

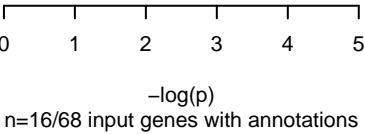
GO:BP  
Elav\_Nvec\_vc1.1\_XM\_001633398.3

fraction genes in fg and expected value

collateral sprouting	GO:0048668
positive regulation of axon regeneration	GO:0048680
regulation of histone H3-K27 methylation	GO:0061085
negative regulation of protein ubiquitin...	GO:0031397
protein heterooligomerization	GO:0051291
stabilization of membrane potential	GO:0030322
nucleobase-containing compound catabolic...	GO:0034655
positive regulation of histone methylati...	GO:0031062
cellular nitrogen compound catabolic pro...	GO:0044270
heterocycle catabolic process	GO:0046700
positive regulation of organelle organiz...	GO:0010638
potassium ion transmembrane transport	GO:0071805
organic cyclic compound catabolic proces...	GO:1901361
aromatic compound catabolic process	GO:0019439
positive regulation of protein modificat...	GO:0031401
nucleotide catabolic process	GO:0009166
positive regulation of chromatin organiz...	GO:1905269
positive regulation of histone modificat...	GO:0031058
nucleoside phosphate catabolic process	GO:1901292
regulation of muscle hypertrophy	GO:0014743
regulation of cardiac muscle hypertrophy	GO:0010611
negative regulation of cell population p...	GO:0008285
positive regulation of secretion by cell	GO:1903532
potassium ion transport	GO:0006813
peptidyl-threonine modification	GO:0018210
regulation of chromatin organization	GO:1902275
positive regulation of chromosome organi...	GO:2001252
protein maturation	GO:0051604
calcium-ion regulated exocytosis	GO:0017156
regulation of muscle adaptation	GO:0043502

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p=4.2E-03	n=2
p=8.3E-03	n=2
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p=1.3E-02	n=2
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p=1.4E-02	n=4
p=1.7E-02	n=3
p=2.0E-02	n=3
p=2.0E-02	n=3
p=2.2E-02	n=5
p=2.7E-02	n=2
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p=3.2E-02	n=4
p=3.3E-02	n=3
p=3.3E-02	n=3
p=3.5E-02	n=2
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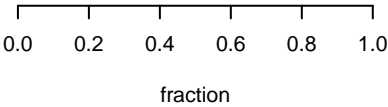
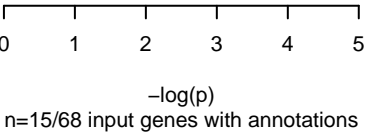
GO:MF  
Elav\_Nvec\_vc1.1\_XM\_001633398.3

fraction genes in fg and expected value

potassium ion leak channel activity	GO:0022841
guanyl ribonucleotide binding	GO:0032561
guanyl nucleotide binding	GO:0019001
protein N-acetylglucosaminyltransferase ...	GO:0016262
acetylglucosaminyltransferase activity	GO:0008375
voltage-gated calcium channel activity i...	GO:0086056
voltage-gated calcium channel activity i...	GO:0086059
voltage-gated calcium channel activity i...	GO:0086007
intracellular sodium activated potassium...	GO:0005228
protein O-GlcNAc transferase activity	GO:0097363
monosaccharide binding	GO:0048029
actin binding	GO:0003779
ribonucleotide binding	GO:0032553
purine ribonucleotide binding	GO:0032555
small molecule binding	GO:0036094
nucleotide binding	GO:0000166
nucleoside phosphate binding	GO:1901265
purine nucleotide binding	GO:0017076
carbohydrate binding	GO:0030246
protein serine/threonine phosphatase act...	GO:0004722
calcium-activated potassium channel acti...	GO:0015269
low voltage-gated calcium channel activi...	GO:0008332
actin monomer binding	GO:0003785
ubiquitin-like protein ligase binding	GO:0044389
ubiquitin protein ligase binding	GO:0031625
carbohydrate derivative binding	GO:0097367
voltage-gated cation channel activity	GO:0022843
RNA polymerase II transcription regulato...	GO:0000977
ribonucleoside binding	GO:0032549
phosphatidylinositol-3,4,5-trisphosphate...	GO:0005547

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p=4.1E-02	n=1
p=5.9E-02	n=2
p=6.1E-02	n=3
p=6.1E-02	n=3
p=6.5E-02	n=4
p=6.8E-02	n=3
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p=8.1E-02	n=1
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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_001633398.3

fraction genes in fg and expected value

euchromatin	GO:0000791
intrinsic component of plasma membrane	GO:0031226
septin filament array	GO:0032160
zymogen granule	GO:0042588
ESC/E(Z) complex	GO:0035098
contractile ring	GO:0070938
presynaptic active zone membrane	GO:0048787
Sin3-type complex	GO:0070822
axoneme	GO:0005930
ciliary plasm	GO:0097014
plasma membrane	GO:0005886
integral component of plasma membrane	GO:0005887
cell periphery	GO:0071944
stress fiber	GO:0001725
septin cytoskeleton	GO:0032156
intrinsic component of the cytoplasmic s...	GO:0031235
plasma membrane bounded cell projection ...	GO:0032838
contractile actin filament bundle	GO:0097517
intercellular bridge	GO:0045171
septin ring	GO:0005940
septin complex	GO:0031105
sperm annulus	GO:0097227
actin filament bundle	GO:0032432
intrinsic component of membrane	GO:0031224
actin cytoskeleton	GO:0015629
cleavage furrow	GO:0032154
filopodium	GO:0030175
actomyosin	GO:0042641
histone deacetylase complex	GO:0000118
cation channel complex	GO:0034703

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p=5.1E-02	n=10
p=6.9E-02	n=5
p=7.4E-02	n=10
p=7.8E-02	n=1
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