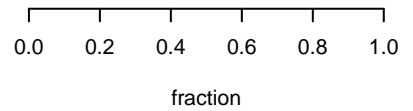
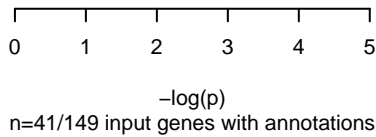


GO:BP
Elav_Nvec_vc1.1_XM_001627049.3

fraction genes in fg and expected value

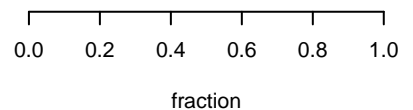
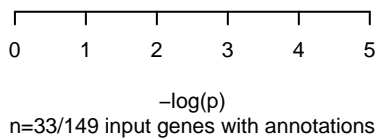
GO term	GO ID	p-value	n	fg	bg
ADP metabolic process	GO:0046031	p=5.5E-04	n=4	fg=0.10	bg=0.01
peptidyl-arginine modification	GO:0018195	p=1.5E-03	n=2	fg=0.05	bg=0.00
glucosamine-containing compound metaboli...	GO:1901071	p=1.5E-03	n=2	fg=0.05	bg=0.00
detection of external stimulus	GO:0009581	p=1.9E-03	n=5	fg=0.12	bg=0.02
nucleotide catabolic process	GO:0009166	p=2.3E-03	n=4	fg=0.10	bg=0.01
detection of abiotic stimulus	GO:0009582	p=2.4E-03	n=5	fg=0.12	bg=0.02
histone H4-K5 acetylation	GO:0043981	p=2.9E-03	n=2	fg=0.05	bg=0.00
histone H4-K8 acetylation	GO:0043982	p=2.9E-03	n=2	fg=0.05	bg=0.00
metanephric renal vesicle morphogenesis	GO:0072283	p=2.9E-03	n=2	fg=0.05	bg=0.00
detection of stimulus involved in sensor...	GO:0050906	p=3.1E-03	n=4	fg=0.10	bg=0.02
regulation of reactive oxygen species bi...	GO:1903426	p=3.3E-03	n=3	fg=0.07	bg=0.01
second-messenger-mediated signaling	GO:0019932	p=3.5E-03	n=6	fg=0.15	bg=0.04
histone H4-K16 acetylation	GO:0043984	p=4.8E-03	n=2	fg=0.05	bg=0.00
cyclic purine nucleotide metabolic proce...	GO:0052652	p=4.8E-03	n=2	fg=0.05	bg=0.00
locomotory behavior	GO:0007626	p=5.0E-03	n=7	fg=0.17	bg=0.05
cell differentiation involved in kidney ...	GO:0061005	p=5.9E-03	n=3	fg=0.07	bg=0.01
regulation of muscle adaptation	GO:0043502	p=6.9E-03	n=3	fg=0.07	bg=0.01
nucleoside diphosphate phosphorylation	GO:0006165	p=6.9E-03	n=3	fg=0.07	bg=0.01
regulation of cAMP-dependent protein kin...	GO:2000479	p=7.1E-03	n=2	fg=0.05	bg=0.00
cardiac muscle hypertrophy in response t...	GO:0014898	p=7.1E-03	n=2	fg=0.05	bg=0.00
cerebellar Purkinje cell differentiation	GO:0021702	p=7.1E-03	n=2	fg=0.05	bg=0.00
motor neuron migration	GO:0097475	p=7.1E-03	n=2	fg=0.05	bg=0.00
negative regulation of striated muscle t...	GO:0045843	p=7.1E-03	n=2	fg=0.05	bg=0.00
cellular response to pH	GO:0071467	p=7.1E-03	n=2	fg=0.05	bg=0.00
growth	GO:0040007	p=7.9E-03	n=12	fg=0.29	bg=0.14
membrane lipid biosynthetic process	GO:0046467	p=8.1E-03	n=3	fg=0.07	bg=0.01
cyclic nucleotide metabolic process	GO:0009187	p=8.9E-03	n=4	fg=0.10	bg=0.01
cellular response to catecholamine stimu...	GO:0071870	p=9.4E-03	n=3	fg=0.07	bg=0.01
cardiac conduction	GO:0061337	p=9.4E-03	n=3	fg=0.07	bg=0.01
positive regulation of BMP signaling pat...	GO:0030513	p=9.7E-03	n=2	fg=0.05	bg=0.00



