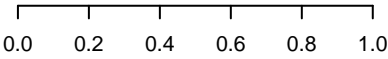
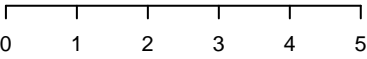


GO:BP
Elav_Nvec_vc1.1_XM_032379457.2

fraction genes in fg and expected value

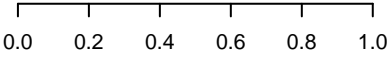
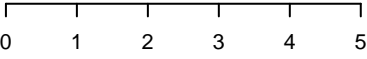
mRNA splicing, via spliceosome	GO:0000398	p=6.4E-04	n=3	fg=0.25	bg=0.02
synaptic vesicle cycle	GO:0099504	p=1.5E-03	n=3	fg=0.25	bg=0.02
carbohydrate derivative catabolic proces...	GO:1901136	p=7.6E-03	n=2	fg=0.17	bg=0.01
cellular response to leukemia inhibitory...	GO:1990830	p=7.6E-03	n=2	fg=0.17	bg=0.01
cellular catabolic process	GO:0044248	p=9.5E-03	n=6	fg=0.50	bg=0.18
epithelial cell differentiation	GO:0030855	p=1.1E-02	n=4	fg=0.33	bg=0.08
import into nucleus	GO:0051170	p=1.1E-02	n=2	fg=0.17	bg=0.01
protein import	GO:0017038	p=1.1E-02	n=2	fg=0.17	bg=0.01
protein import into nucleus	GO:0006606	p=1.1E-02	n=2	fg=0.17	bg=0.01
negative regulation of translation	GO:0017148	p=1.1E-02	n=2	fg=0.17	bg=0.01
intracellular protein transport	GO:0006886	p=1.2E-02	n=4	fg=0.33	bg=0.08
establishment of tissue polarity	GO:0007164	p=1.5E-02	n=2	fg=0.17	bg=0.02
negative regulation of cellular amide me...	GO:0034249	p=1.5E-02	n=2	fg=0.17	bg=0.02
establishment of planar polarity	GO:0001736	p=1.5E-02	n=2	fg=0.17	bg=0.02
morphogenesis of a polarized epithelium	GO:0001738	p=1.5E-02	n=2	fg=0.17	bg=0.02
epithelial cell development	GO:0002064	p=1.9E-02	n=3	fg=0.25	bg=0.05
nuclear transport	GO:0051169	p=2.0E-02	n=2	fg=0.17	bg=0.02
nucleocytoplasmic transport	GO:0006913	p=2.0E-02	n=2	fg=0.17	bg=0.02
establishment of synaptic vesicle locali...	GO:0097480	p=2.0E-02	n=2	fg=0.17	bg=0.02
cellular macromolecule localization	GO:0070727	p=2.0E-02	n=5	fg=0.42	bg=0.15
cellular macromolecule biosynthetic proc...	GO:0034645	p=2.1E-02	n=8	fg=0.67	bg=0.34
macromolecule biosynthetic process	GO:0009059	p=2.3E-02	n=8	fg=0.67	bg=0.35
reproductive behavior	GO:0019098	p=2.8E-02	n=3	fg=0.25	bg=0.06
negative regulation of T cell receptor s...	GO:0050860	p=2.9E-02	n=1	fg=0.08	bg=0.00
nucleoside catabolic process	GO:0009164	p=2.9E-02	n=1	fg=0.08	bg=0.00
purine ribonucleoside monophosphate cata...	GO:0009169	p=2.9E-02	n=1	fg=0.08	bg=0.00
regulation of cellular response to alcoh...	GO:1905957	p=2.9E-02	n=1	fg=0.08	bg=0.00
T cell anergy	GO:0002870	p=2.9E-02	n=1	fg=0.08	bg=0.00
positive regulation of cellular response...	GO:1905959	p=2.9E-02	n=1	fg=0.08	bg=0.00
negative regulation of antigen receptor---	GO:0050858	p=2.9E-02	n=1	fg=0.08	bg=0.00



