

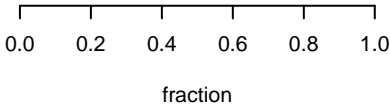
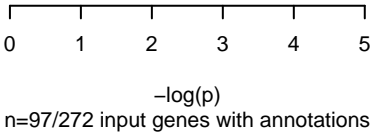
GO:BP
Elav_Nvec_vc1.1_XM_032366790.2

fraction genes in fg and expected value

protein localization to microtubule GO:0035372
wound healing GO:0042060
regulation of postsynaptic membrane orga... GO:1901626
deactivation of rhodopsin mediated signa... GO:0016059
regulation of presynapse assembly GO:1905606
positive regulation of transcription fac... GO:1901485
ovarian follicle cell-cell adhesion GO:0007299
regulation of dopamine receptor signalin... GO:0060159
nervous system process GO:0050877
lens fiber cell differentiation GO:0070306
developmental induction GO:0031128
hyperosmotic response GO:0006972
type B pancreatic cell apoptotic process GO:0097050
positive regulation of long-term synapti... GO:1900454
lung epithelial cell differentiation GO:0060487
bone regeneration GO:1990523
positive regulation of protein localizat... GO:1905477
regulation of filopodium assembly GO:0051489
regulation of Wnt signaling pathway GO:0030111
embryonic digit morphogenesis GO:0042733
cell maturation GO:0048469
positive regulation of transferase activ... GO:0051347
positive regulation of protein polymeriz... GO:0032273
melanotic encapsulation of foreign targe... GO:0035011
3'-UTR-mediated mRNA stabilization GO:0070935
non-canonical Wnt signaling pathway via ... GO:0038031
response to antipsychotic drug GO:0097332
response to clozapine GO:0097338
dosage compensation by hyperactivation o... GO:0009047
R3/R4 cell fate commitment GO:0007464

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p=3.2E-03	n=3
p=3.2E-03	n=4
p=3.7E-03	n=2
p=3.7E-03	n=2
p=3.7E-03	n=2
p=3.7E-03	n=2
p=4.0E-03	n=4
p=4.0E-03	n=4
p=4.4E-03	n=8
p=4.9E-03	n=4
p=5.4E-03	n=9
p=6.4E-03	n=11
p=7.0E-03	n=4
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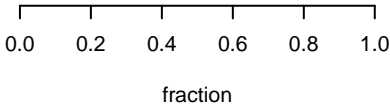
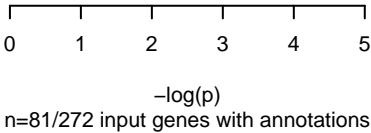
GO:MF
Elav_Nvec_vc1.1_XM_032366790.2

fraction genes in fg and expected value

protein binding GO:0005515
DNA-binding transcription activator acti... GO:0001228
cis-regulatory region sequence-specific ... GO:0000987
RNA polymerase II cis-regulatory region ... GO:0000978
MAP kinase kinase activity GO:0004708
RNA polymerase II transcription regulato... GO:0000977
adrenergic receptor binding GO:0031690
phosphatidic acid binding GO:0070300
dopamine receptor binding GO:0050780
enzyme binding GO:0019899
protein kinase activity GO:0004672
ubiquitin protein ligase binding GO:0031625
phosphotransferase activity, alcohol gro... GO:0016773
scaffold protein binding GO:0097110
identical protein binding GO:0042802
ubiquitin-like protein ligase binding GO:0044389
magnesium ion binding GO:0000287
actin binding GO:0003779
beta-adrenergic receptor kinase activity GO:0047696
phosphatidylcholine transporter activity GO:0008525
nitrite reductase (NO-forming) activity GO:0050421
protein-arginine omega-N symmetric methy... GO:0035243
delta-type opioid receptor binding GO:0031850
kappa-type opioid receptor binding GO:0031851
1-alkenylglycerophosphocholine O-acyltra... GO:0047159
open rectifier potassium channel activit... GO:0005252
voltage-gated calcium channel activity i... GO:0086056
fructose binding GO:0070061
voltage-gated calcium channel activity i... GO:0086059
pre-miRNA binding GO:0070883

p=2.3E-03	n=60
p=3.2E-03	n=8
p=1.3E-02	n=7
p=1.3E-02	n=7
p=1.6E-02	n=2
p=1.8E-02	n=8
p=2.2E-02	n=2
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p=2.2E-02	n=2
p=2.3E-02	n=26
p=2.4E-02	n=9
p=2.4E-02	n=7
p=2.7E-02	n=10
p=2.9E-02	n=3
p=3.0E-02	n=21
p=3.2E-02	n=7
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GO:CC
Elav_Nvec_vc1.1_XM_032366790.2

fraction genes in fg and expected value

cytoplasmic region GO:0099568
stress fiber GO:0001725
cell cortex GO:0005938
presynaptic periaxial zone GO:0036062
plasma membrane region GO:0098590
protein serine/threonine phosphatase com... GO:0008287
plasma membrane bounded cell projection GO:0120025
phosphatase complex GO:1903293
cell projection GO:0042995
synapse GO:0045202
cell junction GO:0030054
magnesium-dependent protein serine/threo... GO:0005963
sperm flagellum GO:0036126
cytoplasmic side of dendritic spine plas... GO:1990780
RCAF complex GO:0035059
core-binding factor complex GO:0016513
septin collar GO:0032173
endoplasmic reticulum tubular network me... GO:0098826
ATF4-CREB1 transcription factor complex GO:1990589
growth cone leading edge GO:0061850
RNA nuclear export complex GO:0042565
6-phosphofructokinase complex GO:0005945
anterior cell cortex GO:0061802
nuclear RNA export factor complex GO:0042272
MSL complex GO:0072487
Schmidt-Lanterman incisure GO:0043220
internode region of axon GO:0033269
dosage compensation complex GO:0046536
compact myelin GO:0043218
dendritic spine head GO:0044327

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p=4.9E-03	n=3
p=7.1E-03	n=9
p=1.3E-02	n=2
p=1.5E-02	n=15
p=1.9E-02	n=3
p=2.6E-02	n=26
p=2.7E-02	n=3
p=2.8E-02	n=26
p=3.1E-02	n=14
p=3.1E-02	n=18
p=3.3E-02	n=2
p=3.5E-02	n=4
p=3.7E-02	n=1
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