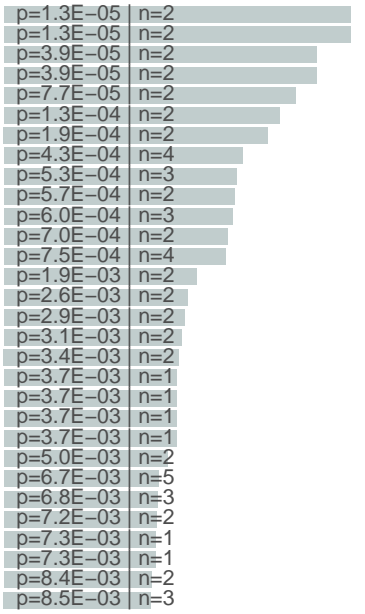


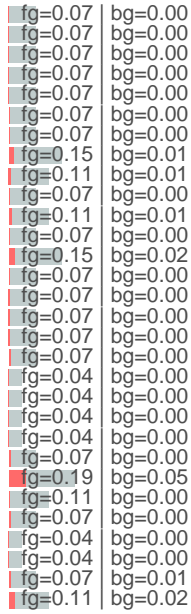
GO:BP  
Metazoa\_gain

cellular response to monosodium glutamat...	GO:1904009
negative regulation of guanylate cyclase...	GO:0031283
protein localization to tricellular tigh...	GO:0061833
positive regulation of transcription fac...	GO:1901485
JUN phosphorylation	GO:0007258
activation of phospholipase D activity	GO:0031584
positive regulation of podosome assembly	GO:0071803
neuron migration	GO:0001764
positive regulation of synapse assembly	GO:0051965
positive regulation of adenylate cyclase...	GO:0045762
negative regulation of angiogenesis	GO:0016525
positive regulation of protein targeting...	GO:0090314
adenylate cyclase-activating G protein-c...	GO:0007189
synaptic vesicle fusion to presynaptic a...	GO:0031629
regulation of postsynaptic neurotransmit...	GO:0099149
cellular response to cadmium ion	GO:0071276
calcineurin-NFAT signaling cascade	GO:0033173
vesicle docking	GO:0048278
regulation of DNA replication origin bin...	GO:1902595
cornified envelope assembly	GO:1903575
positive regulation of axon guidance	GO:1902669
positive regulation of glial cell apopto...	GO:0034352
regulation of voltage-gated calcium chan...	GO:1901385
modulation of chemical synaptic transmis...	GO:0050804
synaptic vesicle membrane organization	GO:0048499
peripheral nervous system development	GO:0007422
protein localization involved in establi...	GO:0090251
secretion by lung epithelial cell involv...	GO:0061033
cerebral cortex development	GO:0021987
inner ear development	GO:0048839



