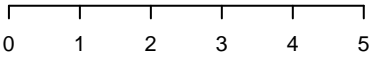


GO:BP
Elav_Nvec_vc1.1_XM_032376736.2

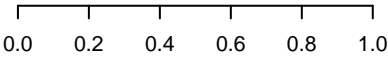
fraction genes in fg and expected value

negative regulation of hippo signaling	GO:0035331	p=1.7E-03	n=3
protein phosphorylation	GO:0006468	p=3.0E-03	n=18
cardiac ventricle formation	GO:0003211	p=4.2E-03	n=2
cardiac myofibril assembly	GO:0055003	p=4.2E-03	n=2
sperm DNA decondensation	GO:0035041	p=4.2E-03	n=2
positive regulation of transcription by ...	GO:0045944	p=5.3E-03	n=14
regulation of respiratory gaseous exchan...	GO:0043576	p=8.1E-03	n=2
G1/S transition of mitotic cell cycle	GO:0000082	p=1.0E-02	n=5
protein autophosphorylation	GO:0046777	p=1.0E-02	n=5
regulation of vascular associated smooth...	GO:1904705	p=1.3E-02	n=2
suckling behavior	GO:0001967	p=1.3E-02	n=2
maturation of SSU-rRNA	GO:0030490	p=1.3E-02	n=2
DNA damage response, signal transduction...	GO:0006977	p=1.3E-02	n=2
regulation of adenylate cyclase activity	GO:0045761	p=1.3E-02	n=2
fucosylation	GO:0036065	p=1.3E-02	n=2
mitotic cell cycle phase transition	GO:0044772	p=1.3E-02	n=8
mitotic DNA damage checkpoint signaling	GO:0044773	p=1.4E-02	n=3
Notch signaling pathway	GO:0007219	p=1.5E-02	n=6
negative regulation of protein-containin...	GO:0031333	p=1.7E-02	n=3
mitotic DNA integrity checkpoint signali...	GO:0044774	p=1.7E-02	n=3
regulation of Notch signaling pathway	GO:0008593	p=1.8E-02	n=5
cell cycle G1/S phase transition	GO:0044843	p=1.8E-02	n=5
vascular associated smooth muscle cell p...	GO:1990874	p=1.9E-02	n=2
histone H3-K9 methylation	GO:0051567	p=1.9E-02	n=2
branched-chain amino acid metabolic proc...	GO:0009081	p=1.9E-02	n=2
branched-chain amino acid catabolic proc...	GO:0009083	p=1.9E-02	n=2
negative regulation of calcium ion-depen...	GO:0045955	p=1.9E-02	n=2
mitotic G1/S transition checkpoint signa...	GO:0044819	p=1.9E-02	n=2
regulation of inclusion body assembly	GO:0090083	p=1.9E-02	n=2
sarcomere organization	GO:0045214	p=1.9E-02	n=2



-log(p)
n=69/177 input genes with annotations

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fg=0.03	bg=0.00
fg=0.07	bg=0.02
fg=0.07	bg=0.02
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fg=0.03	bg=0.00
fg=0.03	bg=0.00
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fg=0.03	bg=0.00
fg=0.12	bg=0.05
fg=0.04	bg=0.01
fg=0.09	bg=0.03
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fg=0.07	bg=0.02
fg=0.03	bg=0.00
fg=0.03	bg=0.00
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fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00

