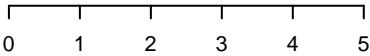


GO:BP
Elav_Nvec_vc1.1_XM_048724387.1

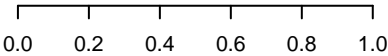
fraction genes in fg and expected value

imaginal disc-derived leg morphogenesis	GO:0007480	p=4.0E-04	n=5
regulation of skeletal muscle tissue dev...	GO:0048641	p=4.1E-04	n=4
negative regulation of double-strand bre...	GO:2000780	p=4.2E-04	n=3
mitotic DNA damage checkpoint signaling	GO:0044773	p=1.1E-03	n=4
regulation of skeletal muscle fiber deve...	GO:0048742	p=1.3E-03	n=2
negative regulation of protein kinase ac...	GO:0044387	p=1.3E-03	n=2
histone H2A K63-linked ubiquitination	GO:0070535	p=1.3E-03	n=2
myoblast proliferation	GO:0051450	p=3.2E-03	n=3
regulation of cellular senescence	GO:2000772	p=3.7E-03	n=2
negative regulation of vulval developmen...	GO:0040027	p=3.7E-03	n=2
SRP-dependent cotranslational protein ta...	GO:0006616	p=3.7E-03	n=2
positive regulation of circadian rhythm	GO:0042753	p=4.4E-03	n=3
positive regulation of canonical Wnt sig...	GO:0090263	p=5.7E-03	n=4
autonomic nervous system development	GO:0048483	p=5.9E-03	n=3
positive regulation of gene expression	GO:0010628	p=6.4E-03	n=20
negative regulation of cell population p...	GO:0008285	p=6.9E-03	n=9
negative regulation of neuron death	GO:1901215	p=7.0E-03	n=6
regulation of skeletal muscle cell diffe...	GO:2001014	p=7.2E-03	n=2
negative regulation of osteoblast differ...	GO:0045668	p=7.2E-03	n=2
3'-UTR-mediated mRNA stabilization	GO:0070935	p=7.2E-03	n=2
regulation of brood size	GO:0060378	p=7.2E-03	n=2
positive regulation of transcription, DN...	GO:0045893	p=7.3E-03	n=15
regulation of striated muscle tissue dev...	GO:0016202	p=8.0E-03	n=4
imaginal disc-derived wing morphogenesis	GO:0007476	p=9.3E-03	n=6
regulation of circadian sleep/wake cycle...	GO:0045187	p=9.7E-03	n=3
response to cocaine	GO:0042220	p=9.7E-03	n=3
spermatid nucleus differentiation	GO:0007289	p=1.2E-02	n=2
DNA damage response, signal transduction...	GO:0006977	p=1.2E-02	n=2
response to epidermal growth factor	GO:0070849	p=1.2E-02	n=2
negative regulation of signaling recepto...	GO:2000272	p=1.2E-02	n=2



-log(p)
n=65/252 input genes with annotations

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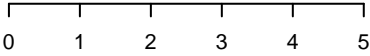


