



Figure S1. Relative logarithmic expression (RLE) boxplots for six samples

Descriptions of Tab S1-3.

Table S1. The list of 90 DEGs.

Table S2. GO enrichment analysis terms of upregulated DEGs.

Table S3. GO enrichment analysis terms of downregulated DEGs.

| GeneSymbol | GeneName | EntrezGeneID | Regulation(C_vs._B) |
|--------------|-----------------------------------------------|--------------|---------------------|
| Akap1 | A-kinase anchoring protein 1 | 114124 | down |
| Alas2 | 5'-aminolevulinate synthase 2 | 25748 | up |
| Arhgap26 | Rho GTPase activating protein 26 | 307459 | down |
| Asic4 | acid sensing ion channel subunit family memt | 63882 | down |
| Bcl3 | B-cell CLL/lymphoma 3 | 680611 | down |
| Bcl6 | B-cell CLL/lymphoma 6 | 303836 | up |
| Bhlhb9 | basic helix-loop-helix family member B9 | 317407 | up |
| Bmx | BMX non-receptor tyrosine kinase | 367786 | up |
| Cacna1c | calcium voltage-gated channel subunit alpha1 | 24239 | down |
| Cdkl3 | cyclin-dependent kinase-like 3 | 60396 | up |
| Celf6 | CUGBP, Elav-like family member 6 | 300758 | down |
| Chd11 | chromodomain helicase DNA binding protein | 310707 | up |
| Chi3l1 | chitinase 3 like 1 | 89824 | up |
| Col9a3 | collagen type IX alpha 3 chain | 362285 | up |
| Cp | ceruloplasmin | 24268 | up |
| Cxcl11 | C-X-C motif chemokine ligand 11 | 305236 | down |
| Dgkh | diacylglycerol kinase, eta | 361076 | down |
| Dlg5 | discs large MAGUK scaffold protein 5 | 305645 | down |
| Dst | dystonin | 316313 | down |
| Enpp2 | ectonucleotide pyrophosphatase/phosphodiect | 84050 | up |
| Erp27 | endoplasmic reticulum protein 27 | 297698 | up |
| Fam180a | family with sequence similarity 180, member | 362336 | up |
| Fam199x | family with sequence similarity 199, X-linked | 679168 | down |
| Fcrl2 | Fc receptor-like 2 | 310694 | up |
| Gpr174 | G protein-coupled receptor 174 | 302373 | up |
| Gprin3 | GPRIN family member 3 | 502784 | down |
| Grap2 | GRB2-related adaptor protein 2 | 366962 | down |
| Grm4 | glutamate metabotropic receptor 4 | 24417 | up |
| Gypa | glycophorin A | 688972 | up |
| Hba1 | hemoglobin, alpha 1 | 25632 | up |
| Hba2 | hemoglobin, alpha 2 | 360504 | up |
| Hbb | hemoglobin subunit beta | 24440 | up |
| Hbb-b1 | hemoglobin, beta adult major chain | 361619 | up |
| Hbe2 | hemoglobin, epsilon 2 | 502359 | up |
| Hira | histone cell cycle regulator | 363849 | down |
| Hunk | hormonally upregulated Neu-associated kinase | 288275 | down |
| Klk1c8 | kallikrein 1-related peptidase C8 | 292866 | down |
| Krtap7-1 | keratin associated protein 7-1 | 363741 | down |
| Ldhc | lactate dehydrogenase C | 29634 | up |
| Lmod2 | leiomodrin 2 | 296935 | down |
| LOC100134871 | beta globin minor gene | 100134871 | up |
| LOC100909803 | uncharacterized LOC100909803 | 100909803 | up |
| LOC100911266 | uncharacterized LOC100911266 | 100911266 | up |
| LOC100912622 | uncharacterized LOC100912622 | 100912622 | down |
| LOC102548015 | uncharacterized LOC102548015 | 102548015 | up |
| LOC102549174 | ankyrin repeat domain-containing protein 26-l | 102549174 | up |
| LOC102549287 | uncharacterized LOC102549287 | 102549287 | up |
| LOC102550495 | uncharacterized LOC102550495 | 102550495 | up |
| LOC103690979 | uncharacterized LOC103690979 | 103690979 | down |

