

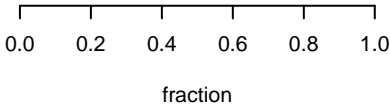
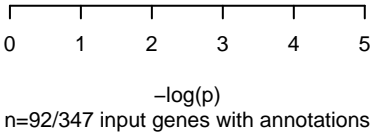
GO:BP
Elav_Nvec_vc1.1_XM_001624716.3

fraction genes in fg and expected value

regulation of mRNA 3'–end processing	GO:0031440
mRNA polyadenylation	GO:0006378
regulation of mitotic cell cycle	GO:0007346
termination of RNA polymerase II transcr...	GO:0006369
positive regulation of translation	GO:0045727
regulation of protein autoubiquitination	GO:1902498
regulation of neuron projection developm...	GO:0010975
endothelial cell apoptotic process	GO:0072577
internal peptidyl–lysine acetylation	GO:0018393
negative regulation of cellular macromol...	GO:2000113
negative regulation of gene expression	GO:0010629
female pregnancy	GO:0007565
mitral valve morphogenesis	GO:0003183
regulation of cell cycle phase transitio...	GO:1901987
negative regulation of vasculature devel...	GO:1901343
platelet degranulation	GO:0002576
response to radiation	GO:0009314
establishment of RNA localization	GO:0051236
positive regulation of transcription, DN...	GO:0045893
regulation of transcription by RNA polym...	GO:0006357
positive regulation of cellular cataboli...	GO:0031331
urogenital system development	GO:0001655
cell part morphogenesis	GO:0032990
negative regulation of nucleobase–contai...	GO:0045934
response to light stimulus	GO:0009416
cell morphogenesis involved in neuron di...	GO:0048667
cellular response to DNA damage stimulus	GO:0006974
positive regulation of transcription by ...	GO:0045944
regulation of neuron differentiation	GO:0045664
negative regulation of transcription by ...	GO:0000122

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p=1.1E–03	n=5
p=1.3E–03	n=14
p=2.3E–03	n=3
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p=2.6E–03	n=2
p=3.1E–03	n=13
p=3.8E–03	n=3
p=5.3E–03	n=6
p=5.3E–03	n=20
p=6.7E–03	n=24
p=7.1E–03	n=5
p=7.4E–03	n=2
p=8.4E–03	n=10
p=8.5E–03	n=3
p=8.5E–03	n=3
p=8.9E–03	n=11
p=9.4E–03	n=6
p=9.5E–03	n=19
p=1.0E–02	n=24
p=1.1E–02	n=10
p=1.1E–02	n=9
p=1.1E–02	n=17
p=1.2E–02	n=19
p=1.2E–02	n=9
p=1.2E–02	n=16
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p=1.4E–02	n=14
p=1.4E–02	n=13

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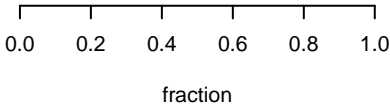
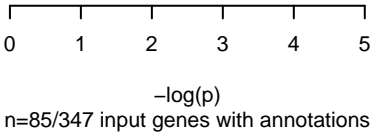
GO:MF
Elav_Nvec_vc1.1_XM_001624716.3

fraction genes in fg and expected value

DNA–binding transcription factor activit...	GO:0000981
microtubule binding	GO:0008017
MHC protein binding	GO:0042287
polynucleotide adenylyltransferase activ...	GO:0004652
manganese ion binding	GO:0030145
tau protein binding	GO:0048156
histone acetyltransferase activity	GO:0004402
magnesium ion binding	GO:0000287
RNA polymerase II cis–regulatory region ...	GO:0000978
heterocyclic compound binding	GO:1901363
organic cyclic compound binding	GO:0097159
histone binding	GO:0042393
nucleic acid binding	GO:0003676
modification–dependent protein binding	GO:0140030
phospholipase binding	GO:0043274
transcription coregulator activity	GO:0003712
transcription coactivator activity	GO:0003713
DNA–binding transcription activator acti...	GO:0001228
DNA–binding transcription activator acti...	GO:0001216
transcription factor binding	GO:0008134
histone deacetylase activity	GO:0004407
polyubiquitin modification–dependent pro...	GO:0031593
protein lysine deacetylase activity	GO:0033558
core promoter sequence–specific DNA bind...	GO:0001046
RNA strand–exchange activity	GO:0034057
guanine nucleotide transmembrane transpo...	GO:0001409
amine transmembrane transporter activity	GO:0005275
ABC–type 3',5'–cyclic GMP transmembrane ...	GO:1905948
poly(G) binding	GO:0034046
activin receptor activity, type II	GO:0016362

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p=1.5E–03	n=8
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p=4.4E–03	n=3
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p=8.2E–03	n=2
p=8.2E–03	n=2
p=9.0E–03	n=6
p=9.1E–03	n=8
p=9.5E–03	n=36
p=1.2E–02	n=36
p=1.2E–02	n=5
p=1.5E–02	n=28
p=1.6E–02	n=4
p=2.5E–02	n=2
p=2.6E–02	n=10
p=3.4E–02	n=7
p=4.0E–02	n=7
p=4.0E–02	n=7
p=4.7E–02	n=11
p=5.0E–02	n=2
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p=5.0E–02	n=3
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GO:CC
Elav_Nvec_vc1.1_XM_001624716.3

fraction genes in fg and expected value

P–body	GO:0000932
U5 snRNP	GO:0005682
platelet alpha granule	GO:0031091
nucleus	GO:0005634
nuclear lumen	GO:0031981
intercalary heterochromatin	GO:0005725
spot adherens junction	GO:0005914
kinetochore	GO:0000776
costamere	GO:0043034
fibrillar center	GO:0001650
nucleolus	GO:0005730
ficolin–1–rich granule lumen	GO:1904813
microtubule	GO:0005874
zymogen granule	GO:0042588
MLL1 complex	GO:0071339
mitotic spindle pole	GO:0097431
spindle pole	GO:0000922
pronucleus	GO:0045120
nuclear body	GO:0016604
transcription factor TFIID complex	GO:0005669
MLL1/2 complex	GO:0044665
nucleoplasm	GO:0005654
ficolin–1–rich granule	GO:0101002
eukaryotic translation initiation factor...	GO:0016281
intracellular transport particle B	GO:0030992
extrinsic component of presynaptic activ...	GO:0098891
extrinsic component of synaptic membrane	GO:0099243
BAT3 complex	GO:0071818
extrinsic component of presynaptic membr...	GO:0098888
ER membrane insertion complex	GO:0072379

p=1.5E–03	n=5
p=2.8E–03	n=2
p=4.5E–03	n=3
p=4.9E–03	n=65
p=8.0E–03	n=42
p=8.2E–03	n=2
p=8.2E–03	n=2
p=8.6E–03	n=4
p=1.6E–02	n=2
p=1.6E–02	n=4
p=2.2E–02	n=13
p=2.3E–02	n=4
p=2.5E–02	n=5
p=2.6E–02	n=2
p=2.6E–02	n=2
p=2.6E–02	n=2
p=3.6E–02	n=4
p=3.7E–02	n=2
p=4.0E–02	n=11
p=5.0E–02	n=2
p=5.0E–02	n=2
p=5.1E–02	n=34
p=5.3E–02	n=4
p=5.4E–02	n=1
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