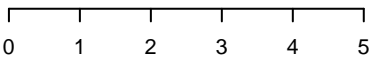


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_001628087.3

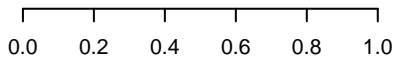
fraction genes in fg and expected value

neuroepithelial cell differentiation	GO:0060563	p=3.2E-03	n=3
positive regulation of Wnt signaling pat...	GO:0030177	p=3.2E-03	n=3
actin cortical patch localization	GO:0051666	p=3.3E-03	n=2
lysine transport	GO:0015819	p=3.3E-03	n=2
regulation of Rac protein signal transdu...	GO:0035020	p=3.3E-03	n=2
protein O-linked glycosylation	GO:0006493	p=3.3E-03	n=2
limb bud formation	GO:0060174	p=3.3E-03	n=2
auditory receptor cell development	GO:0060117	p=3.3E-03	n=2
protein maturation	GO:0051604	p=8.3E-03	n=3
late endosome to vacuole transport	GO:0045324	p=9.6E-03	n=2
ventricular septum morphogenesis	GO:0060412	p=9.6E-03	n=2
histone H3-K4 methylation	GO:0051568	p=9.6E-03	n=2
regulation of protein ubiquitination	GO:0031396	p=1.2E-02	n=3
regulation of protein stability	GO:0031647	p=1.6E-02	n=3
negative regulation of protein ubiquitin...	GO:0031397	p=1.8E-02	n=2
protein heterooligomerization	GO:0051291	p=1.8E-02	n=2
transcription elongation from RNA polym...	GO:0006368	p=1.8E-02	n=2
regulation of transcription elongation f...	GO:0034243	p=1.8E-02	n=2
pancreas development	GO:0031016	p=1.8E-02	n=2
regulation of transcription by RNA polym...	GO:0006357	p=2.1E-02	n=10
biomineral tissue development	GO:0031214	p=2.2E-02	n=3
biomineralization	GO:0110148	p=2.2E-02	n=3
regulation of protein modification by sm...	GO:1903320	p=2.2E-02	n=3
positive regulation of cellular componen...	GO:0051130	p=2.2E-02	n=7
positive regulation of transcription by ...	GO:0045944	p=2.2E-02	n=7
transcription by RNA polymerase II	GO:0006366	p=2.5E-02	n=10
positive regulation of transcription, DN...	GO:0045893	p=2.6E-02	n=8
regulation of RNA metabolic process	GO:0051252	p=2.7E-02	n=12
positive regulation of apoptotic process	GO:0043065	p=2.7E-02	n=5
positive regulation of programmed cell d...	GO:0043068	p=2.7E-02	n=5



-log(p)  
n=24/90 input genes with annotations

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fg=0.12	bg=0.02
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fg=0.08	bg=0.01
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fg=0.08	bg=0.01
fg=0.42	bg=0.22
fg=0.12	bg=0.03
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fg=0.29	bg=0.13
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fg=0.42	bg=0.23
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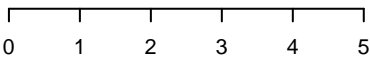


