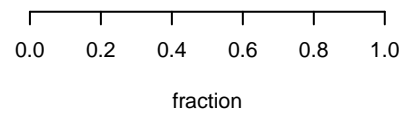
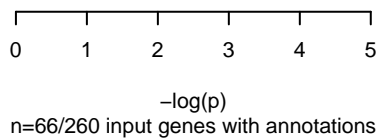
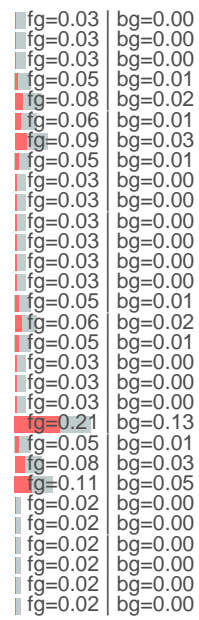


GO:BP
Elav_Nvec_vc1.1_XM_001623098.3

fraction genes in fg and expected value

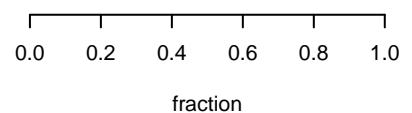
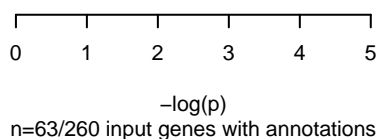
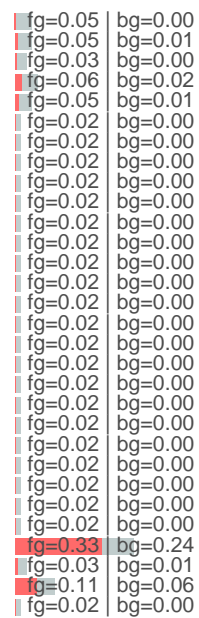
ventricular system development	GO:0021591	p=7.5E-03	n=2
cell-cell adhesion mediated by integrin	GO:0033631	p=7.5E-03	n=2
exploration behavior	GO:0035640	p=1.2E-02	n=2
cardiac ventricle morphogenesis	GO:0003208	p=1.3E-02	n=3
signal transduction by p53 class mediato...	GO:0072331	p=1.5E-02	n=5
positive regulation of small molecule me...	GO:0062013	p=1.5E-02	n=4
detection of stimulus	GO:0051606	p=2.1E-02	n=6
neuromuscular process controlling balanc...	GO:0050885	p=2.2E-02	n=3
positive regulation of translational ini...	GO:0045948	p=2.4E-02	n=2
endochondral ossification	GO:0001958	p=2.4E-02	n=2
synaptic vesicle priming	GO:0016082	p=2.4E-02	n=2
replacement ossification	GO:0036075	p=2.4E-02	n=2
intracellular lipid transport	GO:0032365	p=2.4E-02	n=2
positive regulation of execution phase o...	GO:1900119	p=2.4E-02	n=2
clathrin-dependent endocytosis	GO:0072583	p=2.5E-02	n=3
limb development	GO:0060173	p=2.7E-02	n=4
detection of visible light	GO:0009584	p=2.9E-02	n=3
endochondral bone morphogenesis	GO:0060350	p=3.2E-02	n=2
positive regulation of circadian sleep/w...	GO:0045938	p=3.2E-02	n=2
positive regulation of ATP metabolic pro...	GO:1903580	p=3.2E-02	n=2
regulation of programmed cell death	GO:0043067	p=3.3E-02	n=14
positive regulation of translation	GO:0045727	p=3.4E-02	n=3
gliogenesis	GO:0042063	p=3.5E-02	n=5
positive regulation of cellular cataboli...	GO:0031331	p=3.6E-02	n=7
maternal determination of dorsal/ventral...	GO:0008070	p=3.6E-02	n=1
melanocyte apoptotic process	GO:1902362	p=3.6E-02	n=1
globoside metabolic process	GO:0001575	p=3.6E-02	n=1
regulation of chorionic trophoblast cell...	GO:1901382	p=3.6E-02	n=1
negative regulation of peptidyl-serine p...	GO:0033140	p=3.6E-02	n=1
regulation of peptidyl-serine phosphoryl...	GO:0033139	p=3.6E-02	n=1



