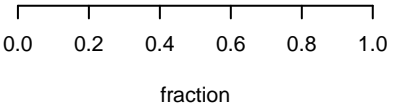
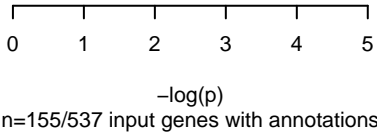


GO:BP
Elav_Nvec_vc1.1_XM_048728028.1

fraction genes in fg and expected value

germarium-derived female germ-line cyst ...	GO:0030727	p=1.7E-03	n=3
regulation of transcription, DNA-templat...	GO:0006355	p=2.0E-03	n=46
forebrain development	GO:0030900	p=2.7E-03	n=14
positive regulation of autophagy of mito...	GO:1903599	p=3.3E-03	n=3
actin cortical patch localization	GO:0051666	p=3.3E-03	n=2
positive regulation of eye pigmentation	GO:0048075	p=3.3E-03	n=2
iris morphogenesis	GO:0061072	p=3.3E-03	n=2
lysine transport	GO:0015819	p=3.3E-03	n=2
tryptophan metabolic process	GO:0006568	p=3.3E-03	n=2
protein maturation by copper ion transfe...	GO:0015680	p=3.3E-03	n=2
negative regulation of oxidative stress-...	GO:1903377	p=3.3E-03	n=2
heat acclimation	GO:0010286	p=3.3E-03	n=2
blood vessel remodeling	GO:0001974	p=3.6E-03	n=4
response to bacterium	GO:0009617	p=4.8E-03	n=13
negative regulation of response to endop...	GO:1903573	p=5.0E-03	n=4
negative regulation of vasoconstriction	GO:0045906	p=5.5E-03	n=3
thermosensory behavior	GO:0040040	p=5.5E-03	n=3
melanocyte differentiation	GO:0030318	p=5.5E-03	n=3
positive regulation of oxidoreductase ac...	GO:0051353	p=5.5E-03	n=3
learning or memory	GO:0007611	p=7.7E-03	n=14
regulation of anoikis	GO:2000209	p=8.4E-03	n=3
regulation of cellular macromolecule bio...	GO:2000112	p=8.4E-03	n=51
cellular response to catecholamine stimu...	GO:0071870	p=8.5E-03	n=5
histone deacetylation	GO:0016575	p=8.7E-03	n=4
positive regulation of oxidative stress-...	GO:1903223	p=9.5E-03	n=2
elastin metabolic process	GO:0051541	p=9.5E-03	n=2
spinal cord motor neuron cell fate speci...	GO:0021520	p=9.5E-03	n=2
ventral spinal cord interneuron specific...	GO:0021521	p=9.5E-03	n=2
negative regulation of vascular associat...	GO:1904706	p=9.5E-03	n=2
negative regulation of engulfment of apo...	GO:1901075	p=9.5E-03	n=2

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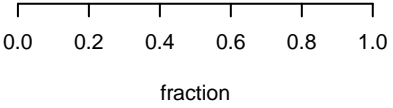
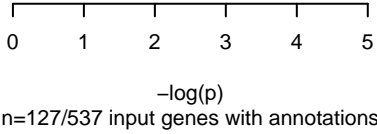


