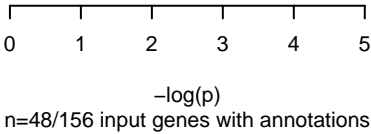
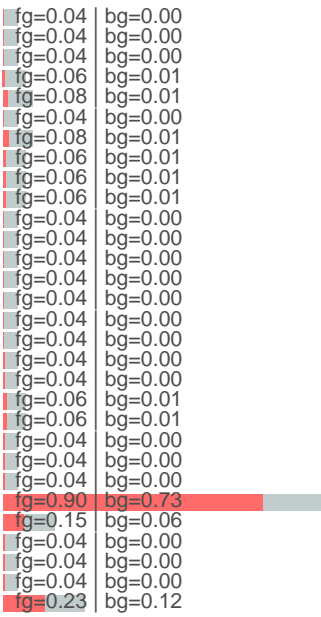


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_048731950.1

neurohypophysis development	GO:0021985	p=2.0E−03	n=2
miRNA catabolic process	GO:0010587	p=2.0E−03	n=2
IMP biosynthetic process	GO:0006188	p=2.0E−03	n=2
cell proliferation in forebrain	GO:0021846	p=2.5E−03	n=3
visual perception	GO:0007601	p=3.1E−03	n=4
glomerular visceral epithelial cell deve...	GO:0072015	p=4.0E−03	n=2
detection of light stimulus	GO:0009583	p=4.8E−03	n=4
phospholipid transport	GO:0015914	p=5.2E−03	n=3
carbohydrate derivative transport	GO:1901264	p=5.2E−03	n=3
epithelial cell apoptotic process	GO:1904019	p=5.2E−03	n=3
regulation of imaginal disc growth	GO:0045570	p=6.5E−03	n=2
isoprenoid metabolic process	GO:0006720	p=6.5E−03	n=2
hypothalamus cell differentiation	GO:0021979	p=6.5E−03	n=2
positive regulation of muscle cell apopt...	GO:0010661	p=6.5E−03	n=2
protein–lipid complex subunit organizati...	GO:0071825	p=6.5E−03	n=2
modulation by host of viral genome repli...	GO:0044827	p=6.5E−03	n=2
positive regulation of necrotic cell dea...	GO:0010940	p=6.5E−03	n=2
eye pigment biosynthetic process	GO:0006726	p=9.6E−03	n=2
negative regulation of innate immune res...	GO:0045824	p=9.6E−03	n=2
clathrin–dependent endocytosis	GO:0072583	p=1.1E−02	n=3
detection of visible light	GO:0009584	p=1.3E−02	n=3
negative regulation of protein tyrosine ...	GO:0061099	p=1.3E−02	n=2
detection of light stimulus involved in ...	GO:0050962	p=1.3E−02	n=2
detection of light stimulus involved in ...	GO:0050908	p=1.3E−02	n=2
biological regulation	GO:0065007	p=1.4E−02	n=43
import into cell	GO:0098657	p=1.7E−02	n=7
cellular oxidant detoxification	GO:0098869	p=1.7E−02	n=2
regulation of release of cytochrome c fr...	GO:0090199	p=1.7E−02	n=2
positive regulation of lipid transport	GO:0032370	p=1.7E−02	n=2
cell migration	GO:0016477	p=2.0E−02	n=11

