

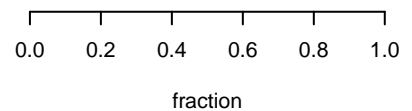
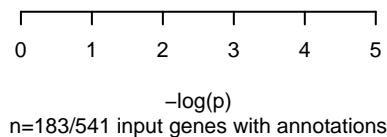
GO:BP
Elav_Nvec_vc1.1_XM_048726885.1

fraction genes in fg and expected value

establishment of mitotic spindle orienta...	GO:0000132
GTP metabolic process	GO:0046039
cell fate determination	GO:0001709
positive regulation of Wnt protein secre...	GO:0061357
male germ cell proliferation	GO:0002176
regulation of single stranded viral RNA ...	GO:0045099
negative regulation of viral transcripti...	GO:0032897
ovarian follicle cell-cell adhesion	GO:0007299
carnitine biosynthetic process	GO:0045329
apoptotic nuclear changes	GO:0030262
myelination in peripheral nervous system	GO:0022011
cellular response to interleukin-4	GO:0071353
hemidesmosome assembly	GO:0031581
negative regulation of axon regeneration	GO:0048681
regulation of protein targeting to membr...	GO:0090313
cochlea development	GO:0090102
lymph gland development	GO:0048542
neuroepithelial cell differentiation	GO:0060563
regulation of cell migration involved in...	GO:0090049
guanosine-containing compound metabolic ...	GO:1901068
somatic muscle development	GO:0007525
urogenital system development	GO:0001655
regulation of programmed cell death	GO:0043067
defense response to fungus	GO:0050832
amino sugar metabolic process	GO:0006040
regulation of execution phase of apoptos...	GO:1900117
regulation of hematopoietic stem cell di...	GO:1902036
vesicle-mediated transport between endos...	GO:0098927
establishment or maintenance of polarity...	GO:0016332
platelet activating factor metabolic pro...	GO:0046469

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p=4.6E-03	n=2
p=4.6E-03	n=4
p=5.3E-03	n=3
p=5.3E-03	n=3
p=5.3E-03	n=3
p=5.3E-03	n=3
p=5.6E-03	n=5
p=7.2E-03	n=5
p=8.0E-03	n=6
p=8.7E-03	n=3
p=9.0E-03	n=4
p=9.1E-03	n=5
p=1.1E-02	n=13
p=1.1E-02	n=33
p=1.2E-02	n=4
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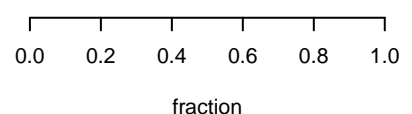
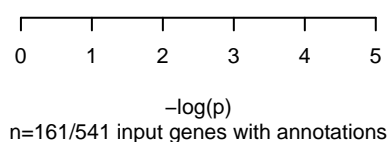
GO:MF
Elav_Nvec_vc1.1_XM_048726885.1

fraction genes in fg and expected value

E-box binding	GO:0070888
inositol bisphosphate phosphatase activi...	GO:0016312
gamma-butyrobetaine dioxygenase activity	GO:0008336
dynein intermediate chain binding	GO:0045505
HMG box domain binding	GO:0071837
RNA polymerase II intronic transcription...	GO:0001162
U2 snRNA binding	GO:0030620
glycolipid binding	GO:0051861
xylosyltransferase activity	GO:0042285
FAD binding	GO:0071949
UDP-xylosyltransferase activity	GO:0035252
potassium channel activity	GO:0005267
ubiquitin binding	GO:0043130
phosphatidylinositol phosphate phosphata...	GO:0052866
dynein light chain binding	GO:0045503
satellite DNA binding	GO:0003696
intronic transcription regulatory region...	GO:0001161
calcium-activated potassium channel acti...	GO:0015269
phosphoric diester hydrolase activity	GO:0008081
pentosyltransferase activity	GO:0016763
GTPase binding	GO:0051020
small GTPase binding	GO:0031267
bicarbonate transmembrane transporter ac...	GO:0015106
MAP kinase kinase activity	GO:0004708
phosphatidylinositol phosphate 5-phospha...	GO:0034595
gamma-tubulin binding	GO:0043015
ribosome binding	GO:0043022
enzyme binding	GO:0019899
ubiquitin-like protein binding	GO:0032182
potassium ion transmembrane transporter ...	GO:0015079

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p=3.4E-02	n=3
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p=4.0E-02	n=2
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p=4.0E-02	n=2
p=4.2E-02	n=4
p=4.3E-02	n=3
p=5.1E-02	n=14
p=5.2E-02	n=12
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GO:CC
Elav_Nvec_vc1.1_XM_048726885.1

fraction genes in fg and expected value

M band	GO:0031430
intraciliary transport particle A	GO:0030991
U5 snRNP	GO:0005682
extracellular exosome	GO:0070062
extracellular vesicle	GO:1903556
extracellular membrane-bounded organelle	GO:0065010
extracellular organelle	GO:0043230
mitotic spindle pole	GO:0097431
endosome	GO:0005768
zonula adherens	GO:0005915
intraciliary transport particle	GO:0030990
ruffle membrane	GO:0032587
ruffle	GO:0001726
early endosome	GO:0005769
protein kinase CK2 complex	GO:0005956
smooth septate junction	GO:0005920
anterior cell cortex	GO:0061802
omegasome membrane	GO:1903349
nuclear RNA export factor complex	GO:0042272
pinosome	GO:0044352
macropinosome	GO:0044354
BAT3 complex	GO:0071818
internode region of axon	GO:0033269
eukaryotic 43S preinitiation complex	GO:0016282
bub1-bub3 complex	GO:1990298
methionyl glutamyl tRNA synthetase compl...	GO:0017102
omegasome	GO:1990462
intrinsic component of endosome membrane	GO:0031302
Ric1-Rgp1 guanyl-nucleotide exchange fac...	GO:0034066
U7 snRNP	GO:0005683

[illegible][illegible]