| | | | |
|--------------|------------------------------------------------|-----------|------|
| LOC103691905 | uncharacterized LOC103691905 | 103691905 | down |
| LOC103692634 | uncharacterized LOC103692634 | 103692634 | down |
| LOC108349347 | disks large homolog 5-like | 108349347 | up |
| LOC108351873 | endogenous retrovirus group K member 9 Pol | 108351873 | down |
| LOC689064 | beta-globin | 689064 | up |
| Lpin1 | lipin 1 | 313977 | up |
| Ly49si2 | immunoreceptor Ly49si2 | 494207 | up |
| Mob3c | MOB kinase activator 3C | 313511 | down |
| Myo1g | myosin IG | 289785 | up |
| Ncf1 | neutrophil cytosolic factor 1 | 114553 | up |
| Nphs1 | NPHS1 nephrin | 64563 | down |
| Nxpe1 | neurexophilin and PC-esterase domain family | 500992 | up |
| Olr59 | olfactory receptor 59 | 170816 | up |
| Opn4 | opsin 4 | 192223 | up |
| Palm | paralemmin | 170673 | down |
| Pbx2 | PBX homeobox 2 | 406164 | down |
| Pcdha3 | protocadherin alpha 3 | 116780 | up |
| Prnd | prion like protein doppel | 113910 | up |
| Rasgrp3 | RAS guanyl releasing protein 3 | 313874 | up |
| Rnf223 | ring finger protein 223 | 680874 | down |
| Sgpp2 | sphingosine-1-phosphate phosphatase 2 | 301543 | down |
| Sh2d1a | SH2 domain containing 1A | 501502 | up |
| Slc4a1 | solute carrier family 4 member 1 | 24779 | up |
| Sorbs2 | sorbin and SH3 domain containing 2 | 114901 | down |
| Stfa2l2 | stefin A2-like 2 | 498087 | up |
| Sult1a1 | sulfotransferase family 1A member 1 | 83783 | up |
| Syne3 | spectrin repeat containing, nuclear envelope f | 299356 | down |
| Synpo2l | synaptopodin 2-like | 305675 | down |
| Tab3 | TGF-beta activated kinase 1 and MAP3K7 bir | 317546 | down |
| Tff2 | trefoil factor 2 | 116592 | down |
| Tmed6 | transmembrane p24 trafficking protein 6 | 291991 | up |
| Tmem235 | transmembrane protein 235 | 688285 | up |
| Tnfaip3 | TNF alpha induced protein 3 | 683206 | down |
| Trim15 | tripartite motif containing 15 | 100910806 | down |
| Uhrf1 | ubiquitin-like with PHD and ring finger doma | 316129 | down |
| Usp35 | ubiquitin specific peptidase 35 | 308834 | down |
| Zbtb16 | zinc finger and BTB domain containing 16 | 353227 | up |
| Zfp37 | zinc finger protein 37 | 115768 | down |
| Zhx3 | zinc fingers and homeoboxes 3 | 311604 | down |
| Znf768 | zinc finger protein 768 | 102553763 | down |
| Zscan10 | zinc finger and SCAN domain containing 10 | 302962 | down |

