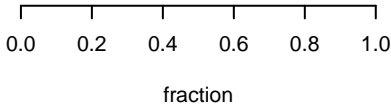
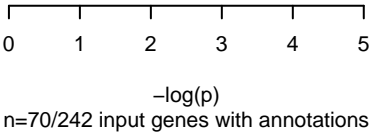


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_001623467.3

fraction genes in fg and expected value

interleukin-12-mediated signaling pathwa...	GO:0035722	p=1.0E-03	n=3
regulation of transcription by RNA polym...	GO:0006357	p=1.1E-03	n=22
positive regulation of glutathione biosy...	GO:1903788	p=1.5E-03	n=2
regulation of cellular response to manga...	GO:1905802	p=1.5E-03	n=2
negative regulation of hematopoietic ste...	GO:1902037	p=1.5E-03	n=2
regulation of macrophage derived foam ce...	GO:0010743	p=1.5E-03	n=2
removal of superoxide radicals	GO:0019430	p=1.5E-03	n=2
response to acid chemical	GO:0001101	p=1.9E-03	n=8
positive regulation of small molecule me...	GO:0062013	p=3.1E-03	n=5
regulation of mRNA splicing, via spliceo...	GO:0048024	p=3.3E-03	n=4
cellular response to glucose starvation	GO:0042149	p=3.9E-03	n=3
regulation of cellular macromolecule bio...	GO:2000112	p=4.0E-03	n=28
positive regulation of neuron differenti...	GO:0045666	p=4.1E-03	n=9
cellular response to manganese ion	GO:0071287	p=4.1E-03	n=4
response to cAMP	GO:0051591	p=4.1E-03	n=4
regulation of stem cell population maint...	GO:2000036	p=4.3E-03	n=2
negative regulation of JUN kinase activi...	GO:0043508	p=4.3E-03	n=2
N-glycan processing	GO:0006491	p=4.3E-03	n=2
COPII-coated vesicle cargo loading	GO:0090110	p=4.3E-03	n=2
positive regulation of neurogenesis	GO:0050769	p=5.1E-03	n=10
regulation of ATP metabolic process	GO:1903578	p=5.1E-03	n=4
regulation of nitrogen compound metaboli...	GO:0051171	p=5.8E-03	n=44
regulation of cytokine production	GO:0001817	p=6.5E-03	n=7
regulation of cellular respiration	GO:0043457	p=7.3E-03	n=3
intracellular mRNA localization	GO:0008298	p=7.4E-03	n=4
positive regulation of establishment of ...	GO:1903749	p=8.4E-03	n=2
chondrocyte development	GO:0002063	p=8.4E-03	n=2
cellular hyperosmotic response	GO:0071474	p=8.4E-03	n=2
negative regulation of nervous system de...	GO:0051961	p=8.8E-03	n=8
response to organic cyclic compound	GO:0014070	p=9.0E-03	n=15

fg=0.04	bg=0.00
fg=0.31	bg=0.16
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.11	bg=0.03
fg=0.07	bg=0.01
fg=0.06	bg=0.01
fg=0.04	bg=0.01
fg=0.40	bg=0.25
fg=0.13	bg=0.05
fg=0.06	bg=0.00
fg=0.06	bg=0.01
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.14	bg=0.06
fg=0.06	bg=0.01
fg=0.63	bg=0.39
fg=0.10	bg=0.03
fg=0.04	bg=0.01
fg=0.06	bg=0.01
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.11	bg=0.04
fg=0.21	bg=0.08

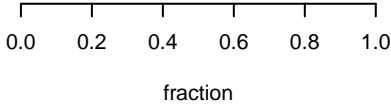
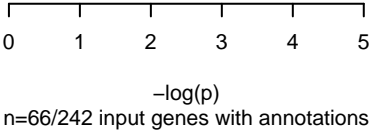


