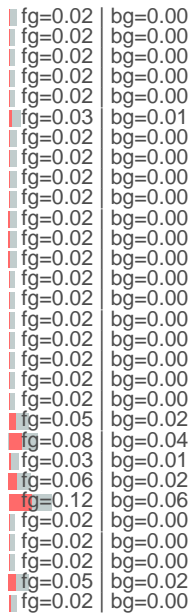
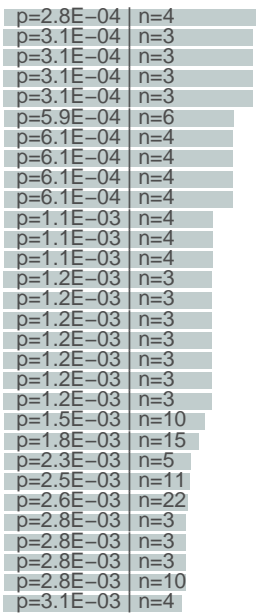


GO:BP
Ncol_Nvec_vc1.1_XM_048729481.1

fraction genes in fg and expected value

torso signaling pathway GO:0008293
positive regulation of CoA-transferase a... GO:1905920
positive regulation of acetylcholine bio... GO:1905923
positive regulation of heart rate involv... GO:0001988
generation of ovulation cycle rhythm GO:0060112
positive regulation of actin filament bu... GO:0032233
ectodermal placode formation GO:0060788
negative regulation of tumor necrosis fa... GO:0032720
signal transduction involved in cellular... GO:1903831
acetylcholine receptor signaling pathway GO:0095500
sensory processing GO:0050893
negative regulation of interleukin-6 pro... GO:0032715
regulation of synapse structural plastic... GO:0051823
cellular response to thyroid hormone sti... GO:0097067
dopamine biosynthetic process GO:0042416
adaptive thermogenesis GO:1990845
regulation of amyloid fibril formation GO:1905906
negative regulation of amyloid-beta form... GO:1902430
negative regulation of interleukin-1 bet... GO:0032691
head segmentation GO:0035287
branching morphogenesis of an epithelial... GO:0048754
regulation of membrane potential GO:0042391
negative regulation of transporter activ... GO:0032410
regulation of animal organ morphogenesis GO:2000027
regulation of anatomical structure size GO:0090066
positive regulation of amyloid-beta form... GO:1902004
dendrite arborization GO:0140059
regulation of norepinephrine secretion GO:0014061
eye photoreceptor cell differentiation GO:0001754
positive regulation of filopodium assemb... GO:0051491



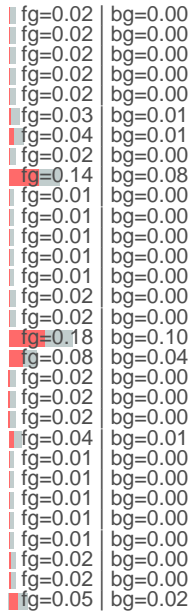
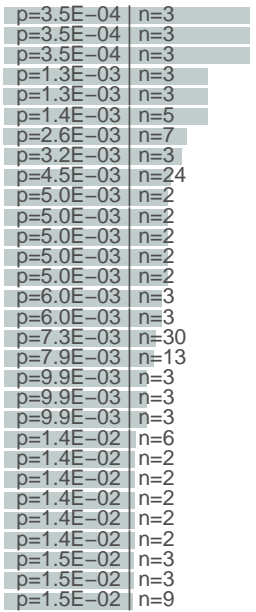
-log(p)
n=183/591 input genes with annotations

fraction

GO:MF
Ncol_Nvec_vc1.1_XM_048729481.1

fraction genes in fg and expected value

acetylcholine binding GO:0042166
acetylcholine-gated cation-selective cha... GO:0022848
acetylcholine receptor activity GO:0015464
cAMP binding GO:0030552
protein kinase A catalytic subunit bindi... GO:0034236
ammonium ion binding GO:0070405
ATPase binding GO:0051117
toxic substance binding GO:0015643
protein domain specific binding GO:0019904
beta-2 adrenergic receptor binding GO:0031698
eukaryotic initiation factor 4E binding GO:0008190
malic enzyme activity GO:0004470
D3 dopamine receptor binding GO:0031750
D4 dopamine receptor binding GO:0031751
protein disulfide isomerase activity GO:0003756
peroxidase activity GO:0004601
signaling receptor binding GO:0005102
phospholipid binding GO:0005543
voltage-gated chloride channel activity GO:0005247
adenylate cyclase binding GO:0008179
chloride channel regulator activity GO:0017081
phosphatidylinositol biphosphate bindin... GO:1902936
D2 dopamine receptor binding GO:0031749
cAMP-dependent protein kinase inhibitor ... GO:0004862
S100 protein binding GO:0044548
U2 snRNA binding GO:0030620
cAMP-dependent protein kinase regulator ... GO:0008603
snRNA binding GO:0017069
protein serine/threonine kinase inhibito... GO:0030291
ion gated channel activity GO:0022839



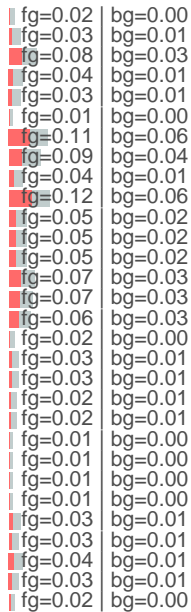
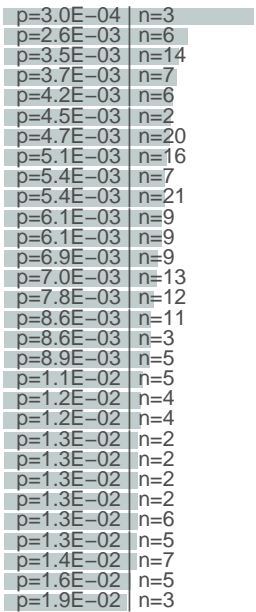
-log(p)
n=168/591 input genes with annotations

fraction

GO:CC
Ncol_Nvec_vc1.1_XM_048729481.1

fraction genes in fg and expected value

acetylcholine-gated channel complex GO:0005892
dendritic shaft GO:0043198
apical plasma membrane GO:0016324
extrinsic component of plasma membrane GO:0019897
extracellular vesicle GO:1903561
DNA polymerase III complex GO:0009360
neuronal cell body GO:0043025
cell leading edge GO:0031252
presynaptic membrane GO:0042734
perinuclear region of cytoplasm GO:0048471
growth cone GO:0030426
actin-based cell projection GO:0098858
dendritic spine GO:0043197
side of membrane GO:0098552
extracellular space GO:0005615
membrane raft GO:0045121
axolemma GO:0030673
lysosomal lumen GO:0043202
extrinsic component of cytoplasmic side ... GO:0031234
stereocilium GO:0032420
stereocilium bundle GO:0032421
cAMP-dependent protein kinase complex GO:0005952
muscle cell projection GO:0036194
muscle cell projection membrane GO:0036195
actin cap GO:0030478
plasma membrane raft GO:0044853
filopodium GO:0030175
postsynaptic membrane GO:0045211
extracellular exosome GO:0070062
Cul3-RING ubiquitin ligase complex GO:0031463



-log(p)
n=182/591 input genes with annotations

fraction