19943 262/19943 156/19943 208/19943 157/19943 35/19943	3.01E-05 3.28E-05 3.59E-05 3.71E-05 3.77E-05 3.86E-05 3.95E-05 3.96E-05 4.11E-05 4.22E-05	0.000411 0.00044 0.000513 0.000528 0.000528 0.000554 0.000554 0.000554 0.000554 0.000554	0.00032025 0.00034224 0.0003721 0.00039917 0.00041118 0.00041654 0.00043151 0.00043151 0.00044654 0.00045582	ThryL/Draf2/Grin1/Ryr2/Hrt2/Pih2A/Jh3A/Akap6/Grin2b/Hrt2a/Pri SYt2/sniL/Gadgx/Cadgs/Ncst/Rins/Rab3a/Canal/Syt7/Car Arhgap4/dirin1/Heav.1/Aask8/JCarm2/Carm2/Cara/Sc/UrChma7/ Ph124/Scn8a/Gabra5/Rab3a/Atp2b2/Scn1a/Kcna1/Srm4/Kcnma1 Syt2/Senpin1/Rims1/Gini1/Moltg4/Ref/Rit2/Tenm2/2j8084/Cam Kifsa/Neh1/Dyra1/Gini3/Moltg4/Ref/Rit2/Tenm2/2j8084/Cam Kifsa/Neh1/Dyra1/Gini3/Moltg4/Ref/Rit2/Cam/X/Dap1b/Dig2 Grm4/Lg75/Dta2/Gp3/Dq12/Rit2/Chma7/Lgma/Map2/Gna3/Adi Syt2/Pap2/Dma1/Giol3/Chba9/Ly21/Cpne4/Kcn1/Syt7 Klf5a/Nehf/Dyrc11/Nehf/MkfK/Scf8asgp1/Map2/Map2/Map1b/Dig2 Cpt4/Syt2/Ris2/Dma1/Rit3S/syt7
8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8	G0:0010976 G0:0045921 G0:0045921 G0:0072655 G0:0048813 G0:0050954 G0:0010970 G0:0010970 G0:0007188 G0:0071882 G0:00718812 G0:0015812	positive regulation of neuron projection cialcuim ion transmerbrane import into positive regulation of socytosis y positive regulation of positiva dendrite morphogenesis sensory perception of mechanical stimul positive regulation of cell projection orgi transport along microtubule adenylate cyclase-modulating 6 protein- cellular response to calcium ion microtubule-based transport regulation of vesicle fusion regulation of vesicle fusion	20/373 12/373 10/373 17/373 13/373 16/373 23/373 12/373 14/373 9/373 12/373 12/373 5/373	151/19943 106/19943 288/19943 282/19943 262/19943 262/19943 156/19943 208/19943 157/19943 25/19943 22/19943	3.01E-05 3.28E-05 3.59E-05 3.71E-05 3.77E-05 3.86E-05 3.95E-05 3.96E-05 4.11E-05 4.22E-05 4.51E-05	0.000411 0.00044 0.000478 0.000513 0.000528 0.000535 0.000554 0.000554 0.000554 0.000574 0.000574	0.00032025 0.00034224 0.0003721 0.0003721 0.0004118 0.0004118 0.00042342 0.00043151 0.00043151 0.00044654 0.000445582 0.00048582	Thru/LDraf2/Grin1/Riv2/Hrt2/Pib2/Jp32/Akap6/Grin2/Hrt2/Pir 592/2001/LGraf2/Cdap5/Nc15/Hrt1/Eyb13/Ant/JRab33/Dop5//Cn194/C Arhgpa4/4/Mt7/Rab32/Com1/Lgb113/Ant/JRab33/Dop5//Cn194/C Arhgpa4/4/Mt7/Rab32/Com1/Lgb113/Ant/JRab33/Dop5//Cn194/C Arhgpa4/4/mt7/Ris2/Lom3/Lgb12/Cn12/Lgb12/Cn12/Lgb14/C Arbgp42/Sc19/Lgb12/Graf2/Dot1/Lgb12/Cn12/Lgb14/C Arbg12/Sc19/Lgb12/Graf2/Dot1/Lgb12/Ch12/Lgb14/C Sr22/Pip2/Lgb12/Graf2/Dot1/Lgb12/Ch12/Lgb14/C Sr22/Pip2/Lgb12/Lgb12/Ch12/Lgb12/Lg
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8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8	G0:010975 G0:0045921 G0:0045921 G0:0045921 G0:0050954 G0:001097C G0:0007188 G0:001097C G0:0099111 G0:003138 G0:001581 G0:0050966 G0:00050966 G0:0007622 G0:0051954	positive regulation of neuron projection cialcuin on transmerbrane import into positive regulation of soxytosis protein localization to plasma membran- denditie morphogenesis sensory perception of mechanical stimulu positive regulation of call projection org, transport along microtubule adenylate cyclase-modulating 6 protein- cellular response to calcium ion microtubule-based transport regulation of vesicle fusion regulation of vesicle fusion inhibitory postypatic potential chyktmic behavior positive regulation of amine transport	20/373 12/373 10/373 17/573 13/373 16/373 23/373 12/373 12/373 12/373 12/373 9/373 5/373 5/373 5/373 5/373 5/373 5/373	151/19943 106/19943 288/19943 262/19943 262/19943 156/19943 208/19943 257/19943 35/19943 22/19943 22/19943 22/19943 22/19943 52/19943	3.01E-05 3.28E-05 3.59E-05 3.71E-05 3.95E-05 3.96E-05 3.96E-05 4.11E-05 4.51E-05 4.51E-05 4.51E-05 4.77E-05 4.91E-05	0.000411 0.00044 0.000478 0.000513 0.000528 0.000554 0.000554 0.000554 0.000554 0.000566 0.000617 0.000617 0.000667	0.00032025 0.00034224 0.0003721 0.0003917 0.00041549 0.00041549 0.00042342 0.00043151 0.00044554 0.00044554 0.00044554 0.00044509 0.00048009 0.00048009 0.00048009	Thru/LDraf2/Grin1/Riv2/Htr2/Pib2/2/bib3/Akap6/Grin2/Htr2/Pib 59/2/sni1/Gabg2/Cadaps/Ncs1/Rins/Rab33/Cons1/Syr1/Car Arngap4/4/In1/Rab32/Carn1/Epb113/Ani:J/Rab33/Dop6//Cin3/4/C Arngap4/4/In1/Rev1/Map8/kb2/Carn2/Lornk2/Carn2/2/Conta/2/Cir Pib12/Sc683/Gabra3/Rab32/Atp222/Scn13/Kcna1/Srm4/Kcnm31 Syr2/Sempin1/Rins/J/Gn1/Mdg4/HrvfRt/T2Tem12/Zb634/Car Klf5a/Neh/Dync11/NeH/Nehr/Klf2/Tem22/Dis3/Atp2/Map12/Dlg2 Grm4/Lg5/Daf2/Gr3/Opd1/Klf5/Rasgrp1/Map2/Map12/Dlg2 Grm4/Lg5/Daf2/Gr3/Opd1/Klf5/Rasgrp1/Map2/Map12/Dlg2 Grm4/Sir2/Daf2/Cirm3/Chg4/Kr4/Klf2/Rasgr01/Map2/Map12/Dlg2 Grm4/Sir2/Daf2/Lf2/Rins2/Ap12/Rab33/Syr7 Grm5/Sir23/Htr2/Sic6611/Hrh3 Phf24/Scn13/Kran1/Grin2/Htr3 Brit2/Lf2/Rins2/Laf2/Rins2/Ag2D/Kd5 Drd2/Ltr12/Kcn32/Map12/D/Kcnm31/Opt1/Lf2/Rab3/Cat Drd2/Ltr12/Kcn32/Map10/Kcnm31/Opt1/Lf2/Rab2/Cat Drd2/Ltr13/Htr22/Nk85P4/D/Kcn32/Dopt1/Lf2/Kb12/Cat
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8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8	G0:0109753 G0:0045921 G0:0045821 G0:0048813 G0:0053954 G0:0053344 G0:0053344 G0:0071287 G0:0007188 G0:007188 G0:007182 G0:0050966 G0:00050966 G0:0007622 G0:0051954 G0:00051954 G0:00051954	positive regulation of neuron projection cialcuin on transmerbrane import into positive regulation of soxytosis protein localization to plasma membran- denditte morphogenesis sensory perception of mechanical stimulu positive regulation of call projection org; transport along microtubule adenylate optase-modulating 6 protein- cellular response to calcium ion microtubule-based transport regulation of vesicle fusion regulation of vesicle fusion microtubule-based transport detection of mechanical stimulus involve inhibitory postypatic potential rhythmic behavior positive regulation of amine transport synaptic transmission, dopaminergic dendritis spine cagnization	20/373 12/373 10/373 17/373 13/373 13/373 13/373 14/373 9/373 12/373 14/373 9/373 5/373 5/373 5/373 5/373 8/373 5/373 8/373 6/373 6/373	151/19943 106/19943 288/19943 262/19943 262/19943 156/19943 156/19943 208/19943 88/19943 35/19943 22/19943 22/19943 22/19943 36/19943	3.01E-05 3.28E-05 3.57E-05 3.77E-05 3.96E-05 3.96E-05 4.94E-05 4.51E-05 4.51E-05 4.51E-05 4.51E-05 4.51E-05 4.51E-05 4.98E-05 6.14E-05	0.000411 0.00044 0.00053 0.000535 0.000535 0.000535 0.000544 0.000574 0.000586 0.000617 0.000617 0.000617 0.00065 0.000666 0.000664	0.00032025 0.00034224 0.0003917 0.00039917 0.00041118 0.0004118 0.00043151 0.00044315 0.00044315 0.0004465 0.00044609 0.000448009 0.00048009 0.00048009 0.00048009 0.00048009 0.00048009 0.00048009 0.0004582	Thy L/Drd2/Grin1/Rw2/Hrt2/Pib2/Jp32/Akap6/Grin2/Hrt2/Pip Srt2/Sw11/Gobg2/CdapS/NE3/Tbirm3/Rab33/Cons1/Sy71/Gar Arngap4/dr1/Hesv1/Abg8/Bc2/Cam2b2/Chm2b2/C
8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8	G0:010975 G0:009755 G0:0045921 G0:0045921 G0:007265 G0:0048813 G0:0050954 G0:0071277 G0:00971277 G0:00971277 G0:00971277 G0:00971277 G0:0051954 G0:0015412 G0:0051954 G0:00019623 G0:0019623 G0:0019623 G0:0019633	positive regulation of neuron projection calculum ion transmembrane import into positive regulation of excyctosis protein localization to plasma membran- dendrite morphogenesis sensory perception of mechanical stimul positive regulation of sell projection orgi transport along microtubule ademyste cyclase-modulating & protein- caliular response to calcium ion microtubule-based transport regulation of viscil fusion gamma-aminobutyric add transport detection of mechanical stimulus involve inhibitory postsynaptic potential rhythmic baehavior positive regulation of sensition of secretion by cell	20/373 12/373 10/373 110/373 13/373 13/373 13/373 12/373 12/373 12/373 9/373 12/373 9/373 5/373 5/373 5/373 5/373 5/373	151/19943 106/19943 288/19943 262/19943 262/19943 156/19943 2508/19943 25/19943 22/19943 22/19943 22/19943 22/19943 22/19943 36/19943 93/19943	3.01E-05 3.28E-05 3.71E-05 3.77E-05 3.96E-05 3.96E-05 4.22E-05 4.21E-05 4.51E-05 4.51E-05 4.51E-05 4.51E-05 4.77E-05 4.91E-05 6.14E-05 6.14E-05	0.000411 0.00044 0.000533 0.000535 0.000554 0.000554 0.000554 0.000554 0.000554 0.000561 0.000617 0.000665 0.000665	0.00032025 0.00032025 0.0003917 0.00039917 0.00041118 0.00041242 0.0004342 0.0004454 0.00044552 0.00044654 0.00048509 0.00048009 0.00048009 0.00048009 0.00048009 0.00048009 0.00051506 0.0005150 0.0005150	ThryL/Draf2/Grin1/Ryr2/Hrt2/Pib2/Jph3/Akap6/Grin2b/Hrt2/Pib Srt2/sni1/Godg/Cadps/Ncs1/Rhtm3/Rab3/Com2b/Srt7/Grin4 Arhgap4/drin1/Rab3/Cam1/Epb4113/aht/JRab3/Dpp5/Kcin4/C Arhgap4/drin1/Hecv1/Map8kB/Cam2b/Cam2b2/Cam2b2/Crt2/Bot4/C Arhgap4/drin1/Hecv1/Map8kB/Cam2b2/Crt2/Bot4/C Arhgap4/drin1/Hecv1/Map8kB/DH/Hrt2/Tam2/TBot4/C Arhgap4/drin1/Hecv1/Ki5/Rasgr1/Map2/Map1b/Dig2 Grm4/Lgf5/Drl2/Gpf3/Dpt4/JRt2/Chm3/Lgf1/Map2/Map1b/Dig2 Grm4/Lgf5/Drl2/Gpf3/Dpt4/JRt2/Chm3/Srt7 Kl5a/Nehf/Dync1i1/Nehf/NKI5/Rasgr1/Map2/Map1b/Dig2 Grm4/Lgf5/Drl2/Gpf3/Dpt4/JRt2/Chm3/Srt7 Kl5a/Nehf/Dync1i1/Nehf/NKI5/Rasgr1/Map2/Map1b/Dig2 Grm4/Lgf5/Drl2/Gpf3/Dpt4/Srt12/Epm4/Lcn1/Srt7 Kl5a/Nehf/Dync1i1/Nehf/NKI5/Rasgr1/Map2/Map1b/Dig2 Grm4/Lgf3/Zhm3/JRt2/Srt7 Art3
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87 88 89 89 80 80 80 80 80 80 80 80 80 80 80 80 80	GC:00102 GC:00102 GC:00102 GC:007553 GC:0045921 GC:0045921 GC:0045921 GC:0045921 GC:0045921 GC:0045921 GC:0051541 GC:0055	positive regulation of neuron projection cicluiun ion transmembrane import into positive regulation of exocytosis protein localization to plasma membrani dendrite morphogenesis sensory preception of mechanical stimuli positive regulation of sell projection orgi transport along imorotubule adenylate cyclase-modulating & protein adenylate cyclase-modulating & protein adenylate cyclase-modulating & protein adenylate cyclase-modulating & protein adenylate cyclase-modulating & protein microtubule-based transport regulation of sells cyclase detection of mechanical stimulus involve inhibitory postsynaptic potential rhytmic babins, dogaminegic dendrite spine organization positive regulation of seventon by cell responte to ethanol positive regulation of seventon by cell responte to ethanol positive regulation of seventon by cell responte to ethanol positive regulation of seventon by cell responte to bistamine syonamet compatic transitision neurotrammitter receptor internalizatio positivar ergulation of protecolluter positivar ergulation of protecolluter responte to histamine spontaneous synaptic transitision neurotrammitter receptor internalization positivar ergulation of protecolluter positivar ergulativar protecolluter positivar ergula	20(373) 10(373) 10(373) 11(3/33) 12(3/3) 12(3/3) 12(3/3) 12(3/3) 12(3/3) 12(3/3) 12(3/3) 12(3	151/19943 106/19943 1288/19943 1280/19943 1267/19943 1267/19943 1256/19943 1257/19943 127/19943 127/19943 127/19943 127/19943 127/19943 1267/19943 1267/19943 137/1994	3.01e.05 3.28e.05 3.59e.05 3.71e.05 3.77e.05 3.78e.05 3.36e.05 3.36e.05 4.22e.05 4.22e.05 4.51e.05 4.51e.05 4.51e.05 4.51e.05 4.51e.05 4.51e.05 6.37e.05 6.37e.05 7.72F.05 7.7	0.000411 0.000528 0.000528 0.000538 0.000558 0.000558 0.000558 0.000558 0.000558 0.000558 0.000558 0.000561 0.000570 0.000561 0.0005700 0.000570000000000	0.00032025 0.00032025 0.0003921 0.0003921 0.0003921 0.0004118 0.00041649 0.00042342 0.0004131 0.0004450 0.0004450 0.00044509 0.00048009 0.00048009 0.00048009 0.00048009 0.0005526 0.0005525 0.0005255 0.0005255 0.0005255 0.0005255 0.0005255 0.0005255 0.0005255 0.0005255 0.0005255 0.0005255 0.0005255 0.0005255 0.0005255 0.0005255 0.0005255 0.0005255 0.0005255 0.0005255 0.00072422 0.0007605 0.00072126 0.00079219 0.0005256 0.00072422 0.0007655 0.00079219 0.0008526 0.000856	Thr.J.(Dra2)Grin1/Riv2/Hrt2/Pib2/Jp32/Akap6/Grin22/Hrt2 SY22/sni1/Gabg2/Cadaps/NE3/ThuSTIA/Bab32/Com215/sr17/Gar Arngap4/drin1/Hev2./Map8kb2/Cam2/bc32/Cam2b2/Grin2/Sc217C/Bb43/Cam Arngap4/drin1/Hev2./Map8kb2/Cam2b2/Grin2/Sc217C/Bb43/Cam Arngap4/drin1/Hev2./Map8kb2/Cam2b2/Grin2/Zb843/Cam Arlgap4/drin1/Hev2./Map8kb2/Cam2b2/Grin2/Zb843/Cam Klf3a/Nefh/Dync11/Nefh/Nefh/Xf2Tam22/Zb843/Cam Klf3a/Nefh/Dync11/Nefh/Nefh/Xf2Tam22/Cas1/Map2/Map1b/Dlg2 Grm4/Lsf5/Dr42/Gr37/Ord1/XirKi/GRasgrp1/Map2/Map1b/Dlg2 Grw1/Sir23/Hrt2/SirB43/LrMab34/Syr2 Frans/LrMar40/Gra3/Dr42/Nefh/SirG8agrp1/Map2/Map1b/Dlg2 Grw1/Sir23/Hrt2/SirB43/Hrt3 Brit2/LrMa1/Grin2/Hrt32/Sr43/Dr42/Cab Dr42/LrMa1/Kr12/SirB431/Hrt3 Brit2/LrMa1/Grin2/LrMab34/Syr7 Grw53231/Hrt2/KirB43/Kr12/Grab2/Chrb2 Dr42/Chrm3/Hrt2/Kr12/Kab23/Cr2 Dr42/Chrm3/Hrt2/Kr12/Kab23/Cr2 Dr42/Chrm3/Hrt2/Kr12/Kab23/Cr2 Dr42/Chrm3/Hrt2/Kr12/Kab23/Cr2 Dr42/Chrm3/Hrt2/Kr12/Kab23/Cr2 Dr42/Chrm3/Hrt2/Kr12/Kr12/Kr12 Br432/Kr12/Arb13/SirCh4/Chrm2/Chrb2/Cht Dr42/Chrm3/Hrt2/Kr12/Kr12/Kr12 Br432/Kr12/Arb13/SirCh4/Chrm2/Chrb2/Cht Dr42/Grin3/Hrt2/Kr12/Kr12/Kr12 Br432/Kr12/Arb13/SirCh4/Chrm2/Chrb2/Kr12 Br432/Kr12/Arb13/SirCh4/Chrm2/Chrb2/Kr12 Br432/Kr12/Arb13/SirCh4/Chrm2/Chrb2/Kr12 Br432/Kr12/Arb13/SirCh4/Chrm2/Chrb2/Kr12 Br432/Kr12/Arb13/SirCh4/Chrm2/Lr02/Min1/Cpfr1 Lrh5/Crth4/SirKi/SirCh3/Chr12/Lr02/Cabb3 Br432/Kr12/Kr12/Kr12/Kr12/Kr12/Kr12/Kr12 Br432/Kr12/Kr12/Kr12/Kr12/Kr12/Kr12/Kr12/Kr1