GO:MF
Elav_Nvec_vc1.1_XM_048728028.1

fraction genes in fg and expected value

histone acetyltransferase binding	GO:0035035	p=2.7E-05	n=6
RNA polymerase II cis-regulatory region ...	GO:0000978	p=1.8E-03	n=11
histone deacetylase binding	GO:0042826	p=2.0E-03	n=6
superoxide dismutase copper chaperone ac...	GO:0016532	p=2.9E-03	n=2
chaperone binding	GO:0051087	p=3.4E-03	n=7
ubiquitin protein ligase activity	GO:0061630	p=4.3E-03	n=10
zinc ion binding	GO:0008270	p=5.6E-03	n=12
SMAD binding	GO:0046332	p=8.7E-03	n=4
DNA secondary structure binding	GO:0000217	p=1.0E-02	n=3
nuclear thyroid hormone receptor binding	GO:0046966	p=1.0E-02	n=3
solute:cation symporter activity	GO:0015294	p=1.1E-02	n=4
core promoter sequence-specific DNA bind...	GO:0001046	p=1.3E-02	n=4
symporter activity	GO:0015293	p=1.3E-02	n=4
histone deacetylase activity	GO:0004407	p=1.4E-02	n=3
DNA-binding transcription activator acti...	GO:0001228	p=1.6E-02	n=9
DNA-binding transcription activator acti...	GO:0001216	p=1.6E-02	n=9
minor groove of adenine-thymine-rich DNA...	GO:0003680	p=1.6E-02	n=2
histone binding	GO:0042393	p=1.8E-02	n=6
protein lysine deacetylase activity	GO:0033558	p=1.8E-02	n=3
hydrolase activity, acting on carbon-nit...	GO:0016811	p=2.3E-02	n=4
deacetylase activity	GO:0019213	p=2.3E-02	n=3
hormone receptor binding	GO:0051427	p=2.5E-02	n=6
endoribonuclease activity, producing 5'-...	GO:0016891	p=2.6E-02	n=2
acetylcholine receptor binding	GO:0033130	p=2.6E-02	n=2
transcription regulator activity	GO:0140110	p=2.9E-02	n=20
DNA-binding transcription factor activit...	GO:0000981	p=3.2E-02	n=13
intramolecular oxidoreductase activity	GO:0016860	p=3.5E-02	n=3
TBP-class protein binding	GO:0017025	p=3.5E-02	n=3
intramolecular oxidoreductase activity, ...	GO:0016864	p=3.7E-02	n=2
R-SMAD binding	GO:0070412	p=3.7E-02	n=2

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GO:CC
Elav_Nvec_vc1.1_XM_048728028.1

fraction genes in fg and expected value

integral component of endoplasmic reticu...	GO:0030176	p=2.8E-03	n=9
growth cone filopodium	GO:1990812	p=3.2E-03	n=2
Sin3 complex	GO:0016580	p=3.2E-03	n=2
COPI vesicle coat	GO:0030126	p=9.2E-03	n=2
transcription regulator complex	GO:0005667	p=9.7E-03	n=12
late endosome	GO:0005770	p=1.5E-02	n=8
X chromosome	GO:0000805	p=1.8E-02	n=2
platelet alpha granule membrane	GO:0031092	p=1.8E-02	n=2
NuRD complex	GO:0016581	p=1.8E-02	n=2
CHD-type complex	GO:0090545	p=1.8E-02	n=2
growth cone lamellipodium	GO:1990761	p=1.8E-02	n=2
pericentriolar material	GO:0000242	p=2.9E-02	n=2
fungal-type vacuole	GO:0000324	p=2.9E-02	n=2
fungal-type vacuole membrane	GO:0000329	p=2.9E-02	n=2
trans-Golgi network membrane	GO:0032588	p=3.2E-02	n=5
dendritic shaft	GO:0043198	p=3.3E-02	n=4
smooth endoplasmic reticulum	GO:0005790	p=3.4E-02	n=3
asymmetric synapse	GO:0032279	p=3.6E-02	n=7
neuron to neuron synapse	GO:0098984	p=4.0E-02	n=7
endonuclease complex	GO:1905348	p=4.1E-02	n=2
cell tip	GO:0051286	p=4.1E-02	n=2
endoribonuclease complex	GO:1902555	p=4.1E-02	n=2
cell leading edge	GO:0031252	p=4.3E-02	n=10
centrosome	GO:0005813	p=5.0E-02	n=13
postsynapse	GO:0098794	p=5.4E-02	n=10
storage vacuole	GO:0000322	p=5.6E-02	n=2
cell pole	GO:0060187	p=5.6E-02	n=2
ciliary cap	GO:0061822	p=5.7E-02	n=1
intermediate-density lipoprotein particl...	GO:0034363	p=5.7E-02	n=1
high-density lipoprotein particle	GO:0034364	p=5.7E-02	n=1

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