

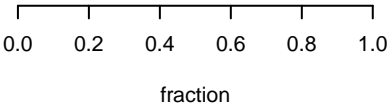
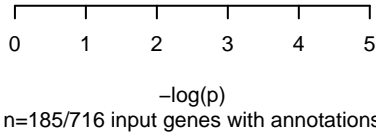
GO:BP
Elav_Nvec_vc1.1_XM_001638266.3

fraction genes in fg and expected value

aging	GO:0007568
response to morphine	GO:0043278
insulin receptor signaling pathway	GO:0008286
Ras protein signal transduction	GO:0007265
appendage morphogenesis	GO:0035107
embryonic morphogenesis	GO:0048598
positive regulation of cytosolic calcium...	GO:0007204
multi-organism reproductive process	GO:0044703
embryo development ending in birth or eg...	GO:0009792
response to nutrient	GO:0007584
response to ketone	GO:1901654
positive regulation of ion transmembrane...	GO:0032414
response to anesthetic	GO:0072347
negative regulation of signal transducti...	GO:0009968
cell fate specification	GO:0001708
response to electrical stimulus	GO:0051602
response to acid chemical	GO:0001101
somatic stem cell population maintenance	GO:0035019
oogenesis	GO:0048477
response to immobilization stress	GO:0035902
R7 cell fate commitment	GO:0007465
cellular response to epidermal growth fa...	GO:0071364
positive regulation of protein localizat...	GO:1903829
regulation of small GTPase mediated sign...	GO:0051056
negative regulation of synapse organizat...	GO:1905809
tube development	GO:0035295
actin-mediated cell contraction	GO:0070252
biological process involved in interspec...	GO:0044419
response to ammonium ion	GO:0060359
maintenance of location in cell	GO:0051651

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p=2.7E-04	n=5
p=3.1E-04	n=10
p=6.4E-04	n=15
p=7.7E-04	n=18
p=8.9E-04	n=27
p=1.2E-03	n=10
p=1.2E-03	n=46
p=1.3E-03	n=32
p=1.3E-03	n=15
p=1.5E-03	n=11
p=1.6E-03	n=6
p=1.7E-03	n=7
p=1.9E-03	n=34
p=2.0E-03	n=11
p=2.1E-03	n=4
p=2.2E-03	n=14
p=2.2E-03	n=6
p=2.8E-03	n=25
p=2.9E-03	n=3
p=2.9E-03	n=3
p=3.2E-03	n=4
p=3.4E-03	n=16
p=3.5E-03	n=10
p=3.6E-03	n=6
p=4.0E-03	n=39
p=4.1E-03	n=7
p=4.2E-03	n=31
p=4.4E-03	n=9
p=4.5E-03	n=10

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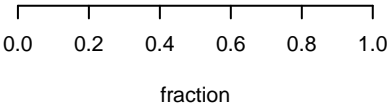
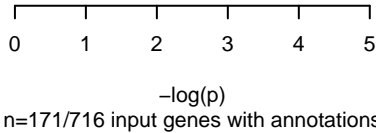
GO:MF
Elav_Nvec_vc1.1_XM_001638266.3