| Term_ID | Term_description | GeneSymbols | P_value | Category |
|------------|----------------------------------|--------------------------|------------|----------|
| GO:0005833 | hemoglobin complex | Hbe2;LOC689064;Hbb-b1;LC | 1.05E-16 | CC |
| GO:0072562 | blood microparticle | LOC689064;Hbb;Cp;Hba-a2; | 7.76E-08 | CC |
| GO:0022627 | cytosolic small ribosomal sub | Hba1;Hba-a2 | 0.00814502 | CC |
| GO:0031256 | leading edge membrane | Myo1g | 0.01565143 | CC |
| GO:0048787 | presynaptic active zone memb | Grm4 | 0.01565143 | CC |
| GO:0043020 | NADPH oxidase complex | Ncf1 | 0.01952692 | CC |
| GO:0032045 | guanyl-nucleotide exchange f | Rasgrp3 | 0.0214591 | CC |
| GO:0031362 | anchored component of extern | Prnd | 0.0310646 | CC |
| GO:0001891 | phagocytic cup | Myo1g | 0.04624302 | CC |
| GO:0005657 | replication fork | Bcl6 | 0.04624302 | CC |
| GO:0005344 | oxygen carrier activity | Hbe2;LOC689064;Hbb-b1;LC | 6.86E-16 | MF |
| GO:0019825 | oxygen binding | Hbe2;LOC689064;Hbb-b1;LC | 3.89E-14 | MF |
| GO:0020037 | heme binding | Hbe2;LOC689064;Hbb-b1;LC | 2.30E-08 | MF |
| GO:0005506 | iron ion binding | Hbe2;LOC689064;Hbb-b1;LC | 6.97E-08 | MF |
| GO:0004601 | peroxidase activity | Hba1;Hbb;Hba-a2 | 9.21E-06 | MF |
| GO:0043325 | phosphatidylinositol-3,4-bisph | Myo1g;Ncf1 | 0.00102297 | MF |
| GO:0005070 | SH3/SH2 adaptor activity | Sh2d1a;Fcr12 | 0.0013941 | MF |
| GO:0005044 | scavenger receptor activity | Fcr12;Enpp2 | 0.00422599 | MF |
| GO:0000166 | nucleotide binding | Sult1a1;Chd11 | 0.00511068 | MF |
| GO:0005507 | copper ion binding | Cp;Prnd | 0.00548639 | MF |
| GO:0016616 | oxidoreductase activity, acting | Ldhc | 0.0098713 | MF |
| GO:0004551 | nucleotide diphosphatase acti | Enpp2 | 0.0098713 | MF |
| GO:0050294 | steroid sulfotransferase activit | Sult1a1 | 0.0098713 | MF |
| GO:0004062 | aryl sulfotransferase activity | Sult1a1 | 0.0098713 | MF |
| GO:0004322 | ferroxidase activity | Cp | 0.0098713 | MF |
| GO:0030492 | hemoglobin binding | Hbb | 0.0098713 | MF |
| GO:0047391 | alkylglycerophosphoethanolar | Enpp2 | 0.01183418 | MF |
| GO:0016176 | superoxide-generating NADP | Ncf1 | 0.01574865 | MF |
| GO:0008020 | G-protein coupled photorecep | Opn4 | 0.01574865 | MF |
| GO:0004568 | chitinase activity | Chi311 | 0.01574865 | MF |
| GO:0016175 | superoxide-generating NADP | Ncf1 | 0.01574865 | MF |
| GO:0015108 | chloride transmembrane transp | Slc4a1 | 0.01770024 | MF |
| GO:0008061 | chitin binding | Chi311 | 0.01770024 | MF |
| GO:0008510 | sodium:bicarbonate symporter | Slc4a1 | 0.01770024 | MF |
| GO:0008066 | glutamate receptor activity | Grm4 | 0.01770024 | MF |
| GO:0050662 | coenzyme binding | Alas2 | 0.01964807 | MF |
| GO:0001206 | transcriptional repressor activi | Zbtb16 | 0.02159216 | MF |
| GO:0005088 | Ras guanyl-nucleotide exchan | Rasgrp3 | 0.02546914 | MF |
| GO:0008195 | phosphatidate phosphatase act | Lpin1 | 0.02546914 | MF |
| GO:0015106 | bicarbonate transmembrane tr | Slc4a1 | 0.02740203 | MF |
| GO:0016594 | glycine binding | Alas2 | 0.02933121 | MF |
| GO:0030247 | polysaccharide binding | Enpp2 | 0.03317844 | MF |
| GO:0042975 | peroxisome proliferator activa | Lpin1 | 0.03701088 | MF |
| GO:0004622 | lysophospholipase activity | Enpp2 | 0.03701088 | MF |
| GO:0015301 | anion:anion antiporter activity | Slc4a1 | 0.03892158 | MF |
| GO:0005452 | inorganic anion exchanger act | Slc4a1 | 0.03892158 | MF |
| GO:0017016 | Ras GTPase binding | Rasgrp3 | 0.04082859 | MF |
| GO:0030506 | ankyrin binding | Slc4a1 | 0.04082859 | MF |
| GO:0004003 | ATP-dependent DNA helicase | Chd11 | 0.04273194 | MF |
| GO:0030246 | carbohydrate binding | Chi311;Ly49si2 | 0.04881282 | MF |
| GO:0015671 | oxygen transport | Hbe2;LOC689064;Hbb-b1;LC | 6.40E-16 | BP |