GO:MF
Elav_Nvec_vc1.1_XM_001627049.3

fraction genes in fg and expected value

mRNA binding	GO:0003729	p=2.8E-03	n=5	fg=0.15	bg=0.03
transcription corepressor activity	GO:0003714	p=3.2E-03	n=4	fg=0.12	bg=0.02
acetylglucosaminyltransferase activity	GO:0008375	p=4.0E-03	n=2	fg=0.06	bg=0.00
poly(U) RNA binding	GO:0008266	p=4.0E-03	n=2	fg=0.06	bg=0.00
histone methyltransferase activity	GO:0042054	p=5.9E-03	n=2	fg=0.06	bg=0.00
intracellular ligand-gated ion channel a...	GO:0005217	p=1.7E-02	n=1	fg=0.06	bg=0.00
calcium ion transmembrane transporter ac...	GO:0015085	p=1.7E-02	n=3	fg=0.09	bg=0.02
mRNA 3'-UTR binding	GO:0003730	p=2.0E-02	n=2	fg=0.06	bg=0.01
arginine N-methyltransferase activity	GO:0016273	p=2.1E-02	n=1	fg=0.03	bg=0.00
protein-arginine N-methyltransferase act...	GO:0016274	p=2.1E-02	n=1	fg=0.03	bg=0.00
[myelin basic protein]-arginine N-methyl...	GO:0016277	p=2.1E-02	n=1	fg=0.03	bg=0.00
histone methyltransferase activity (H3-K...	GO:0046976	p=2.1E-02	n=1	fg=0.03	bg=0.00
RNA uridylyltransferase activity	GO:0050265	p=2.1E-02	n=1	fg=0.03	bg=0.00
histone methyltransferase activity (H4-R...	GO:0044020	p=2.1E-02	n=1	fg=0.03	bg=0.00
small molecule sensor activity	GO:0140299	p=2.1E-02	n=1	fg=0.03	bg=0.00
protein-arginine omega-N monomethyltrans...	GO:0035241	p=2.1E-02	n=1	fg=0.03	bg=0.00
protein-arginine omega-N symmetric methy...	GO:0035243	p=2.1E-02	n=1	fg=0.03	bg=0.00
TFIIIF-class transcription factor complex...	GO:0001096	p=2.1E-02	n=1	fg=0.03	bg=0.00
protein O-GlcNAc transferase activity	GO:0097363	p=2.1E-02	n=1	fg=0.03	bg=0.00
uridylyltransferase activity	GO:0070569	p=2.1E-02	n=1	fg=0.03	bg=0.00
oxygen sensor activity	GO:0019826	p=2.1E-02	n=1	fg=0.03	bg=0.00
histone-arginine N-methyltransferase act...	GO:0008469	p=2.1E-02	n=1	fg=0.03	bg=0.00
AMP deaminase activity	GO:0003876	p=2.1E-02	n=1	fg=0.03	bg=0.00
3-chloroallyl aldehyde dehydrogenase act...	GO:0004028	p=2.1E-02	n=1	fg=0.03	bg=0.00
aldehyde dehydrogenase (NAD+) activity	GO:0004029	p=2.1E-02	n=1	fg=0.03	bg=0.00
protein N-acetylglucosaminyltransferase ...	GO:0016262	p=2.1E-02	n=1	fg=0.03	bg=0.00
adenosine-phosphate deaminase activity	GO:0047623	p=2.1E-02	n=1	fg=0.03	bg=0.00
intracellular phosphatidylinositol-3,5-b...	GO:0097682	p=2.1E-02	n=1	fg=0.03	bg=0.00
aldehyde dehydrogenase [NAD(P)+] activit...	GO:0004030	p=2.1E-02	n=1	fg=0.03	bg=0.00
N-methyltransferase activity	GO:0008170	p=2.4E-02	n=2	fg=0.06	bg=0.00