59 59 59 59 59 59 59 59 59 59 59 59 59 5	GC:0010976 GC:0010976 GC:002752 GC:0045921 GC:002763 GC:002768 GC:002768 GC:0021542 GC:0	positive regulation of neuron projection ciclumio in citraminembrane import into positive regulation of excyclosis protein localization to plasma membran- dendrite morphogenesis sensory perception of mechanical stimul positive regulation of call projection orgi transport along microtubule adenylate cyclase-modulating & protein- deliular response to calcium ion microtubule-based transport regulation of visual transport detection of mechanical stimulus involve inhibitory postsynaptic potential rytymic tambwairor positive regulation of savet on y cell response to ethanol regulation of severation by cell response to ethanol response to ethanol positive regulation of severation y cell response to ethanol regulation of respraptic cytosolic calciu positive regulation of severation calcius positive regulation of severation calcius positive regulation of severation calcius positive regulation of severation calcius positive regulation of severation calcius cytosteleton-dependent intracellular tra- positive regulation of response to dramol colitive regulation of response to dramol colitive regulation of response to dramol cellular response to intramic substance regulation of postrymaptic transmission, gluti intragenic anion transmethrane transpo- long-term memory	20(373) 10(373) 10(373) 113(373) 113(373) 113(373) 113(373) 123(37	151/19943 106/19943 288/19943 188/19943 180/19943 262/19943 262/19943 262/19943 156/19943 252/19943 22/19943 22/19943 22/19943 22/19943 36/19943 36/19943 36/19943 36/19943 36/19943 13/19943 13/19943 13/19943 13/19943 14/19943 14/19943 14/19943 14/19943	3.01e.05 3.28e.05 3.71e.05 3.71e.05 3.77e.05 3.38e.05 3.38e.05 3.38e.05 3.38e.05 3.38e.05 4.21e.05 4.21e.05 4.21e.05 4.451e.05 4.451e.05 4.451e.05 4.451e.05 4.451e.05 4.451e.05 4.451e.05 4.451e.05 4.451e.05 4.451e.05 4.451e.05 4.451e.05 4.451e.05 4.451e.05 4.451e.05 4.451e.05 4.451e.05 4.451e.05 4.451e.05 4.571e.05 7.728e.05 7.728e.05 7.728e.05 7.738e.05 7.748e.057.748e.05 7.748e.05 7.748e.057.748e.05 7.748e.05 7.748e.057.748e.05 7.748e.05 7.748e.057.748e.05 7.748e.057.748e.05 7.748e.057.748e.05 7.748e.057.748e.05 7.748e.057.748e.05 7.748e.057.748e.05 7.748e.057.748e.05 7.748e.057.748e.05 7.748e.057.748e.057.7486 7.74860.05786.0578	0.000411 0.000743 0.000743 0.000513 0.000513 0.000554 0.000555 0.0	0.00032025 0.00032205 0.0003921 0.0003921 0.0004118 0.0004138 0.0004138 0.00043242 0.00043151 0.00044809 0.0004809 0.0004809 0.0004809 0.0004809 0.0005189 0.0005189 0.0005250 0.0005250 0.0005250 0.0007216 0.0007265 0.000755 0.000755 0.000755 0.000755 0.000755 0.000755 0.000755 0.000755 0.000755 0.000755 0.000755 0.000755 0.000755 0.000755 0.000	Thr.J.(Dra2)Grin1/Riv2/Hrt2/Pib2/Jp32/Akap6/Grin22/Hrt2 SY22/sni1/Gabg2/Cadaps/NE3/Thu3/Rab33/Cosa15/sy71/Gar Arngap4/drin1/Hesv1/Map8kb2/Cam2)Cam2b2/Gnt2/Sc12/Rab34/Cam2 Phf24/Sc683/Gabra3/Rab34/Atg222/Sc13/Kcna1/Srm4/Kcnm31 Syt2/Sempin1/Rim3/Gni1/Mid94/Hrt9/Rit2/Tem2/Zf8843/Cam Klf3a/Nefh/Dync11/Nefh/Wefm/Klf2/Tem2/Zf8434/Cam Klf3a/Nefh/Dync11/Nefh/Wefm/Klf2/Tem2/Zf8434/Cam Klf3a/Nefh/Dync11/Nefh/Wefm/Klf2/Tem2/Zf8434/Cam Klf3a/Nefh/Dync11/Nefh/Wefm/Klf2/Tem2/Zf8434/Cam Syt2/Hpea/Data1/Sc12/Sc12/Gna4/Kcn11/Syt7 Klf3a/Nefh/Dync11/Nefh/Klf3/Klf3/Rasgr1/Map2/Map1b/Dlg2 Grk1/Syt2/Hicz/Iken3/Grk12/Sc12/Gna4/Kcn11/Syt7 Klf3a/Nefh/Dync11/Nefh/Klf3/Klf3/Rasgr1/Map2/Map1b/Dlg2 Grk1/Syt2/Hicz/Iken3/UrAb34/Syt7 Grm4/Sit231/Htz2/Klf3/Rab34/Syt7 Grm4/Sit231/Htz2/Klf3/Rab34/Syt7 Grm4/Sit231/Htz2/Klf3/Klf3/Gabg10/Dp11/Chrb3/Chat Drd2/Chrna4/Htz2/Klf3/Chrb3/Chrb2 Drd2/Chrb4/Htz2/Klf3/Chrb3/Chrb2 Drd2/Chrb4/Htz2/Nt81/Chrb3/Chrb2 Drd2/Chrb4/Htz3/Klf3/Chrb3/Chrb2 Drd2/Chrb4/Htz3/Klf3/Chrb3/Chrb2 Drd2/Chrb4/Htz3/Klf3/Chrb3/Chrb2 Drd2/Chrb4/Htz3/Klf3/Chrb3/Chrb2 Drd2/Chrb4/Htz3/Klf3/Chrb3/Chrb2 Drd2/Chrb4/Htz3/Klf3/Chrb3/Chrb2 Drd2/Chrb4/Htz3/Klf3/Chrb3/Chrb2 Drd2/Chrb4/Htz3/Klf3/Chrb3/Chrb2 Drd2/Chrb4/Htz3/Klf3/Chrb3/Chrb2 Drd2/Chrb4/Htz3/Klf3/Chrb3/Chrb2 Drd2/Chrb4/Htz3/Klf3/Chrb3/Chrb2 Drd2/Chrb4/Htz3/Klf3/Chrb3/Chrb2 Drd2/Chrb4/Htz3/Klf3/Chrb3/Chrb2 Drd2/Chrb4/Htz3/Klf3/Chrb3/Chrb3/Chrb1 Drd2/Chrb4/Htz3/Klf3/Chrb3/Chrb3/Chrb3/Chrb1 Drd2/Drd3/Htt2/Kbf3/Klf3/Chrb3/Chrb3 Drd2/Drd3/Htt2/Kbf3/Klf3/Chrb3/Chrb3 Drd2/Drd3/Htt2/Kbf3/Klf3/Chrb3/Chrb3 Drd2/Drd3/Htt2/Kbf3/Klf3/Chrb3/Chrb3/Chrb3/Chrb3/Chrb1 Drd2/Drd3/Htt2/Kbf3/Klf3/Cabb3 Drd2/Drd3/Htt2/Kbf3/Klf3/Cabb3 Drd2/Drd3/Htt2/Kbf3/Klf3/Cabb3 Drd2/Drd3/Htt2/Kbf3/Klf3/Cabb3 Drd2/Drd3/Htt2/Kbf3/Klf3/Cabb3 Drd2/Drd3/Htt2/Kbf3/Klf3/Cabb3 Drd2/Drd3/Htt2/Kbf3/Klf3/Cabb3/

BP BP		regulation of postsynapse organization	10/373 3/373					Rapgef4/Arhgap44/Nptx1/Grin1/Zfp804a/Camk2b/Cbln1/Grip2/G	10
BP		optic nerve morphogenesis positive regulation of synaptic vesicle fur		6/19943 6/19943				Kcna2/Pax2/Chrnb2 Syt2/Rims1/Syt7	3 3
BP	GO:1902630	regulation of membrane hyperpolarizati	3/373	6/19943	0.000124	0.001512	0.00117741	Kenma1/Trpe5/Hen1	3
BP		negative regulation of synaptic transmis		80/19943	0.000125	0.001512	0.00117741	Grm4/Rapgef4/Slc24a2/Drd2/Cbln1/Htr2a/Celf4/Grid2ip	8
BP BP		synaptic vesicle recycling multi-organism behavior	8/373 8/373	81/19943 82/19943				Syt2/Sncb/Stx1b/Rab3a/Pacsin1/Syp/Syt7/Dnm3 Grin1/Crhbp/Mapk8ip2/Grin2b/Shank1/Chrnb2/Nrxn3/Pou4f1	8 8
BP		acetylcholine receptor signaling pathway		28/19943				Chrna4/Chrm2/Hrh3/Chrna7/Chrnb2	5
BP	GO:1903831	signal transduction involved in cellular re	5/373	28/19943	0.000154	0.001825	0.00142082	Chrna4/Chrm2/Hrh3/Chrna7/Chrnb2	5
BP		detection of mechanical stimulus	7/373	62/19943 129/19943				Phf24/Ano3/Atp2b2/Scn1a/Kcna1/Grin2b/Htr2a	7
BP BP		receptor internalization positive regulation of synaptic vesicle ex	10/373	129/19943	0.000159	0.001881	0.00146435	Nsf/Napb/Cacng2/Hpca/Drd2/Cacng3/Pacsin1/Necab2/Nrg1/Dnm Syt2/Rims1/Cacna1b/Syt7	10 4
BP		regulation of calcium ion transmembran		85/19943				Cabp1/Hpca/Drd2/Ryr2/Jph3/Akap6/Oprl1/Cacna2d1	8
BP		regulation of G protein-coupled receptor		132/19943	0.000192	0.002242	0.00174504	Phf24/Drd2/Rgs7/Camk2b/Chga/Syp/Mrap2/Necab2/Oprl1/Tub	10
BP BP		adenylate cyclase-activating G protein-co regulation of cAMP-mediated signaling		133/19943 65/19943				Lgr5/Drd2/Gpr3/Rit2/Chga/Mrap2/Gnas/Adcy1/Opr11/Htr4 Gpr3/Pex5l/Gpr61/Chga/Mrap2/Gnas/Opr11	10 7
BP		positive regulation of synaptic transmiss		7/19943				Drd2/Nat8l/Chrnb2	3
BP	GO:0045110	intermediate filament bundle assembly	3/373	7/19943	0.000215	0.002437	0.00189682	Nefh/Nefl/Nefm	3
BP BP		synaptic transmission, glycinergic	3/373 3/373	7/19943				Gira2/Gira1/Sic6a5	3
BP		rhythmic synaptic transmission potassium ion homeostasis	5/373	7/19943 30/19943				Scn9a/Cacna2d2/Chat Drd2/Sic12a5/Atp1a3/Kcnma1/Sic12a3	3 5
BP	GO:1905144	response to acetylcholine	5/373	30/19943	0.000216	0.002437	0.00189682	Chrna4/Chrm2/Hrh3/Chrna7/Chrnb2	5
BP		cellular response to acetylcholine	5/373	30/19943				Chrna4/Chrm2/Hrh3/Chrna7/Chrnb2	5
BP BP		negative regulation of cell projection org response to anesthetic	13/3/3 10/373	215/19943 134/19943				Thy1/Rit2/RGD1307443/Stx1b/Slit1/Cit/Grin2b/Map2/Pfn2/LOC1( Hpca/Drd2/Nefh/Grin1/Crhbp/Tac3/Grin2b/Htr2a/Prkce/Chrnb2	13 10
BP		neurotransmitter uptake	6/373	47/19943		0.002589	0.00201524	Drd2/Slc17a6/Slc6a5/Nat8l/Slc6a11/Sv2b	6
BP		negative regulation of cyclase activity	4/373	17/19943	0.000236	0.00264	0.00205558	Hpca/Drd2/Hrh3/Akap6	4
BP BP		regulation of receptor-mediated endocy detection of mechanical stimulus involve		111/19943 48/19943	0.00024	0.002677	0.00208397	Nsf/Napb/Hpca/Drd2/Pacsin1/Necab2/Sgip1/Nrg1/Aak1 Phf24/Atp2b2/Scn1a/Kcna1/Grin2b/Htr2a	9 6
BP		circadian behavior	7/373	48/19943 68/19943				Drd2/Hcrtr2/Kcna2/Mapk10/Kcnma1/Oprl1/Chrnb2	7
BP		regulation of cellular component size	19/373	410/19943				Nefl/Nefm/Spire2/Slc12a5/Atp2b2/Slit1/Cit/Kcnma1/Nrg1/Map2/	19
BP		presynapse assembly	6/373	49/19943				Lrfn5/Slitrk3/Clstn3/Cbln1/Cntn5/Bsn	6
BP BP		neuromuscular synaptic transmission neuromuscular process controlling postu	5/373 4/373	32/19943 18/19943				Slc5a7/Chrna4/Rab3a/Chrnb2/Chat Glra1/Scn1a/Atp8a2/Pou4f1	5 4
BP		visual learning	7/373	69/19943				Tafa2/Drd2/Grin1/Ndrg4/Atp1a3/Neto1/Chrnb2	7
BP	GO:1903307	positive regulation of regulated secretor	7/373	69/19943	0.000302	0.003285	0.00255737	Syt2/Cadps/Rims1/Rab3a/Cacna1b/Syt7/Cacna1i	7
BP BP		vesicle fusion	8/373 15/373	91/19943 283/19943				Cplx1/Nsf/Syt2/Rims1/Stx1b/Vamp1/Rab3a/Syt7	8 15
BP		regulation of calcium ion transport nonassociative learning	3/373	283/19943 8/19943				Cabp1/Thy1/Hpca/Drd2/Oprd1/Grin1/Ryr2/Atp2b2/Camk2a/Jph3 Mapk8ip2/Grin2b/Shank1	3
BP		cerebellar Purkinje cell layer developme		33/19943	0.000344	0.003679	0.0028642	Sez6l2/Atp2b2/Klhl1/Cend1/Sptbn2	5
BP		regulation of cell morphogenesis involve		350/19943	0.000345	0.003687	0.00287066	Arhgap44/Thy1/Grin1/Dmtn/Nefl/Nefm/Hecw1/Camk2b/Slit1/Cit,	17
BP BP		regulation of receptor internalization long-term synaptic potentiation	7/373 12/373	71/19943 198/19943				Nsf/Napb/Hpca/Drd2/Pacsin1/Necab2/Nrg1 Slc24a2/Drd2/Rims1/Calb2/Syt12/Camk2b/Adcy1/Grin2b/Chrna7/	7 12
BP		positive regulation of cation transmemb		170/19943				Cacng2/Thy1/Cacng3/Ryr2/Rgs7/Dpp6/Kcnc1/Kcna1/Akap6/Cacna	11
BP		negative regulation of lyase activity	4/373	19/19943	0.000374	0.003933	0.00306165	Hpca/Drd2/Hrh3/Akap6	4
BP BP		regulation of delayed rectifier potassium	4/373 7/373	19/19943 72/19943				Kons2/Konab1/Akap6/Kong1 Tofo2/Ded/Cyin1/Akap6/Kong1	4 7
BP		visual behavior response to insecticide	5/373	34/19943				Tafa2/Drd2/Grin1/Ndrg4/Atp1a3/Neto1/Chrnb2 Kif5a/Nefh/Nefl/Ddc/Map1b	5
BP		organelle membrane fusion	8/373	96/19943				Cplx1/Nsf/Syt2/Rims1/Stx1b/Vamp1/Rab3a/Syt7	8
BP	GO:0048284	organelle fusion	9/373	121/19943				Cplx1/Nsf/Syt2/Gdap1/Rims1/Stx1b/Vamp1/Rab3a/Syt7	9
BP BP		response to amphetamine anterograde axonal protein transport	6/373 3/373	54/19943 9/19943				Drd2/Grin1/Rasgrf1/Rgs7/Grin2b/Rgs17 Kif5a/Kif5c/Dlg2	6 3
BP		protein localization to presynapse	3/373	9/19943	0.000501	0.005141	0.00400232	Kif5a/Kif5c/Dlg2	3
BP		regulation of synaptic transmission, GAB		36/19943	0.000521	0.005296	0.00412253	Phf24/Drd2/Cntnap4/Car7/Prkce	5
BP BP		positive regulation of cAMP-mediated si modification of synaptic structure	5/373 5/373	36/19943 36/19943				Gpr3/Gpr61/Chga/Mrap2/Gnas Cabp1/Arhgap44/Dlgap3/Pfn2/LOC100909840	5 5
BP		neuropeptide signaling pathway	5/3/3 8/373	99/19943 99/19943				Gira2/Scg5/Oprd1/Hcrtr2/Gira1/Hcrtr1/Tac3/Oprl1	8
BP	GO:0008090	retrograde axonal transport	4/373	21/19943	0.00056	0.005611	0.0043683	Kif5a/Nefl/Dlg2/Bsn	4
BP		regulation of endocytosis	15/373	300/19943		0.005637	0.00438844	Nsf/Napb/Hpca/Drd2/Rit2/Stx1b/Pacsin1/Necab2/Sgip1/Nrg1/Mc	15
BP BP		response to amine axo-dendritic transport	7/373 7/373	77/19943 78/19943	0.000592	0.0059	0.00459309	Drd2/Grin1/Rasgrf1/Rgs7/Kcnc1/Grin2b/Rgs17 KifSa/Nefl/Nefm/KifSc/Map2/Dlg2/Bsn	7
BP		catecholamine metabolic process	6/373	57/19943	0.000668	0.006597	0.00513601	Drd2/Sncb/Htr2c/Ddc/Chrna7/Chrnb2	6
BP	GO:0009712	catechol-containing compound metaboli		57/19943	0.000668	0.006597	0.00513601	Drd2/Sncb/Htr2c/Ddc/Chrna7/Chrnb2	6
BP BP		presynapse organization homophilic cell adhesion via plasma mer	6/373	57/19943 128/19943	0.000668	0.006597	0.00513601	Lrfn5/Slitrk3/Clstn3/Cbln1/Cntn5/Bsn Cntn4/Clstn3/Cdh12/Cdh7/Ptprt/Clstn2/Pcdha4/Celsr3/L1cam	6 9
BP		amino acid transport	10/373					Grm4/Grm1/Sic32a1/Sic17a6/Htr2c/Sic6a5/Sic6a11/Sic7a10/Hrh3	10
BP		cellular response to histamine	3/373	10/19943	0.000706	0.00684	0.00532521	Gabrg2/Gabra1/Gabrb3	з
BP BP		neurotransmitter loading into synaptic v		10/19943 10/19943	0.000706			Slc32a1/Slc17a6/Ddc	3 3
BP		receptor diffusion trapping postsynaptic neurotransmitter receptor	3/373 3/373	10/19943	0.000706			Cacng2/Cacng3/Camk2a Cacng2/Cacng3/Camk2a	3
BP		neurotransmitter receptor diffusion trap		10/19943	0.000706				
BP								Cacng2/Cacng3/Camk2a	3
		response to alkaloid	11/373	184/19943	0.000717	0.006931	0.00539577	Drd2/Nefh/Grin1/Ryr2/Crhbp/Tac3/Ddc/Grin2b/Htr2a/Prkce/Chrr	11
BP BP	GO:0007528	neuromuscular junction development	6/373	184/19943 58/19943	0.000717 0.000733	0.006931 0.007068	0.00539577 0.00550245	Drd2/Nefh/Grin1/Ryr2/Crhbp/Tac3/Ddc/Grin2b/Htr2a/Prkce/Chrr Cacng2/Ky/Cacna2d2/Shank1/Chat/Unc13c	11 6
BP BP	GO:0007528 GO:0072384 GO:0060047	neuromuscular junction development organelle transport along microtubule heart contraction	6/373 7/373 12/373	184/19943 58/19943 80/19943 215/19943	0.000717 0.000733 0.000745 0.000767	0.006931 0.007068 0.007168 0.007326	0.00539577 0.00550245 0.00558028 0.00570293	Drd2/Nefh/Grin1/Ryr2/Crhbp/Tac3/Ddc/Grin2b/Htr2a/Prkce/Chrr Cacng2/Ky/Cacna2d2/Shank1/Chat/Unc13c KifSa/Nefh/Dync111/Nefl/Rasgrp1/Nap2/Map1b Drd2/Ryr2/Atp1a3/Scn4b/Chrm2/Chga/Scn1a/Cacna1b/Akap6/Ch	11 6 7 12
BP BP BP	GO:0007528 GO:0072384 GO:0060047 GO:0034767	neuromuscular junction development organelle transport along microtubule heart contraction positive regulation of ion transmembran	6/373 7/373 12/373 11/373	184/19943 58/19943 80/19943 215/19943 186/19943	0.000717 0.000733 0.000745 0.000767 0.000784	0.006931 0.007068 0.007168 0.007326 0.007479	0.00539577 0.00550245 0.00558028 0.00570293 0.00582221	Drd2/Nefh/Grin1/Rv2/Crhbp/Tac3/Ddc/Grin2D/Htr2a/Prkce/Chrr Gacng2/Ky/Cacna2d2/Shank1/Chst/Unc136 KifSa/Nefh/Dync11/Nefl/Ragrp1/Map2/Map1b Drd2/Rv2/Atp1a3/Scn4b/Chrrn2/Chg3/Scn1a/Cacna1b/Akap6/Ch Cacng2/Thy1/Cacng3/Rv2/Rp2/Dp6/Knc1/Knn1/Akap6/Cacn	11 6 7 12 11
BP BP BP BP	GO:0007528 GO:0072384 GO:0060047 GO:0034767 GO:0048639	neuromuscular junction development organelle transport along microtubule heart contraction positive regulation of ion transmembran positive regulation of developmental gro	6/373 7/373 12/373 11/373 12/373	184/19943 58/19943 80/19943 215/19943 186/19943 216/19943	0.000717 0.000733 0.000745 0.000767 0.000784 0.000798	0.006931 0.007068 0.007168 0.007326 0.007479 0.007596	0.00539577 0.00550245 0.00558028 0.00570293 0.00582221 0.00591321	Drd2/Neh/Grin1/Rvr2/Chebp/Tac3/Ddc/Grin2b/Htr2a/Phcce/Chrr Cacng2/Ky/Cacna2d2/Shank1/Cht/Unc13c KifsJNehf/Dync11J/NeH/Ragrp1/Map2/Map1 Drd2/Rvr2/Atp1a3/Scn4b/Chrm2/Cheg/Scn1a/Cacna1b/Akap6/Ch Cacng2/Thy1/Cacng3/Ryr2/Rgs7/Dpp6/Kcnc1/Kcna1/Akap6/Cacn Syz2/Drd2/Rms1/Atp8a2/Rms2/Akap6/Sgip1/Nrg1/Cacna2d2/Nr	11 6 7 12 11 12