fraction

GO:MF  
Elav\_Nvec\_vc1.1\_XM\_001628087.3

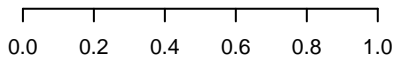
fraction genes in fg and expected value

glutamate receptor binding	GO:0035254	p=3.8E-02	n=2
protein C-terminus binding	GO:0008022	p=3.8E-02	n=2
heterocyclic compound binding	GO:1901363	p=4.8E-02	n=9
guanyl-nucleotide exchange factor activi...	GO:0005085	p=5.1E-02	n=2
sialyltransferase activity	GO:0008373	p=5.5E-02	n=1
acetylglucosaminyltransferase activity	GO:0008375	p=5.5E-02	n=1
phosphatidylinositol 3-kinase activity	GO:0035004	p=5.5E-02	n=1
proline-rich region binding	GO:0070064	p=5.5E-02	n=1
nitric-oxide synthase inhibitor activity	GO:0036487	p=5.5E-02	n=1
(alpha-N-acetylneuraminy-2,3-beta-galac...	GO:0047290	p=5.5E-02	n=1
alpha-N-acetylgalactosaminide alpha-2,6-...	GO:0001665	p=5.5E-02	n=1
phosphatidylinositol bisphosphate kinase...	GO:0052813	p=5.5E-02	n=1
nitric-oxide synthase binding	GO:0050998	p=5.5E-02	n=1
phosphatidylinositol-4,5-bisphosphate 3-...	GO:0046934	p=5.5E-02	n=1
monosaccharide binding	GO:0048029	p=5.5E-02	n=1
protein N-acetylglucosaminyltransferase ...	GO:0016262	p=5.5E-02	n=1
nitric-oxide synthase regulator activity	GO:0030235	p=5.5E-02	n=1
calcium-dependent ATPase activity	GO:0030899	p=5.5E-02	n=1
tau protein binding	GO:0048156	p=5.5E-02	n=1
1-phosphatidylinositol-3-kinase activity	GO:0016303	p=5.5E-02	n=1
GDP-dissociation inhibitor activity	GO:0005092	p=5.5E-02	n=1
phosphatidylinositol kinase activity	GO:0052742	p=5.5E-02	n=1
protein O-GlcNAc transferase activity	GO:0097363	p=5.5E-02	n=1
carbohydrate derivative binding	GO:0097367	p=5.7E-02	n=4
purine ribonucleoside triphosphate bindi...	GO:0035639	p=5.9E-02	n=3
organic cyclic compound binding	GO:0097159	p=6.1E-02	n=9
glycosyltransferase activity	GO:0016757	p=6.6E-02	n=2
histone binding	GO:0042393	p=8.2E-02	n=2
transcription cis-regulatory region bind...	GO:0000976	p=8.7E-02	n=4
binding	GO:0005488	p=9.4E-02	n=18



-log(p)  
n=20/90 input genes with annotations

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fg=0.05	bg=0.00
fg=0.05	bg=0.00
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fg=0.20	bg=0.08
fg=0.15	bg=0.05
fg=0.45	bg=0.27
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fg=0.10	bg=0.02
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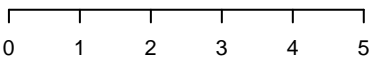


fraction

GO:CC  
Elav\_Nvec\_vc1.1\_XM\_001628087.3

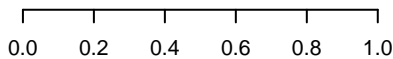
fraction genes in fg and expected value

cell division site	GO:0032153	p=1.5E-03	n=3
cytoplasmic side of plasma membrane	GO:0009898	p=2.1E-03	n=4
cell tip	GO:0051286	p=3.1E-03	n=2
transcription elongation factor complex	GO:0008023	p=3.1E-03	n=2
filopodium	GO:0030175	p=9.1E-03	n=2
fungal-type vacuole membrane	GO:0000329	p=9.1E-03	n=2
nuclear body	GO:0016604	p=4.7E-02	n=3
cell body	GO:0044297	p=4.8E-02	n=6
sperm flagellum	GO:0036126	p=5.5E-02	n=2
9+2 motile cilium	GO:0097729	p=5.5E-02	n=2
axoneme	GO:0005930	p=5.7E-02	n=1
zymogen granule	GO:0042588	p=5.7E-02	n=1
growth cone lamellipodium	GO:1990761	p=5.7E-02	n=1
postsynaptic specialization membrane	GO:0099634	p=5.7E-02	n=1
GTPase complex	GO:1905360	p=5.7E-02	n=1
sperm principal piece	GO:0097228	p=5.7E-02	n=1
NELF complex	GO:0032021	p=5.7E-02	n=1
dendritic spine membrane	GO:0032591	p=5.7E-02	n=1
excitatory synapse	GO:0060076	p=5.7E-02	n=1
septin filament array	GO:0032160	p=5.7E-02	n=1
heterotrimeric G-protein complex	GO:0005834	p=5.7E-02	n=1
ciliary plasm	GO:0097014	p=5.7E-02	n=1
postsynaptic density membrane	GO:0098839	p=5.7E-02	n=1
contractile ring	GO:0070938	p=5.7E-02	n=1
growth cone filopodium	GO:1990812	p=5.7E-02	n=1
apical dendrite	GO:0097440	p=5.7E-02	n=1
motile cilium	GO:0031514	p=7.1E-02	n=2
intracellular membrane-bounded organelle	GO:0043231	p=8.2E-02	n=21
membrane-bounded organelle	GO:0043227	p=9.4E-02	n=21
chromatin	GO:0000785	p=9.8E-02	n=3



-log(p)  
n=23/90 input genes with annotations

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fg=0.09	bg=0.01
fg=0.13	bg=0.04
fg=0.26	bg=0.12
fg=0.09	bg=0.02
fg=0.09	bg=0.02
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
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fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.09	bg=0.02
fg=0.91	bg=0.74
fg=0.91	bg=0.75
fg=0.13	bg=0.05



fraction