0 1 2 3 4 5  
-log(p)  
n=27/46 input genes with annotations

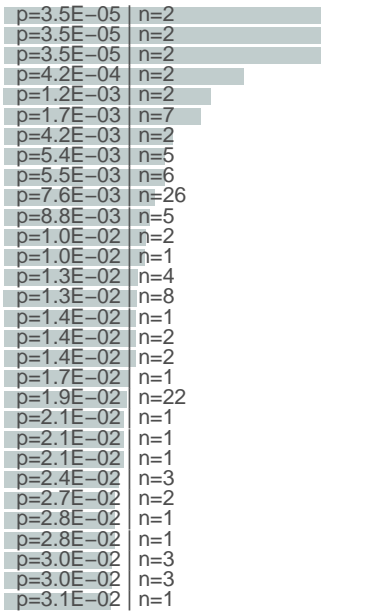
fraction genes in fg and expected value



0.0 0.2 0.4 0.6 0.8 1.0  
fraction

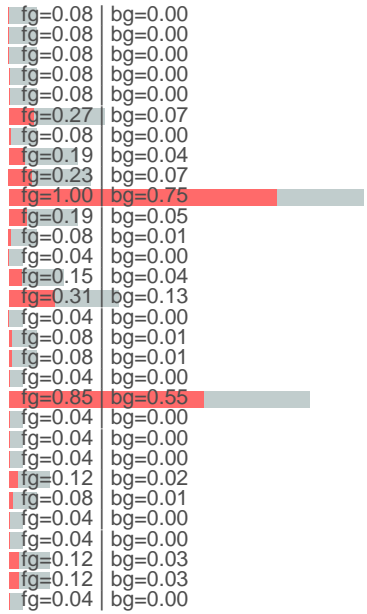
GO:MF  
Metazoa\_gain

JUN kinase activity	GO:0004705
calcium- and calmodulin-regulated 3',5'-...	GO:0048101
calmodulin-dependent cyclic-nucleotide p...	GO:0004117
SNAP receptor activity	GO:0005484
3',5'-cyclic-AMP phosphodiesterase activ...	GO:0004115
cytoskeletal protein binding	GO:0008092
protein serine/threonine/tyrosine kinase...	GO:0004712
calcium ion binding	GO:0005509
kinase binding	GO:0019900
binding	GO:0005488
G protein-coupled receptor activity	GO:0004930
structural constituent of cytoskeleton	GO:0005200
Rho GDP-dissociation inhibitor activity	GO:0005094
actin binding	GO:0003779
molecular function regulator	GO:0098772
histone deacetylase regulator activity	GO:0035033
protein N-terminus binding	GO:0047485
SNARE binding	GO:0000149
myosin head/neck binding	GO:0032028
protein binding	GO:0005515
peptidase activator activity involved in...	GO:0016505
cysteine-type endopeptidase activator ac...	GO:0008656
cytoskeletal anchor activity	GO:0008093
GTP binding	GO:0005525
calcium-dependent protein binding	GO:0048306
chloride channel inhibitor activity	GO:0019869
ATP-dependent protein binding	GO:0043008
guanyl ribonucleotide binding	GO:0032561
guanyl nucleotide binding	GO:0019001
GDP-dissociation inhibitor activity	GO:0005092



0 1 2 3 4 5  
-log(p)  
n=26/46 input genes with annotations

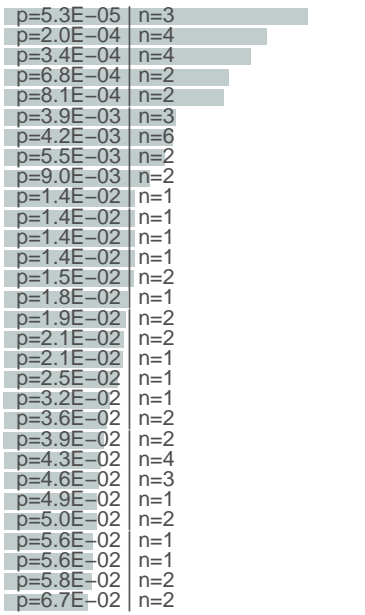
fraction genes in fg and expected value



0.0 0.2 0.4 0.6 0.8 1.0  
fraction

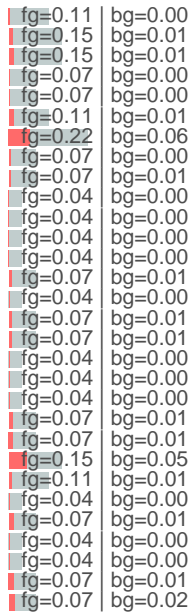
GO:CC  
Metazoa\_gain

dendrite cytoplasm	GO:0032839
perikaryon	GO:0043204
Schaffer collateral - CA1 synapse	GO:0098685
dendritic spine head	GO:0044327
SNARE complex	GO:0031201
synaptic vesicle membrane	GO:0030672
axon	GO:0030424
neuronal cell body membrane	GO:0032809
dendrite membrane	GO:0032590
synaptobrevin 2-SNAP-25-syntaxin-1a-comp...	GO:0070032
synaptobrevin 2-SNAP-25-syntaxin-1a-comp...	GO:0070033
cerebellar climbing fiber to Purkinje ce...	GO:0150053
spectrin-associated cytoskeleton	GO:0014731
intercellular bridge	GO:0045171
asymmetric, glutamatergic, excitatory sy...	GO:0098985
presynaptic active zone membrane	GO:0048787
mitotic spindle	GO:0072686
synaptobrevin 2-SNAP-25-syntaxin-1a comp...	GO:0070044
basal dendrite	GO:0097441
synaptic cleft	GO:0043083
postsynaptic density membrane	GO:0098839
neuromuscular junction	GO:0031594
synaptic membrane	GO:0097060
neuron projection membrane	GO:0032589
podosome	GO:0002102
presynaptic active zone	GO:0048786
axolemma	GO:0030673
M band	GO:0031430
postsynaptic specialization membrane	GO:0099634
spindle	GO:0005819



0 1 2 3 4 5  
-log(p)  
n=27/46 input genes with annotations

fraction genes in fg and expected value



0.0 0.2 0.4 0.6 0.8 1.0  
fraction