

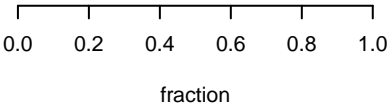
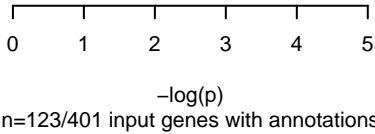
GO:BP
Elav_Nvec_vc1.1_XM_001636464.3

fraction genes in fg and expected value

negative regulation of peptidyl-threonin... GO:0010801
circadian regulation of gene expression GO:0032922
locomotor rhythm GO:0045475
negative regulation of cell population p... GO:0008285
G protein-coupled receptor internalizati... GO:0002031
germarium-derived egg chamber formation GO:0007293
follicle-stimulating hormone signaling p... GO:0042699
negative regulation of protein targeting... GO:0090315
estrogen metabolic process GO:0008210
germline ring canal formation GO:0030725
neuroblast fate specification GO:0014018
protein homooligomerization GO:0051260
adult behavior GO:0030534
response to light stimulus GO:0009416
energy reserve metabolic process GO:0006112
regulation of developmental process GO:0050793
regulation of circadian rhythm GO:0042752
regulation of DNA biosynthetic process GO:2000278
negative regulation of glucose transmemb... GO:0010829
cellular response to platelet-derived gr... GO:0036120
positive regulation of cell cycle G2/M p... GO:1902751
negative regulation of cellular macromol... GO:2000113
cellular polysaccharide metabolic proces... GO:0044264
regulation of actin filament organizatio... GO:0110053
positive regulation of behavior GO:0048520
positive regulation of macromolecule bio... GO:0010557
flavonoid metabolic process GO:0009812
positive regulation of transforming grow... GO:0071636
regulation of dendritic spine maintenanc... GO:1902950
primary miRNA processing GO:0031053

p=8.6E-04	n=3
p=1.1E-03	n=4
p=1.3E-03	n=5
p=1.6E-03	n=15
p=1.7E-03	n=3
p=2.0E-03	n=5
p=2.1E-03	n=2
p=2.1E-03	n=2
p=2.1E-03	n=2
p=2.1E-03	n=2
p=2.1E-03	n=2
p=2.3E-03	n=9
p=2.7E-03	n=10
p=2.9E-03	n=12
p=3.1E-03	n=5
p=3.4E-03	n=40
p=3.7E-03	n=6
p=4.3E-03	n=6
p=4.4E-03	n=3
p=4.4E-03	n=3
p=4.4E-03	n=3
p=4.6E-03	n=24
p=4.6E-03	n=5
p=4.6E-03	n=8
p=5.5E-03	n=5
p=5.8E-03	n=27
p=6.0E-03	n=2
p=6.0E-03	n=2
p=6.0E-03	n=2

fg=0.02	bg=0.00
fg=0.03	bg=0.00
fg=0.04	bg=0.01
fg=0.12	bg=0.05
fg=0.02	bg=0.00
fg=0.04	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.07	bg=0.02
fg=0.08	bg=0.03
fg=0.10	bg=0.04
fg=0.04	bg=0.01
fg=0.33	bg=0.22
fg=0.05	bg=0.01
fg=0.05	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.20	bg=0.11
fg=0.04	bg=0.01
fg=0.07	bg=0.02
fg=0.04	bg=0.01
fg=0.22	bg=0.14
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00



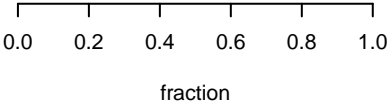
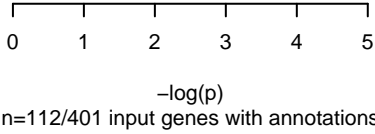
GO:MF
Elav_Nvec_vc1.1_XM_001636464.3

fraction genes in fg and expected value

cAMP response element binding GO:0035497
phosphatidylinositol-3,4,5-trisphosphate... GO:0034485
cAMP response element binding protein bi... GO:0008140
primary miRNA binding GO:0070878
double-stranded RNA binding GO:0003725
D1 dopamine receptor binding GO:0031748
inositol-1,3,4,5-tetrakisphosphate 5-pho... GO:0052659
inositol-polyphosphate 5-phosphatase act... GO:0004445
DNA-binding transcription repressor acti... GO:0001227
phosphatidylinositol-3,4,5-trisphosphate... GO:0005547
identical protein binding GO:0042802
protein kinase B binding GO:0043422
sequence-specific single stranded DNA bi... GO:0098847
acetylcholine receptor binding GO:0033130
arrestin family protein binding GO:1990763
DNA-binding transcription activator acti... GO:0001228
DNA-binding transcription activator acti... GO:0001216
GTPase activity GO:0003924
ribonuclease activity GO:0004540
mRNA 3'-UTR binding GO:0003730
SMAD binding GO:0046332
enzyme inhibitor activity GO:0004857
DEAD/H-box RNA helicase binding GO:0017151
adrenergic receptor binding GO:0031690
ferrous iron binding GO:0008198
lysophospholipase activity GO:0004622
potassium channel inhibitor activity GO:0019870
protein kinase binding GO:0019901
sodium:dicarboxylate symporter activity GO:0017153
oxidoreductase activity, acting on metal... GO:0016724