BP BP BP	GO:0007528 GO:0072384 GO:0060047 GO:0034767 GO:0048639 GO:0098930	neuromuscular junction development organelle transport along microtubule heart contraction positive regulation of ion transmembran positive regulation of developmental gro axonal transport	6/373 7/373 12/373 11/373 12/373 6/373	184/19943 58/19943 80/19943 215/19943 186/19943	0.000717 0.000733 0.000745 0.000767 0.000784 0.000798 0.000803	0.006931 0.007068 0.007168 0.007326 0.007479 0.007596 0.007628	0.00539577 0.00550245 0.00558028 0.00570293 0.00582221 0.00591321 0.00593836	Drd2/Nefi/Gin1/Rw72/Crhbp/Tac3/Ddc/Gin2b/Htr2a/Prkce/Chrr Comp2/ky/Carad2J/Shnk1/ChrtUnc13c Kil5a/Nefi/Dync111/Nefi/Rasgrp1/Nap2/Map1b Drd2/Ry72/Atp1a3/Schub/Chrm2/Chg3/Scn1a/Cacna1b/Akap6/Ch Cacng2/Tin/L/Cacng3/Rv72/Rg71/Dp6/Kncr1/Kna1/Akap6/Ch Cacng2/Tin/L/Cacng3/Rv72/Rg71/Dp6/Kncr1/Kna1/Akap6/Chacn Sv2/Drd2/Rims1/Acap2a/Rims2/Akap6/Sgip1/Nrg1/Cacna2d2/Ni Kif5a/Nef/Kif5A/Nap2/Dg2/Ba	11 6 7 12 11
BP BP BP BP BP BP	GO:0007528 GO:0072384 GO:0060047 GO:0034767 GO:0048639 GO:0098930 GO:0098664 GO:1901385	neuromuscular junction development organelle transport along microtubule heart contraction positive regulation of for transmembran positive regulation of developmental gro axonal transport G protein-coupled serotonin receptor sig regulation of voltage-gated calcium char	6/373 7/373 12/373 11/373 12/373 6/373 5/373 5/373	184/19943 58/19943 80/19943 215/19943 186/19943 216/19943 59/19943 40/19943 40/19943	0.000717 0.000733 0.000745 0.000767 0.000784 0.000798 0.000803 0.000856 0.000856	0.006931 0.007068 0.007168 0.007326 0.007479 0.007596 0.007628 0.008045 0.008045	0.00539577 0.00550245 0.00558028 0.00570293 0.00582221 0.00591321 0.00593836 0.00626309 0.00626309	Drd2/Nehl/Ginin/Riv2/Crhbp/Tac3/Ddc/Grin2b/Htr2a/Prkce/Chrr Caeng2/ky/Carad2J/Shnit/Loht/Unc13c Kil5a/Nehl/Dync111/Net/Rasgrp1/Map2/Map1b Drd2/Riv2/Atpala/Scn4b/Crm2/Chgs/Scn12(Caena1b/Akap6/Cbrd Srd2/Drd2/Rim3/Akap6/Zgn3/Chgs/Scn12/Kap6/Sglp1/Nrg1/Caena2d/Ni Kil5a/Neh/Kif5A/Nap2/Dg2/Sha Htr22/Chrm2/Htr3/Htr24/Htr4 Cabp1/Hog0/Tr2/Dpf1/Caena2d1	11 6 7 12 11 12 6 5 5
BP BP BP BP BP BP BP	G0:0007528 G0:0072384 G0:0060047 G0:0034767 G0:0048639 G0:0098930 G0:0098664 G0:1901385 G0:1990573	neuromuscular junction development organelle transport along microtubule heart contraction positive regulation of ion transmembran positive regulation of developmental gr axonal transport G protein-coupled serotonin receptor sig regulation of voltage-gated calcium cham potassium ion import across plasma men	6/373 7/373 12/373 11/373 12/373 6/373 5/373 5/373 5/373	184/19943 58/19943 80/19943 215/19943 186/19943 216/19943 59/19943 40/19943 40/19943 40/19943	0.000717 0.000733 0.000745 0.000767 0.000784 0.000798 0.000856 0.000856 0.000856	0.006931 0.007068 0.007326 0.007326 0.007479 0.007596 0.007628 0.008045 0.008045 0.008045	0.00539577 0.00550245 0.00558028 0.00570293 0.00582221 0.00591321 0.00593836 0.00626309 0.00626309 0.00626309	Drd2/Nehr/Gein/Riv2/Crheb/Tac3/Det/Gin/2b/Ht/2a/Pirkce/Chrr Coeng2/ky/Carad22/Shnk1/Chr4/Unc13c Klf3A/Nehr/Dync11/Nei/Rasgrb1/Map2/Map1b Drd2/Ry/2A/pta3/Son4b/Chrm2/Chag3/Son14/Carn11/Akap5/Ch Drd2/Ry/2A/pta3/Son4b/Chrm2/Chag3/Son12/Carn14/Akap5/Ch Carn27/ht/Locng3/Ry/2/Rgs7/Dp6/Kncor1/Kna1/Akap5/Coeni Syt2/Drd2/Rivi/Akap52/Rgs7/Dp6/Kncor1/Kna1/Akap5/Coeni Syt2/Drd2/Rivi/Akap52/Rgs7/Dp6/Kncor1/Kna1/Akap5/Coeni Klf3A/Nehr/Klf5C/Map2/Dg2/Ban Htr2C/chrm2/Htr3/Htr3/Htr3 Cabp1/Hpca/Drd2/Op11/Cacn2d1 Kaj3Kl123/Kh13/Kn12/Sit12a3	11 6 7 12 11 12 6 5 5 5 5
BP BP BP BP BP BP	G0:0007528 G0:0072384 G0:006004767 G0:0034767 G0:0048639 G0:0098664 G0:0098664 G0:19008653 G0:1990573 G0:0051209	neuromuscular junction development organelle transport along microtubule heart contraction positive regulation of ion transmembran positive regulation of developmental gro axonal transport G protein-coupled serotonin receptor sig regulation of voltage-gated calcium char potassium ion import across plasma mer release of sequestered calcium ion into o	6/373 7/373 12/373 11/373 12/373 6/373 5/373 5/373 5/373 5/373 9/373	184/19943 58/19943 80/19943 215/19943 186/19943 216/19943 59/19943 40/19943 40/19943	0.000717 0.000733 0.000745 0.000767 0.000784 0.000798 0.000856 0.000856 0.000856 0.000856	0.006931 0.007068 0.007168 0.007326 0.007479 0.007596 0.007628 0.008045 0.008045 0.008045 0.008045	0.00539577 0.00550245 0.00550293 0.00570293 0.00591321 0.00591321 0.005933836 0.00626309 0.00626309 0.00626309	Drd2/Nehl/Gin1/Riv2/Crhbp/Tac3/Ddc/Gin2b/Htr2a/Prkce/Chrr Comp2/kr/Carad2J/ShniL/ChrUnc13c Klf3A/Nehl/Dync111/Nefl/Ragrp1/Map2/Map1b Drd2/Riv2/Atpa13/Scm4J/Crmr2/Chg3/Scn12(Cacna1b/Atap6/Cacni Syd2/Drd2/Rims1/Atpa3/Scm4J/Crmr2/Chg3/Scn12(Cacna1/Atap6/Cacni Syd2/Drd2/Rims1/Atpa3/Scm4J/Crmr2/Kap6/Sglp1/Nrg1/Cacna2d2/Mi Klf3A/N4/Klf3ChA/Rims2/Hatp6 Cabp1/Hpa2/Drd2/Pirt4 Cabp1/Hpa2/Drd2/Drd12/Opt1/Cacna2d1 Knj2/Stc12a5/Atp133/Knj12/Sic12a3	11 6 7 12 11 12 6 5 5 5 9
BP BP BP BP BP BP BP BP BP BP	G0:0007528 G0:0072384 G0:0060047 G0:0034767 G0:0038664 G0:0098664 G0:1901885 G0:1901885 G0:1901873 G0:0051209 G0:20012598	neuromuscular junction development organella transport along microtubule heart contraction positive regulation of on transmembrant positive regulation of developmental gro axonal transport G protein-coupled serotonin receptor ag regulation of voltage-gated aclicum chan potassium ion import across plasma me- relesse of sequestered aclicum ion into positive regulation of dation channel act inorganic anion transport	6/373 7/373 12/373 11/373 12/373 6/373 5/373 5/373 5/373 5/373 9/373 7/373 10/373	184/19943 58/19943 215/19943 215/19943 216/19943 20/19943 40/19943 40/19943 132/19943 132/19943 161/19943	0.000717 0.000733 0.000745 0.000767 0.000784 0.000788 0.000856 0.000856 0.000856 0.000857 0.000857 0.000854 0.000854	0.006931 0.007068 0.007168 0.007326 0.007479 0.007596 0.007628 0.008045 0.008045 0.008045 0.008045 0.008045 0.008045 0.008045	0.00539577 0.00550245 0.00550245 0.00550230 0.00593221 0.00593836 0.00626309 0.00626309 0.00626309 0.00626309 0.00626309 0.00626309	Drd2/Nehl/Gin1/Riv2/Crhbp/Tac3/Ddc/Grin2b/Htr2a/Prkce/Chrr Comp2/kv/Carad2J/ShniL/ChrUnc13c Klf3k/Nehl/Dync111/Nefl/Rasgrp1/Map2/Map1b Drd2/Rv/2Ahg13/Scn4J/Chrn2/Chg3/Scn13/Caran1b/Atap6/Carn Syt2/Drd2/Riv3/Lhg3/Scn4J/Chrn2/Chg3/Scn13/LAap6/Scp1/Ng1/Carna2d2/Mi Kf3k/Nehl/Kf3/Nab2/Dg2/Bu Htr2c/Chrn2/Hth3/Htr2d/Phr4 Cabpl/Hpa2/Drd2/Phr4 Cabpl/Hpa2/Drd2/Phr4 Cabpl/Hpa2/Drd2/Phr4 Scn32/Scn42/Scn3/Skap6/Htr2a/Prkce Cacng2/Cacng3/Knc1/Knap1/Skap6/Htr2a/Prkce Cacng2/Cacng3/Knc1/Knap1/Skap6/Ltr2a/Prkce	11 6 7 12 11 12 6 5 5 5 5 9 7 10
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8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8	GC-0007528 GC-0007528 GC-0002847 GC-0008647 GC-0008646 GC-0008864 GC-0008156 GC-0008166	neuronuscular junction development organells transport along microtubule heart contraction positive regulation of on transmembran positive regulation of odvelopmental gro axonal transport G protein-coupled serotonin receptor ag regulation of voltage-gated calcium chan potassium ion import across plasma mer release of sequestered calcium chan positive regulation of storage-gated calcium neurotransmitter reuptake negative regulation of sequestering of ci positive regulation of sequestering of calcium loss inhibitory synapse assembly dense core granule exocytosis negulation of calcium ion transmembran serotonin receptor signaling pathway heart proces	6/373 7/373 12/373 11/373 11/373 6/373 5/373 5/373 5/373 5/373 5/373 5/373 3/373	184/19943 58/19943 80/19943 215/19943 215/19943 215/19943 216/19943 40/19943 40/19943 40/19943 132/19943 132/19943 134/19943 11/19943 11/19943 11/19943 11/19943 11/19943 13/19943 136/19943 136/19943 136/19943	0.000717 0.000733 0.000745 0.000767 0.00078 0.000803 0.000803 0.000856 0.000856 0.000856 0.000856 0.000858 0.000958 0.000958 0.000958 0.000958 0.000958 0.000958 0.000958 0.000958 0.000958 0.000958 0.000958 0.000958 0.000958 0.000958 0.000958 0.0001046 0.001104	0.006931 0.007168 0.007168 0.007326 0.007429 0.007596 0.007628 0.008045 0.008045 0.008045 0.008045 0.008045 0.008071 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.009594 0.009594 0.009594	0.00539577 0.0055028 0.0055028 0.0055028 0.0055028 0.0052221 0.00531321 0.0052309 0.00628309 0.00628309 0.00628309 0.00628309 0.00628285 0.0074838 0.0074288 0.0074288 0.0074283	Drd2/Nehl/Gin1/Riv2/Crhbp/Tac3/Ddc/Gin2b/Htr2a/Pikce/Chrr Comg2/Ni/Concad2JShnk1/ChrUhD12b Klf5a/Nehl/Dwn211/Nel/Rasgrb1/Map2/Map1b Drd2/Rv2/Apta3/Sicshb2/Chrg3/Chaj2Cara13/Akap6/Cocn Sv2/Drd2/Rv2/Apta3/Sicshb2/Chrg3/Chaj2Cara13/Akap6/Cocn Sv2/Drd2/Rv1/Apta3/Ris2/Ris2/T0p6/Kncc1/Kcn14/Akap6/Cocn Sv2/Drd2/Rv2/Apta3/Kcn12/Sc12A3 Thv3/Drd2/Rv2/Apta3/Kcn12/Sc12A3 Thv3/Drd2/Rv2/Apta3/Kcn12/Sc12A3 Thv3/Drd2/Rv2/Apta3/Kcn12/Sc12A3 Thv3/Drd2/Rv2/Apta3/Kcn12/Sc12A3 Thv3/Drd2/Rv2/Apta3/Kcn12/Sc12A3 Thv3/Drd2/Rv2/Apta3/Kcn12/Sc12A3 Thv3/Drd2/Rv2/Apta3/Kcn12/Sc12A3 Thv3/Drd2/Rv2/Apta3/Kcn12/Sc12A3 Chrd2/Scd3/Nkc12Kcn14/Kap6/Kcn2A21/Hc1 Gabrg2/Gia3/Gabra3/Gabra3/Car7/Gin12/Sc12A5/Gabra3/Sc12A Drd2/Kcd3/Nkc12Kcn14/Kap6/Hc12a/Prkce Chrd3/Rcd2/Lnd2 Gabrg2/Gabra1/Gabra3 Cadpa2/Cadpr1/Unc13c Cadpa2/Cadpr1/Unc13c Cadpa2/Cadpr1/Unc13c Cadp12/Kc14/Ft12/Prk12/Chrm2/Chan231/Hc1 Thv2/Drd2/Rv2/Hr122/Prk12/Chrm2/Chrm2/Chag/Scn21/Tac3/Fcc Drd2/Rv2/Apta3/Scn4b/Hr22/Chrm2/Chag/Scn21/Tac3/Fcc Drd2/Rv2/Apta3/Scn4b/Hr22/Chrm2/Chag/Scn21/Tac3/Fcc Drd2/Rv2/Apta3/Scn4b/Hr22/Chrm2/Chag/Scn21/Tac3/Fcc Drd2/Rv2/Apta3/Scn4b/Hr22/Chrm2/Chag/Scn21/Tac3/Cacn24/ Hr22/Chrm2/Hr32/Hr22/Prk1/Kap5/Hr22/Prkce/Opt1/Lcan2d21 Hr22/Chrm2/Hr32/Hr22/Prk1/Kap5/Hr22/Prkce/Opt1/Lcan2d21 Hr22/Chrm2/Hr33/Scn4b/Hr22/Hr22/Prk2/Cacn24/Lap3/Scn4b/Hr22/Prkce/Opt1/Lcan2d21 Hr22/Chrm2/Hr33/Scn4b/Hr22/Chrm2/Chg2/Scn31/Tac3/Cacn24/Lap3/Scn4b/Hr22/Prkce/Opt1/Lcan2d21 Hr22/Chrm2/Hr33/Scn4b/Hr22/Hr22/Prk2/Cacn24/Lap3/Scn4b/Hr22/Prkce/Opt1/Lcan2d21	11 6 7 12 11 12 6 5 5 9 7 0 4 9 3 3 3 5 6 9 20 10 5 12
8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8	GC-0007528 GC-0007528 GC-00060047 GC-0004663 GC-0008864 GC-008864	neuronuscular junction development organelle transport along microtubule heart contraction positive regulation of ion transmembran positive regulation of olonge- ational transport G protein-coupled serotonian inceptor si regulation of voltage-asted aclium chan potassium ion import across plasma mer release of sequestered calcium chan positive regulation of daton channel act inorganic anion transport neurotransmitter reuptake negative regulation of sacuseting of cu positive regulation of sacuseting of cu positive regulation of sacuseting of cu positive regulation of sacuseting of positive regulation of sacuseting of positive regulation of sacuseting of positive regulation of sacuseting of neuron callular homeostasis regulation of sacuseting of calcium ion blood circulation regulation of sacuseting of calcium ion blood circulation neruon calcium ion transmembran serotonin receptor signaling pathway heart process sequestering of calcium ion	6/373 7/373 12/373 11/373 5/373 5/373 5/373 5/373 5/373 5/373 4/373 4/373 9/373 3/373	184/19943 58/19943 215/19943 215/19943 215/19943 216/19943 216/19943 40/19943 40/19943 40/19943 40/19943 40/19943 132/19943 13/19943 11/19943 11/19943 11/19943 11/19943 41/19943 42/19943 42/19943 164/19943 42/19943 224/19943	0.00717 0.00073 0.000767 0.000767 0.00080 0.000803 0.000856 0.000856 0.000856 0.000856 0.000857 0.000850 0.000951 0.000951 0.000958 0.0000	0.006931 0.007168 0.007168 0.007326 0.007479 0.007596 0.00845 0.008045 0.008045 0.008045 0.008045 0.008045 0.008071 0.008711 0.008711 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008750 0.009596 0.009596 0.009598 0.009598	0.00539577 0.0055028 0.0055028 0.0055028 0.00552028 0.0058228 0.0058228 0.0058228 0.0058280 0.0058280 0.0058280 0.00628309 0.00628309 0.00628309 0.00628205 0.00628285 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00748684 0.0074878 0.00748578 0.00755316	Drd2/Nehr/Gein/Kev2/Cheb/Tac3/Det/Gint2b/Htt2a/Pikce/Chrr Caceg2/Ky/Caced2/Shank/Loku/Unc13c Ktl5a/Nehr/Dync111/Nei/Rasgrb1/Nap2/Map1b Drd2/Ryr2/Apta3/SacA4/Chrr2/Chga/Scn12/Cacn13/Akap6/C Cacn27/Lhy/Cacn23/Syr2/Rgs7/Dp6/Kncc/Lkcn1/Akap6/C Ken1/Kkap2/Rgs7/Rgs7/Dp6/Knc2/Rgs7/Sn12/Cacn22d2/Ni Ktl5a/Nehr/Ktl5c/Map2/Dg2/Ban Htz2/Chrr2/Hhr3/Htz3/Htr4 Cabp1/Hpca/Drd2/Dp1/Lacn2d21 Ken3/Sk123/Knc1/Kcn1/Kap6/Cacn2d2/Htn1 Gabrg2/Gin2/Gabra1/Gabra5/Car7/Gin1/SiC12a5/Gabra3/SiC12a Drd2/Gin2/Gabra1/Gabra5/Car7/Gin1/SiC12a5/Gabra3/SiC12a Drd2/Gin2/Gabra1/Gabra5/Car7/Gin1/SiC12a5/Gabra3/SiC12a Drd2/Gin2/Gabra1/Gabra5/Car7/Gin1/SiC12a5/Gabra3/SiC12a Drd2/Gin2/Gabra1/Gabra5 Car2/Cacn23/Cacn23/Lin2A/Htt2/Pikce Chrna4/Pcp4/Chrnb2 Dpd1/Syk0/Chrn3 Gabrg2/Gabra1/Gabrb3 Na1/Calb2/Att22b3/Cnc11/Cacn21D Nagged4/Fg17/kr2/Dht22/Bab/Cacn21/Hcn1 Thy/Drd2/Ryr2/Htt22/Phck2/Dp3/kap6/Htt22Prkce Drd2/Ryr2/Apta3/Son4UH/t2Chrm2/Cags/Sna1/ac3/Grip2/C Cabp1/Thy1/Hoca/Drd2/Ryr2/Htt22/Phcke/Dp1/Lcan221 Htr2/Chrn2/Htt22/Htt22/Phck2/Dp3/kap6/Htt22Prkce Drd2/Ryr2/Apta3/Son4UH/t2Chrm2/Chg2/Sna1/ac3/Grip2/C Cabp1/Thy1/Hoca/Prk2/Htt22/Phcke/Dp1/Lcan221 Htr2/Chrn2/Htt22/Phck2/Dtr3/Kap6/Htt22Prkce Drd2/Ryr2/Apta3/Son4UH/t2Chrm2/Chg2/Sna1/ac3/Grip2/C Cabp1/Thy1/Hoca/Prk2/Htt22/Phcke/Dp1/Loan221 Htr2/Chrn2/Htt22/Phcke/Dtr3/Kap6/Htt22Prkce	$\begin{array}{c} 11 \\ 6 \\ 7 \\ 12 \\ 11 \\ 12 \\ 6 \\ 5 \\ 5 \\ 5 \\ 9 \\ 7 \\ 10 \\ 4 \\ 9 \\ 3 \\ 3 \\ 3 \\ 3 \\ 3 \\ 5 \\ 6 \\ 9 \\ 200 \\ 5 \\ 12 \\ 9 \end{array}$
