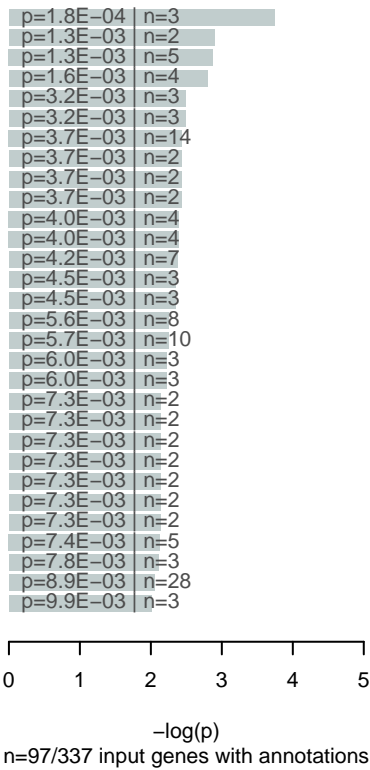


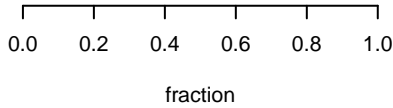
GO:BP
Fox_Nvec_vc1.1_XM_032375280.2

fraction genes in fg and expected value

negative regulation of long-term synapti...	GO:1900272
serotonin receptor signaling pathway	GO:0007210
negative regulation of Notch signaling p...	GO:0045746
Wnt signaling pathway, planar cell polar...	GO:0060071
regulation of epidermal growth factor-ac...	GO:0007176
actin filament depolymerization	GO:0030042
positive regulation of phosphorylation	GO:0042327
asparagine metabolic process	GO:0006528
G protein-coupled opioid receptor signal...	GO:0038003
regulation of receptor binding	GO:1900120
establishment or maintenance of epitheli...	GO:0045197
hormone biosynthetic process	GO:0042446
response to ketone	GO:1901654
glutamine metabolic process	GO:0006541
positive regulation of epidermal growth ...	GO:0045742
regulation of endocytosis	GO:0030100
regulation of protein catabolic process	GO:0042176
membrane protein ectodomain proteolysis	GO:0006509
positive regulation of signaling recepto...	GO:2000273
basal protein localization	GO:0045175
regulation of spontaneous synaptic trans...	GO:0150003
positive regulation of oxidative phospho...	GO:1903862
glycosphingolipid catabolic process	GO:0046479
sensory neuron axon guidance	GO:0097374
regulation of protein localization to ce...	GO:1904776
ceramide catabolic process	GO:0046514
regulation of morphogenesis of an epithe...	GO:1905330
regulation of peptidyl-threonine phospho...	GO:0010799
generation of neurons	GO:0048699
oligosaccharide metabolic process	GO:0009311



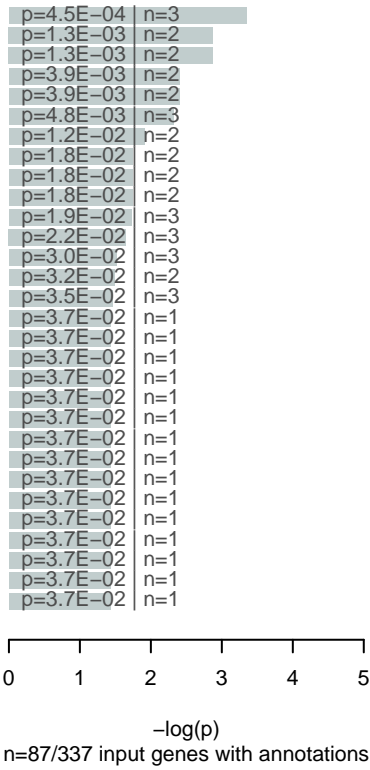
fg=0.03	bg=0.00
fg=0.02	bg=0.00
fg=0.05	bg=0.01
fg=0.04	bg=0.01
fg=0.02	bg=0.00
fg=0.03	bg=0.00
fg=0.14	bg=0.07
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.04	bg=0.01
fg=0.04	bg=0.01
fg=0.07	bg=0.02
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.08	bg=0.03
fg=0.10	bg=0.04
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.05	bg=0.01
fg=0.03	bg=0.00
fg=0.29	bg=0.17
fg=0.03	bg=0.00



