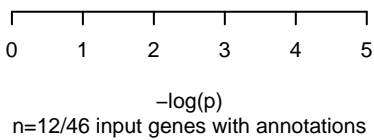
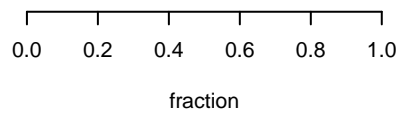


GO:BP
Ncol_Nvec_vc1.1_XM_032372078.2

fraction genes in fg and expected value

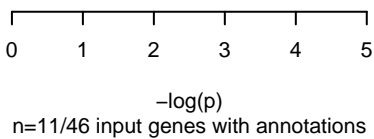
| | | | |
|---|------------|-----------|-----|
| response to amyloid-beta | GO:1904645 | p=4.6E-03 | n=2 |
| negative regulation of protein depolymer... | GO:1901880 | p=7.6E-03 | n=2 |
| ammonium ion metabolic process | GO:0097164 | p=1.1E-02 | n=2 |
| cell junction organization | GO:0034330 | p=1.4E-02 | n=2 |
| positive regulation of cellular amide me... | GO:0034250 | p=1.5E-02 | n=4 |
| regulation of supramolecular fiber organ... | GO:1902903 | p=1.7E-02 | n=3 |
| peptide metabolic process | GO:0006518 | p=1.9E-02 | n=3 |
| embryonic body morphogenesis | GO:0010172 | p=2.0E-02 | n=2 |
| response to cold | GO:0009409 | p=2.0E-02 | n=2 |
| supramolecular fiber organization | GO:0097435 | p=2.2E-02 | n=3 |
| protein localization to plasma membrane | GO:0072659 | p=2.5E-02 | n=2 |
| negative regulation of supramolecular fi... | GO:1902904 | p=2.5E-02 | n=2 |
| body morphogenesis | GO:0010171 | p=2.5E-02 | n=2 |
| negative regulation of cytoskeleton orga... | GO:0051494 | p=2.5E-02 | n=2 |
| regulation of amyloid-beta formation | GO:1902003 | p=2.9E-02 | n=1 |
| positive regulation of amyloid-beta form... | GO:1902004 | p=2.9E-02 | n=1 |
| ecdysone receptor-mediated signaling pat... | GO:0035076 | p=2.9E-02 | n=1 |
| regulation of systemic arterial blood pr... | GO:0003025 | p=2.9E-02 | n=1 |
| positive regulation of CoA-transferase a... | GO:1905920 | p=2.9E-02 | n=1 |
| regulation of acetylcholine biosynthetic... | GO:1905921 | p=2.9E-02 | n=1 |
| positive regulation of acetylcholine bio... | GO:1905923 | p=2.9E-02 | n=1 |
| regulation of amyloid precursor protein ... | GO:1902991 | p=2.9E-02 | n=1 |
| negative regulation of amyloid precursor... | GO:1902992 | p=2.9E-02 | n=1 |
| positive regulation of amyloid precursor... | GO:1902993 | p=2.9E-02 | n=1 |
| regulation of CoA-transferase activity | GO:1905918 | p=2.9E-02 | n=1 |
| myofibroblast differentiation | GO:0036446 | p=2.9E-02 | n=1 |
| positive regulation of translation in re... | GO:0032056 | p=2.9E-02 | n=1 |
| positive regulation of translational ini... | GO:0032058 | p=2.9E-02 | n=1 |
| amyloid-beta metabolic process | GO:0050435 | p=2.9E-02 | n=1 |
| microtubule anchoring | GO:0034453 | p=2.9E-02 | n=1 |

[illegible]

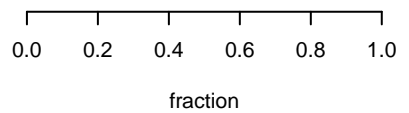
GO:MF
Ncol_Nvec_vc1.1_XM_032372078.2

fraction genes in fg and expected value

| | | | |
|---|------------|-----------|-----|
| ammonium ion binding | GO:0070405 | p=3.9E-04 | n=3 |
| actin filament binding | GO:0051015 | p=3.9E-04 | n=3 |
| phosphatidylcholine binding | GO:0031210 | p=4.8E-03 | n=2 |
| calcium channel activity | GO:0005262 | p=2.7E-02 | n=2 |
| nucleotidyltransferase activity | GO:0016779 | p=3.0E-02 | n=1 |
| postsynaptic neurotransmitter receptor a... | GO:0098960 | p=3.0E-02 | n=1 |
| kinetochore binding | GO:0043515 | p=3.0E-02 | n=1 |
| dystroglycan binding | GO:0002162 | p=3.0E-02 | n=1 |
| choline-phosphate cytidyltransferase a... | GO:0004105 | p=3.0E-02 | n=1 |
| nuclear receptor coactivator activity | GO:0030374 | p=3.0E-02 | n=1 |
| transmitter-gated ion channel activity i... | GO:1904315 | p=3.0E-02 | n=1 |
| acetylcholine binding | GO:0042166 | p=3.0E-02 | n=1 |
| misfolded protein binding | GO:0051787 | p=3.0E-02 | n=1 |
| hydrolase activity, acting on carbon-nit... | GO:0016812 | p=3.0E-02 | n=1 |
| 5-oxoprolinase (ATP-hydrolyzing) activi... | GO:0017168 | p=3.0E-02 | n=1 |
| cytidyltransferase activity | GO:0070567 | p=3.0E-02 | n=1 |
| acetylcholine receptor activity | GO:0015464 | p=3.0E-02 | n=1 |
| chloride channel regulator activity | GO:0017081 | p=3.0E-02 | n=1 |
| toxic substance binding | GO:0015643 | p=3.0E-02 | n=1 |
| neurotransmitter receptor activity invol... | GO:0099529 | p=3.0E-02 | n=1 |
| acetylcholine-gated cation-selective cha... | GO:0022848 | p=3.0E-02 | n=1 |
| kinase binding | GO:0019900 | p=3.3E-02 | n=4 |
| protein kinase binding | GO:0019901 | p=3.3E-02 | n=4 |
| calcium ion transmembrane transporter ac... | GO:0015085 | p=4.6E-02 | n=2 |
| channel regulator activity | GO:0016247 | p=5.4E-02 | n=2 |
| ion channel regulator activity | GO:0099106 | p=5.4E-02 | n=2 |
| phosphatidylethanolamine binding | GO:0008429 | p=6.0E-02 | n=1 |
| high voltage-gated calcium channel activ... | GO:0008331 | p=6.0E-02 | n=1 |
| actin monomer binding | GO:0003785 | p=6.0E-02 | n=1 |
| calcium-dependent phospholipid binding | GO:0005544 | p=6.0E-02 | n=1 |



