

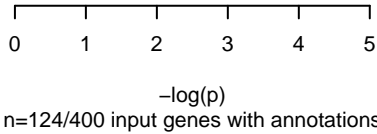
GO:BP
Fox_Nvec_vc1.1_XM_048719424.1

fraction genes in fg and expected value

receptor-mediated endocytosis	GO:0006898
positive regulation of multicellular org...	GO:0040018
actin cytoskeleton organization	GO:0030036
globoside metabolic process	GO:0001575
plasma membrane raft assembly	GO:0044854
lysosomal lumen pH elevation	GO:0035752
pH elevation	GO:0045852
mesectoderm development	GO:0048383
cellular response to exogenous dsRNA	GO:0071360
establishment or maintenance of cytoskel...	GO:0003380
regulation of signal transduction	GO:0009966
neuromuscular process controlling balanc...	GO:0050885
import into cell	GO:0098657
pH reduction	GO:0045851
neuron projection morphogenesis	GO:0048812
intracellular pH reduction	GO:0051452
positive regulation of skeletal muscle t...	GO:0048643
regulation of mitochondrial outer membra...	GO:1901028
cell morphogenesis involved in neuron di...	GO:0048667
cellular response to heat	GO:0034605
negative regulation of biological proces...	GO:0048519
regulation of cell communication by elec...	GO:0010649
positive regulation of protein sumoylati...	GO:0033235
lumen formation, open tracheal system	GO:0035149
post-embryonic body morphogenesis	GO:0040032
microvillus assembly	GO:0030033
glucosylceramide metabolic process	GO:0006678
eye morphogenesis	GO:0048592
negative regulation of mitochondrion org...	GO:0010823
nucleotide-excision repair, DNA gap fill...	GO:0006297

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p=1.7E-03	n=6
p=1.9E-03	n=16
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p=2.6E-03	n=41
p=2.6E-03	n=5
p=2.8E-03	n=14
p=3.0E-03	n=4
p=3.2E-03	n=20
p=3.9E-03	n=4
p=4.5E-03	n=3
p=4.5E-03	n=3
p=4.8E-03	n=19
p=5.2E-03	n=6
p=5.7E-03	n=65
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p=6.2E-03	n=11
p=6.3E-03	n=4
p=6.5E-03	n=3

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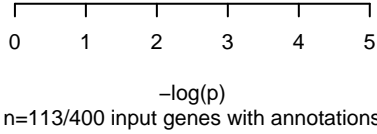
GO:MF
Fox_Nvec_vc1.1_XM_048719424.1

fraction genes in fg and expected value

G-protein beta/gamma-subunit complex bin...	GO:0031683
structural constituent of cytoskeleton	GO:0005200
spectrin binding	GO:0030507
ATPase-coupled ion transmembrane transpo...	GO:0042625
5S rRNA binding	GO:0008097
calcium-dependent protein binding	GO:0048306
phospholipid transporter activity	GO:0005548
calcium channel regulator activity	GO:0005246
signaling receptor binding	GO:0005102
active ion transmembrane transporter act...	GO:0022853
BH domain binding	GO:0051400
intramembrane lipid transporter activity	GO:0140303
proteoglycan binding	GO:0043394
ATPase-coupled cation transmembrane tran...	GO:0019829
histone deacetylase binding	GO:0042826
amino acid binding	GO:0016597
DNA binding	GO:0003677
ubiquitin protein ligase binding	GO:0031625
3R-hydroxyacyl-CoA dehydratase activity	GO:0080023
tRNA-intron endonuclease activity	GO:0000213
purine-specific nucleoside:sodium sympor...	GO:0015390
nucleobase:cation symporter activity	GO:0015391
misfolded RNA binding	GO:0034336
beta-1,4-N-acetylgalactosaminyltransfera...	GO:0033207
pyrimidine nucleobase transmembrane tran...	GO:0005350
mono-olein transacylation activity	GO:0051264
diolein transacylation activity	GO:0051265
BH2 domain binding	GO:0051433
phosphatidylglycerol binding	GO:1901611
cardiolipin binding	GO:1901612

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p=2.7E-02	n=18
p=2.9E-02	n=6
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p=3.0E-02	n=2
p=3.2E-02	n=3
p=3.3E-02	n=4
p=3.8E-02	n=3
p=4.0E-02	n=20
p=4.7E-02	n=8
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GO:CC
Fox_Nvec_vc1.1_XM_048719424.1

fraction genes in fg and expected value

heterotrimeric G-protein complex	GO:0005834
uropod	GO:0001931
collagen and cuticulin-based cuticle ext...	GO:0060102
microvillus membrane	GO:0031528
caveola	GO:0005901
I band	GO:0031674
vacuolar proton-transporting V-type ATPa...	GO:0000221
FAR/SIN/STRIPAK complex	GO:0090443
clathrin-coated pit	GO:0005905
cytosolic large ribosomal subunit	GO:0022625
sarcolemma	GO:0042383
postsynaptic density	GO:0014069
cell leading edge	GO:0031252
recycling endosome membrane	GO:0055038
eukaryotic translation initiation factor...	GO:0071541
somatodendritic compartment	GO:0036477
dendrite	GO:0030425
dendritic tree	GO:0097447
Z disc	GO:0030018
T-tubule	GO:0030315
pericentriolar material	GO:0000242
sperm fibrous sheath	GO:0035686
sensory dendrite	GO:0071683
neuron projection	GO:0043005
axon cytoplasm	GO:1904115
plasma membrane proton-transporting V-ty...	GO:0033181
eukaryotic translation initiation factor...	GO:0005852
postsynaptic membrane	GO:0045211
ATPase complex	GO:1904949
side of membrane	GO:0098552

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p=5.5E-03	n=6
p=5.9E-03	n=2
p=5.9E-03	n=2
p=6.2E-03	n=3
p=6.3E-03	n=5
p=6.3E-03	n=5
p=6.4E-03	n=7
p=1.0E-02	n=10
p=1.1E-02	n=3
p=1.1E-02	n=2
p=1.4E-02	n=18
p=1.4E-02	n=14
p=1.5E-02	n=14
p=1.7E-02	n=5
p=1.8E-02	n=3
p=1.8E-02	n=2
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p=2.7E-02	n=2
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