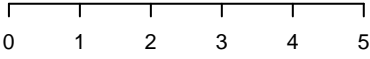


fraction

GO:MF
Elav_Nvec_vc1.1_XM_032376736.2

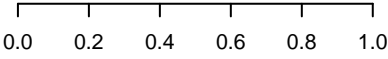
fraction genes in fg and expected value

protein serine/threonine kinase activity	GO:0004674	p=5.8E-04	n=9
RNA polymerase II cis-regulatory region ...	GO:0000978	p=1.1E-03	n=8
DNA-binding transcription activator acti...	GO:0001228	p=7.3E-03	n=7
purine ribonucleoside triphosphate bindi...	GO:0035639	p=7.4E-03	n=9
ATP binding	GO:0005524	p=1.3E-02	n=7
ribonucleotide binding	GO:0032553	p=1.8E-02	n=9
purine ribonucleotide binding	GO:0032555	p=1.8E-02	n=9
carbohydrate derivative binding	GO:0097367	p=2.0E-02	n=10
purine nucleotide binding	GO:0017076	p=2.1E-02	n=9
polynucleotide adenyllyltransferase activ...	GO:0004652	p=2.7E-02	n=2
adenyl ribonucleotide binding	GO:0032559	p=3.2E-02	n=7
adenyl nucleotide binding	GO:0030554	p=3.6E-02	n=7
ribokinase activity	GO:0004747	p=3.8E-02	n=1
adenylate cyclase activator activity	GO:0010856	p=3.8E-02	n=1
[3-methyl-2-oxobutanoate dehydrogenase (...	GO:0047323	p=3.8E-02	n=1
SMC family protein binding	GO:0043221	p=3.8E-02	n=1
uridylyltransferase activity	GO:0070569	p=3.8E-02	n=1
RNA uridylyltransferase activity	GO:0050265	p=3.8E-02	n=1
intracellular sodium activated potassium...	GO:0005228	p=3.8E-02	n=1
endopeptidase activator activity	GO:0061133	p=3.8E-02	n=1
G-protein beta-subunit binding	GO:0031681	p=3.8E-02	n=1
acid-sensing ion channel activity	GO:0044736	p=3.8E-02	n=1
glycolipid transfer activity	GO:0017089	p=3.8E-02	n=1
short-branched-chain-acyl-CoA dehydrogen...	GO:0016937	p=3.8E-02	n=1
MDM2/MDM4 family protein binding	GO:0097371	p=3.8E-02	n=1
nucleotide binding	GO:0000166	p=3.9E-02	n=9
adenylyltransferase activity	GO:0070566	p=4.4E-02	n=2
GDP binding	GO:0019003	p=5.3E-02	n=2
ubiquitin conjugating enzyme activity	GO:0061631	p=6.4E-02	n=2
DNA helicase activity	GO:0003678	p=6.4E-02	n=2



-log(p)
n=61/177 input genes with annotations

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fg=0.15	bg=0.07
fg=0.03	bg=0.00
fg=0.11	bg=0.05
fg=0.11	bg=0.05
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
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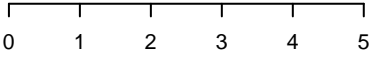


fraction

GO:CC
Elav_Nvec_vc1.1_XM_032376736.2

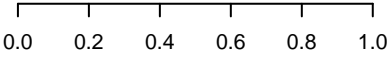
fraction genes in fg and expected value

preribosome, small subunit precursor	GO:0030688	p=1.4E-03	n=2
FAR/SIN/STRIPAK complex	GO:0090443	p=4.1E-03	n=2
nucleus	GO:0005634	p=6.0E-03	n=45
nuclear speck	GO:0016607	p=6.7E-03	n=7
transcription regulator complex	GO:0005667	p=2.3E-02	n=7
cell cortex region	GO:0099738	p=2.8E-02	n=3
desmosome	GO:0030057	p=3.8E-02	n=1
CHRAc	GO:0008623	p=3.8E-02	n=1
ciliary transition fiber	GO:0097539	p=3.8E-02	n=1
ACF complex	GO:0016590	p=3.8E-02	n=1
bleb	GO:0032059	p=3.8E-02	n=1
keratin filament	GO:0045095	p=3.8E-02	n=1
dihydrolipoyl dehydrogenase complex	GO:0045240	p=3.8E-02	n=1
mitochondrial alpha-ketoglutarate dehydr...	GO:0005947	p=3.8E-02	n=1
proteasome complex	GO:0000502	p=6.1E-02	n=2
apical cortex	GO:0045179	p=7.2E-02	n=2
mitochondrial tricarboxylic acid cycle e...	GO:0030062	p=7.4E-02	n=1
tricarboxylic acid cycle enzyme complex	GO:0045239	p=7.4E-02	n=1
cell body fiber	GO:0070852	p=7.4E-02	n=1
NURF complex	GO:0016589	p=7.4E-02	n=1
striated muscle thin filament	GO:0005865	p=7.4E-02	n=1
RSF complex	GO:0031213	p=7.4E-02	n=1
myofilament	GO:0036379	p=7.4E-02	n=1
vacuolar proton-transporting V-type ATPa...	GO:0000220	p=7.4E-02	n=1
proton-transporting two-sector ATPase co...	GO:0033177	p=7.4E-02	n=1
proton-transporting V-type ATPase, V0 do...	GO:0033179	p=7.4E-02	n=1
AP-2 adaptor complex	GO:0030122	p=7.4E-02	n=1
TRAMP complex	GO:0031499	p=7.4E-02	n=1
clathrin coat of endocytic vesicle	GO:0030128	p=7.4E-02	n=1
nuclear lumen	GO:0031981	p=8.9E-02	n=30



-log(p)
n=68/177 input genes with annotations

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fg=0.01	bg=0.00
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fg=0.01	bg=0.00
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fraction