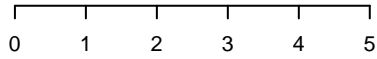


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_001633894.3

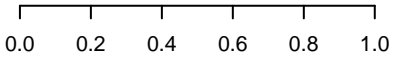
fraction genes in fg and expected value

cell fate commitment	GO:0045165	p=1.4E-03	n=15
negative regulation of cellular process	GO:0048523	p=1.8E-03	n=66
positive regulation of mitotic centrosom...	GO:0046604	p=2.4E-03	n=2
adenylate cyclase-activating G protein-c...	GO:0007189	p=3.8E-03	n=4
regulation of isotype switching	GO:0045191	p=5.5E-03	n=3
negative regulation of cAMP-mediated sig...	GO:0043951	p=5.5E-03	n=3
mitochondrion morphogenesis	GO:0070584	p=5.5E-03	n=3
response to nitrogen compound	GO:1901698	p=6.4E-03	n=23
glial cell migration	GO:0008347	p=6.4E-03	n=4
cellular response to organic substance	GO:0071310	p=6.9E-03	n=35
trans-synaptic signaling, modulating syn...	GO:0099550	p=7.0E-03	n=2
negative regulation of adenylate cyclase...	GO:0007194	p=7.0E-03	n=2
protein kinase C-activating G protein-co...	GO:0007205	p=7.0E-03	n=2
histone arginine methylation	GO:0034969	p=7.0E-03	n=2
tissue homeostasis	GO:0001894	p=7.4E-03	n=8
regulation of centrosome cycle	GO:0046605	p=7.7E-03	n=5
cell surface receptor signaling pathway	GO:0007166	p=7.9E-03	n=35
adherens junction assembly	GO:0034333	p=7.9E-03	n=3
branching involved in open tracheal syst...	GO:0060446	p=7.9E-03	n=3
neuronal stem cell division	GO:0036445	p=8.1E-03	n=4
neuroblast division	GO:0055057	p=8.1E-03	n=4
cell adhesion	GO:0007155	p=8.8E-03	n=14
ribonucleoside metabolic process	GO:0009119	p=1.1E-02	n=5
positive regulation of protein modificat...	GO:0031401	p=1.1E-02	n=19
regulation of G protein-coupled receptor...	GO:0008277	p=1.2E-02	n=5
negative regulation of adenylate cyclase...	GO:0071878	p=1.3E-02	n=2
adenylate cyclase-activating adrenergic ...	GO:0086023	p=1.3E-02	n=2
queuosine biosynthetic process	GO:0008616	p=1.3E-02	n=2
mRNA transcription by RNA polymerase II	GO:0042789	p=1.3E-02	n=2
N-terminal protein amino acid acetylatio...	GO:0006474	p=1.3E-02	n=2



-log(p)  
n=133/432 input genes with annotations

fg=0.11	bg=0.05
fg=0.50	bg=0.36
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fg=0.17	bg=0.10
fg=0.03	bg=0.01
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fg=0.14	bg=0.08
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fg=0.02	bg=0.00

