

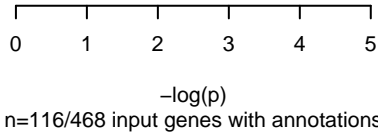
GO:BP  
Elav\_Nvec\_vc1.1\_XM\_032375602.2

fraction genes in fg and expected value

phototransduction	GO:0007602
proximal/distal pattern formation, imagi...	GO:0007449
regulation of 3'-UTR-mediated mRNA stabi...	GO:1905868
serine phosphorylation of STAT protein	GO:0042501
regulation of cilium beat frequency invo...	GO:0060296
negative regulation of leukocyte differe...	GO:1902106
taxis	GO:0042330
regulation of neural retina development	GO:0061074
regulation of retina development in came...	GO:1902866
positive regulation of axon regeneration	GO:0048680
negative regulation of transcription by ...	GO:0000122
renal tubule development	GO:0061326
regulation of synapse organization	GO:0050807
positive regulation of growth	GO:0045927
potassium ion transmembrane transport	GO:0071805
visual perception	GO:0007601
heart valve development	GO:0003170
hindbrain development	GO:0030902
citrulline biosynthetic process	GO:0019240
somite rostral/caudal axis specification	GO:0032525
positive regulation of nervous system de...	GO:0051962
segment specification	GO:0007379
behavior	GO:0007610
sister chromatid cohesion	GO:0007062
ear development	GO:0043583
wing disc dorsal/ventral pattern formati...	GO:0048190
hindbrain morphogenesis	GO:0021575
stabilization of membrane potential	GO:0030322
cystoblast division	GO:0007282
regulation of imaginal disc growth	GO:0045570

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p=1.8E-03	n=2
p=1.8E-03	n=2
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p=3.9E-03	n=4
p=5.0E-03	n=14
p=5.3E-03	n=2
p=5.3E-03	n=2
p=5.4E-03	n=3
p=8.0E-03	n=15
p=8.2E-03	n=6
p=8.2E-03	n=9
p=9.2E-03	n=11
p=9.3E-03	n=5
p=9.3E-03	n=5
p=9.9E-03	n=3
p=1.0E-02	n=6
p=1.0E-02	n=2
p=1.0E-02	n=2
p=1.2E-02	n=13
p=1.3E-02	n=3
p=1.5E-02	n=22
p=1.5E-02	n=4
p=1.6E-02	n=7
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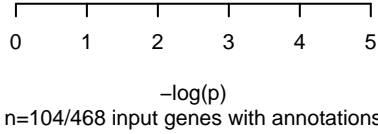
GO:MF  
Elav\_Nvec\_vc1.1\_XM\_032375602.2

fraction genes in fg and expected value

DNA-binding transcription activator acti...	GO:0001228
RNA polymerase II cis-regulatory region ...	GO:0000978
potassium channel activity	GO:0005267
structural constituent of nuclear pore	GO:0017056
voltage-gated potassium channel activity	GO:0005249
cAMP binding	GO:0030552
voltage-gated cation channel activity	GO:0022843
mRNA binding	GO:0003729
RNA methyltransferase activity	GO:0008173
microtubule motor activity	GO:0003777
acetylcholine receptor binding	GO:0033130
leak channel activity	GO:0022840
potassium ion leak channel activity	GO:0022841
narrow pore channel activity	GO:0022842
cyclic nucleotide binding	GO:0030551
E-box binding	GO:0070888
O-methyltransferase activity	GO:0008171
adrenergic receptor binding	GO:0031690
MAP kinase activity	GO:0004707
voltage-gated ion channel activity	GO:0005244
voltage-gated channel activity	GO:0022832
1-alkenylglycerophosphocholine O-acyltra...	GO:0047159
open rectifier potassium channel activit...	GO:0005252
platelet activating factor receptor bind...	GO:0031859
taste receptor binding	GO:0031883
ATP-dependent DNA/DNA annealing activity	GO:0036310
glutamate-5-semialdehyde dehydrogenase a...	GO:0004350
alpha-1A adrenergic receptor binding	GO:0031691
guanine nucleotide transmembrane transpo...	GO:0001409
amine transmembrane transporter activity	GO:0005275

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p=1.3E-03	n=10
p=6.7E-03	n=4
p=7.9E-03	n=3
p=1.1E-02	n=3
p=1.1E-02	n=2
p=1.4E-02	n=4
p=1.5E-02	n=8
p=1.6E-02	n=4
p=1.7E-02	n=3
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p=2.1E-02	n=3
p=2.5E-02	n=2
p=3.5E-02	n=2
p=3.5E-02	n=2
p=3.6E-02	n=4
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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_032375602.2

fraction genes in fg and expected value

photoreceptor inner segment	GO:0001917
hippocampal mossy fiber	GO:0097457
photoreceptor outer segment	GO:0001750
synapse	GO:0045202
voltage-gated potassium channel complex	GO:0008076
exon-exon junction complex	GO:0035145
lipid droplet	GO:0005811
plasma membrane raft	GO:0044853
transverse filament	GO:0000802
spectrosome	GO:0045170
spectrin	GO:0008091
hippocampal mossy fiber expansion	GO:1990026
integral component of pigment granule me...	GO:0090740
pigment granule membrane	GO:0090741
plus-end kinesin complex	GO:0005873
chromatin	GO:0000785
dendrite	GO:0030425
dendritic tree	GO:0097447
cortical actin cytoskeleton	GO:0030864
pigment granule	GO:0048770
dendritic spine	GO:0043197
neuron spine	GO:0044309
caveola	GO:0005901
cortical cytoskeleton	GO:0030863
RNA polymerase III transcription regulat...	GO:0090576
spermatoproteasome complex	GO:1990111
transcription factor TFIIC complex	GO:0000127
BBSome	GO:0034464
tRNA-splicing ligase complex	GO:0072669
calcineurin complex	GO:0005955

p=1.8E-03	n=4
p=1.9E-03	n=2
p=4.2E-03	n=4
p=6.4E-03	n=18
p=7.8E-03	n=3
p=1.1E-02	n=2
p=1.9E-02	n=4
p=4.0E-02	n=4
p=4.4E-02	n=1
p=4.4E-02	n=1
p=4.4E-02	n=1
p=4.4E-02	n=1
p=4.4E-02	n=1
p=5.0E-02	n=10
p=5.1E-02	n=12
p=5.3E-02	n=12
p=5.4E-02	n=3
p=6.8E-02	n=2
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p=7.4E-02	n=5
p=7.6E-02	n=3
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