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|------------|------------------------------------------------------------|------------------------|------------|----|
| GO:0048821 | erythrocyte development | Hba1;Hbb;Bcl6;Hba-a2 | 1.26E-07 | BP |
| GO:0042744 | hydrogen peroxide catabolic process | Hba1;Hbb;Hba-a2 | 5.47E-06 | BP |
| GO:0042542 | response to hydrogen peroxide | Slc4a1;Hbb;Hba-a2;Hba1 | 1.74E-05 | BP |
| GO:0006968 | cellular defense response | Sh2d1a;Ncf1 | 0.00020201 | BP |
| GO:0010942 | positive regulation of cell death | Hba1;Hbb;Hba-a2 | 0.00026258 | BP |
| GO:0031065 | positive regulation of histone methylation | Lpin1;Bcl6 | 0.00043806 | BP |
| GO:0001953 | negative regulation of cell migration | Bcl6;Enpp2 | 0.00049586 | BP |
| GO:0051291 | protein heterooligomerization | Hba1;Hbb;Hba-a2 | 0.00108805 | BP |
| GO:0071276 | cellular response to cadmium | Enpp2;Ncf1 | 0.00156097 | BP |
| GO:0009967 | positive regulation of signal transduction | Sh2d1a;Fcr12 | 0.00276494 | BP |
| GO:0006879 | cellular iron ion homeostasis | Cp;Alas2 | 0.00333701 | BP |
| GO:0043087 | regulation of GTPase activity | Rasgrp3;Bcl6 | 0.00715144 | BP |
| GO:0009812 | flavonoid metabolic process | Sult1a1 | 0.00974316 | BP |
| GO:0014051 | gamma-aminobutyric acid secretion | Grm4 | 0.00974316 | BP |
| GO:0016056 | rhodopsin mediated signaling | Opn4 | 0.00974316 | BP |
| GO:0072606 | interleukin-8 secretion | Chi311 | 0.00974316 | BP |
| GO:0045629 | negative regulation of T-helper cell activation | Bcl6 | 0.00974316 | BP |
| GO:0006584 | catecholamine metabolic process | Sult1a1 | 0.00974316 | BP |
| GO:0030097 | hemopoiesis | Zbtb16;Hbb | 0.01016261 | BP |
| GO:0042541 | hemoglobin biosynthetic process | Alas2 | 0.01168071 | BP |
| GO:0006642 | triglyceride mobilization | Lpin1 | 0.01168071 | BP |
| GO:0051138 | positive regulation of NK T cell activation | Zbtb16 | 0.01168071 | BP |
| GO:0071800 | podosome assembly | Ncf1 | 0.01168071 | BP |
| GO:0002467 | germinal center formation | Bcl6 | 0.01361457 | BP |
| GO:0070741 | response to interleukin-6 | Chi311 | 0.01361457 | BP |
| GO:0038096 | Fc-gamma receptor signaling pathway | Myo1g | 0.01361457 | BP |
| GO:2000394 | positive regulation of lamellipodium formation | Enpp2 | 0.01361457 | BP |
| GO:0014823 | response to activity | Sult1a1;Slc4a1 | 0.01539663 | BP |
| GO:0045986 | negative regulation of smooth muscle cell proliferation | Ncf1 | 0.01554477 | BP |
| GO:0006782 | protoporphyrinogen IX biosynthesis | Alas2 | 0.01554477 | BP |
| GO:0050427 | 3'-phosphoadenosine 5'-phosphoribosyl transferase activity | Sult1a1 | 0.01554477 | BP |
| GO:0001878 | response to yeast | Ncf1 | 0.01554477 | BP |
| GO:0006691 | leukotriene metabolic process | Ncf1 | 0.01554477 | BP |
| GO:0006032 | chitin catabolic process | Chi311 | 0.01554477 | BP |
| GO:0019752 | carboxylic acid metabolic process | Ldhc | 0.01554477 | BP |
| GO:0072678 | T cell migration | Myo1g | 0.01554477 | BP |
| GO:0002829 | negative regulation of type 2 interferon production | Bcl6 | 0.01554477 | BP |
| GO:0002456 | T cell mediated immunity | Myo1g | 0.01554477 | BP |
| GO:0007196 | adenylate cyclase-inhibiting activity | Grm4 | 0.01747129 | BP |
| GO:0050665 | hydrogen peroxide biosynthesis | Ncf1 | 0.01747129 | BP |
| GO:0006898 | receptor-mediated endocytosis | Fcr12;Enpp2 | 0.01788076 | BP |
| GO:0045730 | respiratory burst | Ncf1 | 0.01939416 | BP |
| GO:0006090 | pyruvate metabolic process | Ldhc | 0.01939416 | BP |
| GO:0051923 | sulfation | Sult1a1 | 0.01939416 | BP |
| GO:0018298 | protein-chromophore linkage | Opn4 | 0.01939416 | BP |
| GO:0006825 | copper ion transport | Cp | 0.01939416 | BP |
| GO:0045741 | positive regulation of epidermal cell proliferation | Ncf1 | 0.01939416 | BP |
| GO:0005975 | carbohydrate metabolic process | Chi311;Ldhc | 0.01984801 | BP |
| GO:0032025 | response to cobalt ion | Alas2 | 0.02131338 | BP |