p=1.0E-04	n=3
p=2.2E-03	n=2
p=2.2E-03	n=2
p=2.2E-03	n=2
p=2.4E-03	n=4
p=6.4E-03	n=2
p=6.4E-03	n=2
p=6.4E-03	n=2
p=7.6E-03	n=5
p=8.7E-03	n=4
p=1.2E-02	n=29
p=1.3E-02	n=2
p=2.0E-02	n=2
p=2.0E-02	n=2
p=2.0E-02	n=2
p=2.1E-02	n=8
p=2.1E-02	n=8
p=2.4E-02	n=6
p=3.6E-02	n=4
p=3.7E-02	n=3
p=3.7E-02	n=3
p=4.0E-02	n=6
p=4.0E-02	n=2
p=4.0E-02	n=2
p=4.0E-02	n=2
p=4.0E-02	n=2
p=4.0E-02	n=2
p=4.0E-02	n=2
p=4.0E-02	n=2
p=4.2E-02	n=13
p=4.7E-02	n=1
p=4.7E-02	n=1

fg=0.03	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.04	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.04	bg=0.01
fg=0.04	bg=0.01
fg=0.26	bg=0.17
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.07	bg=0.03
fg=0.07	bg=0.03
fg=0.05	bg=0.02
fg=0.04	bg=0.01
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.05	bg=0.02
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.12	bg=0.07
fg=0.01	bg=0.00
fg=0.01	bg=0.00



GO:CC
Elav_Nvec_vc1.1_XM_001636464.3

fraction genes in fg and expected value

perinuclear region of cytoplasm GO:0048471
dendritic shaft GO:0043198
euchromatin GO:0000791
main axon GO:0044304
mitotic spindle pole GO:0097431
protein phosphatase type 1 complex GO:0000164
PML body GO:0016605
spindle GO:0005819
actin-based cell projection GO:0098858
autophagosome membrane GO:0000421
chromosomal region GO:0098687
intrinsic component of Golgi membrane GO:0031228
spindle midzone GO:0051233
neuron spine GO:0044309
dendritic spine GO:0043197
cell leading edge GO:0031252
cytoskeleton GO:0005856
protein serine/threonine phosphatase com... GO:0008287
spindle pole GO:0000922
transcription regulator complex GO:0005667
postsynapse GO:0098794
intermediate-density lipoprotein particl... GO:0034363
high-density lipoprotein particle GO:0034364
lipoprotein particle GO:1990777
ATF4-CREB1 transcription factor complex GO:1990589
plasma lipoprotein particle GO:0034358
triglyceride-rich plasma lipoprotein par... GO:0034385
amyloid-beta complex GO:0106003
nuclear mitotic cohesin complex GO:0034990
clathrin-sculpted gamma-aminobutyric aci... GO:0061200

p=7.5E-04	n=18
p=2.6E-03	n=5
p=3.9E-03	n=4
p=9.6E-03	n=4
p=1.2E-02	n=3
p=1.9E-02	n=2
p=1.9E-02	n=3
p=2.3E-02	n=9
p=2.7E-02	n=6
p=2.8E-02	n=2
p=2.8E-02	n=8
p=2.9E-02	n=3
p=2.9E-02	n=3
p=3.0E-02	n=6
p=3.0E-02	n=6
p=3.0E-02	n=9
p=3.4E-02	n=26
p=3.4E-02	n=3
p=3.4E-02	n=5
p=3.8E-02	n=9
p=3.8E-02	n=9
p=4.6E-02	n=1
p=4.6E-02	n=1
p=4.6E-02	n=1
p=4.6E-02	n=1
p=4.6E-02	n=1
p=4.6E-02	n=1
p=4.6E-02	n=1
p=4.6E-02	n=1
p=4.6E-02	n=1
p=4.6E-02	n=1

fg=0.15	bg=0.06
fg=0.04	bg=0.01
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.07	bg=0.03
fg=0.05	bg=0.02
fg=0.02	bg=0.00
fg=0.06	bg=0.03
fg=0.02	bg=0.01
fg=0.02	bg=0.01
fg=0.05	bg=0.02
fg=0.07	bg=0.04
fg=0.21	bg=0.15
fg=0.02	bg=0.01
fg=0.04	bg=0.01
fg=0.07	bg=0.04
fg=0.07	bg=0.04
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00

