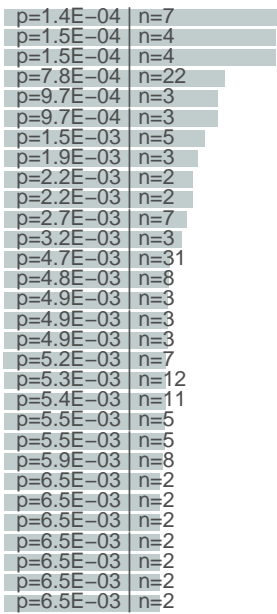


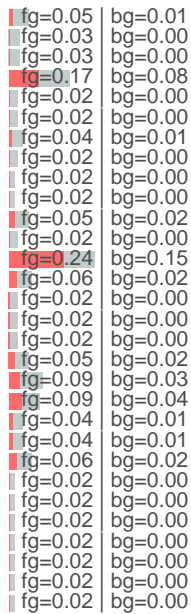
GO:BP
Elav_Nvec_vc1.1_XM_048723351.1

fraction genes in fg and expected value

imaginal disc-derived leg morphogenesis GO:0007480
regulation of cellular senescence GO:2000772
cellular response to parathyroid hormone... GO:0071374
positive regulation of transcription by ... GO:0045944
collateral sprouting GO:0048668
negative regulation of vulval developmen... GO:0040027
locomotor rhythm GO:0045475
negative regulation of double-strand bre... GO:2000780
positive regulation of skeletal muscle c... GO:2001016
platelet activating factor biosynthetic ... GO:0006663
molting cycle GO:0042303
cellular response to glucagon stimulus GO:0071377
positive regulation of gene expression GO:0010628
detection of external stimulus GO:0009581
regulation of cardiac muscle contraction... GO:0010882
cardiac muscle hypertrophy in response t... GO:0014898
positive regulation of cell cycle G2/M p... GO:1902751
feeding behavior GO:0007631
positive regulation of cell cycle proces... GO:0090068
organic anion transport GO:0015711
cell-cell junction assembly GO:0007043
regulation of DNA binding GO:0051101
regulation of DNA-binding transcription ... GO:0051090
cardiac ventricle formation GO:0003211
negative regulation of blood vessel endo... GO:0043537
negative regulation of transcription by ... GO:0016479
phosphatidylcholine acyl-chain remodelin... GO:0036151
phosphatidylglycerol acyl-chain remodeli... GO:0036148
regulation of receptor binding GO:1900120
SRP-dependent cotranslational protein ta... GO:0006616



