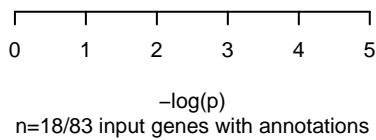


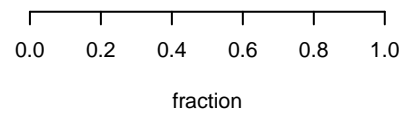
GO:BP  
Elav\_Nvec\_vc1.1\_XM\_032364225.2

fraction genes in fg and expected value

positive regulation of viral transcripti...	GO:0050434	p=1.8E-03	n=2
medium-term memory	GO:0072375	p=1.8E-03	n=2
regulation of defecation	GO:2000292	p=5.4E-03	n=2
muscle organ development	GO:0007517	p=1.6E-02	n=4
cellular response to mechanical stimulus	GO:0071260	p=2.5E-02	n=2
cAMP metabolic process	GO:0046058	p=2.5E-02	n=2
negative regulation of gene expression, ...	GO:0045814	p=2.5E-02	n=2
regulation of locomotion	GO:0040012	p=2.8E-02	n=6
positive regulation of response to exter...	GO:0032103	p=2.8E-02	n=3
regulation of biosynthetic process	GO:0009889	p=3.1E-02	n=10
regulation of cellular biosynthetic proc...	GO:0031326	p=3.1E-02	n=10
regulation of biological process involve...	GO:0043903	p=3.4E-02	n=2
nucleobase-containing compound biosynt...	GO:0034654	p=3.4E-02	n=10
regulation of transcription, DNA-templat...	GO:0006355	p=3.6E-02	n=9
aromatic compound biosynthetic process	GO:0019438	p=3.6E-02	n=10
regulation of nucleic acid-templated tra...	GO:1903506	p=3.8E-02	n=9
regulation of RNA biosynthetic process	GO:2001141	p=3.8E-02	n=9
heterocycle biosynthetic process	GO:0018130	p=3.8E-02	n=10
cellular biosynthetic process	GO:0044249	p=4.0E-02	n=12
organic substance biosynthetic process	GO:1901576	p=4.0E-02	n=12
biosynthetic process	GO:0009058	p=4.2E-02	n=12
muscle structure development	GO:0061061	p=4.4E-02	n=4
actin polymerization or depolymerization	GO:0008154	p=4.4E-02	n=2
actin filament polymerization	GO:0030041	p=4.4E-02	n=2
cGMP metabolic process	GO:0046068	p=4.4E-02	n=2
adherens junction maintenance	GO:0034334	p=4.4E-02	n=1
cell elongation involved in imaginal dis...	GO:0090254	p=4.4E-02	n=1
nucleoside catabolic process	GO:0009164	p=4.4E-02	n=1
purine ribonucleoside monophosphate cata...	GO:0009169	p=4.4E-02	n=1
pharyngeal muscle development	GO:0043282	p=4.4E-02	n=1



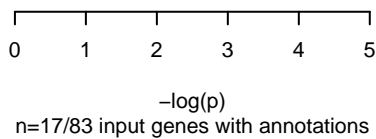
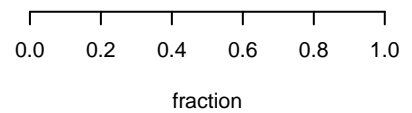
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GO:MF  
Elav\_Nvec\_vc1.1\_XM\_032364225.2