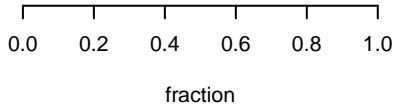
GO:MF
Fox_Nvec_vc1.1_XM_032375280.2

fraction genes in fg and expected value

ephrin receptor binding	GO:0046875
coreceptor activity involved in Wnt sign...	GO:1904929
apolipoprotein binding	GO:0034185
neurexin family protein binding	GO:0042043
mRNA regulatory element binding translat...	GO:0000900
frizzled binding	GO:0005109
acetylcholine receptor binding	GO:0033130
proteoglycan binding	GO:0043394
Wnt-protein binding	GO:0017147
dynein heavy chain binding	GO:0045504
growth factor receptor binding	GO:0070851
oxidoreduction-driven active transmembra...	GO:0015453
growth factor binding	GO:0019838
snRNA binding	GO:0017069
phospholipase activity	GO:0004620
CCR chemokine receptor binding	GO:0048020
myosin II binding	GO:0045159
tRNA 2'-phosphotransferase activity	GO:0000215
testosterone 17-beta-dehydrogenase (NADP...	GO:0047045
mono-olein transacylation activity	GO:0051264
diolefin transacylation activity	GO:0051265
ACP phosphopantetheine attachment site b...	GO:0044620
phosphopantetheine binding	GO:0031177
anaphase-promoting complex binding	GO:0010997
U12 snRNA binding	GO:0030626
alpha-sialidase activity	GO:0016997
steroid dehydrogenase activity, acting o...	GO:0033764
G protein-coupled opioid receptor activi...	GO:0004985
acyl binding	GO:0000035
acyl carrier activity	GO:0000036



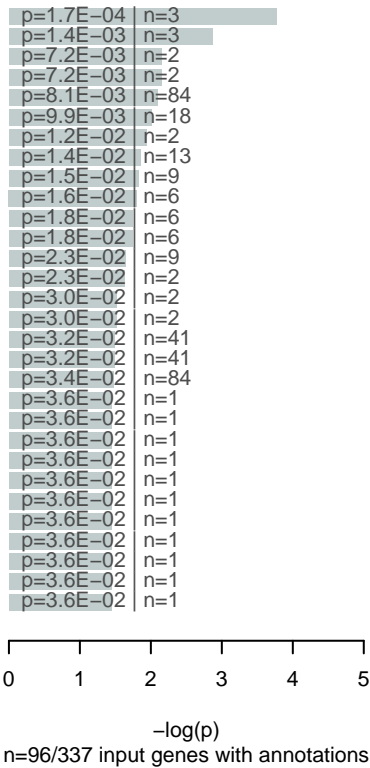
fg=0.03	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.03	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00



GO:CC
Fox_Nvec_vc1.1_XM_032375280.2

fraction genes in fg and expected value

growth cone lamellipodium	GO:1990761
apicolateral plasma membrane	GO:0016327
dendritic spine membrane	GO:0032591
integral component of lumenal side of en...	GO:0071556
intracellular membrane-bounded organelle	GO:0043231
organelle envelope	GO:0031967
presynaptic periaxial zone	GO:0036062
secretory vesicle	GO:0095003
mitochondrial inner membrane	GO:0005743
secretory granule lumen	GO:0034774
vesicle lumen	GO:0031983
cytoplasmic vesicle lumen	GO:0060205
organelle inner membrane	GO:0019866
axonemal dynein complex	GO:0005858
aggresome	GO:0016235
specific granule lumen	GO:0035580
non-membrane-bounded organelle	GO:0043228
intracellular non-membrane-bounded organ...	GO:0043232
cytoplasm	GO:0005737
cytoplasmic side of dendritic spine plas...	GO:1990780
endosome to plasma membrane transport ve...	GO:0070381
lipoprotein particle	GO:1990777
cytoplasmic periphery of the nuclear por...	GO:1990723
Gemini of coiled bodies	GO:0097504
interleukin-5 receptor complex	GO:0005895
amyloid-beta complex	GO:0106003
nuclear pore cytoplasmic filaments	GO:0044614
cyclin E1-CDK2 complex	GO:0097134
cyclin E2-CDK2 complex	GO:0097135
smooth septate junction	GO:0005920



fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.88	bg=0.77
fg=0.19	bg=0.11
fg=0.02	bg=0.00
fg=0.14	bg=0.07
fg=0.09	bg=0.04
fg=0.06	bg=0.02
fg=0.06	bg=0.02
fg=0.06	bg=0.02
fg=0.09	bg=0.04
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.43	bg=0.33
fg=0.43	bg=0.33
fg=0.88	bg=0.80
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00