8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8P 8	GC:0007528 GC:0007528 GC:0002847 GC:0008647 GC:0008647 GC:0008646 GC:0008864 GC:0008864 GC:0008864 GC:0008864 GC:0008810 GC:0008810 GC:0008810 GC:0008810 GC:0008810 GC:000880 GC:00080 GC:0000	neuronuscular junction development organells transport along microtubule heart contraction positive regulation of on transmembran positive regulation of odvelopmental gro axonal transport G protein-coupled serotonin receptor ag regulation of voltage-gated calcium chan potassium ion import across plasma mer release of sequestered calcium chan positive regulation of storage-gated calcium neurotransmitter reuptake negative regulation of sequestering of ci positive regulation of sequestering of calcium loss inhibitory synapse assembly dense core granule exocytosis negulation of calcium ion transmembran serotonin receptor signaling pathway heart proces	6/373 7/373 12/373 11/373 12/373 6/373 5/373 5/373 5/373 5/373 5/373 3/373	184/19943 58/19943 215/19943 215/19943 216/19943 216/19943 40/19943 40/19943 82/19943 82/19943 13/19943 14/19943 11/19943 11/19943 11/19943 11/19943 13/19943 49/319443 136/19943 49/31943 136/19943 42/19943 22/419943 22/419943 12/19943 22/419943	0.00717 0.000745 0.000745 0.000745 0.000784 0.000780 0.000856 0.000856 0.000856 0.000856 0.000856 0.000857 0.000854 0.000926 0.000926 0.000958 0.000159 0.001155 0.001115 0.001115	0.006931 0.007068 0.007168 0.007168 0.007459 0.007596 0.007596 0.008045 0.008045 0.008045 0.008045 0.008045 0.008071 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008771 0.008754 0.009594 0.009594 0.009594 0.009564 0.00956	0.00539577 0.0055028 0.0055028 0.0055028 0.0055028 0.0058028 0.0058028 0.00582291 0.0058280 0.0058280 0.00628309 0.00628309 0.00628309 0.006282815 0.006282815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00682815 0.00678588 0.0074869 0.0074859 0.0075888	Drd2/Nehl/Gin1/Riv2/Crhbp/Tac3/Ddc/Gin2b/Htr2a/Pikce/Chrr Comg2/Ni/Concad2JShnk1/ChrUhD12b Klf5a/Nehl/Dwn211/Nel/Rasgrb1/Map2/Map1b Drd2/Rv2/Apta3/Sicshb2/Chrg3/Chaj2Cara13/Akap6/Cocn Sv2/Drd2/Rv2/Apta3/Sicshb2/Chrg3/Chaj2Cara13/Akap6/Cocn Sv2/Drd2/Rv1/Apta3/Ris2/Ris2/T0p6/Kncc1/Kcn14/Akap6/Cocn Sv2/Drd2/Rv2/Apta3/Kcn12/Sc12A3 Thv3/Drd2/Rv2/Apta3/Kcn12/Sc12A3 Thv3/Drd2/Rv2/Apta3/Kcn12/Sc12A3 Thv3/Drd2/Rv2/Apta3/Kcn12/Sc12A3 Thv3/Drd2/Rv2/Apta3/Kcn12/Sc12A3 Thv3/Drd2/Rv2/Apta3/Kcn12/Sc12A3 Thv3/Drd2/Rv2/Apta3/Kcn12/Sc12A3 Thv3/Drd2/Rv2/Apta3/Kcn12/Sc12A3 Thv3/Drd2/Rv2/Apta3/Kcn12/Sc12A3 Chrd2/Scd3/Nkc12Kcn14/Kap6/Kcn2A21/Hc1 Gabrg2/Gia3/Gabra3/Gabra3/Car7/Gin12/Sc12A5/Gabra3/Sc12A Drd2/Kcd3/Nkc12Kcn14/Kap6/Hc12a/Prkce Chrd3/Rcd2/Lnd2 Gabrg2/Gabra1/Gabra3 Cadpa2/Cadpr1/Unc13c Cadpa2/Cadpr1/Unc13c Cadpa2/Cadpr1/Unc13c Cadp12/Kc14/Ft12/Prk12/Chrm2/Chan231/Hc1 Thv2/Drd2/Rv2/Hr122/Prk12/Chrm2/Chrm2/Chag/Scn21/Tac3/Fcc Drd2/Rv2/Apta3/Scn4b/Hr22/Chrm2/Chag/Scn21/Tac3/Fcc Drd2/Rv2/Apta3/Scn4b/Hr22/Chrm2/Chag/Scn21/Tac3/Fcc Drd2/Rv2/Apta3/Scn4b/Hr22/Chrm2/Chag/Scn21/Tac3/Fcc Drd2/Rv2/Apta3/Scn4b/Hr22/Chrm2/Chag/Scn21/Tac3/Cacn24/ Hr22/Chrm2/Hr32/Hr22/Prk1/Kap5/Hr22/Prkce/Opt1/Lcan2d21 Hr22/Chrm2/Hr32/Hr22/Prk1/Kap5/Hr22/Prkce/Opt1/Lcan2d21 Hr22/Chrm2/Hr33/Scn4b/Hr22/Hr22/Prk2/Cacn24/Lap3/Scn4b/Hr22/Prkce/Opt1/Lcan2d21 Hr22/Chrm2/Hr33/Scn4b/Hr22/Chrm2/Chg2/Scn31/Tac3/Cacn24/Lap3/Scn4b/Hr22/Prkce/Opt1/Lcan2d21 Hr22/Chrm2/Hr33/Scn4b/Hr22/Hr22/Prk2/Cacn24/Lap3/Scn4b/Hr22/Prkce/Opt1/Lcan2d21	11 6 7 12 11 12 6 5 5 9 7 0 4 9 3 3 3 3 5 6 9 20 10 5 12

BP BP	GO:0021695 cerebellar cortex development GO:0018958 phenol-containing compound met	6/373 tabolic 8/373	63/19943 111/19943	0.001138	0.010143	0.00789627	Sez6I2/Atp2b2/Cbln1/KlhI1/Cend1/Sptbn2 Tph2/Drd2/Sncb/Atp2b2/Htr2c/Ddc/Chrna7/Chrnb2	6 8
BP	GO:0009914 hormone transport	17/373	390/19943	0.001154	0.010244	0.00797494	Cplx1/Rapgef4/Vsnl1/Scg5/Drd2/Pex5l/Gpld1/Crhbp/Htr2c/Chga/	17
BP	GO:1904375 regulation of protein localization t GO:0098887 neurotransmitter receptor transp	to cell r 9/373	139/19943 12/19943		0.010937 0.011088	0.00851444	Rapgef4/Arhgap44/Cacng2/Grm1/Dpp6/Camk2b/Mrap2/Camk2a, Arhgap44/Grip2/Lrrc7	9 3
BP	GO:0006898 receptor-mediated endocytosis	12/373	228/19943	0.001273	0.011186	0.00870791	Nsf/Napb/Cacng2/Hpca/Drd2/Cacng3/Pacsin1/Necab2/Sgip1/Nrg	12
BP BP	GO:0098656 anion transmembrane transport GO:0021510 spinal cord development	13/373 9/373	260/19943 140/19943	0.001293 0.001298	0.01126	0.00876588	Gabrg2/Gira2/Gabra1/Gabra5/Gira1/Sic32a1/Sic17a6/Sic12a5/Sic Rapgef4/Gira2/Nefh/Nefl/Nefm/Acan/Sit1/Lhx4/Nova1	13 9
BP	GO:0021510 spinal cord development GO:0060004 reflex	4/373	26/19943	0.001298			Cacng2/Gira1/Kcnma1/Shank1	4
BP	GO:2000311 regulation of AMPA receptor activ	vity 4/373	26/19943	0.0013	0.01126	0.00876588	Cacng2/Cacng3/Mapk8ip2/Shank1	4
BP BP	GO:0021675 nerve development GO:0010107 potassium ion import	7/373 5/373	89/19943 45/19943	0.001401 0.001473	0.012065 0.012583	0.00939238	: Nptx1/Gabra5/Kcna2/Pax2/Chrnb2/Gabrb3/Pou4f1 . Kcnj3/Slc12a5/Atp1a3/Kcnj12/Slc12a3	7 5
BP	GO:0010107 potassium ion import GO:1901381 positive regulation of potassium in		45/19943			0.00979572	. Rgs7/Dpp6/Kcnc1/Kcna1/Akap6	5
BP	GO:2001258 negative regulation of cation char	nnel act 5/373	45/19943	0.001473	0.012583	0.00979572	Cabp1/Fgf12/Drd2/Kcnab1/Oprl1	5
BP BP	GO:1904063 negative regulation of cation tran GO:0097305 response to alcohol	smemt 7/373 18/373	90/19943 437/19943		0.012751 0.013377		Cabp1/Fgf12/Drd2/Hecw1/Kcnab1/Prkce/Oprl1 Gira2/Kif5a/Drd2/Grin1/Gira1/Nefl/Gpld1/Crhbp/Rgs7/Gnas/Cacn	7 18
BP	GO:0002028 regulation of sodium ion transpor		91/19943	0.001594	0.013517	0.01052241	Fgf12/Drd2/Hecw1/Scn4b/Gnas/Neto1/Neto2	7
BP	GO:0048814 regulation of dendrite morphoger		117/19943		0.013584	0.01057497	Arhgap44/Grin1/Hecw1/Camk2b/Cit/Chrnb2/Dnm3/Trpc5	8
BP BP	GO:0099639 neurotransmitter receptor transp GO:1902950 regulation of dendritic spine main	ort, en: 3/373	13/19943 13/19943	0.001615	0.013584		Arhgap44/Grip2/Lrrc7 Grin1/Zfp804a/Grin2b	3 3
BP	GO:0043954 cellular component maintenance		68/19943	0.001615			Grin1/Rab3a/Zfp804a/Grin2b/Dlg2/Bsn	6
BP	GO:0035235 ionotropic glutamate receptor sig	naling 4/373	28/19943		0.014374	0.0111902	Grin1/Atp1a3/Camk2a/Grin2b	4
BP BP	GO:0045761 regulation of adenylate cyclase ac GO:0060384 innervation	tivity 4/373 4/373	28/19943 28/19943		0.014374 0.014374		. Hpca/Drd2/Hrh3/Akap6 .Nptx1/Gabra5/Gabrb3/Pou4f1	4
BP	GO:0099010 modification of postsynaptic struc		28/19943		0.014374		Cabp1/Arhgap44/Pfn2/LOC100909840	4
BP	GO:0008089 anterograde axonal transport	5/373	47/19943		0.014858		Kif5a/Nefl/Kif5c/Map2/Dlg2	5
BP BP	GO:0030431 sleep GO:0032414 positive regulation of ion transme	5/373 mbran 8/373	47/19943 119/19943	0.001793	0.014858 0.014865	0.01156693	. Drd2/Kcna2/Htr2a/Chrnb2/Cacna1i ' Cacng2/Cacng3/Ryr2/Kcnc1/Kcna1/Akap6/Cacna2d1/Hcn1	5 8
BP	GO:0051235 maintenance of location	15/373	339/19943	0.001914	0.015796	0.01229718	Vstm2a/Thy1/Drd2/Pex5l/Epb41l3/Ryr2/Rit2/Htr2c/Mest/Pich2/Jj	15
BP	GO:0048488 synaptic vesicle endocytosis	6/373	70/19943	0.001969	0.016154	0.01257528	Syt2/Sncb/Pacsin1/Syp/Syt7/Dnm3	6
BP	GO:0140238 presynaptic endocytosis GO:0045104 intermediate filament cytoskeleto	6/373 on orga 5/373	70/19943 48/19943	0.001969	0.016154	0.01257528	Syt2/Sncb/Pacsin1/Syp/Syt7/Dnm3 Nefh/Nefl/Nefm/Ina/Atp8a2	6
BP	GO:1900273 positive regulation of long-term s		29/19943	0.001976	0.016154	0.01257528	Drd2/Adcy1/Grin2b/Chrna7	5 4
BP BP	GO:2000310 regulation of NMDA receptor acti		29/19943	0.001976			Rph3a/Rasgrf1/Crhbp/Mapk8ip2	4
BP	GO:0021554 optic nerve development GO:0030007 cellular potassium ion homeostas	3/373 is 3/373	14/19943 14/19943		0.016326	0.01270915	Kcna2/Pax2/Chrnb2 Drd2/Atp1a3/Kcnma1	3
BP	GO:0032252 secretory granule localization	3/373	14/19943	0.002027	0.016326	0.01270915	Kif5a/Rasgrp1/Map2	з
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 GO:0021766 hippocampus development	16/373 8/373	376/19943 123/19943	0.002036	0.0163/3	0.012/45/6	Cplx1/Rapgef4/Vsnl1/Scg5/Drd2/Pex5l/Gpld1/Crhbp/Htr2c/Chga/ Kif5a/Nefh/Nefl/Nefm/Slc32a1/Slc17a6/Kcna1/Grin2b	16 8
BP	GO:0050795 regulation of behavior	7/373	97/19943	0.002301	0.018331	0.0142702	Drd2/Cntnap4/Hcrtr2/Kcna2/Sgip1/Oprl1/Chrnb2	7
BP BP	GO:0042755 eating behavior	5/373	50/19943 418/19943	0.002367	0.018752		i Oprd1/Atp8a2/Hrh3/Sgip1/Oprl1 : Drd2/Glra1/Ryr2/Atp1a3/Scn4b/Chrm2/Chga/Scn1a/Atp8a2/Grip;	5 17
BP	GO:0003012 muscle system process GO:0048511 rhythmic process	17/373 16/373	383/19943	0.0024			<ul> <li>Drd2/Gra1/Kyr2/Atp1a3/Scn4b/Chrm2/Cnga/Scn1a/Atp8a2/Grip.</li> <li>Tph2/Drd2/Hertr2/Grin1/Kena2/Chga/Dde/Adey1/Mapk10/Kenma</li> </ul>	16
BP	GO:0021700 developmental maturation	14/373	314/19943	0.002498	0.019478	0.01516308	Gpr3/Grin1/Nefl/Rab3a/Sez6l2/Camk2b/Grip2/Pax2/Kcnma1/Mar	14
BP	GO:0007194 negative regulation of adenylate		15/19943 15/19943	0.002498			Drd2/Hrh3/Akap6	3
BP	GO:0031340 positive regulation of vesicle fusio GO:1901160 primary amino compound metabo	olic pro 3/373	15/19943	0.002498	0.019478	0.01516308	: Syt2/Rims1/Syt7 : Tph2/Atp2b2/Ddc	3 3
BP	GO:1901386 negative regulation of voltage-gat	ted cak 3/373	15/19943	0.002498	0.019478	0.01516308	Cabp1/Drd2/Oprl1	3
BP BP	GO:1903818 positive regulation of voltage-gate		15/19943 31/19943		0.019478 0.019744		Kcnc1/Kcna1/Akap6 Nefl/Sez6l2/Camk2b/Shank1	3 4
BP	GO:0060074 synapse maturation GO:0009582 detection of abiotic stimulus	4/373 8/373	31/19943 126/19943		0.019744	0.01537005	Netl/Sezbl2/Camk2D/Shank1 Phf24/Ano3/Atp2b2/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/Kene1/Kena1/Akap6/Caena2d1/Hen1	8
BP BP	GO:2000549 regulation of sodium ion transme GO:0008016 regulation of heart contraction	mbran: 5/373 10/373	51/19943 185/19943	0.002584	0.019969	0.01554528	Fgf12/Hecw1/Scn4b/Neto1/Neto2 Drd2/Ryr2/Scn4b/Chrm2/Chga/Cacna1b/Akap6/Chrna7/Cacna2d2	5 10
BP	GO:0021761 limbic system development	9/373	155/19943	0.002607	0.020094	0.01564269	KifSa/Drd2/Nefh/Nefl/Nefm/Slc32a1/Slc17a6/Kcna1/Grin2b	9
BP	GO:0032413 negative regulation of ion transm	embrai 6/373	74/19943	0.002614	0.020094	0.01564269	Cabp1/Fgf12/Drd2/Hecw1/Kcnab1/Oprl1	6
BP BP	GO:0009581 detection of external stimulus GO:0007193 adenviate cyclase-inhibiting G pro	8/373	127/19943 75/19943	0.002702	0.020698	0.01611287	Phf24/Ano3/Atp2b2/Scn1a/Atp8a2/Kcna1/Grin2b/Htr2a Grm4/Drd2/Oprd1/Chrm2/Hrh3/Oprl1	8 6
BP	GO:2001222 regulation of neuron migration	5/373	52/19943	0.002816	0.021493	0.01673216	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 BP	GO:0098884 postsynaptic neurotransmitter re GO:0140239 postsynaptic endocytosis	ceptor 4/373 4/373	32/19943 32/19943	0.002862	0.021619		Hpca/Pacsin1/Nrg1/Dnm3 Hpca/Pacsin1/Nrg1/Dnm3	4
BP	GO:1902074 response to salt	4/373	32/19943	0.002862			Hpca/Nefh/Nefl/Pcp4	4
BP	GO:0098876 vesicle-mediated transport to the		101/19943	0.002892	0.021803	0.01697295	Cplx1/Arhgap44/Nsf/Stx1b/Grip2/Mapk10/Lrrc7	7
BP BP	GO:0051965 positive regulation of synapse ass GO:0001967 suckling behavior	embly 6/373 3/373	76/19943 16/19943				Slitrk3/Clstn3/Syndig1/Cbln1/Lingo4/Clstn2 Grin1/Grin2b/Pou4f1	6 3
BP	GO:0035865 cellular response to potassium ior		16/19943	0.003033	0.022438	0.01746794	Nptx1/Crhbp/Dlg2	з
BP	GO:0098926 postsynaptic signal transduction	3/373	16/19943	0.003033	0.022438	0.01746794	Cabp1/Nrg1/Camk4	3
BP BP	GO:0099527 postsynapse to nucleus signaling GO:0099640 axo-dendritic protein transport	2/373 athwa 3/373	16/19943 16/19943	0.003033	0.022438	0.01746794	Cabp1/Nrg1/Carnk4 Kif5a/Kif5c/Dlg2	3 3
BP	GO:1900271 regulation of long-term synaptic p		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		0.022584		Atp1a3/Syp/Cacna1b/Chrna7/Cacna2d1	5
BP BP	GO:0046717 acid secretion GO:0030072 peptide hormone secretion	8/373 13/373	130/19943 288/19943				Grm4/Drd2/Grm1/Htr2c/Hrh3/Grin2b/Oprl1/Abcc2 Cplx1/Rapgef4/Vsnl1/Drd2/Pex5l/Gpld1/Crhbp/Htr2c/Chga/Stxbp	8 13
BP	GO:0022037 metencephalon development	9/373	160/19943	0.00323	0.023656	0.01841552	Grin1/Ckmt1/Sez6l2/Atp2b2/Kcnc1/Cbln1/Klhl1/Cend1/Sptbn2	9
BP	GO:0045103 intermediate filament-based proc		54/19943	0.003324			Nefh/Nefl/Nefm/Ina/Atp8a2	5
BP BP	GO:0010513 positive regulation of phosphatid GO:0099502 calcium-dependent activation of s		5/19943 5/19943	0.003361	0.02413	0.01878472 0.01878472	Htr2c/Htr2a Svt2/Svt7	2 2
BP	GO:1902952 positive regulation of dendritic sp	ine ma 2/373	5/19943	0.003361	0.02413	0.01878472	Grin1/Zfp804a	2
BP BP	GO:0007009 plasma membrane organization	7/373	104/19943 104/19943	0.003406			Ano3/Epb41l3/Rab3a/Pacsin1/Sgip1/Xkr6/Syt7	7
BP	GO:0010771 negative regulation of cell morph GO:0003407 neural retina development	ogenes 7/373 6/373	104/19943 78/19943		0.024336	0.01894504	Thy1/Dmtn/Slit1/Cit/Map2/Dnm3/Trpc5 Thy1/Slc17a6/Atp2b2/Atp2b3/Atp8a2/Hcn1	6
BP	GO:0009612 response to mechanical stimulus	14/373	326/19943	0.003497	0.024942	0.01941662	Phf24/Ano3/Drd2/Ryr2/Acan/Atp2b2/Scn1a/Kcnc1/Atp8a2/Pax2/	14
BP BP	GO:0042749 regulation of circadian sleep/wak		34/19943 34/19943		0.025388		Drd2/Hcrtr2/Kcna2/Chrnb2 Lrfn5/Slitrk3/Clstn3/Cbln1	4
BP BP	GO:1905606 regulation of presynapse assembl GO:0043268 positive regulation of potassium in		34/19943 55/19943	0.003585	0.025388		- Lrfn5/Slitrk3/Clstn3/Cbin1 : Rgs7/Dpp6/Kcnc1/Kcna1/Akap6	4