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|------------|-----------------------------------|------------------|------------|----|
| GO:0008210 | estrogen metabolic process | Sult1a1 | 0.02131338 | BP |
| GO:0051272 | positive regulation of cellular | Bcl6 | 0.02131338 | BP |
| GO:0042554 | superoxide anion generation | Ncf1 | 0.02131338 | BP |
| GO:0050805 | negative regulation of synaptic | Grm4 | 0.02322895 | BP |
| GO:0097484 | dendrite extension | Cdkl3 | 0.02322895 | BP |
| GO:2000773 | negative regulation of cellular | Bcl6 | 0.02322895 | BP |
| GO:0045591 | positive regulation of regulato | Bcl6 | 0.02322895 | BP |
| GO:0019432 | triglyceride biosynthetic proc | Lpin1 | 0.02322895 | BP |
| GO:0006878 | cellular copper ion homeostas | Prnd | 0.02322895 | BP |
| GO:0009062 | fatty acid catabolic process | Lpin1 | 0.02514087 | BP |
| GO:0007340 | acrosome reaction | Prnd | 0.02704917 | BP |
| GO:0006068 | ethanol catabolic process | Sult1a1 | 0.02704917 | BP |
| GO:0001823 | mesonephros development | Zbtb16 | 0.02704917 | BP |
| GO:0035137 | hindlimb morphogenesis | Zbtb16 | 0.02704917 | BP |
| GO:0031529 | ruffle organization | Lpin1 | 0.02704917 | BP |
| GO:0035136 | forelimb morphogenesis | Zbtb16 | 0.02704917 | BP |
| GO:0061036 | positive regulation of cartilage | Zbtb16 | 0.02704917 | BP |
| GO:0051932 | synaptic transmission, GABA | Grm4 | 0.02704917 | BP |
| GO:0006820 | anion transport | Slc4a1 | 0.02704917 | BP |
| GO:0030324 | lung development | Cp;Chi311 | 0.02740296 | BP |
| GO:0009414 | response to water deprivation | Slc4a1 | 0.02895384 | BP |
| GO:0010447 | response to acidic pH | Slc4a1 | 0.0308549 | BP |
| GO:0007602 | phototransduction | Opn4 | 0.0308549 | BP |
| GO:0007250 | activation of NF-kappaB-indu | Chi311 | 0.0308549 | BP |
| GO:0006754 | ATP biosynthetic process | Ldhc | 0.0308549 | BP |
| GO:0017085 | response to insecticide | Sult1a1 | 0.0308549 | BP |
| GO:0035634 | response to stilbenoid | Hba1 | 0.0308549 | BP |
| GO:0006783 | heme biosynthetic process | Alas2 | 0.0308549 | BP |
| GO:0009395 | phospholipid catabolic proces | Enpp2 | 0.03275233 | BP |
| GO:0045598 | regulation of fat cell differenti | Lpin1 | 0.03464617 | BP |
| GO:0006801 | superoxide metabolic process | Ncf1 | 0.03464617 | BP |
| GO:0032332 | positive regulation of chondro | Zbtb16 | 0.0365364 | BP |
| GO:0031589 | cell-substrate adhesion | Myo1g | 0.0365364 | BP |
| GO:0007283 | spermatogenesis | Pcdha3;Bcl6;Prnd | 0.03737964 | BP |
| GO:0050832 | defense response to fungus | Ncf1 | 0.03842304 | BP |
| GO:0006612 | protein targeting to membrane | Ncf1 | 0.03842304 | BP |
| GO:0008285 | negative regulation of cell pro | Zbtb16;Bcl6;Grm4 | 0.03964269 | BP |
| GO:0048714 | positive regulation of oligoder | Enpp2 | 0.0403061 | BP |
| GO:0046685 | response to arsenic-containing | Slc4a1 | 0.0403061 | BP |
| GO:0015698 | inorganic anion transport | Slc4a1 | 0.0403061 | BP |
| GO:1900745 | positive regulation of p38MA | Ncf1 | 0.0403061 | BP |
| GO:0045638 | negative regulation of myeloic | Zbtb16 | 0.0403061 | BP |
| GO:0035024 | negative regulation of Rho pr | Bcl6 | 0.04218558 | BP |
| GO:0045778 | positive regulation of ossificat | Zbtb16 | 0.04218558 | BP |
| GO:0000266 | mitochondrial fission | Lpin1 | 0.04218558 | BP |
| GO:0030517 | negative regulation of axon ex | Cdkl3 | 0.04406148 | BP |
| GO:0061003 | positive regulation of dendriti | Bhlhb9 | 0.04593382 | BP |
| GO:0015701 | bicarbonate transport | Slc4a1 | 0.04593382 | BP |

