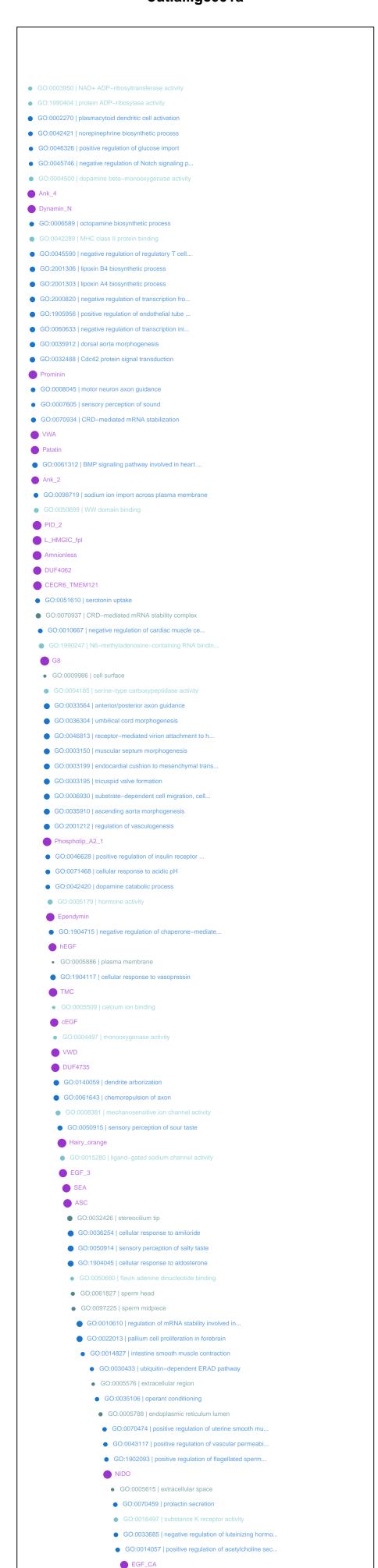
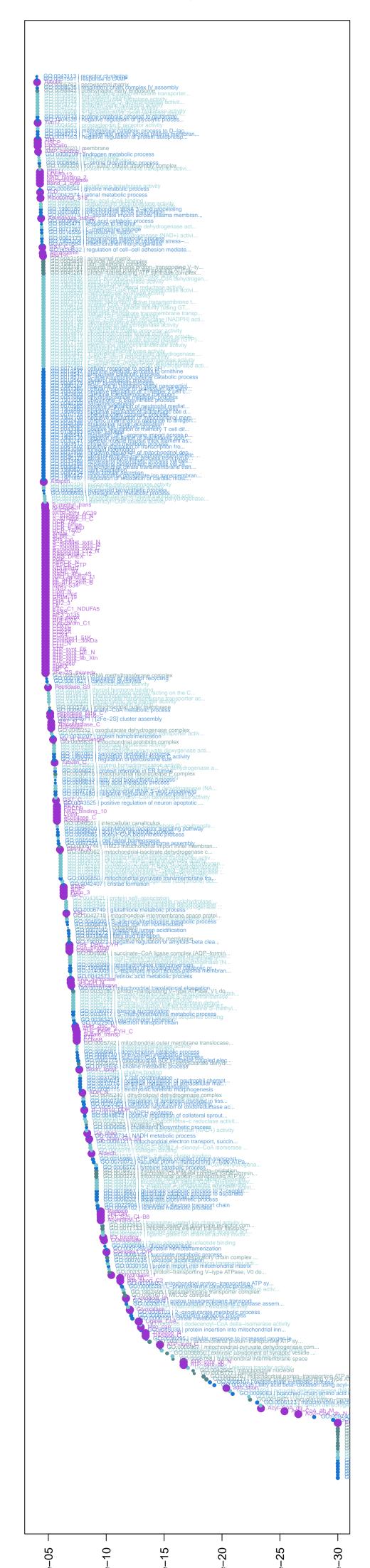
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20G-Fell_Oxy_320G-Fell_Oxy_4

