

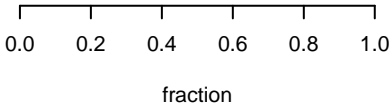
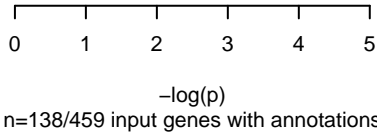
GO:BP
Elav_Nvec_vc1.1_XM_032386356.2

fraction genes in fg and expected value

imaginal disc-derived leg morphogenesis GO:0007480
renal system development GO:0072001
regulation of type B pancreatic cell apo... GO:2000674
age-dependent response to oxidative stre... GO:0001306
platelet activating factor biosynthetic ... GO:0006663
lipid modification GO:0030258
cell proliferation in forebrain GO:0021846
negative regulation of protein polymeriz... GO:0032272
positive regulation by host of viral pro... GO:0044794
phosphatidylcholine acyl-chain remodelin... GO:0036151
establishment of protein localization to... GO:0072594
mesodermal cell migration GO:0008078
response to hydrogen peroxide GO:0042542
positive regulation of canonical Wnt sig... GO:0090263
regulation of B cell activation GO:0050864
spleen development GO:0048536
cellular response to epidermal growth fa... GO:0071364
determination of heart left/right asymme... GO:0061371
epithelial tube formation GO:0072175
positive regulation of macroautophagy GO:0016239
regulation of steroid biosynthetic proce... GO:0050810
secondary alcohol metabolic process GO:1902652
negative regulation of adaptive immune r... GO:0002820
negative regulation of adaptive immune r... GO:0002823
positive regulation of dense core granul... GO:1904811
superoxide anion generation GO:0042554
regulation of dense core granule transpo... GO:1904809
N-terminal protein amino acid acetylatio... GO:0006474
positive regulation of urine volume GO:0035810
limb bud formation GO:0060174

p=1.6E-03	n=6
p=1.7E-03	n=12
p=2.6E-03	n=2
p=2.6E-03	n=2
p=2.6E-03	n=2
p=2.9E-03	n=8
p=3.3E-03	n=4
p=5.7E-03	n=4
p=7.5E-03	n=2
p=7.5E-03	n=2
p=8.3E-03	n=15
p=8.7E-03	n=3
p=8.7E-03	n=6
p=8.9E-03	n=5
p=9.2E-03	n=4
p=1.2E-02	n=3
p=1.2E-02	n=3
p=1.2E-02	n=5
p=1.2E-02	n=7
p=1.4E-02	n=4
p=1.4E-02	n=4
p=1.4E-02	n=5
p=1.5E-02	n=2
p=1.5E-02	n=2
p=1.5E-02	n=2
p=1.5E-02	n=2
p=1.5E-02	n=2
p=1.5E-02	n=2
p=1.5E-02	n=2
p=1.5E-02	n=2

fg=0.04	bg=0.01
fg=0.09	bg=0.03
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.06	bg=0.02
fg=0.03	bg=0.00
fg=0.03	bg=0.01
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.11	bg=0.06
fg=0.02	bg=0.00
fg=0.04	bg=0.01
fg=0.04	bg=0.01
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.04	bg=0.01
fg=0.05	bg=0.02
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.04	bg=0.01
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



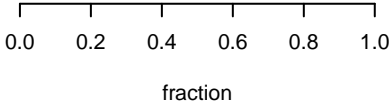
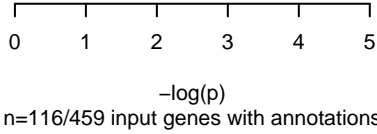
GO:MF
Elav_Nvec_vc1.1_XM_032386356.2

fraction genes in fg and expected value

GTPase activity GO:0003924
1-alkylglycerophosphocholine O-acetyltra... GO:0047192
ribosome binding GO:0043022
GTPase regulator activity GO:0030695
1-acylglycerophosphocholine O-acyltransf... GO:0047184
2-acylglycerol-3-phosphate O-acyltransfe... GO:0047144
minus-end-directed microtubule motor act... GO:0008569
guanyl-nucleotide exchange factor activi... GO:0005085
dynein light intermediate chain binding GO:0051959
ubiquitin-protein transferase activity GO:0004842
GTP binding GO:0005525
ubiquitin-like protein transferase activ... GO:0019787
dynein light chain binding GO:0045503
glucosyltransferase activity GO:0046527
ubiquitin-like protein ligase activity GO:0061659
ubiquitin protein ligase activity GO:0061630
purine ribonucleoside binding GO:0032550
ribonucleoside binding GO:0032549
potassium channel regulator activity GO:0015459
purine nucleoside binding GO:0001883
E-box binding GO:0070888
guanyl ribonucleotide binding GO:0032561
nucleoside binding GO:0001882
guanyl nucleotide binding GO:0019001
dynein intermediate chain binding GO:0045505
1-acylglycerol-3-phosphate O-acyltransfe... GO:0003841
SMAD binding GO:0046332
HMG box domain binding GO:0071837
acylglycerol O-acyltransferase activity GO:0016411
potassium channel inhibitor activity GO:0019870