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		17/19943	0.003632	0.025487	0.01984144	Arhgap44/Grip2/Lrrc7	3
BP	GO:0060041 retina development in camera-typ GO:1990138 neuron projection extension	pe eye 10/373 10/373	194/19943 195/19943	0.003563	0.025663	0.01997851 0.02068513	. Thy1/Hpca/Slc17a6/Atp2b2/Atp2b3/Atp8a2/Pax2/Celf4/Tub/Hcn1 . Syt2/Rims1/Nrn1/Slit1/Rims2/Nrg1/Map2/Map1b/Trpc5/L1cam	10 10
BP	GO:0098659 inorganic cation import across pla	asma m 6/373	80/19943	0.003863	0.026939	0.02097142	Kenj3/Slc12a5/Atp1a3/Kenj12/Slc8a3/Slc12a3	6
BP BP	GO:0099587 inorganic ion import across plasm GO:0061025 membrane fusion	a mem 6/373 8/373	80/19943 135/19943		0.026939		. Kcnj3/Slc12a5/Atp1a3/Kcnj12/Slc8a3/Slc12a3 i Colx1/Nsf/Svt2/Rims1/Stx1b/Vamp1/Rab3a/Svt7	6 8
BP	GO:0061025 membrane fusion GO:0034766 negative regulation of ion transm		135/19943 107/19943		0.027354 0.027679		Cplx1/Nsf/Syt2/Rims1/Stx1b/Vamp1/Rab3a/Syt7 Cabp1/Fgf12/Drd2/Hecw1/Kcnab1/Prkce/Oprl1	8
BP	GO:0045745 positive regulation of G protein-co	oupled 4/373	35/19943	0.003989	0.027679	0.02154746	Drd2/Chga/Mrap2/Necab2	4
BP BP	GO:0031102 neuron projection regeneration GO:0009410 response to xenabiatic stimulus	6/373 16/373	81/19943 404/19943	0.004108	0.028457	0.02215356	: Thy1/Nefh/Nefl/Nefm/Nrg1/Map1b : Hpca/Drd2/Nefh/Grin1/Rasgrf1/Ryr2/Crhbp/Rgs7/Tac3/Grin2b/Ht	6 16
BP	GO:0009410 response to xenoblotic stimulus GO:0090150 establishment of protein localizat		230/19943		0.028806	0.02242501	Cplx1/Arhgap44/Nsf/Cacng2/Hpca/Dmtn/Stx1b/Grip2/Mapk10/Sg	10
BP	GO:0014051 gamma-aminobutyric acid secreti	ion 3/373	18/19943	0.004298	0.0295	0.02296492	. Grm4/Htr2c/Hrh3	з
BP	GO:0021681 cerebellar granular layer develop	ment 3/3/3	18/19943	0.004298	0.0295	u.uzz96492	Atp2b2/Cbln1/Cend1	з

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	G0:0051703 G0:0020102 G0:1902305 G0:0022410 G0:0039174 G0:0030707 G0:0030300 G0:0033000 G0:0033000 G0:003710 G0:0035077 G0:1900451 G0:0035102 G0:0031279 G0:0045475 G0:002548 G0:0025478	Intraspecies interaction between organi cochea development regulation of sodium ion transmembraan ciccatian stegolwake cycle process regulation of presynapse organization regulation of activitic localization to plas regulation of activitic localization to plas regulation of activitic localization to positive regulation of datecholamine sec negative regulation of datecholamine sec negative regulation of datecholamine sec activitic regulation of datecholamine sec activitic regulation of datecholamine sec activitic regulation of glutamate recepto cardiac muscide cell contraction hindbrain development regulation of cycles activity negative regulation of four transport collum-modifiest dignaling using intrace	5/373 5/373 5/373 4/373 4/373 7/373 10/373 18/373 3/373 3/373 3/373 3/373 3/373 10/373	60/19943 60/19943 60/19943 38/19943 38/19943 114/19943 207/19943 20/19943 20/19943 20/19943	0.005242 0.005242 0.005382 0.005382 0.005382 0.005635 0.005757 0.005837 0.005841	0.033846 0.033846 0.033846 0.034592 0.034592 0.036168 0.036844 0.037001	0.02634842 0.02634842 0.02634842 0.02692929 0.02692929 0.0281564 0.0286828	Grin1/Mapk&p2/Shank1/Chmb2/Mrxn3 Pvalb/Gabra5/Atp2b2/Pax2/Gabrb3 Fg12/Hecw152cdb/Neto2 Drd2/Hcrt2/Kcna2/Chmb2 Lrfn5/Slitr13/Cbin3/Cbin1 Arhgap44/Grm1/Dpp6/Camk2b/Mrap2/Camk2a/Dpp10
9 + 6 6 7 + 7 + 6 6 7 + 7 + 6 6 7 + 7 + 6 6 7 + 7 +	G0:0090102 G0:1902305 G0:0022410 G0:0029114 G0:0099174 G0:0050770 G0:0033605 G0:0033605 G0:0050774 G0:0090451 G0:0086003 G0:0030902 G0:0032584 G0:0045475 G0:0025584	cochie development regulation of odiumi (on transmembran- circadian sleep/wale cycle process regulation of prosymaps organization regulation of prosymaps organization regulation of action of catcholamine see negative regulation of datcholamine see negative regulation of datcholamine see negative regulation of datcholamine see negative regulation of datcholamine see cardiac muscle call contraction hindbrain development regulation of cycles activity negative regulation of jours activity negative regulation of jours activity negative regulation of jours activity negative regulation of jours activity	5/373 5/373 4/373 4/373 10/373 3/373 3/373 3/373 3/373 5/373 10/373	60/19943 60/19943 38/19943 38/19943 114/19943 207/19943 20/19943 20/19943 20/19943	0.005242 0.005242 0.005382 0.005382 0.005635 0.005757 0.005837 0.005841	0.033846 0.033846 0.034592 0.034592 0.036168 0.036844 0.037001	0.02634842 0.02634842 0.02692929 0.02692929 0.0281564 0.0286828	Pvalb/Cabina5/Atq2b2/Pax2/Cabin3 Epf12/Hecv1/Scn4b/Neto1/Neto2 Drd2/Hortr2/Kcna2/Chrnb2 Lrfn5/Siltrk3/Clstn3/Cbin1 Arhgap44/Grm1/Dppb/Camk2b/Mrap2/Camk2a/Dpp10
9. 9. 61 69 99 99 99 99 99 99 99 99 99 99 99 99	GO:1902305 GO:0022410 GO:0099174 GO:1903076 GO:0050770 GO:0033050 GO:0033050 GO:0033050 GO:0033050 GO:00320574 GO:0090450 GO:003584 GO:0045475 GO:0099188 GO:00921549	regulation of sodium ion transmembran- circadian steep/wake cycle process regulation of presynapse organization regulation of archicle localization to plass regulation of active localization to plass regulation of active localization to positive regulation of active morphop positive regulation of active morphop positive regulation of glutamate recepto cardiac muscide cell contraction hindbrain development regulation of cycles activity negative regulation of nortansport calcium-modiates dignaling using intrace	5/373 4/373 4/373 7/373 10/373 18/373 3/373 3/373 3/373 3/373 3/373 3/373 5/373 10/373	60/19943 38/19943 38/19943 114/19943 207/19943 495/19943 20/19943 20/19943 20/19943	0.005242 0.005382 0.005382 0.005635 0.005757 0.005837 0.005841	0.033846 0.034592 0.034592 0.036168 0.036844 0.037001	0.02634842 0.02692929 0.02692929 0.0281564 0.0286828	Fgf12/Hecw1/Scn4b/Neto1/Neto2 Drd2/Hortr2/Kcna2/Chrnb2 Urn5/SitrR3/Cistn3/Cbin1 Arhgap44/Grm1/Dpp6/Camk2b/Mrap2/Camk2a/Dpp10
9 P G G P P G G P P G G P P G G P P P G G P P P G G P P P G G P P P G G P P P G G P P P G G P P P G G P P P G G P P G G P P G G P P G G P P G G P P G G P P G G P P G G P P G G P P G G P P G G P P G G P P G G P P P P G G P P P P G P P P P G P P P P G P P P P G P P P P G P	GO:0022410 GO:0099174 GO:1903076 GO:0030900 GO:0030900 GO:0030770 GO:0050774 GO:0097107 GO:1900451 GO:0086003 GO:0030902 GO:0031279 GO:0032584 GO:0045475 GO:0099188 GO:0021549	circadian sleep/wale cycle process regulation of prostin localization to plass regulation of prostin localization to plass regulation of aconogenesis positive regulation of datcholamine see negative regulation of datcholamine see negative regulation of datcholamine see positive regulation of gulamater recepto cardiac muscle cell contraction hindbrain development regulation of cyclass activity negative regulation of jour transport calcium-mediates dignaing using intrace	4/373 4/373 7/373 10/373 18/373 3/373 3/373 3/373 3/373 3/373 3/373 5/373 10/373	38/19943 38/19943 114/19943 207/19943 495/19943 20/19943 20/19943 20/19943	0.005382 0.005382 0.005635 0.005757 0.005837 0.005841	0.034592 0.034592 0.036168 0.036844 0.037001	0.02692929 0.02692929 0.0281564 0.0286828	Drd2/Hcrtr2/Kcna2/Chrnb2 Lrfn5/Slitrk3/Clstn3/Cbln1 Arhgap44/Grm1/Dpp6/Camk2b/Mrap2/Camk2a/Dpp10
p         p         g	GO:0099174 GO:1903076 GO:0050770 GO:0050770 GO:0050774 GO:0050774 GO:1900451 GO:0086003 GO:0030902 GO:0031279 GO:0043271 GO:0035884 GO:0021588 GO:0021549	regulation of presynapse organization regulation of protein localization to plass regulation of axonogenesis forskrain development positive regulation of dendrite morphog positive regulation of dendrite morphog positive regulation of dendrite morphog positive regulation of dendrite morphog cardiac muscle cell contraction hindbrain development regulation of cyclase activity negative regulation of intransport calcium-modiates dignaing using intrace	4/373 7/373 10/373 18/373 3/373 3/373 3/373 3/373 3/373 3/373 5/373 10/373	38/19943 114/19943 207/19943 495/19943 20/19943 20/19943 20/19943	0.005382 0.005635 0.005757 0.005837 0.005841	0.034592 0.036168 0.036844 0.037001	0.02692929 0.0281564 0.0286828	Lrfn5/Slitrk3/Clstn3/Cbln1 Arhgap44/Grm1/Dpp6/Camk2b/Mrap2/Camk2a/Dpp10
P         Gi         Gi           P         Gi         Gi           P         Gi         P         Gi           P         Gi         P         Gi         P           P         Gi         P         Gi         P           P         Gi         P         Gi         P           Gi         P         Gi         P         Gi           P         Gi         P         Gi         P           Gi         P         Gi         P         Gi           P         Gi         P         Gi         P           Gi         P         Gi         P         Gi           P         Gi         P         Gi         P           Gi         P         Gi         P         Gi           P         Gi         P         Gi         P           P         Gi         P         Gi         P           Gi         P         Gi         P         Gi           P         Gi         P         Gi         P           Gi         P         Gi         P         Gi           P         Gi <td>GO:1903076 GO:0050770 GO:0030900 GO:0033605 GO:0050774 GO:0097107 GO:1900451 GO:0030902 GO:0031279 GO:0031279 GO:0043271 GO:003584 GO:003584 GO:009188 GO:0021549</td> <td>regulation of protein localization to plass regulation of acknogenesis forebrain development positive regulation of catcholamine see negative regulation of elandrite morphog positive regulation of glutamate recepto cardiac muscle cell contraction hindbrain development regulation of cyclase activity negative regulation of four transport calcium-mediates dignaing using intrace</td> <td>7/373 10/373 18/373 3/373 3/373 3/373 3/373 3/373 3/373 5/373 10/373</td> <td>114/19943 207/19943 495/19943 20/19943 20/19943 20/19943</td> <td>0.005635 0.005757 0.005837 0.005841</td> <td>0.036168 0.036844 0.037001</td> <td>0.0281564 0.0286828</td> <td>Arhgap44/Grm1/Dpp6/Camk2b/Mrap2/Camk2a/Dpp10</td>	GO:1903076 GO:0050770 GO:0030900 GO:0033605 GO:0050774 GO:0097107 GO:1900451 GO:0030902 GO:0031279 GO:0031279 GO:0043271 GO:003584 GO:003584 GO:009188 GO:0021549	regulation of protein localization to plass regulation of acknogenesis forebrain development positive regulation of catcholamine see negative regulation of elandrite morphog positive regulation of glutamate recepto cardiac muscle cell contraction hindbrain development regulation of cyclase activity negative regulation of four transport calcium-mediates dignaing using intrace	7/373 10/373 18/373 3/373 3/373 3/373 3/373 3/373 3/373 5/373 10/373	114/19943 207/19943 495/19943 20/19943 20/19943 20/19943	0.005635 0.005757 0.005837 0.005841	0.036168 0.036844 0.037001	0.0281564 0.0286828	Arhgap44/Grm1/Dpp6/Camk2b/Mrap2/Camk2a/Dpp10
P         Gi         Gi           P         Gi         Gi           P         Gi         Gi           P         Gi         P           Gi         P         Gi	GC:0030900 GO:0033605 GO:0050774 GO:0097107 GO:0086003 GO:0030902 GO:003279 GO:0043271 GO:0043271 GO:0043271 GO:0043275 GO:0045475 GO:0099188 GO:0021549	forebrain development positive regulation of catecholamine see negative regulation of dendrite morphog postsynaptic density assembly positive regulation of glutamate recepto cardiae muscle cell contraction hindbrain development regulation of cyclase activity negative regulation of ion transport calcium-mediated signaling using intrace	18/373 3/373 3/373 3/373 3/373 3/373 3/373 5/373 10/373	207/19943 495/19943 20/19943 20/19943 20/19943	0.005757 0.005837 0.005841	0.036844 0.037001	0.0286828	
P         Gi         Gi           P         Gi         Gi           P         Gi         Gi         P           Gi         P         Gi         P         Gi           P         Gi         P         Gi         P           Q         P         Gi         P         Gi           P         Gi         P         Gi         P           Gi         P         Gi         P         Gi           P         Gi         P         Gi         P           Gi         P         Gi         P         Gi           P         Gi         P         Gi         P           Gi         P         Gi         P         Gi           P         Gi         P         Gi         P           Q         P         Gi         P         Gi           P         Gi	GO:0033605 GO:0050774 GO:0097107 GO:1900451 GO:0086003 GO:0030902 GO:0031279 GO:0043271 GO:0035584 GO:0045475 GO:0099188 GO:0021549	positive regulation of catecholamine see negative regulation of dendrite morphog postsynaptic dendity assembly positive regulation of glutamate recepto cardiac muscle cell contraction hindbrain davelopment regulation of cyclase activity negative regulation of ion transport colcium-mediated signaling using Intrace	3/373 3/373 3/373 3/373 3/373 5/373 10/373	20/19943 20/19943 20/19943	0.005841	0.037001		Thy1/Grin1/Nefl/Nefm/Slit1/Nrg1/Map2/Map1b/Trpc5/L1cam
P         Gr         Gr	GO:0050774 GO:0097107 GO:1900451 GO:0086003 GO:0030902 GO:0031279 GO:0035584 GO:0045475 GO:0095188 GO:0021549	negative regulation of dendrite morphog postsynaptic density assembly positive regulation of glutamate recepto cardiae muscle cell contraction hindbrain development regulation of cyclase activity negative regulation of ion transport calcium-mediated signaling using intrace	3/373 3/373 3/373 3/373 5/373 10/373	20/19943 20/19943			0.02880497	Kif5a/Drd2/Nefh/Grin1/Nefl/Nefm/Slc32a1/Slc17a6/Atp1a3/Kcn