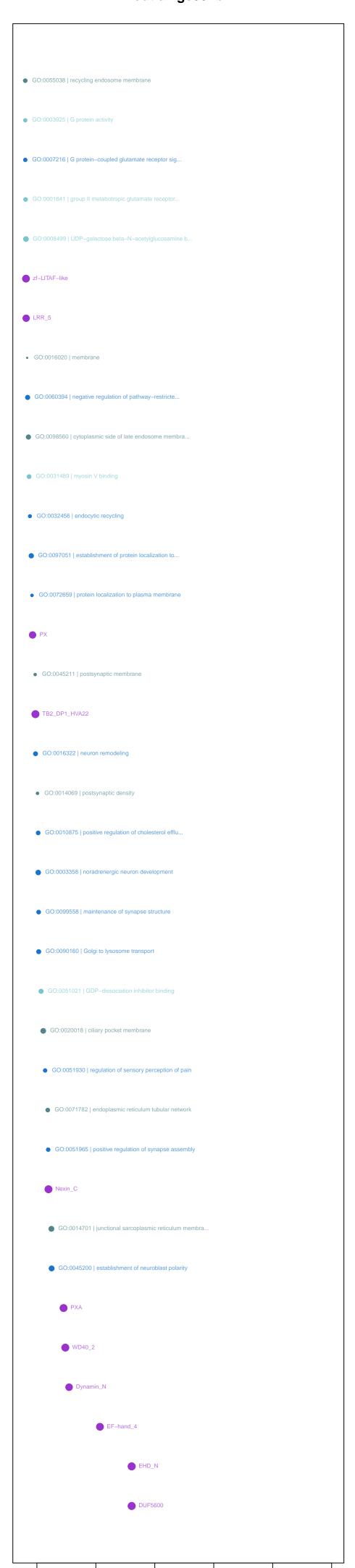
Pyr_redox_3

out.all.gc002a

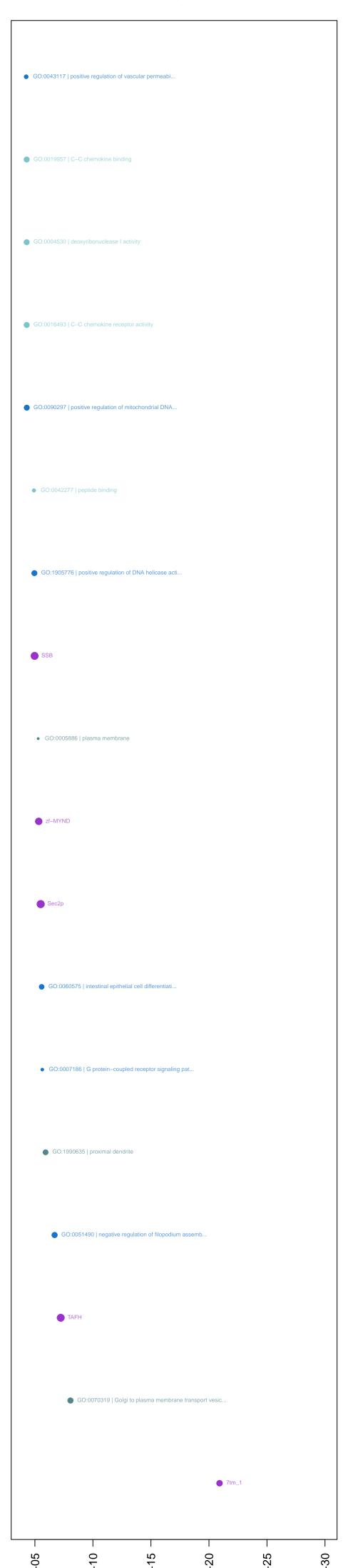


p-value

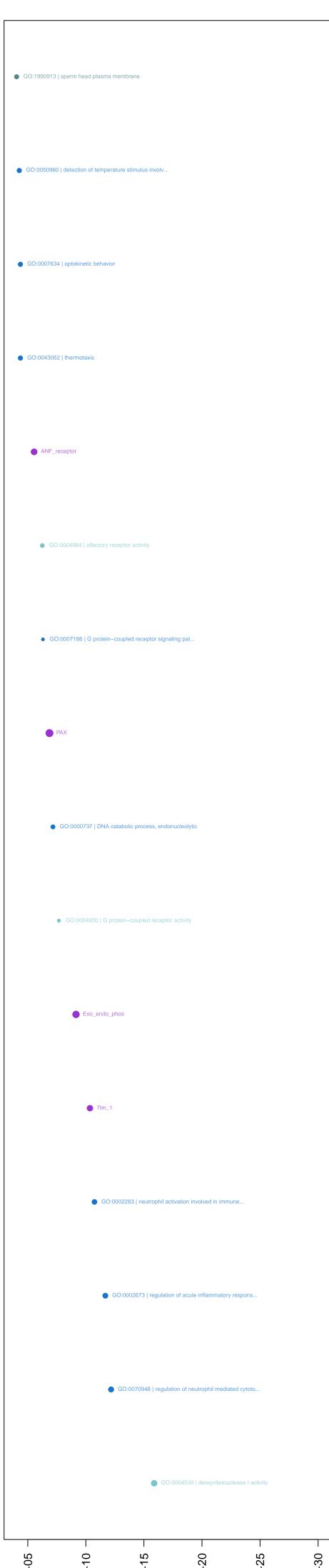
out.all.gc002b



out.all.gc003a



out.all.gc003b



```
STAT_int
STAT_bind
GO:0030425 | dendrite
                        GO:0061891 | calcium ion sensor activity
GO:0031528 | microvillus membrane
                        GO:0031528 | microvillus membrane
GO:0035254 | glutamate receptor binding
GO:2000766 | negative regulation of cytoplasmic trans.
                        GO:0043204 | perikaryon / phosphatise GO:0016239 | positive regulation of cytoplasmic trans chocostal conditions and conditions are regulated by the conditions are regulation of a cell differential conditions are regulated by the cell differential conditions are regulated by the cell differential conditions are regulated by the cell differential cell differenti
                                        Rad60–SLD 2
                                                                              t 0005249 voltage—gated potassium channel activity 0004117 calmodulin—dependent cyclic—nucleotide p. 0048101 calcium— and calmodulin—regulated 3',5'—... 0017098 sulfonylurea receptor binding 0042975 peroxisome proliferator activated recept... 0003677
                           GO:0017093
GO:0042975
GO:0042975
GO:002677
GO:1902667
GO:002867
GO:0002851
GO:0002851
GO:0002851
GO:0032981
GO:003281
GO:003284
GO:003290
GO:003284
GO:003290
GO:00329
••••••••••••••••••••
                                        NTP_transf_7
GO:0031201 | SNARE complex
                                           GO:0005525 GTP binding
GO:0099576 regulation of protein catabolic process ...
GO:190417 cellular response to vasopressin
GO:0001917 photoreceptor inner segment
GO:0047555 3;5-cyclic-GMP phosphodiesterase act
                                              GO:0047555 | 3
Serpin
GO:0097110 |
GO:0042149
GO:0046827
GO:0006171 |
GO:0030514 |
STAT_alpha
RRM_7
PAX
                                                                                                                                                                                             scaffold protein binding
cellular response to glucose starvation
positive regulation of protein export fr...
cAMP biosynthetic process
negative regulation of BMP signaling pat...
                                                   PAX
CEBP_ZZ
GO:009523 | presynaptic cytosol
GO:0048278 | vesicle docking
GO:0032009 | early phagosome
GO:004878 | cytoskeleton of presynaptic active zone
GTPase binding

The constituent of presynaptic ac.
                                                        GO:0098882 structural constituent of presynaptic ac
GO:0060216 definitive hemopoiesis
                                                   GO:0060216 definitive hemopoiesis regulation of centromere complex assembl... regulation of centromere complex assembls... regulation of centromere complex assembls... regulation of centromere complex assembly... regulation of complex assembly... regulation of complex assembly... regulation of complex assembly... regulation of nuclear-transcrib... removed in female pre... reproduction of nuclear-transcrib... reproduction of nuclear-transcrib... reproduction of nuclear-transcrib... reproduction of nuclear-transcrib... reproduction reproduction of nuclear-transcrib... reproduction of nuclear-transc
                     ••••••••••
                                                        GO:0098888 | extrinsic component of presynapus memor.

1.1
GO:2000562 | negative regulation of CD4-positive, alp...
GO:0008016 | regulation of heart contraction
GO:000300 | regulation of synaptic vesicle exocytosi...
GO:0045669 | positive regulation of osteoblast differ...
GO:0048841 | cell volume homeostasis
Yippee-Mis18
PAS 9
GO:0048541 | Peyer's patch development
GO:0044306 | negative regulation of cold-induced ther...
GO:00120163 | positive regulation of autophagy
GO:0003924 | GTPase activity
                                                                      GO:000324
GO:0003516
GO:0003516
GO:0008140
AMP response element binding protein bi.
maintenance of presynaptic active zone s..
cellular response to epidermal growth fa...
GO:0046935
1-phosphatidylinositol—3-kinase regulato.
                                                                         GO:0045935 | 1-phosphatidylinositol-3-kinase re
GO:0010813 | neuropeptide catabolic process
GO:0032794 | GTPase activating protein binding
GO:0042588 | zymogen granule
GO:001093 | TEIIB-class transcription factor bir
                                                                              GO:0000149
GO:0032713
GO:1900452
GO:004320
GO:00452
GO:004320
GO:004320
GO:007260
GO:0
                                                                                                                                    2H2_6
0001227 | DNA-binding transcription repressor acti.
                                                                                              GO:0001227 phosphatidylserine binding
GO:0048787 presynaptic active zone membrane
GO:0045668 negative regulation of osteoblast differ...
GO:0071277 cellular response to calcium ion
GO:008978 | glutamatergic synapse
                                                                                                    HNOBA
GO:0070382 | exocytic vesicle
                                                                                                      GO:0042043 | neurexin family protein binding
GO:0046039 | GTP metabolic process
GO:0043679 | axon terminus
GO:0032793 | positive regulation of CREB transcriptio...
GO:0010801 | negative regulation of peptidyl-threonin...
GO:0010807 | regulation of synaptic vesicle priming
GO:0042307 | positive regulation of protein import in...
GO:0035902 | response to immobilization stress
                                                                                                                 GO:0035902 | response to minioconda.
Atg8
GO:0000981 | DNA-binding transcription factor activit...
GO:1904707 | positive regulation of vascular associat...
GO:0045956 | positive regulation of calcium ion-depen.
GO:0048294 | negative regulation of isotype switching...
zf-RING_11
PTPlike_phytase
PP1c_bdg
Jun
                                                                                                                               PP1c_bdg
Jun
DUF2353
CBF_beta
BTG_
BTB_3
APP_N
APP_E2
APP_Cu_bd
GO:0031696
                                                                                                                               GO:0031696 | alpha=2B adrenergic receptor binding blanes. Complex addrenergic receptor binding alpha=2B adrenergic receptor binding adrenergic receptor binding alpha=2B adrenergic receptor binding alpha=2B adrenergic receptor binding positive regulation of response to drug receptor binding strength and receptor binding strength adrenergic receptor binding adrenergic receptor binding adrenergic receptor binding strength adrenergic receptor binding strenergic receptor binding strength addrenergic receptor binding p
                                                                                                                                            GO:0042826 histone deaucrys—
STPPase N
GO:001553 | luteinization
GO:1904692 positive regulation of type B pancreatic...
positive regulation of CDB-positive, alp...
GO:0032792 | protein phosphatase 1 binding
GO:0003176 protein-coupled receptor internalizati...
GO:003145 | dense core granule
GO:0003714 | transcription corepressor activity

SO:0004151 | 3.5-cyclic-AMP phosphodiesterase act
                                                                                                                                                                          GO:0001447 | Cellular response to hydroperoxide GO:0033864 | cellular response to hydroperoxide GO:0033864 | cellular response to hydroperoxide GO:0099626 | voltage-gated calcium channel activity i...
                                                                                                                                                                                  GO:009626 | voltage-gated calcium channel activity i...
FYVE 2
GO:0007212 | dopamine receptor signaling pathway
GO:0008021 | synaptic vesicle
Pkinase
cNMP_binding
GO:0033138 | positive regulation of peptidyl-serine p...
GO:0150037 | regulation of calcium-dependent activati...
GO:0016513 | core-binding factor complex
GO:1990441 | negative regulation of transcription fro...
GO:0043371 | negative regulation of CD4-positive, alp...
RIIa
GO:0031821 | G protein-coupled serotonin receptor bin
                                                                                                                                                                                                                                RIIa
GO:0031821 | G protein–coupled serotonin receptor bin...
GO:0005544 | calcium–dependent phospholipid binding
GO:0017075 | syntaxin–1 binding
GO:0031683 | G–protein beta/gamma–subunit complex bin...
GO:0061669 | spontaneous neurotransmitter secretion
GO:0005891 | voltage–gated calcium channel complex
GO:0005886 | plasma membrane
GO:0005831 | high voltage–gated calcium channel activ...
bZIP Maf
                                                                                                                                                                                                                                                                                                                       ZIP_1
GO:0045944 | positive regulation of transcription by ...
| BTB_2
GO:0000122 | negative regulation of transcription by ...
GO:0046872 | metal ion binding
GO:0001228 | DNA-binding transcription activator acti.

    PDEase_I
    GO:0099502 | calcium–dependent activation of synaptic...
    GO:0005834 | heterotrimeric G–protein complex
    GO:0000978 | RNA polymerase
```

1e-05 1e-05 1e-15 1e-10 1e-15 1e-10 1e





-value

out.all.gc007a GO:0140535 | intracellular protein-containing complex GO:0045947 | negative regulation of translational ini... • GO:0017069 | snRNA binding • GO:0006413 | translational initiation GO:0035279 | mRNA cleavage involved in gene silencing... GO:0090625 | mRNA cleavage involved in gene silencing... GO:0070551 | endoribonuclease activity, cleaving siRN... GO:0090624 | endoribonuclease activity, cleaving miRN... GO:0070180 | large ribosomal subunit rRNA binding GO:0060316 | positive regulation of ryanodine–sensiti... GO:0060315 | negative regulation of ryanodine-sensiti... • GO:0003729 | mRNA binding • GO:1990446 | U1 snRNP binding GO:0003684 | damaged DNA binding GO:0030422 | production of siRNA involved in RNA inte... GO:0019774 | proteasome core complex, beta-subunit co... ● GO:0050610 | methylarsonate reductase activity GO:0045174 | glutathione dehydrogenase (ascorbate) ac... • GO:0000398 | mRNA splicing, via spliceosome • GO:0098794 | postsynapse GO:0034719 | SMN–Sm protein complex • GO:0003743 | translation initiation factor activity GO:0034715 | pICIn–Sm protein complex GO:0000340 | RNA 7-methylguanosine cap binding GO:0005685 | U1 snRNP GO:0019773 | proteasome core complex, alpha-subunit c... GO:0005845 | mRNA cap binding complex GO:0120115 | Lsm2-8 complex GO:0005688 | U6 snRNP GO:0034709 | methylosome GO:0031369 | translation initiation factor binding GO:0071007 | U2-type catalytic step 2 spliceosome GST_N_3 GO:0035278 | miRNA mediated inhibition of translation GO:0000932 | P-body GO:0005689 | U12-type spliceosomal complex GO:0071013 | catalytic step 2 spliceosome Proteasome_A_N GO:0005687 | U4 snRNP GO:0006364 | rRNA processing GO:0005686 | U2 snRNP GO:0140513 | nuclear protein–containing complex GO:0005844 | polysome GO:0071005 | U2-type precatalytic spliceosome GO:0000387 | spliceosomal snRNP assembly RRM_1 GO:0005730 | nucleolus • GO:0003723 | RNA binding GO:0046540 | U4/U6 x U5 tri-snRNP complex Proteasome LSM • GO:0005634 | nucleus GO:0042788 | polysomal ribosome • GO:0005654 | nucleoplasm GO:0022627 | cytosolic small ribosomal subunit