p=1.9E-03	n=8
p=2.4E-03	n=2
p=3.7E-03	n=4
p=6.2E-03	n=11
p=6.9E-03	n=2
p=6.9E-03	n=2
p=6.9E-03	n=2
p=1.2E-02	n=6
p=1.3E-02	n=2
p=1.7E-02	n=11
p=1.9E-02	n=6
p=2.0E-02	n=11
p=2.2E-02	n=2
p=2.2E-02	n=2
p=2.2E-02	n=8
p=2.2E-02	n=8
p=2.3E-02	n=6
p=2.3E-02	n=3
p=2.3E-02	n=6
p=2.8E-02	n=6
p=2.8E-02	n=3
p=3.0E-02	n=6
p=3.0E-02	n=6
p=3.0E-02	n=6
p=3.1E-02	n=2
p=3.1E-02	n=2
p=4.0E-02	n=3
p=4.3E-02	n=2
p=4.3E-02	n=2
p=4.3E-02	n=2

fg=0.07	bg=0.02
fg=0.02	bg=0.00
fg=0.03	bg=0.01
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=0.05	bg=0.02
fg=0.02	bg=0.00
fg=0.05	bg=0.02
fg=0.09	bg=0.05
fg=0.05	bg=0.02
fg=0.09	bg=0.05
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.07	bg=0.03
fg=0.07	bg=0.03
fg=0.05	bg=0.02
fg=0.05	bg=0.02
fg=0.03	bg=0.01
fg=0.05	bg=0.02
fg=0.03	bg=0.01
fg=0.05	bg=0.02
fg=0.05	bg=0.02
fg=0.05	bg=0.02
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



GO:CC
Elav_Nvec_vc1.1_XM_032386356.2

fraction genes in fg and expected value

lipid droplet GO:0005811
mitochondrial nucleoid GO:0042645
mitochondrial protein-containing complex GO:0098798
inner dynein arm GO:0036156
cytoplasm GO:0005737
protein-containing complex GO:0032991
organelle membrane GO:0031090
organelle inner membrane GO:0019866
plasma membrane proton-transporting V-ty... GO:0033181
TIM23 mitochondrial import inner membran... GO:0005744
cytoplasmic region GO:0099568
phagocytic vesicle GO:0045335
cell cortex GO:0005938
axonemal dynein complex GO:0005858
vacuolar proton-transporting V-type ATPa... GO:0016471
mitochondrial inner membrane GO:0005743
intracellular organelle GO:0043229
translation release factor complex GO:0018444
apoplast GO:0048046
plastid GO:0009536
plasmodesma GO:0009506
chloroplast GO:0009507
plus-end kinesin complex GO:0005873
mitochondrial isocitrate dehydrogenase c... GO:0005962
actin rod GO:0031002
condensin complex GO:0000796
centralspindlin complex GO:0097149
UTP-C complex GO:0034456
eukaryotic 48S preinitiation complex GO:0033290
astrocyte end-foot GO:0097450

p=5.5E-03	n=5
p=8.1E-03	n=3
p=1.1E-02	n=8
p=1.4E-02	n=2
p=1.5E-02	n=117
p=1.9E-02	n=69
p=2.5E-02	n=42
p=3.0E-02	n=11
p=3.2E-02	n=2
p=3.2E-02	n=2
p=3.5E-02	n=12
p=3.7E-02	n=4
p=4.1E-02	n=9
p=4.4E-02	n=2
p=4.4E-02	n=2
p=4.4E-02	n=10
p=4.5E-02	n=120
p=5.0E-02	n=1
p=5.0E-02	n=1
p=5.0E-02	n=1
p=5.0E-02	n=1
p=5.0E-02	n=1
p=5.0E-02	n=1
p=5.0E-02	n=1
p=5.0E-02	n=1
p=5.0E-02	n=1
p=5.0E-02	n=1
p=5.0E-02	n=1
p=5.0E-02	n=1
p=5.0E-02	n=1
p=5.0E-02	n=1
p=5.0E-02	n=1

fg=0.04	bg=0.01
fg=0.02	bg=0.00
fg=0.06	bg=0.02
fg=0.01	bg=0.00
fg=0.87	bg=0.80
fg=0.51	bg=0.42
fg=0.31	bg=0.24
fg=0.08	bg=0.04
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.09	bg=0.05
fg=0.03	bg=0.01
fg=0.07	bg=0.03
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.07	bg=0.04
fg=0.90	bg=0.83
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