fraction

GO:MF
Elav_Nvec_vc1.1_XM_048724387.1

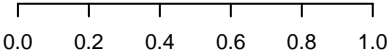
fraction genes in fg and expected value

protein kinase binding	GO:0019901	p=1.0E-03	n=12
DNA-binding transcription factor binding	GO:0140297	p=3.3E-03	n=6
promoter-specific chromatin binding	GO:1990841	p=3.5E-03	n=3
deaminase activity	GO:0019239	p=4.0E-03	n=2
hydrolase activity, acting on carbon-nit...	GO:0016814	p=7.7E-03	n=2
RNA polymerase II-specific DNA-binding t...	GO:0061629	p=1.2E-02	n=5
ephrin receptor binding	GO:0046875	p=1.3E-02	n=2
cis-regulatory region sequence-specific ...	GO:0000987	p=1.7E-02	n=6
RNA polymerase II cis-regulatory region ...	GO:0000978	p=1.7E-02	n=6
galactosyltransferase activity	GO:0008378	p=1.8E-02	n=2
potassium channel inhibitor activity	GO:0019870	p=1.8E-02	n=2
UDP-galactose:beta-N-acetylglucosamine b...	GO:0008499	p=1.8E-02	n=2
UDP-galactosyltransferase activity	GO:0035250	p=1.8E-02	n=2
beta-1,3-galactosyltransferase activity	GO:0048531	p=1.8E-02	n=2
outward rectifier potassium channel acti...	GO:0015271	p=2.5E-02	n=2
phosphotyrosine residue binding	GO:0001784	p=3.3E-02	n=2
metalloendopeptidase activity	GO:0004222	p=3.3E-02	n=2
beta-endorphin binding	GO:0031626	p=3.7E-02	n=1
4-hydroxy-2-oxoglutarate aldolase activi...	GO:0008700	p=3.7E-02	n=1
phosphopantothenate--cysteine ligase act...	GO:0004632	p=3.7E-02	n=1
7S RNA binding	GO:0008312	p=3.7E-02	n=1
adenosine-phosphate deaminase activity	GO:0047623	p=3.7E-02	n=1
adenosine deaminase activity	GO:0004000	p=3.7E-02	n=1
1-alkylglycerophosphocholine O-acyltrans...	GO:0047191	p=3.7E-02	n=1
aldehyde-lyase activity	GO:0016832	p=3.7E-02	n=1
cannabinoid receptor binding	GO:0031717	p=3.7E-02	n=1
type 1 cannabinoid receptor binding	GO:0031718	p=3.7E-02	n=1
5'-3' DNA helicase activity	GO:0043139	p=3.7E-02	n=1
signal recognition particle binding	GO:0005047	p=3.7E-02	n=1
platelet-derived growth factor receptor ...	GO:0005161	p=3.7E-02	n=1



-log(p)
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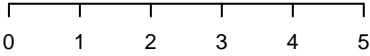


fraction

GO:CC
Elav_Nvec_vc1.1_XM_048724387.1

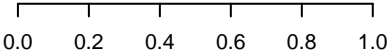
fraction genes in fg and expected value

site of double-strand break	GO:0035861	p=2.3E-03	n=3
secondary lysosome	GO:0005767	p=2.5E-02	n=2
Rb-E2F complex	GO:0035189	p=3.6E-02	n=1
signal recognition particle	GO:0048500	p=3.6E-02	n=1
RNA polymerase II transcription represso...	GO:0090571	p=3.6E-02	n=1
signal recognition particle, endoplasmic...	GO:0005786	p=3.6E-02	n=1
voltage-gated potassium channel complex	GO:0008076	p=4.0E-02	n=2
potassium channel complex	GO:0034705	p=4.0E-02	n=2
autophagosome	GO:0005776	p=4.9E-02	n=3
transcription regulator complex	GO:0005667	p=5.8E-02	n=6
nuclear stress granule	GO:0097165	p=7.2E-02	n=1
activating signal cointegrator 1 complex	GO:0099053	p=7.2E-02	n=1
mRNA cleavage and polyadenylation specif...	GO:0005847	p=7.2E-02	n=1
mRNA cleavage factor complex	GO:0005849	p=7.2E-02	n=1
cytosolic ribosome	GO:0022626	p=9.0E-02	n=2
inaD signaling complex	GO:0016027	p=1.1E-01	n=1
subrhabdomeral cisterna	GO:0016029	p=1.1E-01	n=1
EARP complex	GO:1990745	p=1.1E-01	n=1
GARP complex	GO:0000938	p=1.1E-01	n=1
phagophore assembly site	GO:0000407	p=1.1E-01	n=1
photoreceptor disc membrane	GO:0097381	p=1.1E-01	n=1
endoplasmic reticulum cisternal network	GO:0071781	p=1.1E-01	n=1
skeletal muscle myofibril	GO:0098723	p=1.1E-01	n=1
CD40 receptor complex	GO:0035631	p=1.1E-01	n=1
Hrd1p ubiquitin ligase ERAD-L complex	GO:0000839	p=1.1E-01	n=1
smooth endoplasmic reticulum cisterna	GO:0120082	p=1.1E-01	n=1
RNA polymerase II transcription regulato...	GO:0090575	p=1.2E-01	n=3
nuclear body	GO:0016604	p=1.2E-01	n=7
microbody lumen	GO:0031907	p=1.4E-01	n=1
chromatoid body	GO:0033391	p=1.4E-01	n=1



-log(p)
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fraction