9 9 9 9 9 9 9 9 9 9 9 9 9 9	GO:0097107 GO:1900451 GO:0086003 GO:0030902 GO:0031279 GO:0043271 GO:0035584 GO:0045475 GO:0099188 GO:0021549	postsynaptic density assembly positive regulation of glutamate recepto cardiac muscle cell contraction hindbrain development regulation of cyclase activity negative regulation of ion transport calcium-mediated signaling using intrace	3/373 3/373 5/373 10/373	20/19943	0.005841			Chrna4/Pcp4/Chrnb2
P         Gi	GO:1900451 GO:0086003 GO:0030902 GO:0031279 GO:0043271 GO:0035584 GO:0045475 GO:0099188 GO:0021549	positive regulation of glutamate recepto cardiac muscle cell contraction hindbrain development regulation of cyclase activity negative regulation of ion transport calcium-mediated signaling using intrace	3/373 5/373 10/373					Cit/Dnm3/Trpc5 Nptx1/Cbln1/Shank1
P G G P G G P P G G P P F G P P G P F F F P F F P F P F F P F F P F F P F F P F P F F P F	GO:0086003 GO:0030902 GO:0031279 GO:0043271 GO:0035584 GO:0045475 GO:0099188 GO:0021549	cardiac muscle cell contraction hindbrain development regulation of cyclase activity negative regulation of ion transport calcium-mediated signaling using intrace	5/373 10/373	20/19943	0.005841	0.037001	0.02880497	Cacng2/Cacng3/Necab2
P G P G G P P G G P G G P G G P G G P P G G P P G G P P G G P P G G P P G G C P P G G C P P G G C P D C P D C P D C P D C P D C P D C P D C P D C C C C C C C C C C C C C C C C C C C	GO:0030902 GO:0031279 GO:0043271 GO:0035584 GO:0045475 GO:0099188 GO:0021549	hindbrain development regulation of cyclase activity negative regulation of ion transport calcium-mediated signaling using intrace	10/373	62/19943				Ryr2/Scn4b/Scn1a/Akap6/Cacna2d1
P GG P GG P GG P GG P GG P GG P GG P GG	GO:0031279 GO:0043271 GO:0035584 GO:0045475 GO:0099188 GO:0021549	regulation of cyclase activity negative regulation of ion transport calcium-mediated signaling using intrace	4.10.750	209/19943	0.006149	0.038782	0.03019107	Grin1/Ckmt1/Sez6l2/Atp2b2/Kcnc1/Cbln1/Klhl1/Cend1/Sptbn2/F
Р G Р G Р G Р G Р G Р C G Р P G G P P C G G C C G C C C C C C C C C	GO:0035584 GO:0045475 GO:0099188 GO:0021549	calcium-mediated signaling using intrace	4/373	40/19943				Hpca/Drd2/Hrh3/Akap6
P G P G P G P G P G P G P G P G P G P G	GO:0045475 GO:0099188 GO:0021549		9/373	179/19943				Cabp1/Fgf12/Drd2/Hecw1/Kcnab1/Hrh3/Htr2a/Prkce/Oprl1
P G P G P G P G P G P G P G G P G F P G G P G F P G G F P F G G F P F F G G F P F F G G F P F F G G F F F F F F F F F F F F F F F F	GO:0099188 GO:0021549	locomotor rhythm		21/19943	0.006722	0.041964	0.03266815	Dmtn/Ryr2/Tenm2
P G P G P G P G P G P G P G P G P G P G	GO:0021549		3/373	21/19943 21/19943				Mapk10/Kcnma1/Oprl1
P G P G P G P G P G P G P G P G P G P G			3/373 8/373	148/19943				Nefl/ina/Camk2b Ckmt1/Sez6l2/Atp2b2/Kcnc1/Cbin1/Kihl1/Cend1/Sptbn2
P G P G P G P G P G P G P G P G P G P G			13/373	316/19943				Vsnl1/Scg5/Drd2/Pex5l/Gpld1/Crhbp/Htr2c/Chga/Gnas/Stxbp5l/
P G P G P G P G P G P G P G P G P G P G	GO:0034764	positive regulation of transmembrane tr			0.006836	0.041964	0.03266815	Cacng2/Thy1/Cacng3/Ryr2/Rgs7/Dpp6/Kcnc1/Kcna1/Akap6/Cacr
.P Gi .P Gi .P Gi .P Gi .P Gi .P Gi .P Gi			2/373	7/19943	0.006885	0.041964	0.03266815	Grin1/Chrnb2
PGI PGI PGI PGI PGI PGI PGI PGI	GO:0010511	regulation of phosphatidylinositol biosyr		7/19943	0.006885	0.041964	0.03266815	Htr2c/Htr2a
P G P G P G P G P G P G	GO:0021578	hindbrain maturation	2/373	7/19943				Grin1/Cend1
P GI P GI P GI P GI P GI P GI			2/373	7/19943				Slc12a5/Abcc2
P GI P GI P GI P GI P GI		sensory perception of touch positive regulation of neurotransmitter u	2/373	7/19943 7/19943			0.03266815	Rab3a/Kona1 Drd2/Nat8l
.P GI .P GI .P GI .P GI		neurotransmitter receptor transport, po		7/19943				Cacng2/Cacng3
P GI P GI			2/373	7/19943				Pfn2/L0C100909840
P G			2/373	7/19943			0.03266815	
P G		calcium ion export across plasma memb		7/19943				Atp2b3/Slc8a3
	GO:1990709	presynaptic active zone organization	2/373	7/19943			0.03266815	
		negative regulation of neuron projection		180/19943	0.00693	0.042178	0.03283479	Thy1/Rit2/RGD1307443/Stx1b/Slit1/Cit/Map2/Dnm3/Trpc5
			4/373	41/19943				Atp2b2/Cbln1/Cend1/Sptbn2
			3/373	22/19943				Grin1/Zfp804a/Grin2b
			3/373 4/373	22/19943 42/19943				Rab3a/Dig2/Bsn Drd2/Hertr2/Kena2/Chroh2
		circadian sleep/wake cycle negative regulation of calcium ion transr		42/19943 42/19943				Drd2/Hcrtr2/Kcna2/Chrnb2 Cabp1/Drd2/Prkce/Oprl1
			7/373	42/19943				Cabp1/Urd2/Price/Opr11 Arhgap44/Slc12a5/Camk2b/Camk2a/Nrg1/Shank1/Dnm3
			80/373	493/19943				Grm4/Rph3a/Magee1/Gabrg2/Glra2/Gabra1/Scn8a/Kcnj3/Lrfn5/
		intrinsic component of synaptic membra		254/19943	4.45E-40	9.69E-37		Grm4/Gabrg2/Gabra1/Scn8a/Kcnj3/Lrfn5/Cacng2/Drd2/Slitrk3/C
C GI			58/373	354/19943			1.3214E-34	Rph3a/Magee1/Gabrg2/Gira2/Gabra1/Scn8a/Lrfn5/Cacng2/Cadp
		integral component of synaptic membra		235/19943		5.09E-34	3.9647E-34	Grm4/Gabrg2/Gabra1/Scn8a/Kcnj3/Lrfn5/Cacng2/Drd2/Slitrk3/C
			62/373	452/19943	1.35E-35	1.18E-32		Cabp1/Rapgef4/Gabrg2/Gabra1/Arhgap44/Nsf/Scn8a/Lrfn5/Cacr
			45/373	212/19943				Grm4/Scn8a/Kcnj3/Cadps2/Drd2/Oprd1/Gabra5/Rims1/Chrna4/
			50/373 51/373	294/19943 314/19943	2.71E-33 6.13E-33	1.69E-30 3.34E-30	1.3134E-30	Gabrg2/Glra2/Gabra1/Scn8a/Kcnj3/Cacng2/Gabra5/Chrna4/Pex5 Gabrg2/Glra2/Gabra1/Scn8a/Kcnj3/Cacng2/Gabra5/Chrna4/Pex5
			51/373 51/373	314/19943 321/19943	6.13E-33 1.86E-32	3.34E-30 9E-30		
			55/373	421/19943	1.86E-32 1.82E-30	9E-30 6.62E-28		Gabrg2/Glra2/Gabra1/Scn8a/Kcnj3/Cacng2/Gabra5/Chrna4/Pex5 Cabp1/Rapgef4/Arhgap44/Nsf/Scn8a/Lrfn5/Cacng2/Drd2/Nefh/N
		intrinsic component of presynaptic mem		135/19943	3.44E-30	9.99E-28		Grm4/Scn8a/Kcnj3/Drd2/Oprd1/Gabra5/Chrna4/Cntnap4/Grin1/
			56/373	445/19943	3.7E-30			Cabp1/Rapgef4/Arhgap44/Nsf/Scn8a/Lrfn5/Cacng2/Drd2/Nefh/h
C G		intrinsic component of postsynaptic mer	39/373	185/19943	8.19E-30	2.1E-27	1.6353E-27	Gabrg2/Gabra1/Scn8a/Lrfn5/Cacng2/Drd2/Slitrk3/Oprd1/Gabra5
C G			54/373	417/19943	1.01E-29	2.45E-27	1.9101E-27	Cabp1/Rapgef4/Arhgap44/Nsf/Scn8a/Lrfn5/Cacng2/Drd2/Nefh/M
C G		integral component of presynaptic mem	32/373	122/19943	7.32E-28		9.9358E-26	Grm4/Scn8a/Kcnj3/Drd2/Oprd1/Gabra5/Chrna4/Cntnap4/Grin1/
C GI	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/
		integral component of postsynaptic men		175/19943		5.56E-25		Gabrg2/Gabra1/Scn8a/Lrfn5/Cacng2/Drd2/Slitrk3/Oprd1/Gabra5
		cation channel complex	39/373	221/19943	9.8E-27	1.33E-24		Scn8a/Kcnj3/Cacng2/Pex5l/Kcns2/Kcnab2/Grin1/Cacng3/Dlgap3/
			39/373 40/373	222/19943 245/19943	1.1/E-26	1.545-24	1.202E-24	Cpix1/Grm4/Rapgef4/Syt2/Pvalb/Drd2/Ncs1/Syn1/Oprd1/Kcnabi Cpix1/Grm4/Rapgef4/Syt2/Pvalb/Drd2/Ncs1/Syn1/Oprd1/Kcnabi
		intrinsic component of postsynaptic spec						Cpix1/Grm4/Rapget4/Syt2/Pvalb/Drd2/Ncs1/Syn1/Oprd1/Kcnab. Gabrg2/Gabra1/Scn8a/Lrfn5/Cacng2/Slitrk3/Oprd1/Gabra5/Clstr
		postsynaptic specialization membrane		139/19943	1.1F-24	1.09F-23	8.4608F-23	Gabrg2/Gabra1/Scn8a/Lrfn5/Cacng2/Siltrk3/Oprd1/Gabra5/Cistr Gabrg2/Gabra1/Scn8a/Lrfn5/Cacng2/Siltrk3/Oprd1/Gabra5/Cistr
		integral component of postsynaptic spec			4.55E-23	3.54E-21	2.7545E-21	Gabrg2/Gabra1/Scn8a/Lrfn5/Cacng2/Slitrk3/Oprd1/Gabra5/Clstr Gabrg2/Gabra1/Scn8a/Lrfn5/Cacng2/Slitrk3/Oprd1/Gabra5/Clstr
			25/373					Gabrg2/Gabra1/Lrfn5/Drd2/Slitrk3/Gabra5/Rims1/Clstn3/Cntnap
C G			21/373	76/19943	3.33E-19	2.34E-17	1.8233E-17	Grm4/Rapgef4/Scn8a/Kcnj3/Cadps2/Grin1/Cacng3/Slc17a6/Calb
C G	GO:0044304	main axon	21/373	86/19943	5.56E-18	3.73E-16	2.9017E-16	Scn8a/Thy1/Kcnab2/Epb41l3/Crhbp/Ank1/Kcna2/Kcnc3/Scn1a/K
		intrinsic component of postsynaptic den		81/19943				Scn8a/Lrfn5/Cacng2/Slitrk3/Oprd1/Clstn3/Grin1/Cacng3/Rgs7bp
C G		neuron projection membrane	19/373	74/19943				Gabrg2/Gabra1/Lamp5/Thy1/Hpca/Oprd1/Gabra5/Grin1/Epb41
			21/373	99/19943				Scn8a/Lrfn5/Cacng2/Slitrk3/Oprd1/Clstn3/Grin1/Cacng3/Rgs7bp
:C G(	GO:0098839		23/373	126/19943 75/19943				Cplx1/Grm4/Syt2/Pvalb/Syn1/Grin1/Calb2/Sncb/Vamp1/Rab3a/F Scn8a/Lrfn5/Cacng2/Slitrk3/Oprd1/Clstn3/Grin1/Cacng3/Grm1/A

CC		synaptic vesicle	28/373			4.62E-13	3.5965E-13	Rph3a/Syt2/Lamp5/Drd2/Syn1/Oprd1/Slc5a7/Rab3c/Grin1/Slc32a	28
CC	GO:0098688 GO:0043204	parallel fiber to Purkinje cell synapse	13/373 24/373	33/19943 177/19943	1.14E-14 3.34E-14			Grm4/Scn8a/Kcnj3/Cadps2/Grin1/Calb2/Atp2b2/Atp2b3/Cbln1/Kc	13 24
CC		neuron spine	26/373	217/19943		2.84E-12	2.2075E-12	Rbfox3/Kif5a/Pcsk2/Hpca/Drd2/Nefh/Serpini1/Slc5a7/Rgs7bp/Glr- Rph3a/Rapgef4/Arhgap44/Hpca/Drd2/Oprd1/Grin1/Rgs7bp/Grm1	24
CC		leading edge membrane	23/373	171/19943	1.38E-13	6.76E-12	5.2596E-12	Gabrg2/Gabra1/Arhgap44/Lamp5/Thy1/Hpca/Oprd1/Gabra5/Grin	23
CC		voltage-gated potassium channel compl- synaptic vesicle membrane	17/373 20/373	83/19943 127/19943	1.93E-13 2.69E-13			Kcnj3/Kcns2/Kcnab2/Kcnc3/Dpp6/Kcnip4/Kcnc1/Kcnab1/Kc Rph3a/Syt2/Lamp5/Drd2/Syn1/Oprd1/Rab3c/Slc32a1/Slc17a6/Ga	17 20
CC		exocytic vesicle membrane	20/373	127/19943	2.69E-13	1.24E-11		Rph3a/Syt2/Lamp5/Drd2/Syn1/Oprd1/Rab3c/Sic32a1/Sic17a6/Ga	20
CC	GO:0043197	dendritic spine	25/373	214/19943	3.09E-13	1.4E-11		Rph3a/Rapgef4/Arhgap44/Hpca/Drd2/Oprd1/Grin1/Rgs7bp/Grm1	25
CC		exocytic vesicle	28/373 17/373	280/19943 91/19943	5.6E-13 9.52E-13	2.49E-11 4.07E-11		Rph3a/Syt2/Lamp5/Drd2/Syn1/Oprd1/Slc5a7/Rab3c/Grin1/Slc32a Grm4/Arhgap44/Scn8a/Syn1/Rims1/Slc32a1/Stx1b/Rab3a/Atp2b2	28 17
CC		presynaptic active zone potassium channel complex	17/373	91/19943	9.52E-15 1.66E-12	4.07E-11 6.75E-11		Kcnj3/Kcns2/Kcnab2/Kcna2/Kcnc3/Dpp6/Kcnip4/Kcnc1/Kcnab1/Kc	17
CC	GO:0030133	transport vesicle	32/373	390/19943		1.07E-10	8.3664E-11	Rph3a/Nptx1/Syt2/Pcsk2/Lamp5/Drd2/Syn1/Oprd1/Sic5a7/Rab3c	32
CC CC		dendrite membrane neuromuscular junction	13/373 16/373	48/19943 99/19943	2.97E-12 4.49E-11	1.17E-10 1.59E-09		Gabrg2/Gabra1/Lamp5/Thy1/Hpca/Oprd1/Gabra5/Grin1/Slc12a5/ Rph3a/Syt2/Slc5a7/Nefl/Nefm/Dlgap3/Stx1b/Vamp1/Kcnc3/Syp/S	13 16
CC		transport vesicle membrane	21/373	186/19943	4.45E-11 4.87E-11			Rph3a/Syt2/JicSa//Weir/Weir/Ogap3/Stctb/Vamp1/kcicS/3yp/3 Rph3a/Syt2/Lamp5/Drd2/Syn1/Oprd1/Rab3c/Sic32a1/Sic17a6/Ga	21
CC		Schaffer collateral - CA1 synapse	17/373	119/19943	8.39E-11	2.79E-09	2.1718E-09	Cplx1/Cacng2/Nefh/Syn1/Cacng3/Nefl/Grm1/Ina/Syp/Camk2a/Ad	17
CC		cell projection membrane cytoplasmic vesicle membrane	26/373 29/373	321/19943 397/19943	4.23E-10 4.65E-10	1.27E-08 1.39E-08	9.9046E-09	Gabrg2/Gabra1/Lamp5/Thy1/Hpca/Drd2/Oprd1/Gabra5/Grin1/Dr Rph3a/Gabrg2/Gabra1/Syt2/Lamp5/Drd2/Cadps/Syn1/Oprd1/Rat	26 29
CC		vesicle membrane	29/373	423/19943	2.01E-09	5.73E-08		Rph3a/Gabrg2/Gabra1/Syt2/Lamp5/Drd2/Cadps/Syn1/Opro1/Rat Rph3a/Gabrg2/Gabra1/Syt2/Lamp5/Drd2/Cadps/Syn1/Oprd1/Rat	29
CC	GO:0030673		8/373	22/19943	3.53E-09	9.63E-08	7.4942E-08	Thy1/Epb41l3/Ank1/Kene3/Kene1/Kenh1/Nrg1/Chrna7	8
CC CC		dendritic shaft	12/373 11/373	67/19943 56/19943	3.65E-09 5.93E-09	9.89E-08 1.57E-07		Grm4/Nsf/Rgs7bp/Slc12a5/Syndig1/Zfp804a/Grip2/Cacna1b/Htr2: Cacng2/Grin1/Cacng3/Dlgap3/Olfm3/Nrn1/Grin2b/Lrrc7/Shank1/I	12 11
CC	GO:0008328 GO:0098981	ionotropic glutamate receptor complex cholinergic synapse	7/373	16/19943	7.49E-09	1.95E-07		Rph3a/Chrna4/Nefl/Digap3/Chrm2/Chrna7/Chrnb2	7
CC	GO:0060077	inhibitory synapse	8/373	24/19943	7.87E-09	2.04E-07	1.5887E-07	Gabrg2/Rims1/Glra1/Slc32a1/Gad2/Rims2/Bsn/Gabrb3	8
CC		juxtaparanode region of axon	6/373 11/373	10/19943 58/19943	8.11E-09 8.77E-09	2.09E-07 2.25E-07		Kcnab2/Epb41l3/Kcna2/Kcnab1/Kcna1/Dlg2	6 11
CC		neurotransmitter receptor complex intrinsic component of synaptic vesicle r		58/19943 67/19943	4.26E-08	1.03E-06		Cacng2/Grin1/Cacng3/Dlgap3/Olfm3/Nrn1/Grin2b/Lrrc7/Shank1/I Syt2/Syn1/Oprd1/Rab3c/Slc32a1/Slc17a6/Vamp1/Rab3a/Syp/Sv2I	11
CC	GO:0044305	calyx of Held	8/373	30/19943	5.68E-08	1.34E-06	1.0408E-06	Cplx1/Ncs1/Gira1/Kcna2/Atp1a3/Kcnc1/Kcna1/Unc13c	8
CC		axon initial segment	7/373	21/19943	7.02E-08	1.65E-06		Scn8a/Ank1/Scn1a/Scn2a/Kcnq2/Map2/Lrrc7	7
CC CC		cell leading edge apical dendrite	26/373 7/373	414/19943 26/19943	8.23E-08 3.66E-07	1.91E-06 7.68E-06		Gabrg2/Gabra1/Arhgap44/Lamp5/Thy1/Hpca/Oprd1/Gabra5/Grin Kif5a/Rasgrf1/Slc7a10/Grin2b/Map2/Map1b/Hcn1	26 7
CC		plasma membrane receptor complex	16/373	185/19943	4.26E-07	8.83E-06		Cacng2/Chrna4/Grin1/Cacng3/Grm1/Dlgap3/Olfm3/Nrn1/Gabbr2	16
CC		dense core granule	7/373	27/19943	4.87E-07	1E-05		Syt2/Cadps/Ncs1/Oprd1/Crhbp/Stxbp5l/Syt7	7
CC		growth cone presynaptic cytoskeleton	17/373 5/373	219/19943 11/19943	8.58E-07 9.38E-07	1.72E-05 1.86E-05		Rapgef4/Kif5a/Lamp5/Thy1/Nefl/Rasgrf1/Nrsn1/Sncb/Tenm2/Zfp: Rims1/Nefl/Nefm/Rims2/Bsn	17 5
CC			17/373	222/19943	1.04E-06	2.04E-05		Rapgef4/Kif5a/Lamp5/Thy1/Nefl/Rasgrf1/Nrsn1/Sncb/Tenm2/Zfpi	17
CC	GO:0005883	neurofilament	5/373	12/19943			2.3468E-05	Nefh/Nefl/Nefm/Ina/Pcp4	5
cc		GABA receptor complex	6/373	21/19943	1.76E-06	3.29E-05		Gabrg2/Gabra1/Gabra5/Gabra3/Gabbr2/Gabrb3	6
CC		receptor complex integral component of synaptic vesicle n	23/373	399/19943 47/19943	2.04E-06 2.31E-06	3.78E-05 4.25E-05		Gabrg2/Gabra1/Cacng2/Gabra5/Chrna4/Pex5l/Grin1/Cacng3/Grm Syt2/Oprd1/Slc32a1/Slc17a6/Vamp1/Syp/Sv2b/Sv2c	23 8
cc		neuronal cell body membrane	7/373	35/19943	3.24E-06	5.65E-05	4.3976E-05	Thy1/Hpca/Gabra5/Kcna2/Kcnc3/Atp2b2/Kcnc1	7
CC	GO:0001518	voltage-gated sodium channel complex	5/373	14/19943	3.88E-06	6.71E-05		Scn8a/Scn4b/Scn1a/Scn2a/Scn9a	5
CC		cell body membrane neuron projection cytoplasm	7/373 10/373	37/19943 90/19943	4.8E-06	8.21E-05 0.000117		Thy1/Hpca/Gabra5/Kcna2/Kcnc3/Atp2b2/Kcnc1 Kif5a/Hpca/Dync1i1/Nefl/Kcnab1/Camk2a/Kif5c/Map2/Dlg2/Bsn	7 10
CC		anchored component of membrane	12/373	132/19943		0.000119		Cntn4/Cntn3/Thy1/Syn1/Rab3c/Rgs7bp/Gad2/Rab3a/Nrn1/Cntn5	12
CC	GO:0034707	chloride channel complex	7/373	42/19943	1.16E-05		0.00014761	Gabrg2/Gira2/Gabra1/Gabra5/Gira1/Gabra3/Gabrb3	7