GO:0051966 regulation of synaptic transmi:Grm4

0.0478026 BP

| Term_ID | Term_description | GeneSymb | P_value | Category |
|------------|--------------------------|------------|----------|----------|
| GO:0014069 | postsynaptic density | Palm;Dst;I | 5.65E-05 | CC |
| GO:0030018 | Z disc | Cacna1c;S | 0.001057 | CC |
| GO:0009898 | cytoplasmic side of pl | Palm;Dst | 0.003534 | CC |
| GO:1990454 | L-type voltage-gated c | Cacna1c | 0.011435 | CC |
| GO:0005634 | nucleus | Palm;Pbx2 | 0.012813 | CC |
| GO:0036057 | slit diaphragm | Nphs1 | 0.013058 | CC |
| GO:0044309 | neuron spine | Palm | 0.013058 | CC |
| GO:0097512 | cardiac myofibril | Lmod2 | 0.014678 | CC |
| GO:0034993 | LINC complex | Syne3 | 0.014678 | CC |
| GO:0030056 | hemidesmosome | Dst | 0.016296 | CC |
| GO:0000791 | euchromatin | Uhrf1 | 0.016296 | CC |
| GO:0042383 | sarcolemma | Cacna1c;D | 0.017544 | CC |
| GO:0005865 | striated muscle thin fil | Lmod2 | 0.017912 | CC |
| GO:0030061 | mitochondrial crista | Akap1 | 0.019525 | CC |
| GO:0032591 | dendritic spine membe | Palm | 0.019525 | CC |
| GO:0097038 | perinuclear endoplasr | Dst | 0.024348 | CC |
| GO:0005635 | nuclear envelope | Syne3;Dst | 0.02725 | CC |
| GO:0031527 | filopodium membrane | Palm | 0.027551 | CC |
| GO:0005665 | DNA-directed RNA p | Znf768 | 0.029148 | CC |
| GO:0035371 | microtubule plus-end | Dst | 0.032336 | CC |
| GO:0005640 | nuclear outer membra | Syne3 | 0.033926 | CC |
| GO:0016327 | apicolateral plasma m | Palm | 0.033926 | CC |
| GO:0043234 | protein complex | Hira;Cacn | 0.034446 | CC |
| GO:0015629 | actin cytoskeleton | Synpo2l;D | 0.036099 | CC |
| GO:0005657 | replication fork | Uhrf1 | 0.038681 | CC |
| GO:0005891 | voltage-gated calcium | Cacna1c | 0.038681 | CC |
| GO:0031430 | M band | Lmod2 | 0.044985 | CC |
| GO:0005720 | nuclear heterochromat | Uhrf1 | 0.044985 | CC |
| GO:0032590 | dendrite membrane | Palm | 0.044985 | CC |
| GO:0045211 | postsynaptic membran | Cacna1c;A | 0.046299 | CC |
| GO:0051393 | alpha-actinin binding | Cacna1c;N | 0.000828 | MF |
| GO:0019904 | protein domain specifi | Akap1;Cac | 0.00374 | MF |
| GO:0008092 | cytoskeletal protein bi | Dlg5;Syne | 0.006294 | MF |
| GO:0004843 | thiol-dependent ubiqu | Tnfaip3;U | 0.007907 | MF |
| GO:0048248 | CXCR3 chemokine re | Cxcl11 | 0.009275 | MF |
| GO:0003779 | actin binding | Synpo2l;D | 0.009322 | MF |
| GO:0061578 | Lys63-specific deubiq | Tnfaip3 | 0.01112 | MF |
| GO:0030346 | protein phosphatase 2l | Akap1 | 0.016635 | MF |
| GO:0042379 | chemokine receptor bi | Cxcl11 | 0.018467 | MF |
| GO:0004143 | diacylglycerol kinase | Dgkh | 0.018467 | MF |
| GO:0051010 | microtubule plus-end | Dst | 0.022121 | MF |
| GO:0008331 | high voltage-gated cal | Cacna1c | 0.022121 | MF |
| GO:0005272 | sodium channel activi | Asic4 | 0.027577 | MF |
| GO:0005523 | tropomyosin binding | Lmod2 | 0.027577 | MF |
| GO:0003714 | transcription corepres | Hira;Zhx3 | 0.028946 | MF |
| GO:0003951 | NAD+ kinase activity | Dgkh | 0.031197 | MF |
| GO:0046872 | metal ion binding | Tab3;Zsca | 0.031672 | MF |
| GO:0008327 | methyl-CpG binding | Uhrf1 | 0.033003 | MF |
| GO:0031491 | nucleosome binding | Hira | 0.036604 | MF |