GO:MF
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AP-2 adaptor complex binding	GO:0035612	p=5.6E-04	n=3
integrin binding	GO:0005178	p=1.0E-02	n=3
collagen binding	GO:0005518	p=2.1E-02	n=2
cell adhesion molecule binding	GO:0050839	p=2.5E-02	n=4
protease binding	GO:0002020	p=3.2E-02	n=3
uridylyltransferase activity	GO:0070569	p=4.0E-02	n=1
long-chain fatty acid transporter activi...	GO:0005324	p=4.0E-02	n=1
phosphatidylinositol phosphate kinase ac...	GO:0016307	p=4.0E-02	n=1
1-phosphatidylinositol-4-phosphate 5-kin...	GO:0016308	p=4.0E-02	n=1
1-phosphatidylinositol-5-phosphate 4-kin...	GO:0016309	p=4.0E-02	n=1
1-phosphatidylinositol-3-phosphate 4-kin...	GO:0052811	p=4.0E-02	n=1
UDP-N-acetylglucosamine-dolichyl-phospha...	GO:0003975	p=4.0E-02	n=1
adenosine-phosphate deaminase activity	GO:0047623	p=4.0E-02	n=1
[phosphorylase] phosphatase activity	GO:0050196	p=4.0E-02	n=1
fibronectin binding	GO:0001968	p=4.0E-02	n=1
neuregulin binding	GO:0038132	p=4.0E-02	n=1
RNA uridylyltransferase activity	GO:0050265	p=4.0E-02	n=1
insulin-like growth factor I binding	GO:0031994	p=4.0E-02	n=1
glycogen binding	GO:2001069	p=4.0E-02	n=1
DNA binding, bending	GO:0008301	p=4.0E-02	n=1
interferon binding	GO:0019961	p=4.0E-02	n=1
interferon-gamma binding	GO:0019964	p=4.0E-02	n=1
phorbol ester receptor activity	GO:0001565	p=4.0E-02	n=1
AMP deaminase activity	GO:0003876	p=4.0E-02	n=1
ankyrin repeat binding	GO:0071532	p=4.0E-02	n=1
non-sequence-specific DNA binding, bendi...	GO:0044378	p=4.0E-02	n=1
enzyme binding	GO:0019899	p=6.3E-02	n=21
potassium channel regulator activity	GO:0015459	p=6.7E-02	n=2
transcription coregulator activity	GO:0003712	p=7.7E-02	n=7
dipeptidyl-peptidase activity	GO:0008239	p=7.8E-02	n=1



GO:CC
Elav_Nvec_vc1.1_XM_001623098.3

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clathrin-coated pit	GO:0005905	p=3.6E-03	n=3
recycling endosome membrane	GO:0055038	p=3.6E-03	n=3
early endosome	GO:0005769	p=1.3E-02	n=7
clathrin-coated vesicle membrane	GO:0030665	p=1.7E-02	n=3
synaptic membrane	GO:0097060	p=2.5E-02	n=5
nuclear body	GO:0016604	p=2.5E-02	n=9
plasma membrane protein complex	GO:0098797	p=2.6E-02	n=6
clathrin-coated vesicle	GO:0030136	p=3.0E-02	n=4
cell junction	GO:0030054	p=3.3E-02	n=15
RNA polymerase II transcription regulato...	GO:0090575	p=3.3E-02	n=4
neuromuscular junction	GO:0031594	p=3.3E-02	n=4
integrin alpha3-beta1 complex	GO:0034667	p=3.8E-02	n=1
katanin complex	GO:0008352	p=3.8E-02	n=1
Ski complex	GO:0055087	p=3.8E-02	n=1
integrin alpha6-beta4 complex	GO:0034676	p=3.8E-02	n=1
integrin alpha7-beta1 complex	GO:0034677	p=3.8E-02	n=1
anchored component of synaptic vesicle m...	GO:0098993	p=3.8E-02	n=1
cation channel complex	GO:0034703	p=4.2E-02	n=3
potassium channel complex	GO:0034705	p=4.2E-02	n=2
clathrin coat	GO:0030118	p=4.2E-02	n=2
clathrin-coated endocytic vesicle	GO:0045334	p=4.2E-02	n=2
voltage-gated potassium channel complex	GO:0008076	p=4.2E-02	n=2
ion channel complex	GO:0034702	p=5.2E-02	n=3
basal part of cell	GO:0045178	p=5.2E-02	n=5
coated vesicle membrane	GO:0030662	p=5.9E-02	n=3
adherens junction	GO:0005912	p=6.0E-02	n=4
cytosol	GO:0005829	p=6.3E-02	n=33
presynaptic membrane	GO:0042734	p=6.5E-02	n=3
synapse	GO:0045202	p=6.6E-02	n=11
smooth endoplasmic reticulum	GO:0005790	p=7.2E-02	n=2