cc		calcium channel complex	8/373	60/19943	1.52E-05 2.09E-05			Cacng2/Ryr2/Cacna1b/Akap6/Cacna2d2/Trpc5/Cacna2d1/Cacna1i	8 5
CC		GABA-A receptor complex sarcolemma	5/373 13/373	19/19943 171/19943	2.09E-05			Gabrg2/Gabra1/Gabra5/Gabra3/Gabrb3 Kcnj3/Rtn2/Ryr2/Ank1/Atp1a3/Scn1a/Gnas/Kcnj12/Akap6/Scn2a/	13
CC	GO:0048787	presynaptic active zone membrane	7/373	47/19943	2.5E-05	0.000371	0.00028852	Grm4/Scn8a/Stx1b/Atp2b2/Kcnma1/Nrg1/Cacna2d1	7
CC	GO:0043083	synaptic cleft	5/373	20/19943		0.000405		Nptx1/Grin1/Cbln1/Grin2b/Dnm3	5
CC		intrinsic component of presynaptic activ hippocampal mossy fiber to CA3 synapse		33/19943 49/19943	2.97E-05 3.31E-05			Grm4/Scn8a/Atp2b2/Kcnma1/Nrg1/Cacna2d1 Rapgef4/Cacng2/Grin1/Adcy1/Grin2b/Syt7/Bsn	6 7
CC		presynaptic active zone cytoplasmic con		21/19943				Rims1/Rims2/Erc2/Bsn/Unc13c	ś
CC	GO:0099571	postsynaptic cytoskeleton	5/373	21/19943	3.54E-05	0.000511	0.00039761	Nefh/Nefl/Nefm/Ina/Sptbn2	5
CC	GO:0032839 GO:0030315	dendrite cytoplasm	6/373 8/373	34/19943 69/19943				Kif5a/Hpca/Kcnab1/Camk2a/Kif5c/Map2	6 8
CC		NMDA selective glutamate receptor con		12/19943		0.000594	0.00046262	Kcnj3/Rtn2/Scn1a/Kcnj12/Akap6/Scn2a/Prkce/Cacna2d1 Grin1/Dlgap3/Grin2b/Shank1	4
CC	GO:0034706	sodium channel complex	5/373	24/19943	7.07E-05	0.000933	0.00072635	Scn8a/Scn4b/Scn1a/Scn2a/Scn9a	5
CC		glycinergic synapse	4/373	13/19943	7.53E-05 0.000104			Gira2/Gira1/Sic6a5/Chrna7	4
CC	GO:0016528 GO:0048788	cytoskeleton of presynaptic active zone	8/373 3/373	78/19943 6/19943				Rtn2/Ryr2/Ank1/Camk2b/Jph3/Akap6/Slc8a3/Cacna2d1 Rims1/Rims2/Bsn	8 3
CC		integral component of presynaptic active		28/19943	0.000154	0.001825	0.00142082	Grm4/Scn8a/Atp2b2/Kcnma1/Nrg1	5
CC		dendritic spine head	4/373	16/19943				Hpca/Rgs7bp/Atp1a3/Dnm3	4
CC CC		anchored component of plasma membra spectrin-associated cytoskeleton	3/373	65/19943 7/19943				Cntn3/Thy1/Rgs7bp/Nrn1/Cntn5/Dlg2/Cacna2d1 Dmtn/Ank1/Sptbn2	7 3
CC		AMPA glutamate receptor complex	5/373	30/19943	0.000216	0.002437	0.00189682	Cacng2/Cacng3/Olfm3/Nrn1/Vwc2l	5
CC		node of Ranvier	4/373	18/19943	0.000299	0.003278	0.00255172	Scn8a/Scn1a/Scn2a/Kcnq2	4
CC		secretory granule anchored component of synaptic memb	18/373	382/19943 19/19943				Rph3a/Syt2/Pcsk2/Scg5/Drd2/Cadps/Ncs1/Serpini1/Oprd1/Ica1// Rgs7bp/Cntn5/Dlg2/Cacna2d1	18 4
CC		dendrite terminus	4/373	20/19943				Sic32a1/Rgs7/Map2/Licam	4
CC	GO:1904115	axon cytoplasm	6/373	55/19943	0.00055	0.005551	0.00432169	KifSa/Dync1i1/Nefl/Kif5c/Dlg2/Bsn	6
CC		cortical cytoskeleton anchored component of postsynaptic me	9/373	128/19943 10/19943	0.000687 0.000706			Pvalb/Rims1/Dmtn/Calb2/Ank1/Cap2/Rims2/Bsn/Sptbn2 Rgs7bp/Dig2/Cacna2d1	9
CC		intrinsic component of postsynaptic membr		245/19943		0.007218	0.00561898	Kgs/bp/Dig2/Cacha2d1 Syt2/Gdap1/Syn1/Oprd1/Rab3c/Slc32a1/Slc17a6/Vamp1/Rab3a/S	13
CC	GO:0005891	voltage-gated calcium channel complex	5/373	39/19943	0.00076	0.007284	0.00567022	Cacng2/Cacna1b/Cacna2d2/Cacna2d1/Cacna1i	5
CC		neuronal dense core vesicle	3/373	12/19943	0.001259			Cadps/Oprd1/Stxbp5l	3
CC CC		presynaptic cytosol membrane raft	4/373 17/373	26/19943 396/19943	0.0013 0.00136			Ncs1/Sncb/Camk2a/Prkce Thy1/Oprd1/Slc5a7/Asah2/Rit2/Rgs7/Atp2b2/Atp2b3/Gnas/Akapi	4 17
CC		membrane microdomain	17/373		0.001397	0.012057	0.00938584	Thy1/Oprd1/Slc5a7/Asah2/Rit2/Rgs7/Atp2b2/Atp2b3/Gnas/Akapi	17
CC		sarcoplasmic reticulum	6/373	66/19943				Rtn2/Ryr2/Ank1/Camk2b/Akap6/Cacna2d1	6
CC CC		anchored component of presynaptic me membrane region	3/373 17/373	13/19943 411/19943				Rgs7bp/Cntn5/Cəcnə2d1 Thy1/Oprd1/Sic5a7/Asah2/Rit2/Rgs7/Atp2b2/Atp2b3/Gnas/Akapi	3 17
CC	GO:0044448	cell cortex part	11/373	212/19943	0.002239	0.01787	0.01391128	Pvalb/Rims1/Dmtn/Calb2/Ank1/Cap2/Rims2/Erc2/Bsn/Unc13c/Sp	11
CC	GO:0032588	trans-Golgi network membrane	4/373	31/19943		0.019744	0.01537005	Lgr5/Cabp7/Caln1/Gnas	4
CC		plasma membrane raft acetylcholine-gated channel complex	8/373					Sic5a7/Asah2/Akap6/Kcnma1/Htr2a/Chrna7/Add2/Chrnb2 Chrna4/Chrna7/Chrnb7	8
CC		acetylcholine-gated channel complex dopaminergic synapse	3/373 3/373					Chrna4/Chrna7/Chrnb2 Drd2/Chrna4/Chrnb2	3 3
CC	GO:0044307	dendritic branch	2/373	5/19943	0.003361	0.02413	0.01878472	Grin1/Map2	2
CC		cone cell pedicle	2/373		0.003361	0.02413	0.01878472	Rapgef4/Slc32a1	2
CC		neurofibrillary tangle	2/373 5/373	5/19943 55/19943			0.01878472	Nefh/Nefm Rims1/Rims2/Erc2/Bsn/Unc13c	2
CC	GO:0033270	paranode region of axon	3/373					Epb41l3/Kcna1/Scn2a	3
CC	GO:0097444	spine apparatus	2/373	6/19943	0.004979	0.032778	0.0255171	Oprd1/Chrna7	2
CC CC		anchored component of postsynaptic sp anchored component of postsynaptic de					0.0255171 0.0255171		2
CC			17/373		0.005373	0.034592	0.02692929	Rgs/bp/Ug2 Cabp1/Lgr5/Camk1g/Clstn3/Asah2/Gad2/Tmem59l/GaInt9/Cabp7	17
CC	GO:0019898	extrinsic component of membrane	13/373	309/19943	0.005689	0.036458	0.02838196	Rph3a/Hpca/Cadps/Syn1/Kcnab2/Ryr2/Cdh12/Tenm2/Cdh7/Kcna	13
CC		anchored component of synaptic vesicle						Syn1/Rab3c/Rab3a	3
	GU:0032838	plasma membrane bounded cell projecti	10/2/3	200/19943	0.005951	0.03764	0.02930186	Kif5a/Hpca/Dync1i1/Nefl/Kcnab1/Camk2a/Kif5c/Map2/Dlg2/Bsn	10

CC	GO:0099522 region of cytosol GO:0031301 integral component of organelle memb	4/373 br: 10/373	42/19943 218/19943	0.007698			Ncs1/Sncb/Camk2a/Prkce Syt2/Gdap1/Oprd1/Slc32a1/Slc17a6/Vamp1/Syp/Sv2b/Sv2c/Chrn:	4
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 50/373	337/19943 406/19943	2.35E-28 1.6E-26	4.46E-26 2.05E-24	3.4711E-26	Gabrg2/Glra2/Gabra1/Scn8a/Kcnj3/Cacng2/Kcnab3/Ncs1/Gabra5, Gabrg2/Glra2/Gabra1/Scn8a/Kcnj3/Cacng2/Slc24a2/Kcnab3/Ncs1	48 50
MF	GO:0005216 ion channel activity GO:0022838 substrate-specific channel activity	50/373	406/19943	5.56E-26	6.55E-24	1.5989E-24 5.0976E-24	Gabrg2/Gira2/Gabra1/ScnBa/Kcnj3/Cacng2/Sic24a2/Kcnab3/Ncs1 Gabrg2/Gira2/Gabra1/ScnBa/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/Slc24a2/Kcnab3/Ncs1/Chrna4/Pex5l/Kcns2/k	43
MF	GO:0015267 channel activity	50/373	447/19943 447/19943	1.36E-24 1.36E-24	1.26E-22	9.8249E-23	Gabrg2/Glra2/Gabra1/Scn8a/Kcnj3/Cacng2/Slc24a2/Kcnab3/Ncs1	50 50
ME	GO:0022803 passive transmembrane transporter ac GO:0005244 voltage-gated ion channel activity	34/373	195/19943	1.36E-24 3E-23	1.26E-22 2.38E-21		Gabrg2/Glra2/Gabra1/Scn8a/Kcnj3/Cacng2/Slc24a2/Kcnab3/Ncs1 Scn8a/Kcnj3/Cacng2/Kcnab3/Ncs1/Kcns2/Kcnab2/Grin1/Cacng3/K	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/Kcns2/Kcnab2/Grin1/Cacng3/K	34
MF	GO:0046873 metal ion transmembrane transporter		430/19943	1.01E-22	7.72E-21	6.01E-21	Scn8a/Kenj3/Cacng2/Slc24a2/Kenab3/Nes1/Slc5a7/Kens2/Kenab2/	47
MF	GO:0022843 voltage-gated cation channel activity GO:0035254 glutamate receptor binding	27/373 19/373	146/19943 67/19943	2.2E-19 9.9E-18	1.57E-17 6.54E-16	1.2255E-17	Kcnj3/Cacng2/Kcnab3/Ncs1/Kcns2/Kcnab2/Grin1/Cacng3/Kcna2/k Cabp1/Nsf/Cacng2/Drd2/Grin1/Cacng3/Rasgrf1/Atp2b2/Syndig1/l	27 19
MF	GO:0015079 potassium ion transmembrane transpo		161/19943	3.81E-15	2.15E-13	1.6775E-13	<ul> <li>Kenj3/Slc24a2/Kenab3/Kens2/Kenab2/Slc12a5/Kena2/Kenc3/Atp1;</li> </ul>	24
MF	GO:0015077 monovalent inorganic cation transmer	nt 34/373	375/19943	2.99E-14	1.57E-12	1.2242E-12	Scn8a/Kcnj3/Slc24a2/Kcnab3/Slc5a7/Kcns2/Kcnab2/Slc32a1/Slc12	34
MF	GO:0005249 voltage-gated potassium channel activi GO:0030594 neurotransmitter receptor activity	it: 18/373 20/373	88/19943 119/19943	3.83E-14 7.51E-14	1.96E-12 3.72E-12		. Kcnj3/Kcnab3/Kcns2/Kcnab2/Kcna2/Kcnc3/Kcnc1/Kcnab1/Kcna1/I Gabrg2/Glra2/Gabra1/Drd2/Gabra5/Chrna4/Grin1/Glra1/Grm1/H	18 20
MF	GO:0005267 potassium channel activity	20/373	127/19943	2.69E-13	1.24E-11		Keni3/Kenab3/Kens2/Kenab2/Kena2/Kena2/Kenip4/Kene1/Kenab1/	20
MF	GO:0015276 ligand-gated ion channel activity	20/373	131/19943	4.92E-13	2.21E-11		Gabrg2/Glra2/Gabra1/Kcnj3/Gabra5/Chrna4/Pex5l/Grin1/Glra1/R	20
MF	GO:0022834 ligand-gated channel activity	20/373 11/373	134/19943 30/19943	7.63E-13 3.36E-12	3.32E-11 1.3E-10	2.5876E-11	Gabrg2/Glra2/Gabra1/Kcnj3/Gabra5/Chrna4/Pex5l/Grin1/Glra1/R	20 11
MF	GO:0098918 structural constituent of synapse GO:0098960 postsynaptic neurotransmitter recepto		30/19943 57/19943	3.36E-12 3.24E-11	1.3E-10 1.19E-09	9.7409E-10	Nefh/Rims1/Nefl/Ina/Camk2b/Rims2/Erc2/Dlg2/Dnm3/Bsn/Sptbn Gabrg2/Glra2/Gabra1/Gabra5/Chrna4/Grin1/Glra1/Grm1/Gabra3	11
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/Pcp4/Ca	20
MF	GO:0042165 neurotransmitter binding	13/373	61/19943	8.13E-11	2.75E-09	2.137E-09	Glra2/Slc5a7/Chrna4/Grin1/Glra1/Crhbp/Htr2c/Slc6a11/Grin2b/H	13
MF MF	GO:1904315 transmitter-gated ion channel activity i GO:0099529 neurotransmitter receptor activity invo		52/19943 55/19943	1.62E-10 3.27E-10	5.18E-09 1.01E-08	4.0356E-09 7.8677E-09	Gabrg2/Glra2/Gabra1/Gabra5/Chrna4/Grin1/Glra1/Gabra3/Grin2 Gabrg2/Glra2/Gabra1/Gabra5/Chrna4/Grin1/Glra1/Gabra3/Grin2	12 12
MF	GO:0035255 ionotropic glutamate receptor binding		44/19943	3.73E-10	1.13E-08		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/Glra1/Gabra3/Grin2	12
MF	GO:0022835 transmitter-gated channel activity GO:0015085 calcium ion transmembrane transporte	12/373	58/19943 134/19943	6.32E-10 4.46E-09	1.86E-08 1.19E-07	1.4467E-08	Gabrg2/Glra2/Gabra1/Gabra5/Chrna4/Grin1/Glra1/Gabra3/Grin2 Cacng2/Slc24a2/Ncs1/Grin1/Cacng3/Ryr2/Atp2b2/Atp2b3/Jph3/C	12 16
MF	GO:0015085 calcium for transmembrane transporte GO:0005230 extracellular ligand-gated ion channel a		70/19943	4.46E-09 6.16E-09	1.62E-07	1.2594E-07	Gabrg2/Glra2/Gabra1/Gabra5/Chrna4/Grin1/Glra1/Gabra3/Grin2	10
MF	GO:0099095 ligand-gated anion channel activity	7/373	20/19943	4.76E-08	1.14E-06	8.8687E-07	Gabrg2/Gira2/Gabra1/Gabra5/Gira1/Gabra3/Gabrb3	7
MF	GO:0070405 ammonium ion binding	11/373	79/19943	2.45E-07	5.36E-06	4.17E-06	Drd2/Slc5a7/Chrna4/Htr2c/Gpr12/Rasgrp1/Htr2a/Chrna7/Pcyt1b/	11
MF	GO:0099094 ligand-gated cation channel activity GO:0005262 calcium channel activity	12/373 13/373	99/19943 119/19943	3.29E-07 3.64E-07	7.03E-06 7.66E-06		Kcnj3/Chrna4/Pex5l/Grin1/Ryr2/Jph3/Kcnj12/Kcnh7/Grin2b/Chrna Cacng2/Slc24a2/Ncs1/Grin1/Cacng3/Ryr2/Jph3/Cacna1b/Grin2b/C	12 13
MF	GO:0016247 channel regulator activity	14/373	141/19943	4.24E-07	8.83E-06		Fgf12/Lynx1/Cacng2/Kcnab2/Cacng3/Gpld1/Scn4b/Dpp6/Kcnip4/I	14
MF	GO:0005237 inhibitory extracellular ligand-gated ior	n (6/373	17/19943	4.28E-07	8.83E-06	6.8747E-06	Gabrg2/Glra2/Gabra1/Gabra5/Glra1/Gabra3	6
MF MF	GO:0005251 delayed rectifier potassium channel act GO:0005248 voltage-gated sodium channel activity	tiv 7/373 6/373	29/19943 20/19943	8.28E-07 1.28E-06	1.67E-05 2.46E-05	1.3012E-05	Kcna2/Kcnc3/Kcnc1/Kcna1/Kcnh1/Kcnq2/Kcng1 Scn8a/Scn4b/Scn1a/Scn2a/Scn9a/Hcn1	7 6
MF	GO:0099186 structural constituent of postsynapse	6/373	20/19943	1.28E-06	2.46E-05		Nefh/Nefl/Ina/Camk2b/Dlg2/Dnm3	6
MF	GO:0099508 voltage-gated ion channel activity invo	lv 4/373	6/19943	1.75E-06	3.29E-05	2.5621E-05	Kene1/Kena1/Kenh1/Sen2a	4
MF MF	GO:0016917 GABA receptor activity GO:0022851 GABA-gated chloride ion channel activi	6/373	22/19943 13/19943	2.38E-06 2.53E-06	4.34E-05 4.58E-05		Gabrg2/Gabra1/Gabra5/Gabra3/Gabbr2/Gabrb3 Gabrg2/Gabra1/Gabra5/Gabra3/Gabrb3	6 5
MF	GO:0022851 GABA-gated chloride fon channel activi GO:0015081 sodium ion transmembrane transporte		141/19943	2.53E-06	4.58E-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/Cxxc4/Atp2b3/Cit/Kcnj12/Erc2/	12
MF	GO:0044325 ion channel binding	13/373	143/19943	2.98E-06	5.27E-05	4.1063E+05	Cabp1/Fgf12/Rims1/Kcnab2/Ank1/Scn4b/Kcnc1/Kcnab1/Dpp10/K	13
MF	GO:0098882 structural constituent of presynaptic ac GO:0005543 phospholipid binding	23/373 23/373	7/19943 424/19943	4.03E-06 5.59E-06	6.94E-05 9.49E-05		Rims1/Rims2/Erc2/Bsn Rph3a/Arhgap44/Syt2/Thy1/Cadps/Syt12/Pla2g4e/Pacsin1/Cpne4	4 23
MF	GO:0099181 structural constituent of presynapse	4/373	9/19943	1.41E-05		0.00017506	Rims1/Rims2/Erc2/Bsn	4
MF	GO:0004890 GABA-A receptor activity	5/373	19/19943	2.09E-05			Gabrg2/Gabra1/Gabra5/Gabra3/Gabrb3	5 7
MF	GO:0099528 G protein-coupled neurotransmitter re- GO:0008503 benzodiazepine receptor activity	c∈ 7/373 4/373	47/19943 11/19943	2.5E-05 3.58E-05			. Grm1/Htr2c/Chrm2/Hrh3/Gabbr2/Htr2a/Htr4 . Gabrg2/Gabra1/Gabra5/Gabra3	7
MF	GO:0005245 voltage-gated calcium channel activity	7/373	50/19943	3.78E-05			Cacng2/Ncs1/Cacng3/Cacna1b/Cacna2d2/Cacna2d1/Cacna1i	7
MF	GO:0005231 excitatory extracellular ligand-gated io	n 6/373	35/19943	4.22E-05	0.000586		Glra2/Chrna4/Glra1/Grin2b/Chrna7/Chrnb2	6
MF	GO:0015464 acetylcholine receptor activity GO:0000149 SNARE binding	5/373 10/373	22/19943 115/19943	4.51E-05 6.06E-05	0.000617 0.000816	0.00048009	Chrna4/Chrm2/Hrh3/Chrna7/Chrnb2 Cplx1/Nsf/Napb/Syt2/Stx1b/Syt12/Syp/Stxbp5l/Syt7/Unc13c	5 10
MF	GO:0000149 SNARE binding GO:0031402 sodium ian binding	4/373	13/19943				Scn8a/Scn1a/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 MF	GO:0015108 chloride transmembrane transporter a	ct 9/373 7/373	97/19943 58/19943				Gabrg2/Gira2/Gabra1/Gabra5/Gira1/Sic12a5/Gabra3/Sic12a3/Gal Nefh/Nefi/Ina/Tuba8/Camk2b/Add2/Sotbn2	9
MF	GO:0005200 structural constituent of cytoskeleton GO:0019905 syntaxin binding	8/373	58/19943 79/19943	0.0001			Colx1/Nsf/Napb/Svt2/Svp/Stxbp5l/Svt7/Unc13c	8
MF	GO:0004683 calmodulin-dependent protein kinase a	ac 5/373	27/19943	0.000128	0.001551	0.00120764	Camk1g/Camk2b/Camk2a/Camk1d/Camk4	5
MF	GO:0008022 protein C-terminus binding	14/373	234/19943		0.001683	0.00131033	Rbfox1/Nsf/Nefl/Rasgrf1/Rab3a/Atp2b2/Grip2/Cacna1b/Sgtb/Lrrc	14