● GO:0002181 | cytopla

-value

GO:0140236 | translation at presynapse

GO:0140242 | translation at postsynapse

GO:0022625 | cytosoli

• GO:0003735 | structu

out.all.gc007b

 GO:0006334 | nucleosome assembly GO:0043021 | ribonucleoprotein complex binding SIMPL Mago_nashi GO:0007004 | telomere maintenance via telomerase GO:0035145 | exon-exon junction complex GO:0099631 | postsynaptic endocytic zone cytoplasmic ... GO:0031439 | positive regulation of mRNA cleavage GO:2000975 | positive regulation of pro-B cell differ... XPG_I DNA_pol_E_B CSN8_PSD8_EIF3K GO:0050821 | protein stabilization GO:0000413 | protein peptidyl-prolyl isomerization GO:0051168 | nuclear export HMG box GO:1900087 | positive regulation of G1/S transition o... GO:0007339 | binding of sperm to zona pellucida GO:0008622 | epsilon DNA polymerase complex GO:0061574 | ASAP complex GO:0051225 | spindle assembly GO:0000027 | ribosomal large subunit assembly GO:0090661 | box H/ACA telomerase RNP complex GO:1904667 | negative regulation of ubiquitin protein... GO:0031298 | replication fork protection complex GO:0005854 | nascent polypeptide-associated complex GO:1990723 | cytoplasmic periphery of the nuclear por... GO:0070182 | DNA polymerase binding GO:1990189 | peptide-serine-N-acetyltransferase activ.. GO:0043111 | replication fork arrest GO:0034421 | post-translational protein acetylation Prp19 PAC4 NUDIX 2 Metallophos_2 Ctf8 Clathrin_lg_ch GO:0008541 | proteasome regulatory particle, lid subc... GO:2000622 | regulation of nuclear-transcribed mRNA c. • GO:0005813 | centrosome GO:0003755 | peptidyl-prolyl cis-trans isomerase acti. GO:0005971 | ribonucleoside-diphosphate reductase com... ● GO:0004748 | ribonucleoside-diphosphate reductase act.. GO:0071006 | U2-type catalytic step 1 spliceosome GO:0005658 | alpha DNA polymerase:primase complex GO:0006269 | DNA replication, synthesis of RNA primer GO:0032040 | small-subunit processome GO:0001650 | fibrillar center GO:0061077 | chaperone-mediated protein folding GO:0005850 | eukaryotic translation initiation factor... NTF2 NAC LZ3wCH GO:0006231 | dTMP biosynthetic process ■ GO:0006272 | leading strand elongation GO:1903934 | positive regulation of DNA primase activ... GO:0000974 | Prp19 complex GO:0006260 | DNA replication GO:0031429 | box H/ACA snoRNP complex GO:0034513 | box H/ACA snoRNA binding Ribosomal_L7Ae CBFD_NFYB_HMF GO:0005844 | polysome • GO:0006413 | translational initiation GO:1990948 | ubiquitin ligase inhibitor activity GO:0002183 | cytoplasmic translational initiation GO:0106068 | SUMO ligase complex GO:0005665 | RNA polymerase II, core complex GO:0001731 | formation of translation preinitiation c... GO:0002199 | zona pellucida receptor complex GO:0042393 | histone binding GO:0051290 | protein heterotetramerization GO:0071541 | eukaryotic translation initiation factor... • GO:0031428 | box C/D RNP complex ■ GO:1990501 | exon-exon junction subcomplex mago-y14 GO:0008250 | oligosaccharyltransferase complex GO:0001651 | dense fibrillar component ion of SSU-rRNA from tricistro GO:0006335 | DNA replication-dependent nucleosome a GO:0000932 | P-body Pro_isomerase GO:0005697 | telomerase holoenzyme complex GO:0016272 | prefoldin complex GO:0006268 | DNA unwinding involved in DNA replicatio... GO:1990498 | mitotic spindle microtubule GO:0006364 | rRNA processing GO:0017116 | single-stranded DNA helicase activity GO:0032299 | ribonuclease H2 complex GO:1904851 | positive regulation of establishment of ... GO:0000381 | regulation of alternative mRNA splicing,... GO:1905907 | negative regulation of amyloid fibril fo... GO:0140662 | ATP-dependent protein folding chaperone GO:0016607 | nuclear speck GO:0000243 | commitment complex GO:0090204 | protein localization to nuclear pore GO:0071004 | U2-type prespliceosome GO:0000785 | chromatin GO:0019774 | proteasome core complex, beta-subunit co... GO:0003689 | DNA clamp loader activity • GO:0005634 | nucleus GO:0031390 | Ctf18 RFC-like complex GO:0070652 | HAUS complex GO:0005832 | chaperonin-containing T-complex GO:0048025 | negative regulation of mRNA splicing, vi... GO:0006457 | protein folding Cpn60_TCP1 GO:1900264 | positive regulation of DNA-directed DNA ... GO:0048026 | positive regulation of mRNA splicing, vi... GO:0006298 | mismatch repair GO:0005662 | DNA replication factor A complex GO:0042788 | polysomal ribosome GO:1990726 | Lsm1-7-Pat1 complex GO:0005683 | U7 snRNP GO:0022627 | cytosolic small ribosomal subunit GO:0003743 | translation initiation factor act • GO:0000398 | mRNA splicing, via spliceosome GO:0034719 | SMN-Sm protein complex GO:0071013 | catalytic step 2 spliceosome ■ GO:0019773 | proteasome core complex, alpha-subunit c... • GO:0005730 | nucleolus GO:0051082 | unfolded protein binding RRM_1 GO:0005682 | U5 snRNP GO:0000387 | spliceosomal snRNP assembly Proteasome_A_N GO:1990446 | U1 snRNP binding ● GO:0034715 | plCln-Sm protein complex GO:0120115 | Lsm2-8 complex GO:0005688 | U6 snRNP GO:0005689 | U12-type spliceosomal com GO:0071007 | U2-type catalytic step 2 s GO:0005686 | U2 snRNP GO:0140236 | translation at presynaps GO:0005654 | nucleoplasm GO:0140242 | translation at postsyr GO:0034709 | methylosome GO:0005685 | U1 snRNP