0 1 2 3 4 5
-log(p)
n=128/443 input genes with annotations

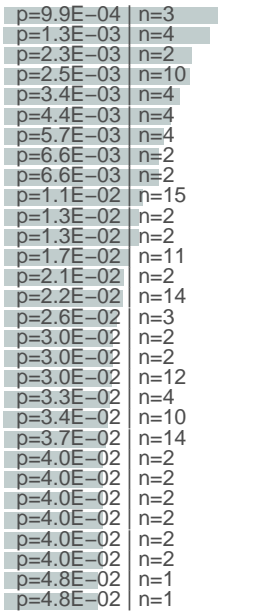


0.0 0.2 0.4 0.6 0.8 1.0
fraction

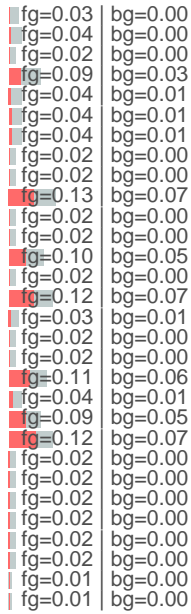
GO:MF
Elav_Nvec_vc1.1_XM_048723351.1

fraction genes in fg and expected value

ephrin receptor binding GO:0046875
promoter-specific chromatin binding GO:1990841
1-alkylglycerophosphocholine O-acetyltra... GO:0047192
RNA polymerase II cis-regulatory region ... GO:0000978
phospholipid transporter activity GO:0005548
ATPase-coupled cation transmembrane tran... GO:0019829
ATPase-coupled ion transmembrane transpo... GO:0042625
1-acylglycerophosphocholine O-acyltransf... GO:0047184
2-acylglycerol-3-phosphate O-acyltransfe... GO:0047144
DNA-binding transcription factor activit... GO:0003700
nucleotide-sugar transmembrane transport... GO:0005338
minor groove of adenine-thymine-rich DNA... GO:0003680
ubiquitin-like protein transferase activ... GO:0019787
P-type calcium transporter activity GO:0005388
protein kinase binding GO:0019901
E-box binding GO:0070888
1-acylglycerol-3-phosphate O-acyltransfe... GO:0003841
tumor necrosis factor receptor binding GO:0005164
DNA-binding transcription factor activit... GO:0000981
histone deacetylase binding GO:0042826
ubiquitin-protein transferase activity GO:0004842
kinase binding GO:0019900
peptidase activator activity GO:0016504
UDP-galactose:beta-N-acetylglucosamine b... GO:0008499
HMG box domain binding GO:0071837
UDP-galactosyltransferase activity GO:0035250
acylglycerol O-acyltransferase activity GO:0016411
MAP kinase kinase kinase activity GO:0004709
phosphatidylcholine transporter activity GO:0008525
myosin II binding GO:0045159



0 1 2 3 4 5
-log(p)
n=113/443 input genes with annotations

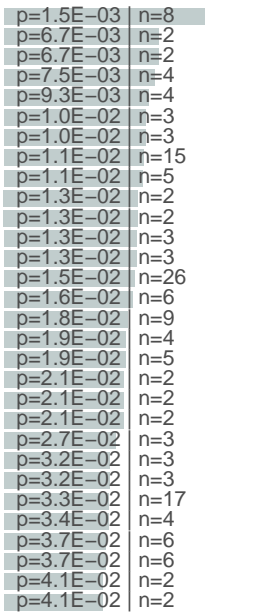


0.0 0.2 0.4 0.6 0.8 1.0
fraction

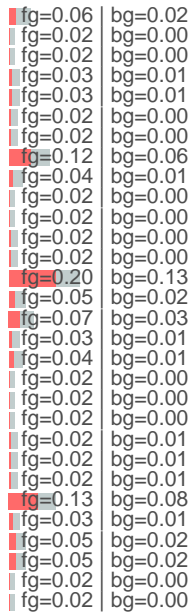
GO:CC
Elav_Nvec_vc1.1_XM_048723351.1

fraction genes in fg and expected value

Golgi stack GO:0005795
cAMP-dependent protein kinase complex GO:0005952
ciliary rootlet GO:0035253
actomyosin GO:0042641
transcription repressor complex GO:0017053
stress fiber GO:0001725
contractile actin filament bundle GO:0097517
nuclear body GO:0016604
ciliary transition zone GO:0035869
nucleotide-activated protein kinase comp... GO:0031588
RNA polymerase II transcription represso... GO:0090571
actin filament bundle GO:0032432
mitotic spindle pole GO:0097431
endoplasmic reticulum GO:0005783
neuromuscular junction GO:0031594
nuclear speck GO:0016607
rough endoplasmic reticulum GO:0005791
Golgi cisterna GO:0031985
septin cytoskeleton GO:0032156
fungal-type vacuole GO:0000324
fungal-type vacuole membrane GO:0000329
ciliary base GO:0097546
Golgi medial cisterna GO:0005797
germ cell nucleus GO:0043073
synapse GO:0045202
cation channel complex GO:0034703
neuron spine GO:0044309
dendritic spine GO:0043197
storage vacuole GO:0000322
germinal vesicle GO:0042585



0 1 2 3 4 5
-log(p)
n=130/443 input genes with annotations



0.0 0.2 0.4 0.6 0.8 1.0
fraction