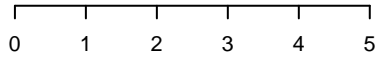


fraction

GO:MF  
Elav\_Nvec\_vc1.1\_XM\_001633894.3

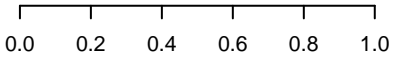
fraction genes in fg and expected value

BH domain binding	GO:0051400	p=2.1E-03	n=3
vinculin binding	GO:0017166	p=7.0E-03	n=2
proteasome binding	GO:0070628	p=7.9E-03	n=3
voltage-gated channel activity	GO:0022832	p=1.2E-02	n=5
voltage-gated ion channel activity	GO:0005244	p=1.2E-02	n=5
voltage-gated cation channel activity	GO:0022843	p=2.1E-02	n=4
potassium ion transmembrane transporter ...	GO:0015079	p=2.4E-02	n=4
cytokine receptor binding	GO:0005126	p=2.4E-02	n=4
calcium channel regulator activity	GO:0005246	p=2.9E-02	n=3
protein heterodimerization activity	GO:0046982	p=3.3E-02	n=12
SMAD binding	GO:0046332	p=4.1E-02	n=3
protein kinase activator activity	GO:0030295	p=4.1E-02	n=3
AMP binding	GO:0016208	p=4.3E-02	n=2
cation channel activity	GO:0005261	p=4.8E-02	n=7
kinase activator activity	GO:0019209	p=4.8E-02	n=3
vascular endothelial growth factor recep...	GO:0043184	p=4.9E-02	n=1
GBD domain binding	GO:0032427	p=4.9E-02	n=1
URM1 activating enzyme activity	GO:0042292	p=4.9E-02	n=1
juvenile hormone epoxide hydrolase activ...	GO:0008096	p=4.9E-02	n=1
beta-galactosidase activity	GO:0004565	p=4.9E-02	n=1
fructose binding	GO:0070061	p=4.9E-02	n=1
misfolded RNA binding	GO:0034336	p=4.9E-02	n=1
[cytochrome c]-arginine N-methyltransfer...	GO:0016275	p=4.9E-02	n=1
pyrroline-5-carboxylate reductase activi...	GO:0004735	p=4.9E-02	n=1
Roundabout binding	GO:0048495	p=4.9E-02	n=1
netrin receptor activity	GO:0005042	p=4.9E-02	n=1
6-phosphofructokinase activity	GO:0003872	p=4.9E-02	n=1
calcitonin family receptor activity	GO:0097642	p=4.9E-02	n=1
intracellular sodium activated potassium...	GO:0005228	p=4.9E-02	n=1
alkylglycerophosphoethanolamine phosphod...	GO:0047391	p=4.9E-02	n=1



-log(p)  
n=117/432 input genes with annotations

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fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.10	bg=0.06
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.06	bg=0.03
fg=0.03	bg=0.01
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
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fg=0.01	bg=0.00
fg=0.01	bg=0.00

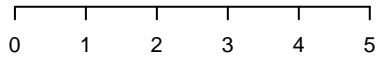


fraction

GO:CC  
Elav\_Nvec\_vc1.1\_XM\_001633894.3

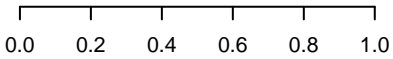
fraction genes in fg and expected value

cytoplasmic side of plasma membrane	GO:0009898	p=5.6E-03	n=8
membrane coat	GO:0030117	p=2.0E-02	n=4
coated membrane	GO:0048475	p=2.0E-02	n=4
midbody	GO:0030496	p=2.3E-02	n=6
intrinsic component of the cytoplasmic s...	GO:0031235	p=2.4E-02	n=2
postsynaptic density membrane	GO:0098839	p=2.4E-02	n=2
postsynaptic specialization membrane	GO:0099634	p=2.4E-02	n=2
extrinsic component of organelle membran...	GO:0031312	p=2.6E-02	n=3
nuclear outer membrane-endoplasmic retic...	GO:0042175	p=2.6E-02	n=17
adherens junction	GO:0005912	p=2.7E-02	n=7
presynaptic active zone	GO:0048786	p=2.8E-02	n=4
focal adhesion	GO:0005925	p=2.8E-02	n=4
lipid droplet	GO:0005811	p=3.2E-02	n=4
ESCRT III complex	GO:0000815	p=3.4E-02	n=2
heterotrimeric G-protein complex	GO:0005834	p=3.4E-02	n=2
GTPase complex	GO:1905360	p=3.4E-02	n=2
dendrite	GO:0030425	p=4.0E-02	n=14
dendritic tree	GO:0097447	p=4.1E-02	n=14
plasma membrane protein complex	GO:0098797	p=4.2E-02	n=8
endoplasmic reticulum membrane	GO:0005789	p=4.3E-02	n=16
somatodendritic compartment	GO:0036477	p=4.6E-02	n=18
presynaptic active zone membrane	GO:0048787	p=4.7E-02	n=2
cell-substrate junction	GO:0030055	p=4.7E-02	n=4
plasma membrane	GO:0005886	p=4.8E-02	n=45
cell cortex	GO:0005938	p=5.0E-02	n=9
EKC/KEOPS complex	GO:0000408	p=5.1E-02	n=1
ER membrane insertion complex	GO:0072379	p=5.1E-02	n=1
apical cytoplasm	GO:0090651	p=5.1E-02	n=1
BAT3 complex	GO:0071818	p=5.1E-02	n=1
anchored component of the cytoplasmic si...	GO:0098753	p=5.1E-02	n=1



-log(p)  
n=139/432 input genes with annotations

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fg=0.01	bg=0.00
fg=0.02	bg=0.00
fg=0.12	bg=0.07
fg=0.05	bg=0.02
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fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.10	bg=0.06
fg=0.10	bg=0.06
fg=0.06	bg=0.03
fg=0.12	bg=0.07
fg=0.13	bg=0.09
fg=0.01	bg=0.00
fg=0.03	bg=0.01
fg=0.32	bg=0.23
fg=0.06	bg=0.03
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00



fraction