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|------------|--------------------------|------------|----------|----|
| GO:0003700 | DNA binding transcrip | Bcl3;Zhx3 | 0.037023 | MF |
| GO:0003677 | DNA binding | Zfp37;Tnf | 0.03794 | MF |
| GO:0034237 | protein kinase A regul | Akap1 | 0.0384 | MF |
| GO:0070530 | K63-linked polyubiqu | Tnfaip3 | 0.040193 | MF |
| GO:0031369 | translation initiation f | Cacna1c | 0.043768 | MF |
| GO:0017022 | myosin binding | Nphs1 | 0.04733 | MF |
| GO:0000987 | proximal promoter sec | Uhrf1 | 0.04733 | MF |
| GO:0003785 | actin monomer bindin | Lmod2 | 0.04733 | MF |
| GO:0030011 | maintenance of cell pc | Dlg5;Dst | 4.30E-05 | BP |
| GO:0007010 | cytoskeleton organizat | Syne3;Palr | 0.00125 | BP |
| GO:0006351 | transcription, DNA-te | Zscan10;H | 0.001326 | BP |
| GO:0060999 | positive regulation of | Dlg5;Palm | 0.001749 | BP |
| GO:0030838 | positive regulation of | Nphs1;Lm | 0.00322 | BP |
| GO:0070098 | chemokine-mediated s | Cxcl11;Tff | 0.004483 | BP |
| GO:0016579 | protein deubiquitinatio | Tnfaip3;U | 0.006646 | BP |
| GO:0086045 | membrane depolarizat | Cacna1c | 0.008601 | BP |
| GO:0042536 | negative regulation of | Bcl3 | 0.008601 | BP |
| GO:0050728 | negative regulation of | Tff2;Tnfai | 0.009836 | BP |
| GO:0010216 | maintenance of DNA | Uhrf1 | 0.010312 | BP |
| GO:0060455 | negative regulation of | Tff2 | 0.010312 | BP |
| GO:0002455 | humoral immune resp | Bcl3 | 0.010312 | BP |
| GO:0051101 | regulation of DNA bir | Bcl3 | 0.010312 | BP |
| GO:0051534 | negative regulation of | Akap1 | 0.010312 | BP |
| GO:0043031 | negative regulation of | Tff2 | 0.010312 | BP |
| GO:0031581 | hemidesmosome asser | Dst | 0.010312 | BP |
| GO:0007015 | actin filament organiz | Sorbs2;Lm | 0.010496 | BP |
| GO:0050869 | negative regulation of | Tnfaip3 | 0.012021 | BP |
| GO:0072205 | metanephric collectin | Dlg5 | 0.012021 | BP |
| GO:0086012 | membrane depolarizat | Cacna1c | 0.012021 | BP |
| GO:0002467 | germinal center forma | Bcl3 | 0.012021 | BP |
| GO:2000347 | positive regulation of | Tnfaip3 | 0.012021 | BP |
| GO:0030252 | growth hormone secre | Cacna1c | 0.012021 | BP |
| GO:1900246 | positive regulation of | Trim15 | 0.012021 | BP |
| GO:0045088 | regulation of innate in | Tnfaip3 | 0.013727 | BP |
| GO:0051694 | pointed-end actin filar | Lmod2 | 0.013727 | BP |
| GO:0035331 | negative regulation of | Dlg5 | 0.013727 | BP |
| GO:0001505 | regulation of neurotra | Celf6 | 0.013727 | BP |
| GO:0090286 | cytoskeletal anchoring | Syne3 | 0.013727 | BP |
| GO:0045010 | actin nucleation | Lmod2 | 0.013727 | BP |
| GO:0032836 | glomerular basement m | Nphs1 | 0.01543 | BP |
| GO:0046620 | regulation of organ gr | Cacna1c | 0.01543 | BP |
| GO:0060074 | synapse maturation | Palm | 0.01543 | BP |
| GO:0010818 | T cell chemotaxis | Cxcl11 | 0.01543 | BP |
| GO:0002315 | marginal zone B cell c | Bcl3 | 0.01543 | BP |
| GO:0045176 | apical protein localiza | Dlg5 | 0.01713 | BP |
| GO:0061337 | cardiac conduction | Cacna1c | 0.01713 | BP |
| GO:0072015 | glomerular visceral ep | Nphs1 | 0.01713 | BP |
| GO:0042088 | T-helper 1 type immu | Bcl3 | 0.01713 | BP |