fraction genes in fg and expected value

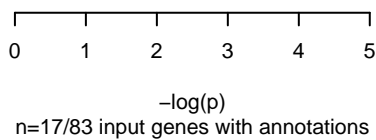
MAP kinase kinase kinase activity	GO:0004709	p=6.0E-03	n=2
GAF domain binding	GO:0036004	p=4.7E-02	n=1
TPR domain binding	GO:0030911	p=4.7E-02	n=1
JUN kinase kinase kinase activity	GO:0004706	p=4.7E-02	n=1
sphingolipid binding	GO:0046625	p=4.7E-02	n=1
chemoattractant activity	GO:0042056	p=4.7E-02	n=1
adipokinetic hormone receptor activity	GO:0097003	p=4.7E-02	n=1
adiponectin binding	GO:0055100	p=4.7E-02	n=1
ubiquitin-protein transferase regulator ...	GO:0055106	p=4.7E-02	n=1
ubiquitin-protein transferase activator ...	GO:0097027	p=4.7E-02	n=1
racemase and epimerase activity	GO:0016854	p=4.7E-02	n=1
racemase and epimerase activity, acting ...	GO:0016857	p=4.7E-02	n=1
beta-catenin binding	GO:0008013	p=4.7E-02	n=1
chondroitin-glucuronate 5-epimerase acti...	GO:0047757	p=4.7E-02	n=1
cGMP-stimulated cyclic-nucleotide phosph...	GO:0004118	p=4.7E-02	n=1
histone binding	GO:0042393	p=6.1E-02	n=2
JUN kinase binding	GO:0008432	p=9.1E-02	n=1
myosin heavy chain binding	GO:0032036	p=9.1E-02	n=1
protein-hormone receptor activity	GO:0016500	p=9.1E-02	n=1
adenylate cyclase activity	GO:0004016	p=9.1E-02	n=1
actin monomer binding	GO:0003785	p=9.1E-02	n=1
signaling receptor regulator activity	GO:0030545	p=9.1E-02	n=1
signaling receptor activator activity	GO:0030546	p=9.1E-02	n=1
microfilament motor activity	GO:0000146	p=9.1E-02	n=1
receptor ligand activity	GO:0048018	p=9.1E-02	n=1
structural constituent of muscle	GO:0008307	p=1.3E-01	n=1
single-stranded RNA binding	GO:0003727	p=1.3E-01	n=1
cAMP binding	GO:0030552	p=1.3E-01	n=1
cGMP binding	GO:0030553	p=1.3E-01	n=1
methylated histone binding	GO:0035064	p=1.3E-01	n=1

[illegible]

**GO:CC**  
**Elav\_Nvec\_vc1.1\_XM\_032364225.2**

fraction genes in fg and expected value

actin cytoskeleton	GO:0015629	p=1.7E-02	n=3
hippocampal mossy fiber	GO:0097457	p=4.2E-02	n=1
heterotrimeric G-protein complex	GO:0005834	p=4.2E-02	n=1
GTPase complex	GO:1905360	p=4.2E-02	n=1
filamentous actin	GO:0031941	p=4.2E-02	n=1
actin filament	GO:0005884	p=4.2E-02	n=1
ISWI-type complex	GO:0031010	p=4.2E-02	n=1
dentate gyrus mossy fiber	GO:0044302	p=4.2E-02	n=1
RSF complex	GO:0031213	p=4.2E-02	n=1
cytoplasmic side of plasma membrane	GO:0009898	p=7.4E-02	n=2
myosin II complex	GO:0016460	p=8.3E-02	n=1
unconventional myosin complex	GO:0016461	p=8.3E-02	n=1
heterochromatin	GO:0000792	p=8.3E-02	n=1
myosin complex	GO:0016459	p=8.3E-02	n=1
SWI/SNF superfamily-type complex	GO:0070603	p=8.3E-02	n=1
intrinsic component of the cytoplasmic s...	GO:0031235	p=8.3E-02	n=1
myosin V complex	GO:0031475	p=8.3E-02	n=1
myosin VI complex	GO:0031476	p=8.3E-02	n=1
myosin VII complex	GO:0031477	p=8.3E-02	n=1
beta-catenin-TCF complex	GO:1990907	p=8.3E-02	n=1
polytene chromosome interband	GO:0005705	p=8.3E-02	n=1
muscle myosin complex	GO:0005859	p=8.3E-02	n=1
ATPase complex	GO:1904949	p=8.3E-02	n=1
intercalary heterochromatin	GO:0005725	p=8.3E-02	n=1
cytoplasmic side of membrane	GO:0098562	p=1.0E-01	n=2
nuclear ubiquitin ligase complex	GO:0000152	p=1.2E-01	n=1
PRC1 complex	GO:0035102	p=1.2E-01	n=1
filopodium	GO:0030175	p=1.2E-01	n=1
rhabdome	GO:0016028	p=1.2E-01	n=1
nuclear protein-containing complex	GO:0140513	p=1.4E-01	n=3



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