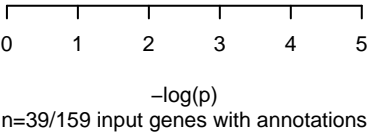


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_048724319.1

fraction genes in fg and expected value

negative regulation of ossification	GO:0030279	p=3.0E-03	n=3
heart valve morphogenesis	GO:0003179	p=3.0E-03	n=3
axon guidance	GO:0007411	p=3.3E-03	n=8
cell fate determination	GO:0001709	p=3.8E-03	n=4
regulation of cell development	GO:0060284	p=4.4E-03	n=11
negative regulation of cell motility	GO:2000146	p=6.5E-03	n=5
mononuclear cell differentiation	GO:1903131	p=6.5E-03	n=5
positive regulation of blood vessel endo...	GO:0043536	p=7.1E-03	n=3
ventricular septum development	GO:0003281	p=7.1E-03	n=3
autonomic nervous system development	GO:0048483	p=7.1E-03	n=3
regulation of neuron migration	GO:2001222	p=7.1E-03	n=3
regulation of nervous system development	GO:0051960	p=8.3E-03	n=11
ectodermal placode morphogenesis	GO:0071697	p=8.9E-03	n=2
mesodermal cell migration	GO:0008078	p=8.9E-03	n=2
animal organ maturation	GO:0048799	p=8.9E-03	n=2
regulation of nephron tubule epithelial ...	GO:0072182	p=8.9E-03	n=2
nephric duct formation	GO:0072179	p=8.9E-03	n=2
spinal cord motor neuron differentiation	GO:0021522	p=8.9E-03	n=2
embryonic viscerocranium morphogenesis	GO:0048703	p=8.9E-03	n=2
metanephric renal vesicle morphogenesis	GO:0072283	p=8.9E-03	n=2
negative regulation of insulin receptor ...	GO:0046627	p=8.9E-03	n=2
uterus development	GO:0060065	p=8.9E-03	n=2
endoderm formation	GO:0001706	p=8.9E-03	n=2
positive regulation of cardiac muscle ce...	GO:0060045	p=8.9E-03	n=2
parathyroid hormone secretion	GO:0035898	p=8.9E-03	n=2
negative regulation of interleukin-2 pro...	GO:0032703	p=8.9E-03	n=2
cardiac ventricle formation	GO:0003211	p=8.9E-03	n=2
cardiac right ventricle morphogenesis	GO:0003215	p=8.9E-03	n=2
negative regulation of osteoblast differ...	GO:0045668	p=8.9E-03	n=2
lymphoid progenitor cell differentiation	GO:0002320	p=8.9E-03	n=2

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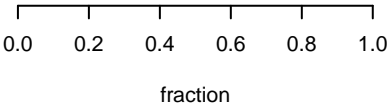
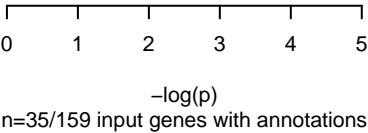