GO:MF
Elav_Nvec_vc1.1_XM_032379457.2

fraction genes in fg and expected value

mRNA regulatory element binding translat...	GO:0000900	p=2.0E-03	n=2	fg=0.20	bg=0.01
mRNA 3'-UTR binding	GO:0003730	p=4.0E-03	n=2	fg=0.20	bg=0.01
calcium channel activity	GO:0005262	p=2.2E-02	n=2	fg=0.20	bg=0.03
mRNA 3'-UTR AU-rich region binding	GO:0035925	p=2.7E-02	n=1	fg=0.10	bg=0.00
ephrin receptor binding	GO:0046875	p=2.7E-02	n=1	fg=0.10	bg=0.00
chemoattractant activity	GO:0042056	p=2.7E-02	n=1	fg=0.10	bg=0.00
GAF domain binding	GO:0036004	p=2.7E-02	n=1	fg=0.10	bg=0.00
cGMP-stimulated cyclic-nucleotide phosph...	GO:0004118	p=2.7E-02	n=1	fg=0.10	bg=0.00
translation factor activity, RNA binding	GO:0008135	p=2.7E-02	n=1	fg=0.10	bg=0.00
TPR domain binding	GO:0030911	p=2.7E-02	n=1	fg=0.10	bg=0.00
beta-glucuronidase activity	GO:0004566	p=2.7E-02	n=1	fg=0.10	bg=0.00
SNAP receptor activity	GO:0005484	p=2.7E-02	n=1	fg=0.10	bg=0.00
epidermal growth factor receptor binding	GO:0005154	p=2.7E-02	n=1	fg=0.10	bg=0.00
poly(U) RNA binding	GO:0008266	p=2.7E-02	n=1	fg=0.10	bg=0.00
poly-pyrimidine tract binding	GO:0008187	p=2.7E-02	n=1	fg=0.10	bg=0.00
calcium ion transmembrane transporter ac...	GO:0015085	p=3.9E-02	n=2	fg=0.20	bg=0.03
tau-protein kinase activity	GO:0050321	p=5.4E-02	n=1	fg=0.10	bg=0.01
ribosome binding	GO:0043022	p=5.4E-02	n=1	fg=0.10	bg=0.01
carbohydrate binding	GO:0030246	p=5.4E-02	n=1	fg=0.10	bg=0.01
gamma-tubulin binding	GO:0043015	p=5.4E-02	n=1	fg=0.10	bg=0.01
phosphatidylinositol 3-kinase binding	GO:0043548	p=5.4E-02	n=1	fg=0.10	bg=0.01
phosphatidylinositol 3-kinase regulatory...	GO:0036312	p=5.4E-02	n=1	fg=0.10	bg=0.01
receptor ligand activity	GO:0048018	p=5.4E-02	n=1	fg=0.10	bg=0.01
miRNA binding	GO:0035198	p=5.4E-02	n=1	fg=0.10	bg=0.01
double-stranded RNA binding	GO:0003725	p=5.4E-02	n=1	fg=0.10	bg=0.01
regulatory RNA binding	GO:0061980	p=5.4E-02	n=1	fg=0.10	bg=0.01
signaling receptor regulator activity	GO:0030545	p=5.4E-02	n=1	fg=0.10	bg=0.01
signaling receptor activator activity	GO:0030546	p=5.4E-02	n=1	fg=0.10	bg=0.01
protein domain specific binding	GO:0019904	p=7.5E-02	n=3	fg=0.30	bg=0.10
ribonucleoprotein complex binding	GO:0043021	p=8.0E-02	n=1	fg=0.10	bg=0.01



GO:CC
Elav_Nvec_vc1.1_XM_032379457.2

fraction genes in fg and expected value

distal axon	GO:0150034	p=4.8E-03	n=4	fg=0.33	bg=0.07
ribonucleoprotein complex	GO:1990904	p=7.6E-03	n=3	fg=0.25	bg=0.04
nucleus	GO:0005634	p=8.3E-03	n=10	fg=0.83	bg=0.46
perinuclear region of cytoplasm	GO:0048471	p=1.1E-02	n=4	fg=0.33	bg=0.08
presynapse	GO:0098793	p=1.3E-02	n=4	fg=0.33	bg=0.08
presynaptic active zone	GO:0048786	p=2.1E-02	n=2	fg=0.17	bg=0.02
messenger ribonucleoprotein complex	GO:1990124	p=3.0E-02	n=1	fg=0.08	bg=0.00
Cajal body	GO:0015030	p=3.0E-02	n=1	fg=0.08	bg=0.00
polysomal ribosome	GO:0042788	p=3.0E-02	n=1	fg=0.08	bg=0.00
male germ cell nucleus	GO:0001673	p=3.0E-02	n=1	fg=0.08	bg=0.00
SNARE complex	GO:0031201	p=3.0E-02	n=1	fg=0.08	bg=0.00
condensed nuclear chromosome	GO:0000794	p=3.0E-02	n=1	fg=0.08	bg=0.00
synaptonemal complex	GO:0000795	p=3.0E-02	n=1	fg=0.08	bg=0.00
synaptonemal structure	GO:0099086	p=3.0E-02	n=1	fg=0.08	bg=0.00
hippocampal mossy fiber	GO:0097457	p=3.0E-02	n=1	fg=0.08	bg=0.00
lateral element	GO:0000800	p=3.0E-02	n=1	fg=0.08	bg=0.00
dentate gyrus mossy fiber	GO:0044302	p=3.0E-02	n=1	fg=0.08	bg=0.00
transverse filament	GO:0000802	p=3.0E-02	n=1	fg=0.08	bg=0.00
lysosomal lumen	GO:0043202	p=3.0E-02	n=1	fg=0.08	bg=0.00
organelle lumen	GO:0043233	p=4.8E-02	n=7	fg=0.58	bg=0.32
membrane-enclosed lumen	GO:0031974	p=4.8E-02	n=7	fg=0.58	bg=0.32
intracellular organelle lumen	GO:0070013	p=4.8E-02	n=7	fg=0.58	bg=0.32
growth cone	GO:0030426	p=5.3E-02	n=2	fg=0.17	bg=0.03
cell junction	GO:0030054	p=5.3E-02	n=5	fg=0.42	bg=0.19
chromosome, centromeric region	GO:0000775	p=5.9E-02	n=1	fg=0.08	bg=0.01
ribosome	GO:0005840	p=5.9E-02	n=1	fg=0.08	bg=0.01
condensed chromosome, centromeric region	GO:0000779	p=5.9E-02	n=1	fg=0.08	bg=0.01
polysome	GO:0005844	p=5.9E-02	n=1	fg=0.08	bg=0.01
condensed chromosome	GO:0000793	p=5.9E-02	n=1	fg=0.08	bg=0.01
cytoplasmic stress granule	GO:0010494	p=5.9E-02	n=1	fg=0.08	bg=0.01