MF	GO:0016594 glycine binding GO:1902936 phosphatidylinositol bisphosphate bind	4/373	16/19943 108/19943	0.000183	0.002154		GIra2/Grin1/GIra1/Grin2b Rph3a/Cadps/Kcnh1/Clvs1/Pfn2/LOC100909840/Amer3/Syt7/Hcn	4 9
MF	GO:0099106 ion channel regulator activity	9/373	115/19943	0.000313	0.003386	0.00263607	Lynx1/Cacng2/Kcnab2/Dpp6/Kcnip4/Kcnab1/Dpp10/Cacna2d2/Nr	9
MF	GO:0005254 chloride channel activity	7/373	70/19943	0.00033	0.003557	0.00276887	Gabrg2/Glra2/Gabra1/Gabra5/Glra1/Gabra3/Gabrb3	7
MF	GO:0005544 calcium-dependent phospholipid bindir GO:0005326 neurotransmitter transporter activity	ng 6/373 6/373	52/19943 53/19943	0.000405	0.004233		Rph3a/Syt2/Syt12/Pla2g4e/Cpne4/Syt7 Colx1/Sic5a7/Sic32a1/Sic17a6/Sic6a5/Sic6a11	6 6
MF	GO:1990763 arrestin family protein binding	3/373	9/19943	0.000501			Gpr61/Chrm2/Gpr135	3
MF	GO:0097110 scaffold protein binding	7/373	75/19943	0.000504	0.005157	0.00401467	Kif5a/Dlgap3/Ryr2/Clt/Grin2b/Chrna7/Shank1	7
MF	GO:0005546 phosphatidylinositol-4,5-bisphosphate GO:0031420 alkali metal ion binding	b 7/373 4/373	76/19943 21/19943	0.000546	0.005526 0.005611	0.00430161	Rph3a/Cadps/Pfn2/LOC100909840/Amer3/Syt7/Hcn1 Scn8a/Scn1a/Scn2a/Scn9a	7 4
MF	GO:0031420 aikaii metai ion binding GO:0032947 protein-containing complex scaffold ac		21/19943	0.00056	0.005611		Mapk8ip2/Grip2/Ksr2/Shank1	4
MF	GO:0008509 anion transmembrane transporter activ	vi 15/373	311/19943	0.000815	0.007724	0.00601319	Gabrg2/Gira2/Gabra1/Gabra5/Gira1/Sic32a1/Sic17a6/Sic12a5/Sic	15
MF MF	GO:0005253 anion channel activity GO:0004993 G protein-coupled serotonin receptor a	7/373	83/19943 41/19943	0.000928			Gabrg2/Gira2/Gabra1/Gabra5/Gira1/Gabra3/Gabrb3 Htr2c/Chrm2/Hrh3/Htr2a/Htr4	7
MF	GO:0004555 G protein-coupled serotonin receptor a GO:0099589 serotonin receptor activity	5/373	41/19943	0.00096			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/HapIn1/HapIn4/Ddc/Grin2b/C	12
MF	GO:0015103 inorganic anion transmembrane transp	on 9/373	136/19943	0.001059	0.009594	0.00746894	Gabrg2/Gira2/Gabra1/Gabra5/Gira1/Sic12a5/Gabra3/Sic12a3/Gal	9
MF	GO:0035256 G protein-coupled glutamate receptor GO:0050780 dopamine receptor binding	4/373	12/19943 26/19943	0.001259 0.0013	0.011088		Cabp1/Necab2/Dnm3 Nsf/Atp1a3/Gnas/Grin2b	3 4
MF	GO:0099604 ligand-gated calcium channel activity	4/373	26/19943	0.0013	0.01126	0.00876588	Grin1/Ryr2/Jph3/Grin2b	4
MF	GO:0017075 syntaxin-1 binding	4/373	27/19943		0.012796	0.00996183	Cplx1/Nsf/Syp/Unc13c	4
MF	GO:0008066 glutamate receptor activity GO:0015643 toxic substance binding	4/373 3/373	28/19943 14/19943	0.001728	0.014374		. Grm4/Grin1/Grm1/Grin2b . Nefh/Nefm/Chrna7	4
MF	GO:0016595 glutamate binding	3/3/3	14/19943	0.002027			Grin1/Gad2/Grin2b	3
MF	GO:0031748 D1 dopamine receptor binding	3/373	14/19943	0.002027	0.016326	0.01270915	Nsf/Atp1a3/Gnas	3
MF	GO:0016597 amino acid binding	6/373	71/19943			0.01323139	Glra2/Grin1/Glra1/Gad2/Ddc/Grin2b	6
MF	GO:0031406 carboxylic acid binding GO:0022804 active transmembrane transporter acti	11/373 ivi 15/373	211/19943 346/19943	0.002158	0.017286 0.018517	0.0134572	Glra2/Grin1/Glra1/Gad2/Acan/Hapln1/Hapln4/Ddc/Grin2b/Ogfod Slc24a2/Slc5a7/Slc32a1/Slc17a6/Slc12a5/Atp1a3/Atp2b2/Slc6a5//	11 15
MF	GO:0015459 potassium channel regulator activity	5/373	50/19943	0.002367	0.018752	0.01459826	Kcnab2/Dpp6/Kcnip4/Kcnab1/Dpp10	5
MF	GO:0008179 adenylate cyclase binding	3/373	15/19943	0.002498	0.019478	0.01516308	Cap2/Akap6/Chrna7 SIc24a2/Sic5a7/Sic32a1/Sic17a6/Sic12a5/Sic6a5/Sic6a11/Sic12a3	3
MF	GO:0015293 symporter activity GO:0005217 intracellular ligand-gated ion channel a	8/373 ct 4/373	128/19943 32/19943	0.002837			SIc24a2/Sic5a7/Sic32a1/Sic17a6/Sic12a5/Sic6a5/Sic6a11/Sic12a3 Pex5l/Rvr2/Jph3/Hcn1	8 4
MF	GO:0005416 amino acid:cation symporter activity	3/373	16/19943	0.003033	0.022438	0.01746794	Slc32a1/Slc6a5/Slc6a11	3
MF	GO:0022848 acetylcholine-gated cation-selective ch		16/19943	0.003033	0.022438	0.01746794	Chrna4/Chrna7/Chrnb2	3
MF	GO:0042166 acetylcholine binding GO:0008227 G protein-coupled amine receptor activ	3/373 vi1 6/373	16/19943 77/19943	0.003033	0.022438	0.01746794	Chrna4/Chrna7/Chrnb2 Drd2/Htr2c/Chrm2/Hrh3/Htr2a/Htr4	3 6
MF	G0:0015185 gamma-aminobutyric acid transmembr	ra 2/373	5/19943	0.003361	0.02413	0.01878472	Slc32a1/Slc6a11	2

MF	GO:0016933 extracellularly glycine-gated ion channel 2/373	5/19943	0.003361 0.02413	3 0.01878472 Gira2/Gira1	2
MF	GO:0016934 extracellularly glycine-gated chloride chr 2/373	5/19943	0.003361 0.02413	8 0.01878472 Gira2/Gira1	2
MF	GO:0022849 glutamate-gated calcium ion channel act 2/373	5/19943	0.003361 0.02413	3 0.01878472 Grin1/Grin2b	2
MF	GO:0098973 structural constituent of postsynaptic ac 2/373	5/19943	0.003361 0.02413	3 0.01878472 Ina/Camk2b	2
MF	GO:1901981 phosphatidylinositol phosphate binding 9/373	162/19943	0.003507 0.024973	0.01944111 Rph3a/Cadps/Kcnh1/Clvs1/Pfn2/LOC100909840/Amer3/Syt7/Hcn	9
MF	GO:0030507 spectrin binding 4/373	34/19943	0.003585 0.025388	3 0.0197643 Dync1i1/Dmtn/Ank1/Add2	4
MF	GO:0043492 ATPase activity, coupled to movement o 8/373	133/19943	0.003589 0.025388	3 0.0197643 Atp1a3/Atp8b3/Atp2b2/Atp2b3/Atp8a2/Abca5/Abcg4/Abcc2	8
MF	GD:0003779 actin binding 16/373	406/19943	0.004312 0.029548	3 0.02300242 Hpca/Syn1/Dmtn/Epb41I3/Spire2/Cap2/Kcnma1/Coro2a/Map2/Pr	16
MF	GO:0042277 peptide binding 13/373	302/19943	0.004713 0.031942	2 0.02486603 Cabp1/Oprd1/Pex5l/Hcrtr2/Grin1/Hcrtr1/Digap3/Crhbp/Atp1a3/C	13
MF	GO:0031802 type 5 metabotropic glutamate receptor 2/373	6/19943	0.004979 0.032778	8 0.0255171 Necab2/Dnm3	2
MF	GO:0033265 choline binding 2/373	6/19943	0.004979 0.032778	8 0.0255171 Slc5a7/Chat	2
MF	GO:0099507 ligand-gated ion channel activity involve 2/373	6/19943	0.004979 0.032778	3 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 activi 3/373	20/19943	0.005841 0.037003	L 0.02880497 Kcnj3/Kcnj12/Kcnh7	3
MF	GO:0005540 hyaluronic acid binding 3/373	21/19943	0.006722 0.041964	0.03266815 Acan/Hapin1/Hapin4	з
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	1 0.03266815 Chrm2/Hrh3	2
MF	GO:0019992 diacylglycerol binding 2/373	7/19943	0.006885 0.041964	0.03266815 Raserp1/Unc13c	2

Activated	genes_KEGG							
ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	genelD	Count
rno04080	Neuroactive ligand-receptor interaction	27/98	284/6610	2.41849E-15	2.51523E-13	2.01116E-13	Grm4/Gabrg2/Glra2/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/Chrm2/0	20
rno04720	Long-term potentiation	8/98	69/6610	6.95357E-06	0.000241057	0.000192748	Rps6ka6/Grin1/Grm1/Camk2b/Camk2a/Adcy1	/ 8
rno04540	Gap junction	8/98	89/6610	4.60497E-05	0.001197292	0.000957349	Gjd2/Drd2/Grm1/Htr2c/Tuba8/Gnas/Adcy1/H	. 8
rno04972	Pancreatic secretion	8/98	104/6610	0.000139958	0.002632948	0.002105292	Ryr2/Atp1a3/Pla2g4e/Atp2b2/Atp2b3/Gnas/A	c 8
rno04010	MAPK signaling pathway	13/98	269/6610	0.000151901	0.002632948	0.002105292	Fgf12/Rps6ka6/Cacng2/Cacng3/Rasgrf1/Pla2g	1 13
rno05414	Dilated cardiomyopathy	7/98	88/6610	0.000302343	0.004491952	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	0.002827798	0.029409096	0.02351537	Nefh/Grin1/Nefl/Nefm/Grin2b	5
rno04912	GnRH signaling pathway	6/98	99/6610	0.003363685	0.031802111	0.025428813	Pla2g4e/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/Cacna2d1	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.

	-	n v
GO term	p.adjust	gene
ion channel complex	1.69×10 <sup>-30</sup>	Gabrg2/Glra2/Gabra1/Scn8a/Kcnj3/Cacng2/Gabra5/Chrna4/Pex5l/Kcns2/Kcnab2/Grin 1/Cacng3/Glra1/Dlgap3/Ryr2/Olfm3/Kcna2/Kcnc3/Scn4b/Dpp6/Kcnip4/Nrn1/Scn1a/Kc nc1/Gabra3/Kcnab1/Kcna1/Dpp10/Kcnh1/Cacna1b/Akap6/Scn2a/Kcnma1/Scn9a/Grin 2b/Chrna7/Kcnq2/Lrrc7/Cacna2d2/Shank1/Chrnb2/Dlg2/Trpc5/Vwc2l/Cacna2d1/Kcng 1/Hcn1/Cacna1i/Gabrb3
GABA-ergic synapse	6.68×10 <sup>-19</sup>	Gabrg2/Gabra1/Lrfn5/Drd2/Slitrk3/Gabra5/Rims1/Clstn3/Cntnap4/Slc32a1/Acan/Atp2 b2/Gabra3/Atp2b3/Slc6a11/Rims2/Cntn5/Gabbr2/Nrg1/Erc2/Camk4/Syt7/Bsn/Nrxn3/ Gabrb3
synaptic transmission, GABAergic	9.40×10 <sup>-10</sup>	Phf24/Grm4/Gabrg2/Gabra1/Drd2/Gabra5/Cistn3/Cntnap4/Car7/Grm1/Gabra3/Prkce /Gabrb3
GABA receptor complex	3.29×10 <sup>-5</sup>	Gabrg2/Gabra1/Gabra5/Gabra3/Gabbr2/Gabrb3
GABA-gated chloride ion channel activity	4.58×10 <sup>-5</sup>	Gabrg2/Gabra1/Gabra5/Gabra3/Gabrb3
GABA-A receptor complex	3.20×10 <sup>-4</sup>	Gabrg2/Gabra1/Gabra5/Gabra3/Gabrb3
chloride transport	3.53×10 <sup>-4</sup>	Gabrg2/Gira2/Gabra1/Gabra5/Car7/Gira1/Sic12a5/Gabra3/Sic12a3/Gabrb3
chloride transmembrane transporter activity	1.09×10 <sup>-3</sup>	Gabrg2/Glra2/Gabra1/Gabra5/Glra1/Slc12a5/Gabra3/Slc12a3/Gabrb3

## Table S3. Antibodies.

antibody	company	cat#	Application
Purified anti-GABRA1 Antibody (m)	Biolegend	832301	WB, IF
Anti-GABA A Receptor alpha 3/GABRA3 antibody (R)	Abcam	ab72446	WB, IF
Anti-GABA A Receptor alpha 5/GABRA5 antibody (R)	Abcam	ab10098	WB, IF
Anti-GABA A Receptor beta 3/GABRB3 antibody [N87/25] (m)	Abcam	ab98968	WB, IF
GABRG2 Antibody (R)	Proteintech	14104-1-AP	WB, IF
KCC2 Monoclonal Antibody (S1-12) (m)	Invitrogen	MA5-27610	WB, IF
Anti-K+/Cl- Cotransporter (KCC2) Antibody (R)	millpore	07-432	WB, IF
Monoclonal Anti-HA, clone HA-7, produced in mouse, ascites fluid (m)	sigma	H9658-200UL	WB, IF
HA tag Rabbit Polyclonal Antibody (R)	Proteintech	51064-2-AP-100ul	WB, IF
Anti-FLAG <sup>a</sup> Antibody produced in rabbit (R)	Sigma	F74252MG	WB
Flag tag Antibody (m)	Proteintech	20543-1-AP	IF
Anti-NeuN Antibody, clone A60 (m)	millpore	MAB377	WB, IF
Recombinant Anti-NeuN antibody [EPR12763] - Neuronal Marker (R)	Abcam	ab177487-40ul	WB, IF
Anti-MAP2 antibody (chicken)	Abcam	ab5392	WB, IF
BDNF Monoclonal Antibody (m)	Proteintech	66292-1-lg	WB
GAPDH 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
Donkey 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 (SN6), PE, eBioscience**	invitrogen	12-1057-41	Flow
CD90 (Thy-1) Monoclonal Antibody (eBio5E10 (5E10)), 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 <sup>35</sup>	invitrogen	15-0118-41	Flow
CD45 Monoclonal Antibody (HI30), 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 <sup>™</sup>	Invitrogen	Cat # 11-9956-41	Flow
CD34 Monoclonal Antibody (4H11), APC, eBioscience <sup>™</sup>	Invitrogen	Cat # 17-0349-41	Flow

## Table S4. Primers.

<b>54.11</b> mict 5.	
Table S3. Primers	
Primer Name	Sequence
Fwd Gabrg2(r) RT01	CTCCAGTTATGGTTATCCT
Rev Gabrg2(r) RT01	TCCATGACCTTGTGTCTC
Fwd Gabra5(r) RT01	TGCTTTACAACTGGGAAG
Rev_Gabra5(r)_RT01	ATTGAGGCTGTACCCACA
Fwd Gabrb3(r) RT01	TTCTCCATTGTGGAGCAC
Rev Gabrb3(r) RT01	CCGAAAACTCAATGAGAG
Fwd_Slc12a5(r)_RT01	GGAGACAGACCCAGAGAAGG
Rev Slc12a5(r) RT01	TTGATCCCCTCCGAGGAGA
Fwd Gabra1(r) RT01	ACCATAGAACCGGAAAGAA
Rev_Gabra1(r) RT01 Fwd Gabra3(r) RT01	CGCTGTTAAAGGTTTTCT ACTGTCATTCTGTCACAAGT
Rev Gabra3(r) RT01	TGACACAAGACTGTGC
Fwd Gabra4(r) RT01	ATCAGECEGGCATTET
Rev Gabra4(r) RT01	TATGAACCAATCCATGGC
Fwd Gabrb1(r) RT01	AGCAAACAAGACCAGAGT
Rev Gabrb1(r) RT01	AACCTGGACTTTGTTCAT
Fwd Gabrb2(r) RT01	TGTAAAAGCCATTGACATG
Rev Gabrb2(r) RT01	AAGAAGATGTAGTTGACCAA
Fwd Gabrg3(r) RT01	TAACCATGACCACACTCAGC
Rev Gabrg3(r) RT01	GTGACATAGGACACCCGA
Fwd_Gabrd(R)_RT01	GCGCCAGAGCAATGAATGAC
Rev Gabrd(R) RT01	GCGTAGCCCTCCATTAGTCC
Fwd Gad1(R) RT01	GATGGTTTTCGATGGT
Rev_Gad1(R)_RT01	CCATGGTTGTTCCTGA
Fwd Gabbr1(R) RT01	CTCTCGGGCTGGATGGTTAC
Rev-Gabbr1(R) RT01	GGCTCTAGGGTCTTCCTCCA
Fwd_Gabbr2(R)_RT01	CAGGGAAGACTCCACAGCAG
Rev-Gabbr2(R) RT01	AGGCGTACCCATGGAACTTG
Fwd_Gabra2(R)_RT01 Rev_Gabra2(R)_RT01	CGTATGGTTTCCGCTGCTTG GTAATGCTGTCTCCCAGTCCT
Fwd Gad2(R) RT02	ATTATISCACTETECCAGGCAACA
Rev Gad2(R) RT02	GAAATGCGAGAGTGGGCCTTT
Fwd Gabrg1(R) RT03	TCTGGTTTACTGGGTTGG
Rev Gabrg1(R) RT03	CGAAGTGATTATATTGGACT
Fwd_slc6a1(r)_RT01	TGTGTAGGCAATCTACCAGC
Rev slc6a1(r) RT01	AGCAGGTAGATGCCTCAG
Fwd Slc12a2(r) RT02	CTCTGTCATCCTAAGTGGAC
Rev_Slc12a2(r)_RT02	CGAAACACAGGCTCTCA
Fwd Slc32a1(r) RT01	TGCCCAGCCTCTTCCACTT
Rev Slc32a1(r) RT01	AGATGCCGCCGATGACGAA
Fwd_28srRNA(m)_RT01	GTGACGCCGCATGAATGGA
Rev 28srRNA(m) RT01 dsDNA: 3XFlag-MCS-3XHA	TGTGGTTTCGCTGGATAGTAGGT CAATTGGCCACCATGGACTACAAGGACCATGACGGAGACTACAAGGACCATGACATCGACTACAAGGACGACGATGACAAGGAATTCCTC
OSDIVA: SAFIAB-WC3-SAFIA	GAGACTAGTICTAGAGCGGCCGCGGGATCCGTACCGAGACTACGAGGCCATGACATGCGGGGCTATCCCTATGAGGGCGCCCGGGACTATGCAGGAT
	CGTATCCTTATGACGTTCCAGATTACGCTGGGTCCTAAAGATCT
Flag-HA F	GAGCGCAGTCGAGAAGGTACCCAATTGTGGCCACCATGGACTACAAGGACCATGACG
Flag-HA R Gabra1 F	AGAGGTTGATTATCGATAAGCTTTTAGGACCCAGCGTAATCTGGAA GGACGACGATGACAAGGAATTCatgaagaaaagtcggggtct
Gabra1 P Gabra1 R	
Gabra3 F	
Gabra3 R	GonConConTonConContent In California Califor
rGABRA5-E	GGACGACGATGACAAGGAATTCatggacaatggaatgctctctaga
rGABRA5-R	GAACATCGTATGGGTACGGATCctttrgagagetagcccct
rKCC2-F	GGACGACGACGAAGGAATTCatgctcaacaacctgacggact
rKCC2-R	GAACATCGTATGGGTACGGATCggggtagatggtgatggcct
Fwd Gabrb3(R) EcoRI one step cloning02	GACGACGATGACAAGGAATTCATGTGGGGGCTTTGCGGGAGG
Rev Gabrb3 (R) BamHI one step cloning	ACATCGTATGGGTACGGATCCCAGTTAACATAGTACAGCCAG
Fwd Gabrg2(R) EcoRI one step cloning02	GACGACGATGACAAGGAATTCATGTGGGGGCTTTGCGGGAGG
Rev Gabrg2(R) BamHI one step cloning	ACATCGTATGGGTACGGATCCCACAGATAAAGATAGGAGAC
Fwd Kpn1 3XFLAG-2	GAGCGCAGTCGAGAAGGTACCGAATTCGGATCCCCATGGGACTACAAGGACCATGACGG
Rev HindIII 3XFLAG	AGGTTGATTATCGATAAGCTTtcaCTTGTCATCGTCGTCCTTGT
Fwd Kpn1 3XHA	GAGCGCAGTCGAGAAGGTACCCCCATGGGAATTCCTCGAGACTAGTTC
Fwd-c-3XFLAG-KCC2(r)-Kpnl	GAGCGCAGTCGAGAAGGTAACCatgctcaacaacctgacggact
Rev-c-3XFLAG-KCC2(r)-BamHI	CTTGTAGTCCCATGGGATCCggagtagatgatgatgatcactc
Rev-c-3XHA-KCC2(r)-EcoRI Fwd Bdnf(r)-EcoRI one step cloning	AGAACTAGTCTCGAGGAATTCggggtagatggtggtggtggtggtggtggtggtggtggtg
Rev Bdnf(r)-Ecoki one step cloning	GALGAIGA IGALAAGGAAT I Latgickgeotcoggigtetg AGAGGGCGGGATCGCGGCGCCCtatattetettitating
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