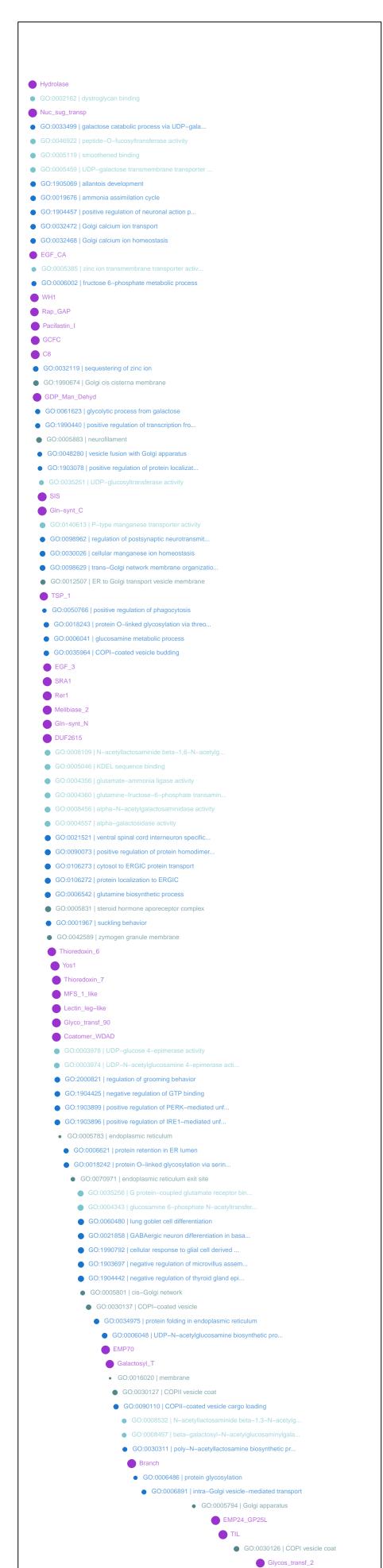
le-10 - le-25 - le-30 - le-30

p-value

GO:0022625 | cytosolic large ribo

GO:0003723 | RNA bindingGO:0005687 | U4 snRNP

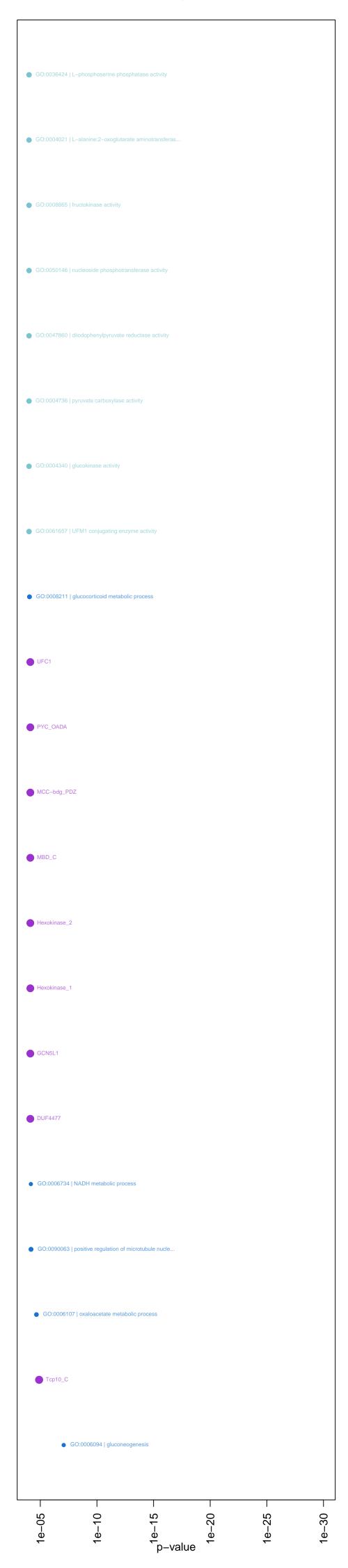
Proteasome

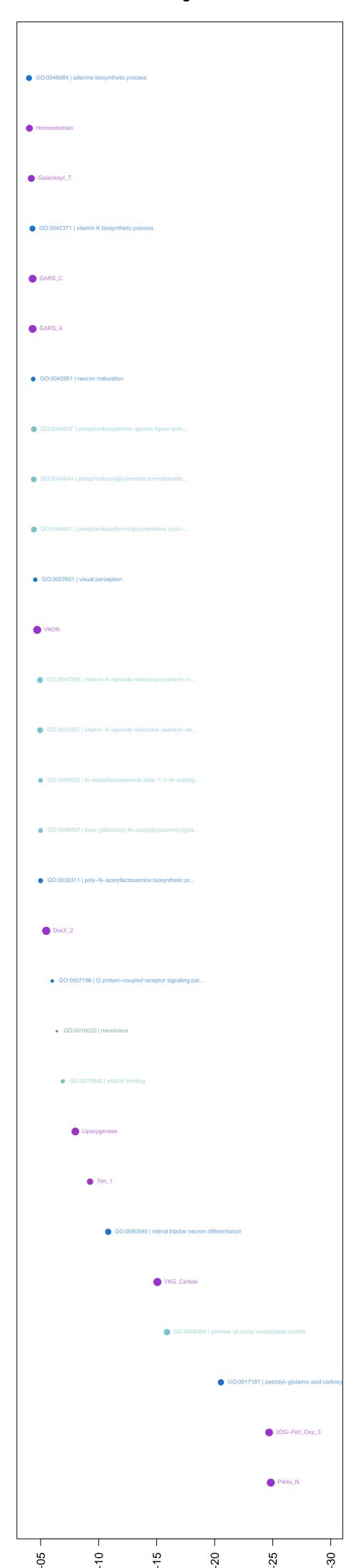


p-value

Ricin_B_lectin

GO:0030134 | COPII-coated E
 GO:0005793 | endoplasmic
 GO:0000139 | Golgi membra
 GO:0006890 | retrograde ve
 GO:0006888 | endoplasmic





out.all.gc011a



-value

```
    GO:0021904 | dorsal/ventral neural tube patterning

    GO:0070459 | prolactin secretion

    GO:0033685 | negative regulation of luteinizing hormo...

    GO:0009651 | response to salt stress

   GO:0014057 | positive regulation of acetylcholine sec...
   GO:0014827 | intestine smooth muscle contraction
   GO:0045776 | negative regulation of blood pressure

    GO:1903265 | positive regulation of tumor necrosis fa...

   GO:0048016 | inositol phosphate-mediated signaling

    GO:0007218 | neuropeptide signaling pathway

   GO:0060252 | positive regulation of glial cell prolif...

    GO:0042311 | vasodilation

Homeodomain
   GO:0032722 | positive regulation of chemokine product...
   GO:0032056 | positive regulation of translation in re...
   GO:0006821 | chloride transport

    GO:0071482 | cellular response to light stimulus

    GO:0032715 | negative regulation of interleukin–6 pro...

 LIM
    GO:2000463 | positive regulation of excitatory postsy...
    GO:0019722 | calcium-mediated signaling

    GO:0009986 | cell surface

    GO:0050709 | negative regulation of protein secretion

    GO:0098641 | cadherin binding involved in cell-cell a...

    GO:0098882 | structural constituent of presynaptic ac...

  • GO:0009791 | post-embryonic development
  ● GO:0048788 | cytoskeleton of presynaptic active zone

    GO:0004698 | calcium-dependent protein kinase C activ

    GO:0031210 | phosphatidylcholine binding

    GO:0021517 | ventral spinal cord development

  ● GO:0046069 | cGMP catabolic process
  Pvr redox dim

    GO:0050482 Larachidonic acid secretion.

    GO:0043951 | negative regulation of cAMP-mediated sig...

  Rhomboid
     GO:0008285 | negative regulation of cell population p...
   • GO:0050805 | negative regulation of synaptic transmis...

    GO:0033025 | regulation of mast cell apoptotic proces...

   ● GO:0010842 | retina layer formation
      GO:1990913 | sperm head plasma membrane
       GO:0045741 | positive regulation of epidermal growth ...
    PDEase_I
    ● GO:0070528 | protein kinase C signaling

    GO:0021702 | cerebellar Purkinje cell differentiation

    GO:0035106 | operant conditioning

    GO:0061827 | sperm head

       GO:0097573 | glutathione oxidoreductase activity

    GO:0030673 | axolemma

    GO:0050960 | detection of temperature stimulus involv...

     ● GO:0034351 | negative regulation of glial cell apopto..
     DM
        GO:0021520 | spinal cord motor neuron cell fate speci...
     ● GO:0060539 | diaphragm development

    GO:0043052 | thermotaxis

    GO:0007634 | optokinetic behavior

      PP-2
      ADAM17_MPD

    GO:0070474 | positive regulation of uterine smooth mu...

      • GO:0043117 | positive regulation of vascular permeabi...

    GO:0010744 | positive regulation of macrophage derive...

    GO:1902093 | positive regulation of flagellated sperm...

    GO:0097060 | synaptic membrane

    GO:0031018 | endocrine pancreas development

    GO:0004791 | thioredoxin-disulfide reductase activity

    GO:0090190 | positive regulation of branching involve...

    GO:0015643 | toxic substance binding

    GO:0014049 | positive regulation of glutamate secreti.

    GO:0002438 | acute inflammatory response to antigenic...

    GO:0007608 | sensory perception of smell

    GO:0060124 | positive regulation of growth hormone se...

    GO:0021871 | forebrain regionalization

    GO:0048703 | embryonic viscerocranium morphogenesis

         ● GO:0048793 | pronephros development
            GO:0031702 | type 1 angiotensin receptor binding

    GO:0051932 | synaptic transmission, GABAergic

            GO:0005138 | interleukin-6 receptor bir

    GO:0061205 | paramesonephric duct development

          ■ GO:0035624 | receptor transactivation
          ■ GO:0071403 | cellular response to high density lipopr...
             GO:0035633 I maintenance of blood-br
             GO:0060068 | vagina development
              GO:1902712 | G protein-coupled GABA receptor complex
              GO:0033602 | negative regulation of dopamine secretio.
              GO:0014053 | negative regulation of gamma-aminobutyri...
              GO:1990430 | extracellular matrix protein binding
              GO:0150099 | neuron-glial cell signaling
              GO:0032525 | somite rostral/caudal axis specification
              GO:0032811 | negative regulation of epinephrine secre..
              GO:1905564 | positive regulation of vascular endothel...
               GO:0007193 | adenylate cyclase-inhibiting G protein-c.
               GO:0008074 | guanylate cyclase complex, soluble
               GO:0043197 | dendritic spine
                GO:0098978 | glutamatergic synapse
                GO:0090009 | primitive streak formation

    GO:0050861 | positive regulation of B cell receptor s...

              ■ GO:0060059 | embryonic retina morphogenesis in camera...
                 GO:0072197 | ureter morphogenesis
                 GO:0007189 | adenylate cyclase-activating G protein-
                  GO:0098982 | GABA-ergic synapse
                 GO:0042622 | photoreceptor outer segment membrane
                  GO:0017046 | peptide hormone binding
               ● GO:0031698 | beta-2 adrenergic receptor binding

    GO:1902239 | negative regulation of intrinsic apoptot...

                    GO:0007194 | negative regulation of adenylate cyclase...
                     GO:0007602 | phototransduction
                     GO:1990384 | hyaloid vascular plexus regression
                     GO:0048382 | mesendoderm development

    GO:0072283 | metanephric renal vesicle morphogenesis

    GO:0021527 | spinal cord association neuron different.

                       GO:0004965 | G protein-coupled GABA receptor activity
                       GO:0038039 | G protein-coupled receptor heterodimeric...
                       GO:0043198 | dendritic shaft

    GO:0016941 | natriuretic peptide receptor act

                      • GO:0045211 | postsynaptic membrane
                        GO:0007202 | activation of phospholipase C activity
                         GO:0008020 | G protein-coupled photoreceptor activity
                         GO:0004930 | G protein-coupled receptor activity

    GO:0007214 | gamma-aminobutyric acid signaling pathwa...

                          GO:0007601 | visual perception
                          GO:0072049 | comma-shaped body morphogenesis
                         ■ GO:2000543 | positive regulation of gastrulation
                            GO:0035849 | nephric duct elongation
                            GO:0035847 | uterine epithelium development
                            GO:2000744 | positive regulation of anterior head dev..
                            GO:0097477 | lateral motor column neuron migration
                            GO:2000768 | positive regulation of nephron tubule ep...

    GO:0072284 | metanephric S-shaped body morphogenesis

                            GO:0060067 | cervix development
                            GO:0001705 | ectoderm formation
                          GO:0021937 | cerebellar Purkinje cell-granule cell pr..
                            GO:0042734 | presynaptic membrane
                              GO:0098685 | Schaffer collateral - CA1 synapse
                                 GO:0008045 | motor neuron axon guidance
                                   ANF_receptor
                                     7tm_3
                                  NIT
                                              GO:0019934 | cGMP-mediated signaling
                                                       GO:0006182 | cGMP biosynthetic process
                                                         GO:0007168 | receptor guanylyl cyclase signaling path...

    GO:0005886 | plasma membrane
```