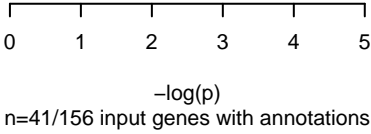


fraction genes in fg and expected value

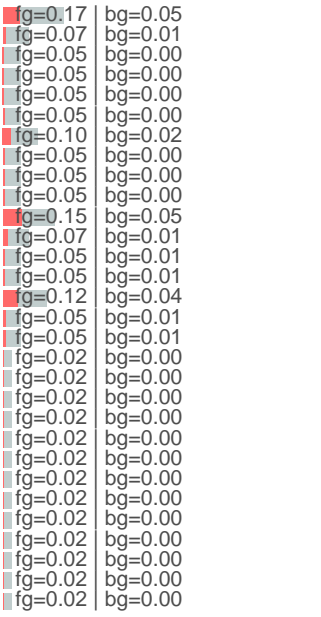


GO:MF  
Elav\_Nvec\_vc1.1\_XM\_048731950.1

ATP hydrolysis activity	GO:0016887	p=2.4E−03	n=7
phospholipid transporter activity	GO:0005548	p=3.8E−03	n=3
lipid transfer activity	GO:0120013	p=6.2E−03	n=2
Wnt–protein binding	GO:0017147	p=6.2E−03	n=2
ABC–type transporter activity	GO:0140359	p=6.2E−03	n=2
antioxidant activity	GO:0016209	p=9.1E−03	n=2
active ion transmembrane transporter act...	GO:0022853	p=1.2E−02	n=4
protein–disulfide reductase (NAD(P)) act...	GO:0047134	p=1.3E−02	n=2
adrenergic receptor binding	GO:0031690	p=1.3E−02	n=2
oxidoreductase activity, acting on a sul...	GO:0016668	p=1.3E−02	n=2
lipid binding	GO:0008289	p=1.7E−02	n=6
translation regulator activity	GO:0045182	p=1.7E−02	n=3
translation initiation factor binding	GO:0031369	p=2.1E−02	n=2
protein–disulfide reductase activity	GO:0015035	p=2.1E−02	n=2
phospholipid binding	GO:0005543	p=2.5E−02	n=5
alcohol binding	GO:0043178	p=2.6E−02	n=2
histone acetyltransferase binding	GO:0035035	p=2.6E−02	n=2
amidophosphoribosyltransferase activity	GO:0004044	p=2.6E−02	n=1
sodium:phosphate symporter activity	GO:0005436	p=2.6E−02	n=1
platelet activating factor receptor bind...	GO:0031859	p=2.6E−02	n=1
follicle–stimulating hormone receptor bi...	GO:0031762	p=2.6E−02	n=1
SMC family protein binding	GO:0043221	p=2.6E−02	n=1
purine nucleobase transmembrane transpor...	GO:0005345	p=2.6E−02	n=1
UDP–N–acetylglucosamine–dolichyl–phospha...	GO:0003975	p=2.6E−02	n=1
selenium binding	GO:0008430	p=2.6E−02	n=1
N6–methyladenosine–containing RNA bindin...	GO:1990247	p=2.6E−02	n=1
adenosine–phosphate deaminase activity	GO:0047623	p=2.6E−02	n=1
type 2A serotonin receptor binding	GO:0031826	p=2.6E−02	n=1
ABC–type sterol transporter activity	GO:0034041	p=2.6E−02	n=1
opsin binding	GO:0002046	p=2.6E−02	n=1

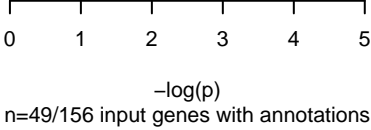


fraction genes in fg and expected value



GO:CC  
Elav\_Nvec\_vc1.1\_XM\_048731950.1

polysome	GO:0005844	p=3.5E−03	n=3
cytoplasmic ribonucleoprotein granule	GO:0036464	p=5.8E−03	n=5
cytoplasmic microtubule	GO:0005881	p=1.8E−02	n=2
synapse	GO:0045202	p=1.9E−02	n=10
polymeric cytoskeletal fiber	GO:0099513	p=2.3E−02	n=4
endosome	GO:0005768	p=2.4E−02	n=9
cell junction	GO:0030054	p=2.5E−02	n=12
integral component of pigment granule me...	GO:0090740	p=2.7E−02	n=1
pigment granule membrane	GO:0090741	p=2.7E−02	n=1
axonemal microtubule	GO:0005879	p=2.7E−02	n=1
exoribonuclease complex	GO:1905354	p=2.7E−02	n=1
hippocampal mossy fiber to CA3 synapse	GO:0098686	p=2.7E−02	n=1
exosome (RNase complex)	GO:0000178	p=2.7E−02	n=1
tubulin folding cofactor complex	GO:1990727	p=2.7E−02	n=1
cuticular plate	GO:0032437	p=2.7E−02	n=1
UTP–C complex	GO:0034456	p=2.7E−02	n=1
CURI complex	GO:0032545	p=2.7E−02	n=1
smooth endoplasmic reticulum	GO:0005790	p=4.0E−02	n=2
P granule	GO:0043186	p=4.0E−02	n=2
pole plasm	GO:0045495	p=4.6E−02	n=2
germ plasm	GO:0060293	p=4.6E−02	n=2
integral component of organelle membrane	GO:0031301	p=5.2E−02	n=5
microtubule	GO:0005874	p=5.3E−02	n=3
NSL complex	GO:0044545	p=5.3E−02	n=1
TRAMP complex	GO:0031499	p=5.3E−02	n=1
ESCRT IV complex	GO:1990621	p=5.3E−02	n=1
filamentous actin	GO:0031941	p=5.3E−02	n=1
intrinsic component of organelle membran...	GO:0031300	p=5.7E−02	n=5
ribonucleoprotein complex	GO:1990904	p=6.7E−02	n=9
ribonucleoprotein granule	GO:0035770	p=7.3E−02	n=6



fraction genes in fg and expected value

