

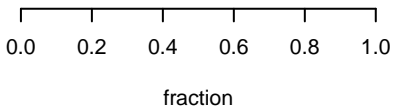
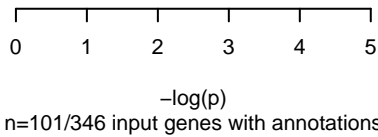
GO:BP
Elav_Nvec_vc1.1_XM_001622271.3

fraction genes in fg and expected value

copper ion transport	GO:0006825
actin cortical patch localization	GO:0051666
tRNA 5'-leader removal	GO:0001682
collagen fibril organization	GO:0030199
negative regulation of mitotic DNA damag...	GO:1904290
primary sex determination, soma	GO:0007539
lysine transport	GO:0015819
protein maturation by copper ion transfe...	GO:0015680
regulation of oxidoreductase activity	GO:0051341
Malpighian tubule morphogenesis	GO:0007443
head involution	GO:0008258
DNA repair	GO:0006281
adrenal gland development	GO:0030325
double-strand break repair	GO:0006302
detection of chemical stimulus	GO:0009593
eating behavior	GO:0042755
regulation of angiogenesis	GO:0045765
regulation of vasculature development	GO:1901342
regulation of long-term neuronal synapti...	GO:0048169
NLS-bearing protein import into nucleus	GO:0006607
norepinephrine metabolic process	GO:0042415
male sex differentiation	GO:0046661
muscle system process	GO:0003012
positive regulation of biosynthetic proc...	GO:0009891
circulatory system development	GO:0072359
cellular response to amino acid stimulus	GO:0071230
chromosome condensation	GO:0030261
peripheral nervous system development	GO:0007422
positive regulation of ATP biosynthetic ...	GO:2001171
cellular response to manganese ion	GO:0071287

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p=1.1E-02	n=3
p=1.2E-02	n=4
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p=1.7E-02	n=5
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p=1.7E-02	n=2
p=1.9E-02	n=6
p=2.1E-02	n=8
p=2.3E-02	n=23
p=2.4E-02	n=14
p=2.5E-02	n=3
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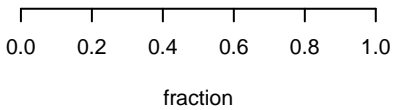
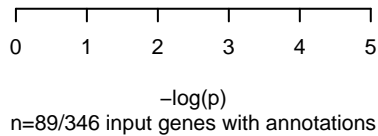
GO:MF
Elav_Nvec_vc1.1_XM_001622271.3

fraction genes in fg and expected value

superoxide dismutase copper chaperone ac...	GO:0016532
copper-dependent protein binding	GO:0032767
vinculin binding	GO:0017166
beta-aspartyl-peptidase activity	GO:0008798
MHC protein binding	GO:0042287
myosin binding	GO:0017022
nucleic acid binding	GO:0003676
nuclear glucocorticoid receptor binding	GO:0035259
DNA-binding transcription factor binding	GO:0140297
microtubule plus-end binding	GO:0051010
mRNA 3'-UTR binding	GO:0003730
zinc ion binding	GO:0008270
myosin heavy chain binding	GO:0032036
phospholipase binding	GO:0043274
ATPase-coupled transmembrane transporter...	GO:0042626
ATPase-coupled ion transmembrane transpo...	GO:0042625
ubiquitin-like protein ligase activity	GO:0061659
ubiquitin protein ligase activity	GO:0061630
protein domain specific binding	GO:0019904
RNA polymerase II-specific DNA-binding t...	GO:0061629
SMAD binding	GO:0046332
beta-catenin binding	GO:0008013
aryl hydrocarbon receptor binding	GO:0017162
cholesterol binding	GO:0015485
RNA binding	GO:0003723
DNA binding	GO:0003677
ATP hydrolysis activity	GO:0016887
sterol binding	GO:0032934
protein serine/threonine kinase inhibito...	GO:0030291
neuropilin binding	GO:0038191

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p=5.9E-03	n=27
p=8.9E-03	n=2
p=1.5E-02	n=8
p=1.7E-02	n=2
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p=2.8E-02	n=2
p=2.8E-02	n=2
p=3.1E-02	n=4
p=3.2E-02	n=3
p=3.6E-02	n=7
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GO:CC
Elav_Nvec_vc1.1_XM_001622271.3

fraction genes in fg and expected value

multimeric ribonuclease P complex	GO:0030681
Lewy body	GO:0097413
M band	GO:0031430
fungal-type vacuole	GO:0000324
fungal-type vacuole membrane	GO:0000329
aggresome	GO:0016235
cell tip	GO:0051286
Golgi cis cisterna	GO:0000137
endonuclease complex	GO:1905348
Golgi trans cisterna	GO:0000138
vacuolar membrane	GO:0005774
Golgi cisterna	GO:0031985
exocytic vesicle membrane	GO:0099501
nucleoplasm	GO:0005654
storage vacuole	GO:0000322
cell pole	GO:0060187
transcription factor TFTC complex	GO:0033276
female germ cell nucleus	GO:0001674
A band	GO:0031672
RNA polymerase II transcription regulato...	GO:0090575
sarcoplasm	GO:0016528
sarcoplasmic reticulum	GO:0016529
lytic vacuole membrane	GO:0098852
vacuole	GO:0005773
focal adhesion	GO:0005925
transcription factor TFIID complex	GO:0005669
SAGA-type complex	GO:0070461
nuclear lumen	GO:0031981
Golgi-associated vesicle lumen	GO:0070931
chromaffin granule	GO:0042583

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p=2.1E-02	n=8
p=2.1E-02	n=5
p=2.3E-02	n=4
p=2.5E-02	n=37
p=2.8E-02	n=2
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