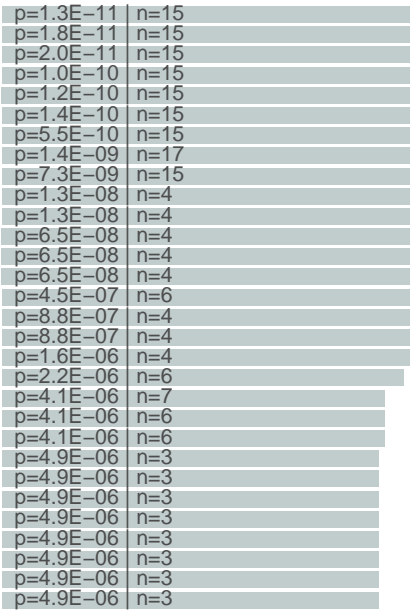


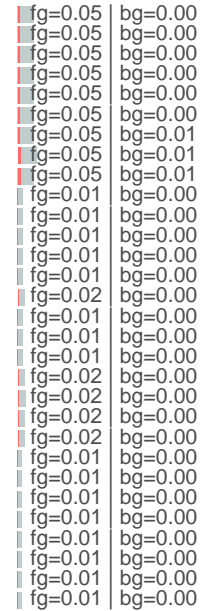
GO:BP
gc001a

fraction genes in fg and expected value

positive regulation of acetylcholine sec...	GO:0014057
negative regulation of luteinizing hormo...	GO:0033685
prolactin secretion	GO:0070459
positive regulation of flagellated sperm...	GO:1902093
positive regulation of vascular permeabi...	GO:0043117
positive regulation of uterine smooth mu...	GO:0070474
operant conditioning	GO:0035106
ubiquitin-dependent ERAD pathway	GO:0030433
intestine smooth muscle contraction	GO:0014827
pallium cell proliferation in forebrain	GO:0022013
regulation of mRNA stability involved in...	GO:0010610
cellular response to aldosterone	GO:1904045
sensory perception of salty taste	GO:0050914
cellular response to amiloride	GO:0036254
sensory perception of sour taste	GO:0050915
chemorepulsion of axon	GO:0061643
dendrite arborization	GO:0140059
cellular response to vasopressin	GO:1904117
negative regulation of chaperone-mediate...	GO:1904715
dopamine catabolic process	GO:0042420
cellular response to acidic pH	GO:0071468
positive regulation of insulin receptor ...	GO:0046628
regulation of vasculogenesis	GO:2001212
ascending aorta morphogenesis	GO:0035910
substrate-dependent cell migration, cell...	GO:0006930
tricuspid valve formation	GO:0003195
endocardial cushion to mesenchymal trans...	GO:0003199
muscular septum morphogenesis	GO:0003150
receptor-mediated virion attachment to h...	GO:0046813
umbilical cord morphogenesis	GO:0036304



