

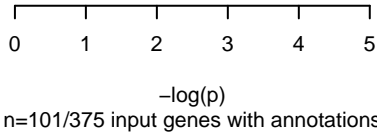
GO:BP  
Fox\_Nvec\_vc1.1\_XM\_032374382.2

fraction genes in fg and expected value

coronary vasculature development	GO:0060976
protein stabilization	GO:0050821
cell migration involved in gastrulation	GO:0042074
negative regulation of gliogenesis	GO:0014014
oligodendrocyte development	GO:0014003
canonical glycolysis	GO:0061621
androgen receptor signaling pathway	GO:0030521
positive regulation of transport	GO:0051050
ammonium ion metabolic process	GO:0097164
negative regulation of protein modificat...	GO:1903321
somatic muscle development	GO:0007525
regulation of protein ubiquitination	GO:0031396
posterior lateral line development	GO:0048916
indole-containing compound metabolic pro...	GO:0042430
bone morphogenesis	GO:0060349
positive regulation of DNA binding	GO:0043388
negative regulation of proteasomal ubiqu...	GO:0032435
glial cell proliferation	GO:0014009
intermediate filament cytoskeleton organ...	GO:0045104
lung-associated mesenchyme development	GO:0060484
limb bud formation	GO:0060174
sphingomyelin metabolic process	GO:0006684
positive regulation of epithelial to mes...	GO:0010718
export from cell	GO:0140352
leukocyte mediated immunity	GO:0002443
organonitrogen compound catabolic proces...	GO:1901565
positive regulation of locomotion	GO:0040017
histone exchange	GO:0043486
regulation of membrane lipid distributio...	GO:0097035
negative regulation of protein ubiquitin...	GO:0031397

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p=7.6E-03	n=3
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p=1.3E-02	n=11
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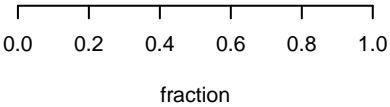
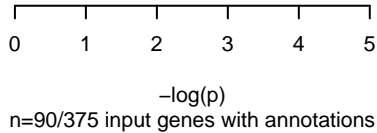
GO:MF  
Fox\_Nvec\_vc1.1\_XM\_032374382.2

fraction genes in fg and expected value

phosphoric diester hydrolase activity	GO:0008081
histone binding	GO:0042393
heparan-alpha-glucosaminide N-acetyltran...	GO:0015019
nitric-oxide synthase binding	GO:0050998
ubiquitin conjugating enzyme activity	GO:0061631
translation initiation factor activity	GO:0003743
ATPase-coupled cation transmembrane tran...	GO:0019829
ubiquitin-like protein conjugating enzym...	GO:0061650
ligase activity, forming carbon-sulfur b...	GO:0016877
misfolded protein binding	GO:0051787
ATPase-coupled ion transmembrane transpo...	GO:0042625
2-oxoglutarate-dependent dioxygenase act...	GO:0016706
nuclear receptor binding	GO:0016922
heparin binding	GO:0008201
dioxygenase activity	GO:0051213
CoA carboxylase activity	GO:0016421
sphingomyelin phosphodiesterase D activi...	GO:0050290
ubiquitin-protein transferase inhibitor ...	GO:0055105
RNA strand-exchange activity	GO:0034057
sodium:phosphate symporter activity	GO:0005436
leptin receptor binding	GO:1990460
glyceraldehyde-3-phosphate dehydrogenase...	GO:0004365
phosphate ion binding	GO:0042301
transferrin receptor binding	GO:1990459
intracellular sodium activated potassium...	GO:0005228
phosphatidylglycerol binding	GO:1901611
cardiolipin binding	GO:1901612
ATPase-coupled intramembrane lipid trans...	GO:0140326
flippase activity	GO:0140327
aminophospholipid flippase activity	GO:0015247

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p=2.6E-02	n=3
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p=2.8E-02	n=2
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p=4.1E-02	n=2
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GO:CC  
Fox\_Nvec\_vc1.1\_XM\_032374382.2

fraction genes in fg and expected value

microvillus membrane	GO:0031528
tertiary granule membrane	GO:0070821
specific granule membrane	GO:0035579
extrinsic component of membrane	GO:0019898
large ribosomal subunit	GO:0015934
lysosomal membrane	GO:0005765
Z disc	GO:0030018
mediator complex	GO:0016592
nuclear membrane	GO:0031965
Cul2-RING ubiquitin ligase complex	GO:0031462
cytosolic large ribosomal subunit	GO:0022625
eukaryotic translation initiation factor...	GO:0005851
9+2 motile cilium	GO:0097729
sperm principal piece	GO:0097228
sperm fibrous sheath	GO:0035686
trans-Golgi network	GO:0005802
brush border membrane	GO:0031526
acrosomal vesicle	GO:0001669
dynein complex	GO:0030286
caveola	GO:0005901
early endosome membrane	GO:0031901
eukaryotic translation initiation factor...	GO:0016281
molybdopterin synthase complex	GO:0019008
RNA polymerase III transcription regulat...	GO:0090576
dihydrolipoyl dehydrogenase complex	GO:0045240
beta-catenin-TCF7L2 complex	GO:0070369
synaptic cleft	GO:0043083
DNA replication factor C complex	GO:0005663
Swi5-Swi2 complex	GO:0034974
transcription factor TFIIC complex	GO:0000127

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p=9.8E-03	n=5
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