GO:CC
Elav_Nvec_vc1.1_XM_001627049.3

fraction genes in fg and expected value

GO term	GO ID	p-value	n	fg	bg
T-tubule	GO:0030315	p=1.2E-03	n=3	fg=0.07	bg=0.01
histone methyltransferase complex	GO:0035097	p=4.9E-03	n=3	fg=0.07	bg=0.01
cation channel complex	GO:0034703	p=1.1E-02	n=3	fg=0.07	bg=0.01
ion channel complex	GO:0034702	p=1.4E-02	n=3	fg=0.07	bg=0.01
extrinsic component of organelle membran...	GO:0031312	p=1.6E-02	n=2	fg=0.05	bg=0.00
Z disc	GO:0030018	p=1.8E-02	n=3	fg=0.07	bg=0.01
I band	GO:0031674	p=2.0E-02	n=3	fg=0.07	bg=0.01
autosome	GO:0030849	p=2.3E-02	n=1	fg=0.02	bg=0.00
RNA polymerase II transcription represso...	GO:0090571	p=2.3E-02	n=1	fg=0.02	bg=0.00
L-type voltage-gated calcium channel com...	GO:1990454	p=2.3E-02	n=1	fg=0.02	bg=0.00
integral component of lysosomal membrane	GO:1905103	p=2.3E-02	n=1	fg=0.02	bg=0.00
extrinsic component of mitochondrial inn...	GO:0031314	p=2.3E-02	n=1	fg=0.02	bg=0.00
methylosome	GO:0034709	p=2.3E-02	n=1	fg=0.02	bg=0.00
neuronal cell body membrane	GO:0032809	p=3.8E-02	n=2	fg=0.05	bg=0.01
sarcomere	GO:0030017	p=4.3E-02	n=3	fg=0.07	bg=0.02
cell body membrane	GO:0044298	p=4.4E-02	n=2	fg=0.05	bg=0.01
integral component of vacuolar membrane	GO:0031166	p=4.5E-02	n=1	fg=0.02	bg=0.00
intrinsic component of vacuolar membrane	GO:0031310	p=4.5E-02	n=1	fg=0.02	bg=0.00
glycosylphosphatidylinositol-N-acetylglu...	GO:0000506	p=4.5E-02	n=1	fg=0.02	bg=0.00
Seh1-associated complex	GO:0035859	p=4.5E-02	n=1	fg=0.02	bg=0.00
NSL complex	GO:0044545	p=4.5E-02	n=1	fg=0.02	bg=0.00
GATOR2 complex	GO:0061700	p=4.5E-02	n=1	fg=0.02	bg=0.00
nuclear speck	GO:0016607	p=4.7E-02	n=4	fg=0.10	bg=0.03
transmembrane transporter complex	GO:1902495	p=5.3E-02	n=3	fg=0.07	bg=0.02
transporter complex	GO:1990351	p=6.0E-02	n=3	fg=0.07	bg=0.02
neuron spine	GO:0044309	p=6.0E-02	n=3	fg=0.07	bg=0.02
dendritic spine	GO:0043197	p=6.0E-02	n=3	fg=0.07	bg=0.02
acetyltransferase complex	GO:1902493	p=6.1E-02	n=2	fg=0.05	bg=0.01
protein acetyltransferase complex	GO:0031248	p=6.1E-02	n=2	fg=0.05	bg=0.01
histone acetyltransferase complex	GO:0000123	p=6.1E-02	n=2	fg=0.05	bg=0.01

