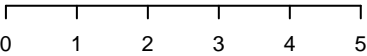


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_032366609.2

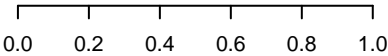
fraction genes in fg and expected value

negative regulation of lymphocyte mediat...	GO:0002707	p=9.4E-04	n=2
cellular iron ion homeostasis	GO:0006879	p=2.8E-03	n=2
regulation of peptide transport	GO:0090087	p=4.5E-03	n=5
regulation of Notch signaling pathway	GO:0008593	p=4.7E-03	n=3
regulation of collagen biosynthetic proc...	GO:0032965	p=5.4E-03	n=2
negative regulation of G1/S transition o...	GO:2000134	p=5.4E-03	n=2
mitotic DNA damage checkpoint signaling	GO:0044773	p=5.4E-03	n=2
cellular response to cAMP	GO:0071320	p=5.4E-03	n=2
negative regulation of transporter activ...	GO:0032410	p=5.4E-03	n=2
macromolecule localization	GO:0033036	p=6.4E-03	n=8
centrosome duplication	GO:0051298	p=8.9E-03	n=2
actin cytoskeleton organization	GO:0030036	p=9.5E-03	n=4
actin filament organization	GO:0007015	p=1.1E-02	n=3
multicellular organism development	GO:0007275	p=1.2E-02	n=11
intracellular mRNA localization	GO:0008298	p=1.3E-02	n=2
regulation of insulin secretion involved...	GO:0061178	p=1.3E-02	n=2
negative regulation of DNA-binding trans...	GO:0043433	p=1.3E-02	n=2
negative regulation of immune response	GO:0050777	p=1.3E-02	n=2
positive regulation of protein ubiquitin...	GO:0031398	p=1.3E-02	n=2
male mating behavior	GO:0060179	p=1.3E-02	n=2
regulation of hormone levels	GO:0010817	p=1.5E-02	n=4
regulation of cellular component size	GO:0032535	p=1.6E-02	n=3
multicellular organismal process	GO:0032501	p=1.7E-02	n=12
positive regulation of protein modificat...	GO:1903322	p=1.8E-02	n=2
regulation of actin polymerization or de...	GO:0008064	p=1.8E-02	n=2
establishment of tissue polarity	GO:0007164	p=1.8E-02	n=2
establishment of planar polarity	GO:0001736	p=1.8E-02	n=2
morphogenesis of a polarized epithelium	GO:0001738	p=1.8E-02	n=2
regulation of actin filament length	GO:0030832	p=1.8E-02	n=2
regulation of actin filament polymerizat...	GO:0030833	p=1.8E-02	n=2



-log(p)  
n=13/52 input genes with annotations

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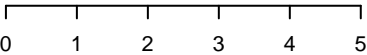