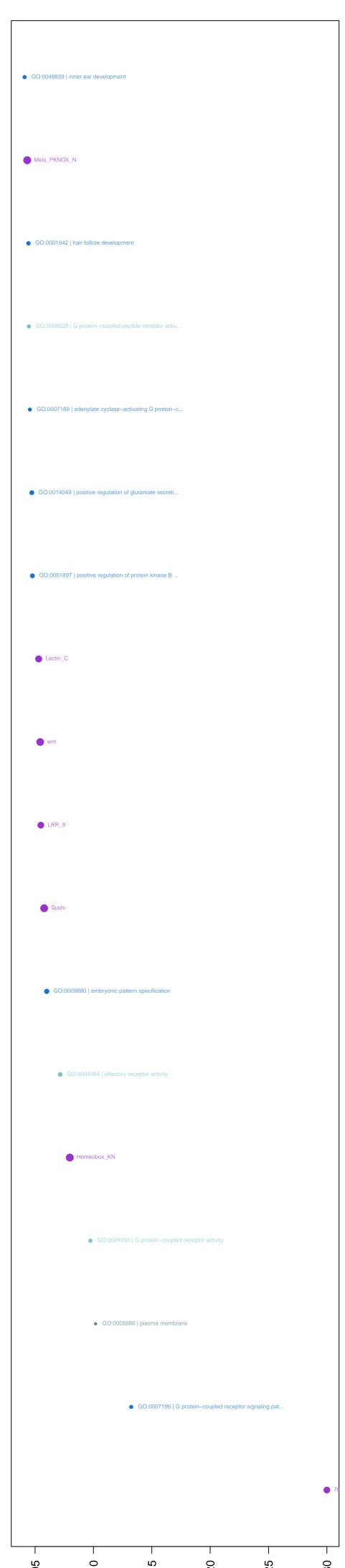
GO:0004383 | guanylate cyclase acGO:0007186 | G proteinGuanylate_cyc



