

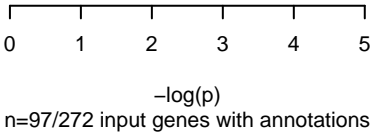
GO:BP  
Elav\_Nvec\_vc1.1\_XM\_048720954.1

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=3.1E–04	n=12
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p=1.3E–03	n=2
p=1.3E–03	n=2
p=2.7E–03	n=19
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p=3.2E–03	n=3
p=3.2E–03	n=4
p=3.7E–03	n=2
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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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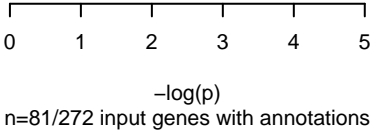
GO:MF  
Elav\_Nvec\_vc1.1\_XM\_048720954.1

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
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p=1.6E–02	n=2
p=1.8E–02	n=8
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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
p=3.3E–02	n=5
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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_048720954.1

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

p=3.8E–03	n=12
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
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