fraction genes in fg and expected value

mRNA regulatory element binding translat...	GO:0000900
phosphotyrosine residue binding	GO:0001784
G protein-coupled receptor binding	GO:0001664
mRNA 3'-UTR binding	GO:0003730
BH3 domain binding	GO:0051434
sodium:phosphate symporter activity	GO:0005436
adenylate cyclase activity	GO:0004016
acid-ammonia (or amide) ligase activity	GO:0016880
DNA-binding transcription factor activit...	GO:0003700
transcription regulatory region nucleic ...	GO:0001067
dopamine receptor binding	GO:0050780
ribosome binding	GO:0043022
phosphate ion transmembrane transporter ...	GO:0015114
double-stranded DNA binding	GO:0003690
lipid binding	GO:0008289
protein-disulfide reductase (NAD(P)) act...	GO:0047134
RNA polymerase II transcription regulato...	GO:0000977
sequence-specific DNA binding	GO:0043565
ATPase-coupled ion transmembrane transpo...	GO:0042625
sequence-specific double-stranded DNA bi...	GO:1990837
DNA binding	GO:0003677
transcription cis-regulatory region bind...	GO:0000976
guanylate cyclase activity	GO:0004383
glycolipid binding	GO:0051861
Lys63-specific deubiquitinase activity	GO:0061578
bHLH transcription factor binding	GO:0043425
oxidoreductase activity, acting on a sul...	GO:0016668
P-type transmembrane transporter activit...	GO:0140358
P-type ion transporter activity	GO:0015662
frizzled binding	GO:0005109

p=3.7E-04	n=3
p=1.5E-03	n=4
p=2.0E-03	n=9
p=4.2E-03	n=5
p=5.2E-03	n=2
p=5.2E-03	n=2
p=5.2E-03	n=2
p=5.2E-03	n=2
p=7.1E-03	n=21
p=1.0E-02	n=17
p=1.0E-02	n=3
p=1.5E-02	n=4
p=1.5E-02	n=2
p=2.0E-02	n=17
p=2.2E-02	n=15
p=2.2E-02	n=3
p=2.3E-02	n=13
p=2.4E-02	n=18
p=2.4E-02	n=4
p=2.5E-02	n=15
p=2.6E-02	n=29
p=2.8E-02	n=14
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p=2.8E-02	n=2
p=3.0E-02	n=3
p=3.0E-02	n=3
p=3.0E-02	n=3

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GO:CC
Elav_Nvec_vc1.1_XM_001638266.3

fraction genes in fg and expected value

mitochondrial permeability transition po...	GO:0005757
plasma membrane	GO:0005886
preribosome	GO:0030684
ciliary rootlet	GO:0035253
TORC1 complex	GO:0031931
TOR complex	GO:0038201
Bcl-2 family protein complex	GO:0097136
dendrite membrane	GO:0032590
DNA repair complex	GO:1990391
proton-transporting V-type ATPase comple...	GO:0033176
intrinsic component of plasma membrane	GO:0031226
plasma membrane region	GO:0098590
Golgi lumen	GO:0005796
myofilament	GO:0036379
guanylate cyclase complex, soluble	GO:0008074
striated muscle thin filament	GO:0005865
dendritic spine membrane	GO:0032591
subapical complex	GO:0035003
growth cone lamellipodium	GO:1990761
proton-transporting two-sector ATPase co...	GO:0016469
cell cortex	GO:0005938
integral component of plasma membrane	GO:0005887
I band	GO:0031674
cell-cell junction	GO:0005911
anchoring junction	GO:0070161
small-subunit processome	GO:0032040
cortical actin cytoskeleton	GO:0030864
sperm midpiece	GO:0097225
plasma membrane proton-transporting V-ty...	GO:0033181
rough endoplasmic reticulum membrane	GO:0030867

p=5.0E-03	n=2
p=5.5E-03	n=60
p=1.4E-02	n=6
p=1.4E-02	n=2
p=1.4E-02	n=2
p=1.4E-02	n=2
p=1.4E-02	n=2
p=1.5E-02	n=3
p=1.5E-02	n=3
p=1.5E-02	n=3
p=1.9E-02	n=21
p=2.1E-02	n=24
p=2.1E-02	n=3
p=2.7E-02	n=2
p=2.7E-02	n=2
p=2.7E-02	n=2
p=2.7E-02	n=2
p=2.7E-02	n=2
p=2.7E-02	n=2
p=2.9E-02	n=3
p=3.1E-02	n=12
p=3.3E-02	n=19
p=4.3E-02	n=6
p=4.7E-02	n=13
p=4.7E-02	n=13
p=4.8E-02	n=3
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