

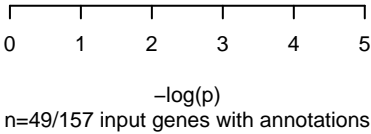
GO:BP
Elav_Nvec_vc1.1_XM_048730757.1

fraction genes in fg and expected value

embryonic body morphogenesis	GO:0010172
anterior neuropore closure	GO:0021506
specification of segmental identity, abd...	GO:0007385
negative regulation of response to gamma...	GO:2001229
cell fate specification	GO:0001708
anatomical structure maturation	GO:0071695
positive regulation of membrane tubulati...	GO:1903527
regulation of stem cell population maint...	GO:2000036
syncytial blastoderm mitotic cell cycle	GO:0035186
regulation of extracellular matrix disas...	GO:0010715
basement membrane organization	GO:0071711
cellular response to nerve growth factor...	GO:1990090
G protein-coupled receptor signaling pat...	GO:0007186
lens morphogenesis in camera-type eye	GO:0002089
cranial nerve formation	GO:0021603
branch elongation of an epithelium	GO:0060602
divalent inorganic anion homeostasis	GO:0072505
phosphate ion homeostasis	GO:0055062
embryonic cranial skeleton morphogenesis	GO:0048701
somatic stem cell population maintenance	GO:0035019
pole cell migration	GO:0007280
Notch receptor processing	GO:0007220
animal organ maturation	GO:0048799
cAMP metabolic process	GO:0046058
mammary gland duct morphogenesis	GO:0060603
blastocyst formation	GO:0001825
positive regulation of animal organ morp...	GO:0110110
inter-male aggressive behavior	GO:0002121
positive regulation of cell death	GO:0010942
gland morphogenesis	GO:0022612

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p=1.3E-03	n=8
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p=2.1E-03	n=2
p=4.1E-03	n=2
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p=5.5E-03	n=3
p=6.7E-03	n=7
p=6.8E-03	n=2
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p=6.8E-03	n=2
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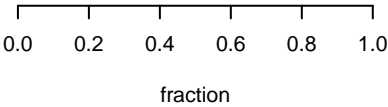
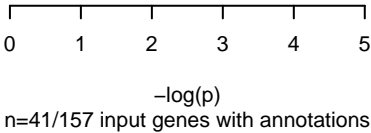
GO:MF
Elav_Nvec_vc1.1_XM_048730757.1

fraction genes in fg and expected value

poly(U) RNA binding	GO:0008266
cysteine-type endopeptidase regulator ac...	GO:0043028
G-protein alpha-subunit binding	GO:0001965
enzyme activator activity	GO:0008047
methylation-dependent protein binding	GO:0140034
methylated histone binding	GO:0035064
D-glucose transmembrane transporter acti...	GO:0055056
rRNA primary transcript binding	GO:0042134
sugar transmembrane transporter activity	GO:0051119
carbohydrate:cation symporter activity	GO:0005402
carbohydrate transmembrane transporter a...	GO:0015144
monosaccharide transmembrane transporter...	GO:0015145
hexose transmembrane transporter activit...	GO:0015149
TFIIIF-class transcription factor complex...	GO:0001096
dystroglycan binding	GO:0002162
beta-1 adrenergic receptor binding	GO:0031697
polypeptide N-acetylgalactosaminy/transf...	GO:0004653
endoribonuclease activity, producing 3'-...	GO:0016892
endonuclease activity, active with eithe...	GO:0016894
carbohydrate:proton symporter activity	GO:0005351
glucose transmembrane transporter activi...	GO:0005355
tRNA-intron endonuclease activity	GO:0000213
riboflavin transmembrane transporter act...	GO:0032217
kinetochore binding	GO:0043515
protein kinase binding	GO:0019901
peptidase regulator activity	GO:0061134
kinase binding	GO:0019900
ribonuclease activity	GO:0004540
protein tyrosine kinase binding	GO:1990782
actin binding	GO:0003779

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GO:CC
Elav_Nvec_vc1.1_XM_048730757.1

fraction genes in fg and expected value

intercalary heterochromatin	GO:0005725
PRC1 complex	GO:0035102
mitochondrial large ribosomal subunit	GO:0005762
cell periphery	GO:0071944
excitatory synapse	GO:0060076
Golgi apparatus subcompartment	GO:0098791
Golgi cisterna membrane	GO:0032580
COPI-coated vesicle	GO:0030137
Golgi apparatus	GO:0005794
chromaffin granule	GO:0042583
chromaffin granule membrane	GO:0042584
centrosomal corona	GO:0031592
RNA polymerase III transcription regulat...	GO:0090576
L-type voltage-gated calcium channel com...	GO:1990454
cortical microtubule cytoskeleton	GO:0030981
exoribonuclease complex	GO:1905354
hippocampal mossy fiber to CA3 synapse	GO:0098686
exosome (RNase complex)	GO:0000178
transcription factor TFIIC complex	GO:0000127
cytoplasmic microtubule plus-end	GO:1904511
apoptosome	GO:0043293
luminal side of Golgi membrane	GO:0098547
cortical microtubule	GO:0055028
tRNA-intron endonuclease complex	GO:0000214
nuclear outer membrane	GO:0005640
AP-3 adaptor complex	GO:0030123
cortical microtubule plus-end	GO:1903754
centrosome	GO:0005813
organelle subcompartment	GO:0031984
plasma membrane region	GO:0098590

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p=1.9E-02	n=12
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