1e-05 1e-05 1e-25 1e-30



-value

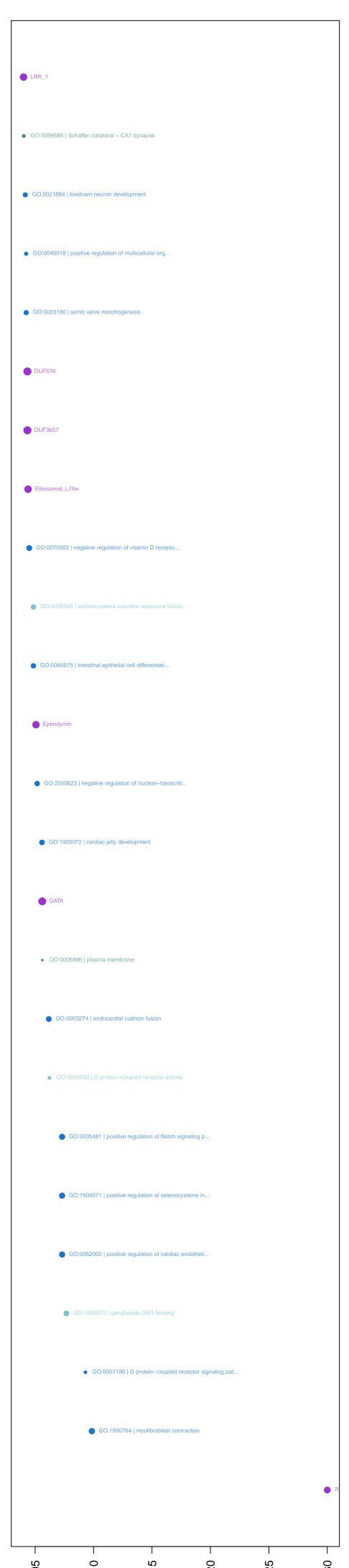




1e-25 | 1e-20 | 1e-25 | 1e-30 | 1e-25 | 1e-25

GO:0098685 | Schaffer collatera
 GO:0004984 | olfactory
 GO:0005886 | plas







-value

 GO:0007266 | Rho protein signal transduction GO:0042472 | inner ear morphogenesis GO:0045211 | postsynaptic membrane GO:2001013 | epithelial cell proliferation involved i... GO:0008360 | regulation of cell shape GO:0007188 | adenylate cyclase-modulating G protein-c... GO:0043410 | positive regulation of MAPK cascade GO:0098978 | glutamatergic synapse GO:0060123 | regulation of growth hormone secretion • GO:0042734 | presynaptic membrane GO:0038022 | G protein-coupled olfactory receptor act... GO:0009952 | anterior/posterior pattern specification GO:0040012 | regulation of locomotion GO:0060999 | positive regulation of dendritic spine d... GO:0016324 | apical plasma membrane GO:0032727 | positive regulation of interferon–alpha ... ● GO:0019236 | response to pheromone GO:0140374 | antiviral innate immune response GO:0007156 | homophilic cell adhesion via plasma memb... ● GO:0001965 | G-protein alpha-subunit binding GO:0098982 | GABA-ergic synapse GO:0009986 | cell surface GO:0051482 | positive regulation of cytosolic calcium... GO:0030165 | PDZ domain binding GO:0005509 | calcium ion binding GO:0051496 | positive regulation of stress fiber asse... GO:0004999 | vasoactive intestinal polypeptide recept... GO:0008285 | negative regulation of cell population p... GO:0004946 | bombesin receptor activity ● GO:1903942 | positive regulation of respiratory gaseo... NCD3G GO:0031989 | bombesin receptor signaling pathway GO:0090290 | positive regulation of osteoclast prolif... GO:0009897 | external side of plasma membrane GO:0035025 | positive regulation of Rho protein signa... ● GO:0016500 | protein-hormone receptor activity GO:0045176 | apical protein localization GO:0032715 | negative regulation of interleukin-6 pro... ● GO:0043198 | dendritic shaft ● GO:0090179 | planar cell polarity pathway involved in... ● GO:0097475 | motor neuron migration GO:0043197 | dendritic spine GO:0043951 | negative regulation of cAMP-mediated sig... GO:0099149 | regulation of postsynaptic neurotransmit... GO:0001942 | hair follicle development GO:0090251 | protein localization involved in establi... GO:0060489 | planar dichotomous subdivision of termin... ● GO:0060488 | orthogonal dichotomous subdivision of te... GO:0060490 | lateral sprouting involved in lung morph... GO:0048105 | establishment of body hair planar orient... GO:0030183 | B cell differentiation GO:0120162 | positive regulation of cold-induced ther... GO:0032060 | bleb assembly GO:0048469 | cell maturation GO:0098693 | regulation of synaptic vesicle cycle GO:0043621 | protein self-association GO:0008344 | adult locomotory behavior GO:0070915 | lysophosphatidic acid receptor activity GO:0045121 | membrane raft GO:0071673 | positive regulation of smooth muscle cel... GO:1904566 | cellular response to 1-oleoyl-sn-glycero... GO:0007202 | activation of phospholipase C activity GO:0002062 | chondrocyte differentiation GO:0007193 | adenylate cyclase-inhibiting G protein-c... GO:0060122 | inner ear receptor cell stereocilium org... GO:0031526 | brush border membrane GO:0007204 | positive regulation of cytosolic calcium... GO:0045453 | bone resorption GO:0008284 | positive regulation of cell population p... GO:0090103 | cochlea morphogenesis GO:0071542 | dopaminergic neuron differentiation GO:0030282 | bone mineralization GO:0004996 | thyroid-stimulating hormone receptor act.. GO:0007187 | G protein-coupled receptor signaling pat... GO:1905229 | cellular response to thyrotropin-releasi... GO:0038194 | thyroid-stimulating hormone signaling pa... GO:1904588 | cellular response to glycoprotein GO:0040018 | positive regulation of multicellular org... GO:0060732 | positive regulation of inositol phosphat... GO:0009755 | hormone–mediated signaling pathway GO:0002076 | osteoblast development GO:0004991 | parathyroid hormone receptor activity GO:0007166 | cell surface receptor signaling pathway GO:0016323 | basolateral plasma membrane GO:0007190 | activation of adenylate cyclase activity GO:0007200 | phospholipase C-activating G prote GO:0005886 | plasma membrane ● GO:0043235 | receptor complex GO:0017046 | peptide hormone GO:0007186 | G protein-co Lectin_C

```
GO:0040038 | polar body extrusion after meiotic divis.
   GO:0097124 | cyclin A2-CDK2 complex
   GO:0000801 | central element
GO:0051455 | monopolar spindle attachment to meiosis ...
   GO:0050774 | negative regulation of dendrite morphoge..
GO:0036089 | cleavage furrow formation
   GO:0015074 | DNA integration
GO:0034773 | histone H4–K20 trimethylation
   GO:0051754 | meiotic sister chromatid cohesion, centr...
GO:0007079 | mitotic chromosome movement towards spin...
   GO:0051257 | meiotic spindle midzone assembly GO:0005818 | aster
    GO:0000785 | chromatin
    GO:0051231 | spindle elongation
    GO:0032147 | activation of protein kinase activity
GO:0051321 | meiotic cell cycle
GO:0042307 | positive regulation of protein import in.
    GO:0090063 | positive regulation of microtubule nucle.
    GO:0032391 | photoreceptor connecting cilium
UQ_con
GO:0000307 | cyclin-dependent protein kinase holoenzy...
      SprT-like
GKAP
      ERG4_ERG24
      Cnd1
      GO:0007099 | centriole replication
      GO:0030951 | establishment or maintenance of microtub...
GO:2000431 | regulation of cytokinesis, actomyosin co...
       GO:0000012 | single strand break repair
    Rad52_Rad22
GO:0043203 | axon hillock
          GO:0120103 | centriolar subdistal appendage
GO:0051298 | centrosome duplication
          GO:0097726 | LEM domain binding
          GO:0097125 | cyclin B1–CDK1 complex
GO:1990385 | meiotic spindle midzone
          GO:0032059 | bleb
          GO:0045870 | positive regulation of single stranded v...
          GO:0099606 | microtubule plus-end directed mitotic ch. GO:1902073 | positive regulation of hypoxia-inducible...
          GO:1905116 | positive regulation of lateral attachmen...
GO:0075713 | establishment of integrated proviral lat...
          GO:0000089 | mitotic metaphase
GO:1905448 | positive regulation of mitochondrial ATP...
          GO:0010609 | mRNA localization resulting in posttrans...
GO:0034772 | histone H4–K20 dimethylation
          GO:0110032 | positive regulation of G2/MI transition ...
GO:1990755 | mitotic spindle microtubule depolymeriza...
          GO:190747 | positive regulation of bleb assembly
GO:0097712 | vesicle targeting, trans–Golgi to perici...
GO:009507 | lateral attachment of mitotic spindle mic...
GO:0051315 | attachment of mitotic spindle microtubul...
           GO:1902425 | positive regulation of attachment of mit..
        GO:0010971 | positive regulation of G2/M transition o.
GO:0070938 | contractile ring
GO:0030953 | astral microtubule organization
             TPX2_importin
             TPX2
              TOPRIM_C
             TACC_C
Spindle_Spc25
             PP1_bind
POLO_box
MKLP1_Arf_bdg
Mito_fiss_reg
             MIIP
              Microtub_bind
             MAP65_ASE1
INCENP_ARK-bind
             HMMR_C
GTSE1_N
             DUF4485
              DNA_topoisoIV
             DNA_gyraseB
              Cnd3
              Cnd1_N
             CKS
             CEP63
             CEP19
             CCSAP
             ALMS_motif
              GO:0005634 | nucleus
               GO:0051010 | microtubule plus-end binding
               GO:0051081 | nuclear membrane disassembly
                GO:0007088 | regulation of mitotic nuclear division
                 GO:0000070 | mitotic sister chromatid segregation
                 GO:0007084 | mitotic nuclear membrane reassembly GO:0031536 | positive regulation of exit from mitosis

    GO:0005815 | microtubule organizing center

                   GO:0007091 | metaphase/anaphase transition of mitotic
                     GO:0016321 | female meiosis chromosome segregation
                     GO:0097539 | ciliary transition fiber
                     GO:0008608 | attachment of spindle microtubules to ki..
                       GO:0070194 | synaptonemal complex disassembly
                       GO:0005721 | pericentric heterochromatin
                       GO:0010369 | chromocenter
                        GO:0005654 | nucleoplasm
GO:0010994 | free ubiquitin chain polymerization
                        GO:1904776 | regulation of protein localization to ce. GO:0008315 | G2/MI transition of meiotic cell cycle
                         GO:0051233 | spindle midzone
                            GO:0005826 | actomyosin contractile ring
GO:0007080 | mitotic metaphase plate congression
                              GO:0007095 | mitotic G2 DNA damage checkpoint signali...
                              GO:0007098 | centrosome cycle
GO:0045171 | intercellular bridge
                              GO:0030261 | chromosome condensation
GO:0000079 | regulation of cyclin–dependent protein s
                                GO:1905786 | positive regulation of anaphase–promotin. GO:0035371 | microtubule plus–end
                                 GO:0097431 | mitotic spindle pole
                                  GO:0031616 | spindle pole centrosome
                                  Pkinase
                                  GO:1901673 | regulation of mitotic spindle assembly GO:0000086 | G2/M transition of mitotic cell cycle
                                  GO:0032154 | cleavage furrow
GO:0060236 | regulation of mitotic spindle organizati.
                                    GO:0051988 | regulation of attachment of spindle micr.
                                    Cyclin_N
                                        GO:0005874 | microtubule
                                         GO:0045842 | positive regulation of mitotic metaphase.

GO:0031106 | septin ring organization
                                             GO:0000132 | establishment of mitotic spindle orienta..
GO:0036064 | ciliary basal body
GO:0060271 | cilium assembly
GO:0051382 | kinetochore assembly
                                                GO:0034501 | protein localization to kinetochore

    GO:1903490 | positive regulation of mitotic cytokines.
    GO:0051383 | kinetochore organization

                                                      GO:0000794 | condensed nuclear chromosome
GO:0070979 | protein K11-linked ubiquitination
                                                        GO:0007057 | spindle assembly involved in female meio. GO:0000776 | kinetochore
                                                          GO:0061673 | mitotic spindle astral microtubule
                                                            GO:0000779 | condensed chromosome, centromeric region
                                                             GO:0031262 | Ndc80 complex

    GO:0090267 | positive regulation of mitotic cell cycl...
    GO:0007052 | mitotic spindle organization

                                                               GO:0090307 | mitotic spindle assembly
GO:0032133 | chromosome passenger complex
                                                                GO:1901970 | positive regulation of mitotic sister ch...
GO:0031145 | anaphase-promoting complex-dependent cat..
                                                                  GO:0005876 | spindle microtubule
                                                                     GO:0005871 | kinesin complex
                                                                      GO:0097149 | centralspindlin complex
                                                                       GO:0000915 | actomyosin contractile ring assembly
GO:1904668 | positive regulation of ubiquitin protein...
                                                                            GO:1904068 positive regulation of ubiquitin protein...
GO:0000322 | spindle pole
GO:00032467 | positive regulation of cytokinesis
GO:0051984 | positive regulation of chromosome segreg..
GO:0000940 | outer kinetochore
GO:0000281 | mitotic cytokinesis
GO:0072686 | mitotic spindle
GO:0010032 | meiotic chromosome condensation

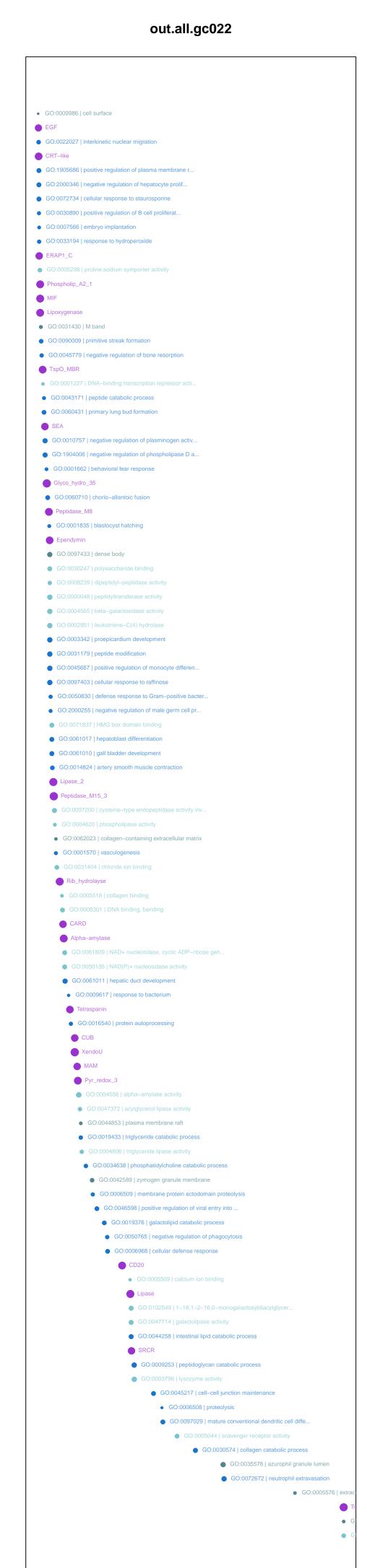
    GO:0034451 | centriolar satellite

                                                                                                ■ GO:0007076 | mitotic chromosome condensation
                                                                                                           ■ GO:0000796 | condensin complex
                                                                                                                        GO:0005680 | anaphase-promoting co
                                                                                                                      GO:1990023 | mitotic spindle midzorGO:1905820 | positive regulation o

    GO:0007094 | mitotic spine

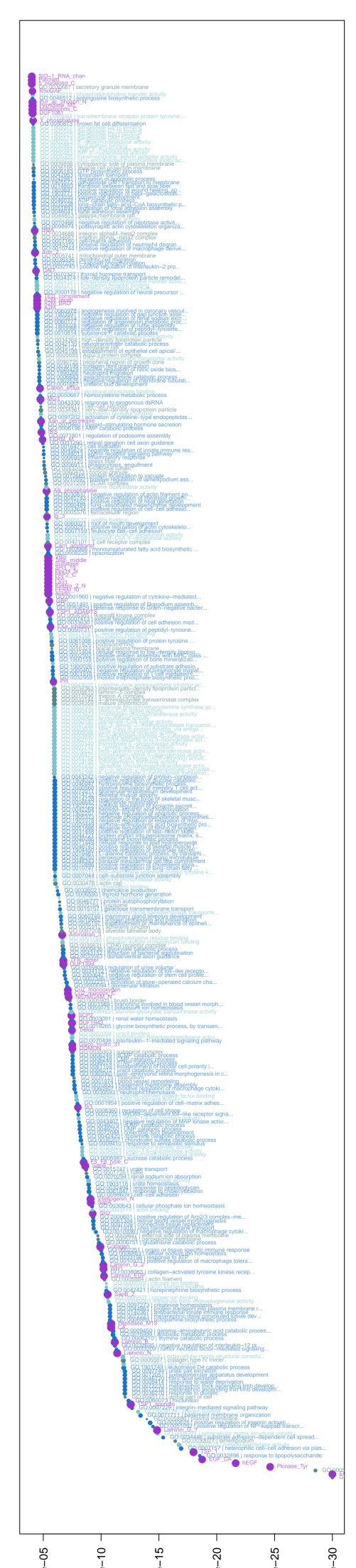
                                                                                                                                                            GO:00058GO:00304
                                                                                                                                                                   GO:005
                                                                                                                                                                    GO:000
                                                                                                                                                                    GO:005
```