0 1 2 3 4 5
-log(p)
n=331/965 input genes with annotations

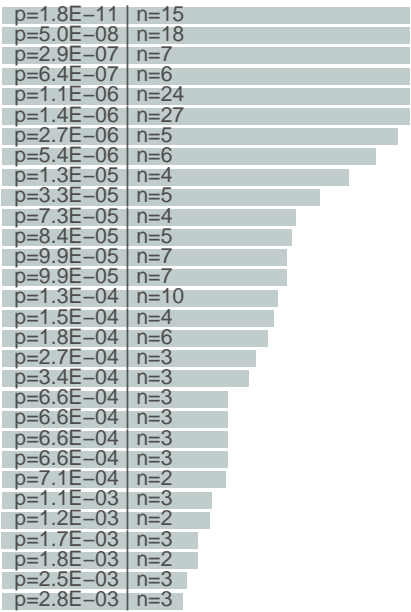


0.0 0.2 0.4 0.6 0.8 1.0
fraction

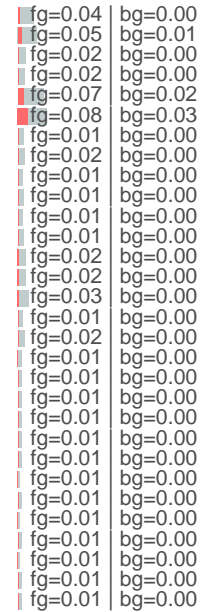
GO:MF
gc001a

fraction genes in fg and expected value

substance K receptor activity	GO:0016497
flavin adenine dinucleotide binding	GO:0050660
ligand-gated sodium channel activity	GO:0015280
mechanosensitive ion channel activity	GO:0008381
monooxygenase activity	GO:0004497
calcium ion binding	GO:0005509
hormone activity	GO:0005179
serine-type carboxypeptidase activity	GO:0004185
N6-methyladenosine-containing RNA binding	GO:1990247
WW domain binding	GO:0050699
MHC class II protein binding	GO:0042289
dopamine beta-monooxygenase activity	GO:0004500
protein ADP-ribosylase activity	GO:1990404
NAD+ ADP-ribosyltransferase activity	GO:0003950
monoamine transmembrane transporter activity	GO:0008504
serotonin:sodium symporter activity	GO:0005335
neurotransmitter transmembrane transport	GO:0005326
BMP receptor binding	GO:0070700
semaphorin receptor binding	GO:0030215
linoleate 13S-lipoxygenase activity	GO:0016165
arachidonate 15-lipoxygenase activity	GO:0050473
arachidonate 12(S)-lipoxygenase activity	GO:0004052
cocaine binding	GO:0019811
L-threonine 3-dehydrogenase activity	GO:0008743
serotonin binding	GO:0051378
glucagon receptor activity	GO:0004967
fibronectin binding	GO:0001968
choline transmembrane transporter activity	GO:0015220
proteoglycan binding	GO:0043394
tumor necrosis factor receptor binding	GO:0005164



0 1 2 3 4 5
-log(p)
n=336/965 input genes with annotations

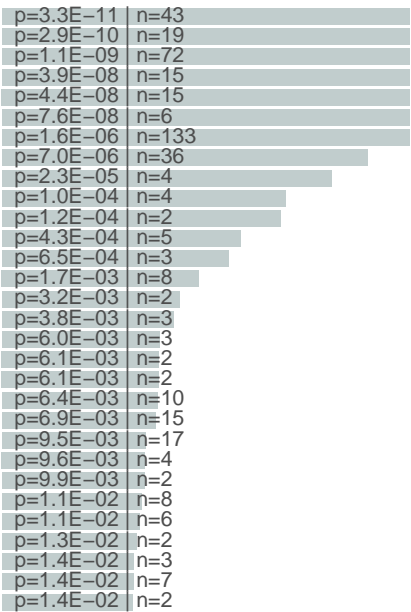


0.0 0.2 0.4 0.6 0.8 1.0
fraction

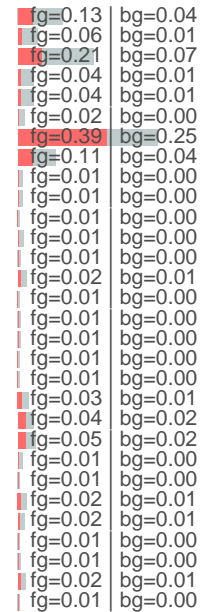
GO:CC
gc001a

fraction genes in fg and expected value

extracellular space	GO:0005615
endoplasmic reticulum lumen	GO:0005788
extracellular region	GO:0005576
sperm midpiece	GO:0097225
sperm head	GO:0061827
stereocilium tip	GO:0032426
plasma membrane	GO:0005886
cell surface	GO:0009986
CRD-mediated mRNA stability complex	GO:0070937
cytolytic granule	GO:0044194
stereocilium coat	GO:0120234
sodium channel complex	GO:0034706
serotonergic synapse	GO:0099154
basement membrane	GO:0005604
muscle tendon junction	GO:0005927
cuticular plate	GO:0032437
nuclear outer membrane	GO:0005640
ciliary inversin compartment	GO:0097543
kinociliary basal body	GO:1902636
external side of plasma membrane	GO:0009897
postsynaptic membrane	GO:0045211
actin cytoskeleton	GO:0015629
smooth endoplasmic reticulum	GO:0005790
apical plasma membrane urothelial plaque	GO:0120001
secretory granule membrane	GO:0030667
endoplasmic reticulum-Golgi intermediate...	GO:0005793
protein phosphatase 4 complex	GO:0030289
Golgi medial cisterna	GO:0005797
sarcolemma	GO:0042383
smooth endoplasmic reticulum membrane	GO:0030868



0 1 2 3 4 5
-log(p)
n=338/965 input genes with annotations



0.0 0.2 0.4 0.6 0.8 1.0
fraction