GO:MF  
Elav\_Nvec\_vc1.1\_XM\_001623467.3

fraction genes in fg and expected value

protein phosphatase binding	GO:0019903	p=5.8E-03	n=5
translation regulator activity	GO:0045182	p=1.1E-02	n=4
mRNA binding	GO:0003729	p=1.4E-02	n=6
GTPase activity	GO:0003924	p=1.5E-02	n=5
poly(U) RNA binding	GO:0008266	p=1.6E-02	n=2
protein phosphatase 2B binding	GO:0030346	p=1.6E-02	n=2
nucleoside-triphosphatase activity	GO:0017111	p=1.8E-02	n=10
oxidoreductase activity, acting on CH-OH...	GO:0016614	p=2.2E-02	n=3
pyrophosphatase activity	GO:0016462	p=2.2E-02	n=10
hydrolase activity, acting on acid anhyd...	GO:0016817	p=2.2E-02	n=10
hydrolase activity, acting on acid anhyd...	GO:0016818	p=2.2E-02	n=10
fibroblast growth factor binding	GO:0017134	p=2.3E-02	n=2
cholesterol binding	GO:0015485	p=2.3E-02	n=2
poly-pyrimidine tract binding	GO:0008187	p=2.3E-02	n=2
RNA binding	GO:0003723	p=2.7E-02	n=11
transition metal ion binding	GO:0046914	p=2.8E-02	n=9
sterol binding	GO:0032934	p=3.1E-02	n=2
translation regulator activity, nucleic ...	GO:0090079	p=3.6E-02	n=3
transcription regulator activity	GO:0140110	p=3.7E-02	n=13
steroid binding	GO:0005496	p=4.0E-02	n=2
Notch binding	GO:0005112	p=4.0E-02	n=2
single-stranded RNA binding	GO:0003727	p=4.1E-02	n=3
histone deacetylase regulator activity	GO:0035033	p=4.2E-02	n=1
phosphofructokinase activity	GO:0008443	p=4.2E-02	n=1
sphingosine N-acyltransferase activity	GO:0050291	p=4.2E-02	n=1
cuprous ion binding	GO:1903136	p=4.2E-02	n=1
steroid dehydrogenase activity	GO:0016229	p=4.2E-02	n=1
pre-mRNA 5'-splice site binding	GO:0030627	p=4.2E-02	n=1
glycogen binding	GO:2001069	p=4.2E-02	n=1
transmembrane receptor protein phosphata...	GO:0019198	p=4.2E-02	n=1

fg=0.08	bg=0.02
fg=0.06	bg=0.01
fg=0.09	bg=0.03
fg=0.08	bg=0.02
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.15	bg=0.07
fg=0.05	bg=0.01
fg=0.15	bg=0.07
fg=0.15	bg=0.07
fg=0.15	bg=0.07
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.17	bg=0.09
fg=0.14	bg=0.07
fg=0.03	bg=0.00
fg=0.05	bg=0.01
fg=0.20	bg=0.12
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.05	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00



GO:CC  
Elav\_Nvec\_vc1.1\_XM\_001623467.3

fraction genes in fg and expected value

COPII vesicle coat	GO:0030127	p=1.5E-03	n=2
perikaryon	GO:0043204	p=7.9E-03	n=4
subsynaptic reticulum	GO:0071212	p=8.7E-03	n=2
polysome	GO:0005844	p=9.9E-03	n=3
Golgi-associated vesicle	GO:0005798	p=1.2E-02	n=5
Golgi-associated vesicle membrane	GO:0030660	p=1.5E-02	n=3
endoplasmic reticulum membrane	GO:0005789	p=1.7E-02	n=11
nuclear outer membrane-endoplasmic retic...	GO:0042175	p=1.9E-02	n=11
Cajal body	GO:0015030	p=2.1E-02	n=2
endoplasmic reticulum subcompartment	GO:0098827	p=2.2E-02	n=11
COPI-coated vesicle	GO:0030137	p=2.8E-02	n=2
U2-type spliceosomal complex	GO:0005684	p=3.6E-02	n=2
6-phosphofructo-2-kinase/fructose-2,6-bi...	GO:0043540	p=3.9E-02	n=1
post-mRNA release spliceosomal complex	GO:0071014	p=3.9E-02	n=1
anchored component of synaptic vesicle m...	GO:0098993	p=3.9E-02	n=1
CCR4-NOT complex	GO:0030014	p=3.9E-02	n=1
CCR4-NOT core complex	GO:0030015	p=3.9E-02	n=1
protein kinase CK2 complex	GO:0005956	p=3.9E-02	n=1
recycling endosome membrane	GO:0055038	p=4.6E-02	n=2
spliceosomal complex	GO:0005681	p=7.2E-02	n=3
nuclear body	GO:0016604	p=7.7E-02	n=8
SMAD protein complex	GO:0071141	p=7.7E-02	n=1
COPI vesicle coat	GO:0030126	p=7.7E-02	n=1
TOR complex	GO:0038201	p=7.7E-02	n=1
COPI-coated vesicle membrane	GO:0030663	p=7.7E-02	n=1
NELF complex	GO:0032021	p=7.7E-02	n=1
mitochondrial crista	GO:0030061	p=7.7E-02	n=1
cytoplasmic cyclin-dependent protein kin...	GO:0000308	p=7.7E-02	n=1
U2-type catalytic step 2 spliceosome	GO:0071007	p=7.7E-02	n=1
TORC1 complex	GO:0031931	p=7.7E-02	n=1

fg=0.03	bg=0.00
fg=0.06	bg=0.01
fg=0.03	bg=0.00
fg=0.04	bg=0.01
fg=0.07	bg=0.02
fg=0.04	bg=0.01
fg=0.15	bg=0.08
fg=0.15	bg=0.08
fg=0.03	bg=0.00
fg=0.15	bg=0.08
fg=0.03	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
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
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00