1e-05 1e-05 1e-25 1e-30 1e-30 1e-30



p-value





p-value

```
GO:1903238 | positive regulation of leukocyte tetheri...
RGM C
GO:0007182 | common-partner SMAD protein phosphorylat...
GO:0035563 | positive regulation of chromatin binding Ribonucleas_3_3
 GBBH-like N
GO:0001337 | epithelial to mesenchymal transition
GO:00045824 | negative regulation of innate immune res...
GO:0009410 | response to xenobiotic stimulus
 GO:0051497 | negative regulation of stress fiber asse. GO:0008336 | gamma-butyrobetaine dioxygenase ac
 GO:0045329 | carnitine biosynthetic process
 GO:0048680 | positive regulation of axon regeneration
 GO:0032587 | ruffle membrane
 GO:0061713 | anterior neural tube closure
 GO:1990712 | HFE-transferrin receptor complex
                   corticotropin-releasing hormone receptor...
 GO:1902624 | positive regulation of neutrophil migrat...
 GO:0098909 | regulation of cardiac muscle cell action...
GO:1902512 | positive regulation of apoptotic DNA fra...
 GO:0035860 | glial cell–derived neurotrophic factor r..
GO:1904698 | negative regulation of acinar cell proli...
 GO:1900826 | negative regulation of membrane depolari..
GO:0072137 | condensed mesenchymal cell proliferation
 GO:0042483 | negative regulation of odontogenesis
GO:0038009 | regulation of signal transduction by rec.
 GO:0051394 | regulation of nerve growth factor recept...
GO:0044337 | canonical Wnt signaling pathway involved..
 GO:0044336 | canonical Wnt signaling pathway involved...
  GO:0070836 | caveola assembly
 GO:0071169 | establishment of protein localization to...
GO:0010936 | negative regulation of macrophage cytoki..
  GO:0048643 | positive regulation of skeletal muscle t...
GO:0099509 | regulation of presynaptic cytosolic calc..
  GO:009909 | regulation of presynaptic cytosolic calc...
Xan_ur_permease
GO:0043242 | negative regulation of protein-containin...
GO:0046716 | muscle cell cellular homeostasis
GO:0015842 | aminergic neurotransmitter loading into ...
   SAM 3
   COF1 HIH
    GO:0070498 | interleukin–1–mediated signaling pathway
    GO:0089718 | amino acid import across plasma membrane GO:0060400 | negative regulation of growth hormone re...
    GO:0061589 | calcium activated phosphatidylserine scr..
    GO:0061591 | calcium activated galactosylceramide scr...
    GO:0061590 | calcium activated phosphatidylcholine sc.
    GO:0007195 | adenylate cyclase–inhibiting dopamine re..
GO:0097368 | establishment of Sertoli cell barrier
    GO:0002280 | monocyte activation involved in immune r...
GO:0045907 | positive regulation of vasoconstriction
     ABC2_membrane
GO:0098839 | postsynaptic density membrane
     GO:0016342 | catenin complex
GO:0042568 | insulin–like growth factor binary comple...
     GO:0042567 | insulin-like growth factor ternary compl...
     GO:2000844 | negative regulation of testosterone secr.
     GO:0038098 | sequestering of BMP from receptor via BM..
     GO:0002755 | MyD88-dependent toll-like receptor signa..
     SH3BGR
      GO:0032695 | negative regulation of interleukin-12 pr...
     GO:0006837 | serotonin transport
GO:0007597 | blood coagulation, intrinsic pathway
      GO:0016323 | basolateral plasma membrane
GO:0010933 | positive regulation of macrophage tolera...
      GO:0031290 | retinal ganglion cell axon guidance
GO:0005903 | brush border
       GO:0032432 | actin filament bundle
      GO:2001046 | positive regulation of integrin-mediated...
       GO:0015848 | spermidine transport
        GO:0021556 | central nervous system formation
        Anoct dimer
        Alkvl sulf C
                        8 | nitric-oxide synthase binding
         HRM
         Kazal 2
          SNF
         OATP
           GO:1902475 | L-alpha-amino acid transmembrane transpo..
           Spectrin
           GO:0110158 | calpain complex
           GO:0015816 | glycine transport
GO:0051016 | barbed-end actin filament capping
           GO:0001504 | neurotransmitter uptake
            Aldolase_II
GO:0010862 | positive regulation of pathway-restricte...
GO:0051092 | positive regulation of NF-kappaB transcr..
            GO:1903078 | positive regulation of protein localizat.
            Smoothelin
            COE1 DRD
             GO:0051693 | actin filament capping
             GO:0007156 | homophilic cell adhesion via plasma memb..
              GO:0015808 | L-alanine transport
GO:0032494 | response to peptidoglycan
               GO:1990779 | glycoprotein lb-IX-V complex
              GO:1905000 | regulation of membrane repolarization du...
GO:0042669 | regulation of inner ear auditory recepto...
               GO:1902396 | protein localization to bicellular tight
               GO:0014816 | skeletal muscle satellite cell different...
               GO:0036032 | neural crest cell delamination
               GO:0010572 | positive regulation of platelet activati
               GO:0030835 | negative regulation of actin filament de..
GO:0000296 | spermine transport
GO:0032437 | cuticular plate
                 EGF_CA
                  GO:0043252 | sodium-independent organic anion transpo.
                   GO:0072531 | pyrimidine–containing compound transmemb...
                   GO:0015132 | prostaglandin trans
               GO:0036122 | BMP binding
GO:0015213 | uridine transmembrane transporter activi.
                   GO:0015860 | purine nucleoside transmembrane transpor...
                    GO:0043194 | axon initial segment
                7tm_2
                    GO:0008091 | spectrin
                     TauD
                      GO:0007026 | negative regulation of microtubule depol.
                      GO:0032238 | adenosine transport
GO:0031852 | mu-type opioid red
                      G0:0070593 | dendrite self–avoidance
G0:0019227 | neuronal action potential propagation
Sugar_tr
G0:0015347 | sodium–independent organic anion te
                                                                  endent organic anion transme.
                           GO:0051610 | serotonin uptake
                                   0015193 | L-proline transmembrane transporter
                             GO:0045162 | clustering of voltage-gated sodium chann...
                             GO:0035524 | proline transmembrane transport
GO:0015824 | proline transport
                               GO:0007520 | myoblast fusion
GO:0043025 | neuronal cell body
                                  GO:0060445 | branching involved in salivary gland mor..
                                      GO:0006874 | cellular calcium ion homeostasis
                                   cEGF
GO:0
                                         GO:0086080 | protein binding involved in heterotypic
                                               GAIN
                                               GO:0033268 | node of Ranvier
                                                GO:0055085 | transmembrane transport
                                                   GO:0030506 | ankyrin binding
                                                     GO:0019

    GO:0098978 | glutamatergic synapse

                                                                                    IgGFc_binding
                                                                                                  GO:0098982 | GABA-ergic synapse
GO:0031594 | neuromuscular junction
                                                                                                                             GO:0048786 | presy
                                                                                                                                          GO:00059
```

p-value



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out.all.gc027 ● GO:0008541 | proteasome regulatory particle, lid subc... GO:0003713 | transcription coactivator activity ● GO:0090571 | RNA polymerase II transcription represso... GO:0090261 | positive regulation of inclusion body as... UbiA HMG_box ● GO:0042659 | regulation of cell fate specification GO:0006367 | transcription initiation from RNA polyme... GO:0035064 | methylated histone binding GO:0001222 | transcription corepressor binding ● GO:0070536 | protein K63-linked deubiquitination GO:1990829 | C-rich single-stranded DNA binding GO:0031208 | POZ domain binding GO:0000183 | rDNA heterochromatin assembly GO:0097067 | cellular response to thyroid hormone sti... GO:1902437 | positive regulation of male mating behav... GO:1903899 | positive regulation of PERK-mediated unf... GO:1903896 | positive regulation of IRE1-mediated unf... GO:0042371 | vitamin K biosynthetic process GO:0031213 | RSF complex GO:0016589 | NURF complex ● GO:0007289 | spermatid nucleus differentiation GO:0005665 | RNA polymerase II, core complex GO:0030512 | negative regulation of transforming grow... GO:0016581 | NuRD complex ● GO:0070734 | histone H3–K27 methylation GO:1990841 | promoter–specific chromatin binding GO:0008623 | CHRAC ● GO:0005787 | signal peptidase complex • GO:0043161 | proteasome-mediated ubiquitin-dependent ... GO:0035851 | Krueppel–associated box domain binding GO:0097150 | neuronal stem cell population maintenanc... ● GO:0061198 | fungiform papilla formation ■ GO:0009234 | menaguinone biosynthetic process GO:0071387 | cellular response to cortisol stimulus GO:0032194 | ubiquinone biosynthetic process via 3,4-... GO:1905213 | negative regulation of mitotic chromosom... GO:0060789 | hair follicle placode formation GO:0090536 | NoRC complex GO:0090535 | WICH complex GO:1902455 | negative regulation of stem cell populat... GO:0035984 | cellular response to trichostatin A GO:0070876 | SOSS complex GO:0000978 | RNA polymerase II cis-regulatory region TMEM33_Pom33 SLIDE Memo GO:0016580 | Sin3 complex GO:0016590 | ACF complex GO:0005677 | chromatin silencing complex ● GO:0017025 | TBP-class protein binding RRM_1 GO:0035019 | somatic stem cell population maintenance Bromodomain GO:0005654 | nucleoplasm GO:0060261 | positive regulation of transcription ini... Prot_ATP_ID_OB GO:1902459 | positive regulation of stem cell populat... GO:0035098 | ESC/E(Z) complex GO:0006338 | chromatin remodeling GO:0032968 | positive regulation of transcription elo... GO:0045944 | positive regulation of transcription by ... GO:0016592 | mediator complex

GO:0072546 | EMC complex

GO:0071816 | tail-anchored membrane protein insertion...