fraction

GO:MF  
Elav\_Nvec\_vc1.1\_XM\_032366609.2

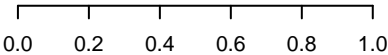
fraction genes in fg and expected value

tubulin binding	GO:0015631	p=6.5E-03	n=3
transmembrane transporter binding	GO:0044325	p=9.4E-03	n=2
phosphatidylinositol binding	GO:0035091	p=1.2E-02	n=3
ATPase-coupled ion transmembrane transpo...	GO:0042625	p=1.4E-02	n=2
ATPase binding	GO:0051117	p=1.4E-02	n=2
ATPase-coupled cation transmembrane tran...	GO:0019829	p=1.4E-02	n=2
primary active transmembrane transporter...	GO:0015399	p=1.9E-02	n=2
ATPase-coupled transmembrane transporter...	GO:0042626	p=1.9E-02	n=2
phosphoprotein binding	GO:0051219	p=2.5E-02	n=2
protein domain specific binding	GO:0019904	p=2.7E-02	n=4
G protein-coupled serotonin receptor bin...	GO:0031821	p=3.3E-02	n=1
alpha-1A adrenergic receptor binding	GO:0031691	p=3.3E-02	n=1
type 2A serotonin receptor binding	GO:0031826	p=3.3E-02	n=1
phosphatidic acid binding	GO:0070300	p=3.3E-02	n=1
clathrin heavy chain binding	GO:0032050	p=3.3E-02	n=1
arrestin family protein binding	GO:1990763	p=3.3E-02	n=1
opsin binding	GO:0002046	p=3.3E-02	n=1
phosphatidic acid transfer activity	GO:1990050	p=3.3E-02	n=1
angiotensin receptor binding	GO:0031701	p=3.3E-02	n=1
type 1 angiotensin receptor binding	GO:0031702	p=3.3E-02	n=1
insulin-like growth factor receptor bind...	GO:0005159	p=3.3E-02	n=1
ecdysis-triggering hormone receptor acti...	GO:0042654	p=3.3E-02	n=1
phosphatidylcholine transporter activity	GO:0008525	p=3.3E-02	n=1
phosphatidylinositol transfer activity	GO:0008526	p=3.3E-02	n=1
WW domain binding	GO:0050699	p=3.3E-02	n=1
follicle-stimulating hormone receptor bi...	GO:0031762	p=3.3E-02	n=1
V2 vasopressin receptor binding	GO:0031896	p=3.3E-02	n=1
HLH domain binding	GO:0043398	p=3.3E-02	n=1
inositol hexakisphosphate binding	GO:0000822	p=3.3E-02	n=1
muscle alpha-actinin binding	GO:0051371	p=3.3E-02	n=1



-log(p)  
n=12/52 input genes with annotations

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fraction

GO:CC  
Elav\_Nvec\_vc1.1\_XM\_032366609.2

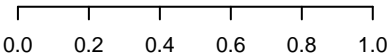
fraction genes in fg and expected value

cell cortex	GO:0005938	p=1.1E-02	n=3
non-motile cilium	GO:0097730	p=1.1E-02	n=2
lysosomal membrane	GO:0005765	p=1.1E-02	n=2
cytoplasmic region	GO:0099568	p=1.3E-02	n=3
microtubule organizing center	GO:0005815	p=1.3E-02	n=3
bounding membrane of organelle	GO:0098588	p=2.5E-02	n=5
cilium	GO:0005929	p=2.6E-02	n=3
lytic vacuole membrane	GO:0098852	p=2.6E-02	n=2
proton-transporting V-type ATPase, V1 do...	GO:0033180	p=3.0E-02	n=1
pseudopodium	GO:0031143	p=3.0E-02	n=1
clathrin-coated pit	GO:0005905	p=3.0E-02	n=1
vacuolar proton-transporting V-type ATPa...	GO:0000221	p=3.0E-02	n=1
proton-transporting two-sector ATPase co...	GO:0033178	p=3.0E-02	n=1
coated membrane	GO:0048475	p=3.0E-02	n=1
intrinsic component of Golgi membrane	GO:0031228	p=3.0E-02	n=1
mitochondrial crista	GO:0030061	p=3.0E-02	n=1
integral component of Golgi membrane	GO:0030173	p=3.0E-02	n=1
membrane coat	GO:0030117	p=3.0E-02	n=1
clathrin coat	GO:0030118	p=3.0E-02	n=1
polycystin complex	GO:0002133	p=3.0E-02	n=1
clathrin coat of coated pit	GO:0030132	p=3.0E-02	n=1
organelle membrane	GO:0031090	p=3.4E-02	n=6
vacuolar membrane	GO:0005774	p=3.9E-02	n=2
membrane protein complex	GO:0098796	p=4.8E-02	n=3
microtubule cytoskeleton	GO:0015630	p=4.8E-02	n=3
plasma membrane proton-transporting V-ty...	GO:0033181	p=5.9E-02	n=1
luminal side of membrane	GO:0098576	p=5.9E-02	n=1
proton-transporting V-type ATPase comple...	GO:0033176	p=5.9E-02	n=1
endoplasmic reticulum cisternal network	GO:0071781	p=5.9E-02	n=1
photoreceptor inner segment	GO:0001917	p=5.9E-02	n=1



-log(p)  
n=12/52 input genes with annotations

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fg=0.08	bg=0.01
fg=0.08	bg=0.01



fraction