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|------------|-------------------------|------------|----------|----|
| GO:0035871 | protein K11-linked de | Tnfaip3 | 0.01713 | BP |
| GO:0031110 | regulation of microtub | Dst | 0.01713 | BP |
| GO:0010225 | response to UV-C | Bcl3 | 0.01713 | BP |
| GO:0008090 | retrograde axonal tran | Dst | 0.018828 | BP |
| GO:0010390 | histone monoubiquitir | Uhrf1 | 0.018828 | BP |
| GO:0002237 | response to molecule c | Tnfaip3 | 0.018828 | BP |
| GO:0035308 | negative regulation of | Akap1 | 0.018828 | BP |
| GO:0098911 | regulation of ventricul | Cacna1c | 0.018828 | BP |
| GO:0032691 | negative regulation of | Tnfaip3 | 0.018828 | BP |
| GO:0008360 | regulation of cell shap | Syne3;Palr | 0.02016 | BP |
| GO:1903364 | positive regulation of | Tnfaip3 | 0.020522 | BP |
| GO:0061049 | cell growth involved i | Sorbs2 | 0.020522 | BP |
| GO:0003094 | glomerular filtration | Nphs1 | 0.020522 | BP |
| GO:0002690 | positive regulation of | Cxcl11 | 0.020522 | BP |
| GO:0032495 | response to muramyl c | Tnfaip3 | 0.020522 | BP |
| GO:0090150 | establishment of prote | Syne3 | 0.020522 | BP |
| GO:0010614 | negative regulation of | Akap1 | 0.020522 | BP |
| GO:0032233 | positive regulation of | Synpo2l | 0.022214 | BP |
| GO:0016574 | histone ubiquitination | Uhrf1 | 0.022214 | BP |
| GO:0045824 | negative regulation of | Tnfaip3 | 0.022214 | BP |
| GO:0016310 | phosphorylation | Dgkh;Akap1 | 0.023542 | BP |
| GO:0043950 | positive regulation of | Cxcl11 | 0.023903 | BP |
| GO:0086002 | cardiac muscle cell ac | Cacna1c | 0.023903 | BP |
| GO:0071625 | vocalization behavior | Celf6 | 0.023903 | BP |
| GO:0030330 | DNA damage respons | Bcl3 | 0.023903 | BP |
| GO:0045104 | intermediate filament | Dst | 0.025589 | BP |
| GO:0045197 | establishment or main | Dlg5 | 0.025589 | BP |
| GO:1902187 | negative regulation of | Trim15 | 0.025589 | BP |
| GO:0030816 | positive regulation of | Cxcl11 | 0.027272 | BP |
| GO:0006939 | smooth muscle contra | Cacna1c | 0.027272 | BP |
| GO:0010738 | regulation of protein k | Akap1 | 0.027272 | BP |
| GO:0032703 | negative regulation of | Tnfaip3 | 0.027272 | BP |
| GO:0032481 | positive regulation of | Trim15 | 0.028952 | BP |
| GO:0032270 | positive regulation of | Uhrf1 | 0.028952 | BP |
| GO:0019229 | regulation of vasocons | Cacna1c | 0.028952 | BP |
| GO:0035418 | protein localization to | Nphs1 | 0.028952 | BP |
| GO:0048870 | cell motility | Dst | 0.03063 | BP |
| GO:0051056 | regulation of small G1 | Arhgap26 | 0.03063 | BP |
| GO:0017156 | calcium ion regulated | Cacna1c | 0.03063 | BP |
| GO:0042692 | muscle cell differentia | Hira | 0.03063 | BP |
| GO:0071257 | cellular response to el | Palm | 0.03063 | BP |
| GO:1903507 | negative regulation of | Hira | 0.033977 | BP |
| GO:0030818 | negative regulation of | Palm | 0.033977 | BP |
| GO:0070536 | protein K63-linked de | Tnfaip3 | 0.035646 | BP |
| GO:0046907 | intracellular transport | Dst | 0.037312 | BP |
| GO:0007520 | myoblast fusion | Nphs1 | 0.037312 | BP |
| GO:0045736 | negative regulation of | Tnfaip3 | 0.037312 | BP |
| GO:0070509 | calcium ion import | Cacna1c | 0.038976 | BP |

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|------------|-------------------------|---------|----------|----|
| GO:0006336 | DNA replication-inde | Hira | 0.038976 | BP |
| GO:0060441 | epithelial tube branchi | Dlg5 | 0.040637 | BP |
| GO:0030041 | actin filament polyme | Lmod2 | 0.040637 | BP |
| GO:1902042 | negative regulation of | Tnfaip3 | 0.042295 | BP |
| GO:0007194 | negative regulation of | Palm | 0.042295 | BP |
| GO:0071108 | protein K48-linked de | Tnfaip3 | 0.042295 | BP |
| GO:0009954 | proximal/distal patter | Pbx2 | 0.04395 | BP |
| GO:0042832 | defense response to pr | Bcl3 | 0.047252 | BP |
| GO:0007205 | protein kinase C-activ | Dgkh | 0.047252 | BP |
| GO:0007586 | digestion | Tff2 | 0.047252 | BP |
| GO:2000352 | negative regulation of | Tnfaip3 | 0.048899 | BP |