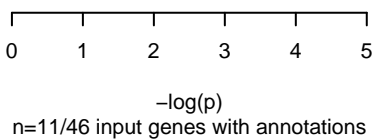
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| fg=0.27 | bg=0.02 |
| fg=0.18 | bg=0.01 |
| fg=0.18 | bg=0.02 |
| fg=0.09 | bg=0.00 |
| fg=0.09 | bg=0.00 |
| fg=0.09 | bg=0.00 |
| fg=0.09 | bg=0.00 |
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| fg=0.09 | bg=0.00 |
| fg=0.09 | bg=0.00 |
| fg=0.09 | bg=0.00 |
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| fg=0.36 | bg=0.12 |
| fg=0.36 | bg=0.12 |
| fg=0.18 | bg=0.03 |
| fg=0.18 | bg=0.04 |
| fg=0.18 | bg=0.04 |
| fg=0.09 | bg=0.01 |
| fg=0.09 | bg=0.01 |
| fg=0.09 | bg=0.01 |
| fg=0.09 | bg=0.01 |



GO:CC
Ncol_Nvec_vc1.1_XM_032372078.2

fraction genes in fg and expected value

| | | | | |
|---|-------------------------------------|------------|-----------|-----|
| | side of membrane | GO:0098552 | p=8.4E-03 | n=3 |
| | cytoplasmic microtubule plus-end | GO:1904511 | p=2.7E-02 | n=1 |
| | kinetochore microtubule | GO:0005828 | p=2.7E-02 | n=1 |
| | glycogen granule | GO:0042587 | p=2.7E-02 | n=1 |
| | acetylcholine-gated channel complex | GO:0005892 | p=2.7E-02 | n= |
| | kinetochore | GO:0000776 | p=2.7E-02 | n=1 |
| | microtubule plus-end | GO:0035371 | p=2.7E-02 | n=1 |
| | cortical microtubule plus-end | GO:1903754 | p=2.7E-02 | n=1 |
| | PML body | GO:0016605 | p=2.7E-02 | n=1 |
| | centrosomal corona | GO:0031592 | p=2.7E-02 | n=1 |
| | cortical microtubule cytoskeleton | GO:0030981 | p=2.7E-02 | n=1 |
| | cortical microtubule | GO:0055028 | p=2.7E-02 | n=1 |
| L-type voltage-gated calcium channel com... | | GO:1990454 | p=2.7E-02 | n=1 |
| | spindle microtubule | GO:0005876 | p=2.7E-02 | n=1 |
| | extrinsic component of membrane | GO:0019898 | p=3.3E-02 | n=2 |
| | cytoplasmic side of plasma membrane | GO:0009898 | p=3.3E-02 | n=2 |
| | cytoplasmic side of membrane | GO:0098562 | p=4.5E-02 | n=2 |
| | growth cone | GO:0030426 | p=4.5E-02 | n=2 |
| | site of polarized growth | GO:0030427 | p=5.2E-02 | n=2 |
| | leading edge membrane | GO:0031256 | p=5.2E-02 | n=2 |
| | sarcoplasm | GO:0016528 | p=5.4E-02 | n=1 |
| | sarcoplasmic reticulum | GO:0016529 | p=5.4E-02 | n=1 |
| | organelle membrane contact site | GO:0044232 | p=5.4E-02 | n=1 |
| | cell cortex region | GO:0099738 | p=5.4E-02 | n=1 |
| | chromosome, centromeric region | GO:0000775 | p=5.4E-02 | n=1 |
| condensed chromosome, centromeric region | | GO:0000779 | p=5.4E-02 | n=1 |
| | microtubule end | GO:1990752 | p=5.4E-02 | n=1 |
| | basal cortex | GO:0045180 | p=5.4E-02 | n=1 |
| | condensed chromosome | GO:0000793 | p=5.4E-02 | n=1 |
| Cul3-RING ubiquitin ligase complex | | GO:0031463 | p=5.4E-02 | n=1 |

[illegible]