GO:0045050 | protein insertion into ER membrane

GO:0070847 | core mediator complex

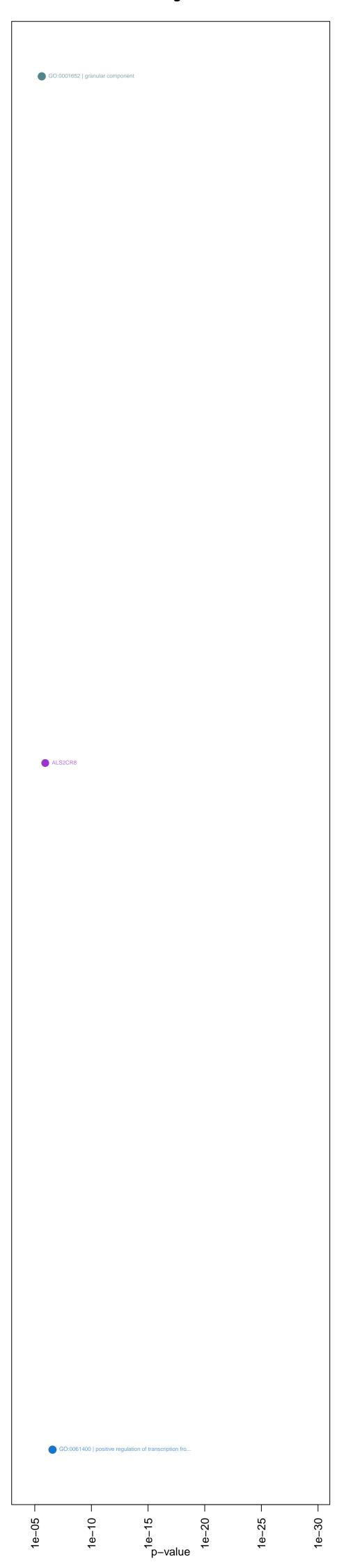
GO:0051123 | RNA polymerase II preinitiation complex ...

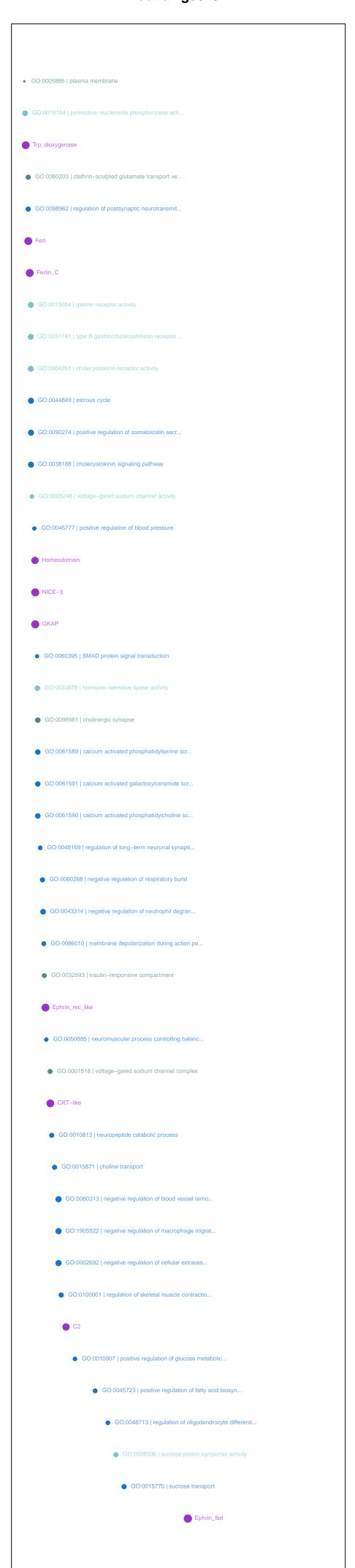
-value

■ GO:0036402 | proteasome–activating activity

GO:0008540 | proteasome regulatory particle, base sub...

GO:0032977 | membrane insertase activity





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Kinesin
GO:0006241 | CTP biosynthetic process
TEX33
       RIB43A
Radial_spoke_3
PPPI_inhib
PPP1R32
       Hydin_ADK
GAS
        FAM47
       EF-hand_11
EDR1
       DUF5578
      DUF5526
DUF5524
DUF4709
DUF4639
      DUF4639
DUF4618
DUF4612
DUF4590
DUF4586
DUF4558
DUF4555
DUF4549
      DUF4549
DUF4541
DUF4490
DUF4486
DUF4483
DUF4464
      DUF4456
       CFAP298
       AKAP28
      ARAC_transp_aux
AAA_17
GO:0042733 | embryonic digit morphogenesis
GO:0005882 | intermediate filament
       GO:000582 | intermediate marriert
Annexin
Tubulin_C
GO:0031021 | interphase microtubule organizing center
GO:0097427 | microtubule bundle
GO:0051122 | hepoxilin biosynthetic process
GO:0031076 | embryonic camera-type eye development
•
         GO:0034451 | centriolar satellite
         GO:0140659 | epidermal stem cell homeostasis
GO:0140659 | cytoskeletal motor regulator activity
GO:0120152 | calcium-dependent outer dynein arm bindi...
GO:0006228 | UTP biosynthetic process
GO:0019372 | lipoxygenase pathway
GO:0007018 | microtubule-based movement
GO:0120222 | regulation of blastocyst development
DUF4572
DED
GO:00045604
              DED
GO:0015631 | tubulin binding
p25-alpha
zf-MYND
GO:0060296 | regulation of cilium beat frequency invo...
GO:007286 | spermatid development
                  Tubulin
FAM183
                    GO:0097500 | receptor localization to non-motile cili...
                   GO:0016165 | linoleate 13S-lipoxygena
GO:0097224 | sperm connecting piece
GO:0009631 | cold acclimation
                    GO:000581 | cold acclimation

LRR_4

GO:0005881 | cytoplasmic microtubule

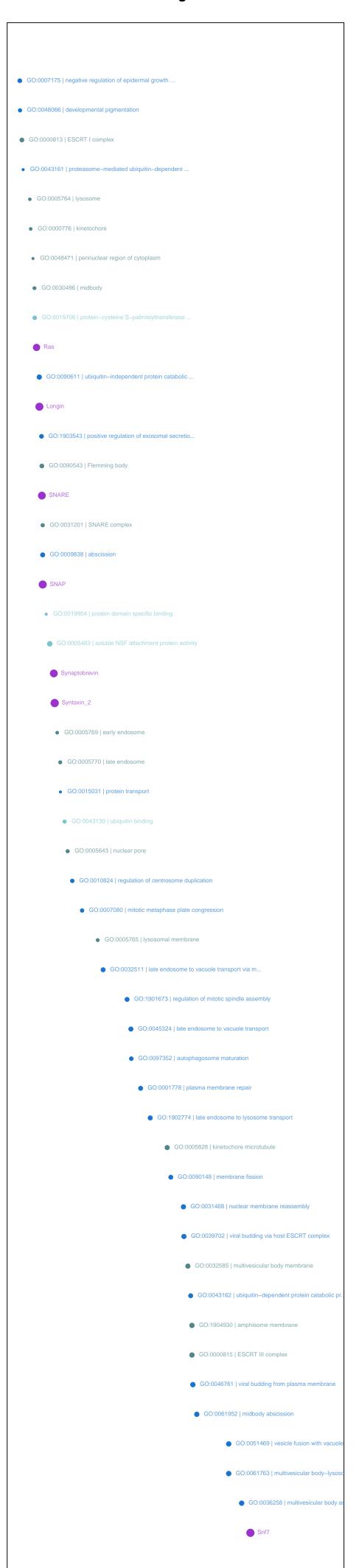
GO:0035686 | sperm fibrous sheath

VWA_3

HDNR

Robl_LC7
                         HDNR
Robl_LC7
GO:0003777 | microtubule motor activity
GO:0005879 | axonemal microtubule
GO:0004127 | cytidylate kinase activity
FAM194
Educate
                                   Enkurin
G0:0044292 | dendrite terminus
G0:0001520 | outer dense fiber
G0:0030286 | dynein complex
G0:0045724 | positive regulation of cilium assembly
G0:0070986 | left/right axis specification
                                          Arm
Tektin
                                     Radial_spoke
DUF4515
Ax_dynein_light
DCX
GO:0060971 | embryonic heart tube left/right pattern ...
GO:1905516 | positive regulation of fertilization
GO:1990718 | axonemal central pair projection
                                                     THEG
NYD-SP28
Dynein_light
DUF4537
                                                      DUF4201
DUF2475
DUF1126
                                                       DUF112b
NDK
GO:0004017 | adenylate kinase acti
GO:1905198 | manchette assembly
TSNAXIP1_N
                                                              GO:0097225 | sperm midpiece
NYD-SP28 assoc
                                                             NYD-SP28_assoc
GO:0001669 | acrosomal vesicle
                                                                  GO:0001669 | acrosomal vesicle
GO:00048487 | beta-tubulin binding
GO:0042073 | intraciliary transport
GO:0005929 | cilium
) GO:0035469 | determination of pancreatic left/right a...
) GO:0071910 | determination of liver left/right asymme...
GO:0120316 | sperm flagellum assembly
CH_2
GO:0120170 | intraciliary transport particle B bindin...
GO:1990716 | axonemal central apparatus
DUF4200
GO:0035735 | intraciliary transport involved in ciliu...
GO:00120229 | protein localization to motile cilium
GO:0060972 | left/right pattern formation
WD40
                                                                                              WD40
GO:0097598 | sperm cytoplasmic droplet
GO:0021591 | ventricular system development
GO:0003352 | regulation of cilium movement
GO:0005858 | axonemal dynein complex
                                                                                                  TTL
GO:0060830 | ciliary receptor clustering involved in ...
GO:0070286 | axonemal dynein complex assembly
GO:0004550 | nucleoside diphosphate kinase activity
                                                                                                              GO:0043014 | alpha-tubulin binding
                                                                                                               Tctex-1
                                                                                                             G::0018095 | protein polygiutamylation |
ADK
G0::0097731 | 9+0 non-motile cilium
G0::0005814 | certriole
G0::006294 | cilium movement involved in cell motilit...
G0::0045503 | dynein light chain binding
                                                                                                                                        •••••••
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