GO:MF  
Elav\_Nvec\_vc1.1\_XM\_048724319.1

fraction genes in fg and expected value

heterocyclic compound binding	GO:1901363	p=6.7E-03	n=16
organic cyclic compound binding	GO:0097159	p=1.1E-02	n=16
transcription coregulator activity	GO:0003712	p=2.3E-02	n=6
translation repressor activity	GO:0030371	p=2.5E-02	n=2
translation regulator activity, nucleic ...	GO:0090079	p=2.5E-02	n=2
mRNA regulatory element binding translat...	GO:0000900	p=2.5E-02	n=2
SMAD binding	GO:0046332	p=2.5E-02	n=2
translation regulator activity	GO:0045182	p=2.5E-02	n=2
cis-regulatory region sequence-specific ...	GO:0000987	p=3.3E-02	n=5
RNA polymerase II cis-regulatory region ...	GO:0000978	p=3.3E-02	n=5
nucleic acid binding	GO:0003676	p=3.3E-02	n=11
mRNA 3'-UTR binding	GO:0003730	p=4.8E-02	n=2
cytokine receptor binding	GO:0005126	p=4.8E-02	n=2
HMG box domain binding	GO:0071837	p=4.8E-02	n=2
sequence-specific DNA binding	GO:0043565	p=5.0E-02	n=7
RNA polymerase II transcription regulato...	GO:0000977	p=5.5E-02	n=6
transcription cis-regulatory region bind...	GO:0000976	p=7.2E-02	n=6
protein tyrosine kinase activity	GO:0004713	p=7.5E-02	n=2
transcription corepressor activity	GO:0003714	p=7.9E-02	n=3
sequence-specific double-stranded DNA bi...	GO:1990837	p=8.2E-02	n=6
double-stranded DNA binding	GO:0003690	p=9.2E-02	n=6
transcription regulatory region nucleic ...	GO:0001067	p=9.2E-02	n=6
phosphatidylinositol 3-kinase activity	GO:0035004	p=9.6E-02	n=1
phosphatidylinositol-4,5-bisphosphate ph...	GO:0106019	p=9.6E-02	n=1
interleukin-2 receptor binding	GO:0005134	p=9.6E-02	n=1
rRNA primary transcript binding	GO:0042134	p=9.6E-02	n=1
inositol trisphosphate phosphatase activ...	GO:0046030	p=9.6E-02	n=1
intronic transcription regulatory region...	GO:0001161	p=9.6E-02	n=1
1-phosphatidylinositol-3-kinase activity	GO:0016303	p=9.6E-02	n=1
RNA polymerase II intronic transcription...	GO:0001162	p=9.6E-02	n=1

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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_048724319.1

fraction genes in fg and expected value

protein-containing complex	GO:0032991	p=2.1E-02	n=19
centrosome	GO:0005813	p=2.6E-02	n=4
nuclear speck	GO:0016607	p=3.1E-02	n=3
nucleus	GO:0005634	p=4.0E-02	n=23
nuclear body	GO:0016604	p=4.3E-02	n=4
dendritic shaft	GO:0043198	p=4.4E-02	n=3
organelle	GO:0043226	p=5.5E-02	n=34
nuclear chromosome	GO:0000228	p=6.6E-02	n=2
perinuclear region of cytoplasm	GO:0048471	p=6.8E-02	n=6
microtubule organizing center	GO:0005815	p=7.9E-02	n=4
intracellular membrane-bounded organelle	GO:0043231	p=8.8E-02	n=32
intracellular organelle	GO:0043229	p=9.3E-02	n=33
Cajal body	GO:0015030	p=9.5E-02	n=1
gut granule	GO:0044840	p=9.5E-02	n=1
gut granule membrane	GO:0044841	p=9.5E-02	n=1
RNA polymerase II transcription represso...	GO:0090571	p=9.5E-02	n=1
excitatory synapse	GO:0060076	p=9.5E-02	n=1
lysosomal lumen	GO:0043202	p=9.5E-02	n=1
polysomal ribosome	GO:0042788	p=9.5E-02	n=1
interphase microtubule organizing center	GO:0031021	p=9.5E-02	n=1
U5 snRNP	GO:0005682	p=9.5E-02	n=1
messenger ribonucleoprotein complex	GO:1990124	p=9.5E-02	n=1
mitotic spindle pole	GO:0097431	p=9.5E-02	n=1
membrane-bounded organelle	GO:0043227	p=1.1E-01	n=32
chromatin	GO:0000785	p=1.1E-01	n=4
microtubule cytoskeleton	GO:0015630	p=1.3E-01	n=5
sarcomere	GO:0030017	p=1.4E-01	n=3
transcription regulator complex	GO:0005667	p=1.4E-01	n=4
cytoskeleton	GO:0005856	p=1.5E-01	n=7
cation channel complex	GO:0034703	p=1.6E-01	n=3

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