

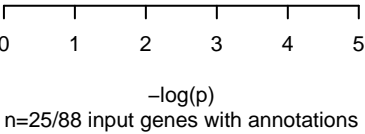
GO:BP
Elav_Nvec_vc1.1_XM_032366482.2

fraction genes in fg and expected value

parathyroid hormone secretion	GO:0035898
otic vesicle formation	GO:0030916
neuron migration	GO:0001764
centriole replication	GO:0007099
fin regeneration	GO:0031101
peptidyl-serine dephosphorylation	GO:0070262
regulation of CD4-positive, alpha-beta T...	GO:0043370
erythrocyte differentiation	GO:0030218
mesodermal cell migration	GO:0008078
animal organ maturation	GO:0048799
positive regulation of animal organ morp...	GO:0110110
positive regulation of myeloid leukocyte...	GO:0002888
positive regulation of mast cell degranu...	GO:0043306
positive regulation of cell division	GO:0051781
posterior lateral line development	GO:0048916
T cell activation involved in immune res...	GO:0002286
ectodermal placode morphogenesis	GO:0071697
mitotic sister chromatid separation	GO:0051306
canonical Wnt signaling pathway	GO:0060070
regulation of extrinsic apoptotic signal...	GO:2001239
negative regulation of embryonic develop...	GO:0045992
regulation of tyrosine phosphorylation o...	GO:0042509
regulation of Wnt signaling pathway	GO:0030111
mammary gland epithelium development	GO:0061180
negative regulation of neural precursor ...	GO:2000178
regulation of fibroblast growth factor r...	GO:0040036
regulation of hematopoietic stem cell di...	GO:1902036
positive regulation of protein kinase B ...	GO:0051897
positive regulation of blood vessel endo...	GO:0043536
camera-type eye development	GO:0043010

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p=1.2E-03	n=4
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p=1.8E-03	n=2
p=2.6E-03	n=3
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p=3.7E-03	n=2
p=3.7E-03	n=2
p=3.7E-03	n=2
p=4.9E-03	n=2
p=4.9E-03	n=4
p=6.2E-03	n=2
p=7.7E-03	n=2
p=7.7E-03	n=2
p=8.1E-03	n=4
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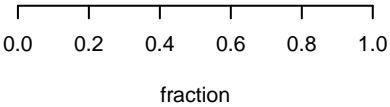
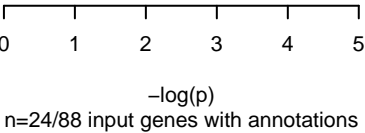
GO:MF
Elav_Nvec_vc1.1_XM_032366482.2

fraction genes in fg and expected value

transcription cis-regulatory region bind...	GO:0000976
ubiquitin protein ligase activity	GO:0061630
growth factor receptor binding	GO:0070851
mannose-6-phosphate isomerase activity	GO:0004476
leptin receptor binding	GO:1990460
intramolecular oxidoreductase activity, ...	GO:0016861
transferrin receptor binding	GO:1990459
mitochondrial promoter sequence-specific...	GO:0001018
ATP-dependent peptidase activity	GO:0004176
SUMO binding	GO:0032183
interleukin-2 receptor binding	GO:0005134
arylformamidase activity	GO:0004061
protein phosphatase regulator activity	GO:0019888
protein serine/threonine phosphatase act...	GO:0004722
phosphatase regulator activity	GO:0019208
enzyme regulator activity	GO:0030234
RNA polymerase II transcription regulato...	GO:0000977
DNA polymerase binding	GO:0070182
protein antigen binding	GO:1990405
ferrous iron transmembrane transporter a...	GO:0015093
angiotensin receptor binding	GO:0031701
type 1 angiotensin receptor binding	GO:0031702
phosphatidate phosphatase activity	GO:0008195
nucleoside-triphosphatase regulator acti...	GO:0060589
protein-containing complex binding	GO:0044877
DNA-binding transcription factor activit...	GO:0003700
G-quadruplex DNA binding	GO:0051880
RNA polymerase II intronic transcription...	GO:0001162
fibroblast growth factor-activated recep...	GO:0005007
mRNA regulatory element binding translat...	GO:0000900

p=8.9E-03	n=5
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p=1.5E-02	n=1
p=1.5E-02	n=2
p=2.0E-02	n=2
p=2.0E-02	n=2
p=2.7E-02	n=6
p=2.8E-02	n=4
p=3.0E-02	n=1
p=3.0E-02	n=1
p=3.0E-02	n=1
p=3.0E-02	n=1
p=3.0E-02	n=1
p=3.5E-02	n=4
p=3.6E-02	n=6
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GO:CC
Elav_Nvec_vc1.1_XM_032366482.2

fraction genes in fg and expected value

protein phosphatase type 2A complex	GO:0000159
centriole	GO:0005814
excitatory synapse	GO:0060076
lamellipodium	GO:0030027
chromaffin granule	GO:0042583
chromaffin granule membrane	GO:0042584
cytosolic region	GO:0099522
postsynaptic cytosol	GO:0099524
T cell receptor complex	GO:0042101
growth cone membrane	GO:0032584
nucleoplasm	GO:0005654
sperm head	GO:0061827
cytoplasmic dynein complex	GO:0005868
organellar large ribosomal subunit	GO:0000315
mitochondrial large ribosomal subunit	GO:0005762
cell leading edge	GO:0031252
receptor complex	GO:0043235
messenger ribonucleoprotein complex	GO:1990124
mitochondrial nucleoid	GO:0042645
nucleoid	GO:0009295
Golgi cisterna membrane	GO:0032580
organellar ribosome	GO:0000313
mitochondrial ribosome	GO:0005761
dynein complex	GO:0030286
cytoplasm	GO:0005737
secretory granule membrane	GO:0030667
large ribosomal subunit	GO:0015934
azurophil granule membrane	GO:0035577
mitochondrion	GO:0005739
nuclear lumen	GO:0031981

p=1.8E-03	n=2
p=2.6E-03	n=3
p=2.7E-03	n=2
p=1.1E-02	n=3
p=1.4E-02	n=1
p=1.4E-02	n=1
p=2.8E-02	n=1
p=2.8E-02	n=1
p=2.8E-02	n=1
p=4.1E-02	n=1
p=5.2E-02	n=11
p=5.4E-02	n=1
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p=5.8E-02	n=3
p=6.7E-02	n=2
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p=8.0E-02	n=1
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