

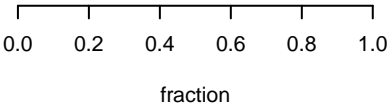
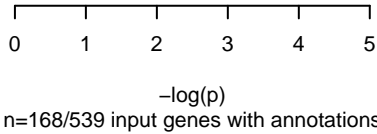
GO:BP
Fox_Nvec_vc1.1_XM_032377897.2

fraction genes in fg and expected value

sensory perception of smell	GO:0007608
melanosome transport	GO:0032402
Fc-gamma receptor signaling pathway invo...	GO:0038096
SRP-dependent cotranslational protein ta...	GO:0006614
suckling behavior	GO:0001967
detection of chemical stimulus	GO:0009593
regulation of organelle transport along ...	GO:1902513
microtubule anchoring at centrosome	GO:0034454
positive regulation of anion transmembra...	GO:1903961
negative regulation of transcription fro...	GO:1990441
positive regulation of bone resorption	GO:0045780
positive regulation of bone remodeling	GO:0046852
adipose tissue development	GO:0060612
regulation of establishment or maintenanc...	GO:0032878
ephrin receptor signaling pathway	GO:0048013
nuclear-transcribed mRNA catabolic proce...	GO:0000184
pseudouridine synthesis	GO:0001522
positive regulation of phosphatidylinosi...	GO:0014068
translational initiation	GO:0006413
locomotion	GO:0040011
regulation of anoikis	GO:2000209
peptide transport	GO:0015833
response to interleukin-2	GO:0070669
regulation of retina development in came...	GO:1902866
regulation of amino acid transmembrane t...	GO:1903789
vestibulocochlear nerve development	GO:0021562
regulation of neural retina development	GO:0061074
maintenance of lens transparency	GO:0036438
negative regulation of transcription by ...	GO:0016479
mitochondrial unfolded protein response	GO:0034514

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p=9.0E-04	n=3
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p=1.9E-03	n=7
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p=3.4E-03	n=4
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p=3.9E-03	n=2
p=4.1E-03	n=3
p=4.8E-03	n=4
p=4.8E-03	n=4
p=5.7E-03	n=7
p=6.9E-03	n=3
p=6.9E-03	n=3
p=9.5E-03	n=9
p=9.9E-03	n=40
p=1.1E-02	n=3
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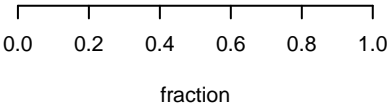
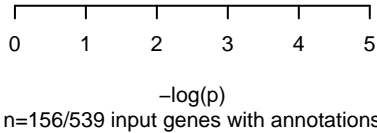
GO:MF
Fox_Nvec_vc1.1_XM_032377897.2

fraction genes in fg and expected value

ephrin receptor binding	GO:0046875
structural molecule activity	GO:0005198
NADPH binding	GO:0070402
signaling adaptor activity	GO:0035591
telomerase RNA binding	GO:0070034
mitogen-activated protein kinase kinase ...	GO:0031435
structural constituent of ribosome	GO:0003735
phosphotyrosine residue binding	GO:0001784
LIM domain binding	GO:0030274
macrolide binding	GO:0005527
FK506 binding	GO:0005528
MAP-kinase scaffold activity	GO:0005078
protein phosphorylated amino acid bindin...	GO:0045309
enzyme binding	GO:0019899
promoter-specific chromatin binding	GO:1990841
cytoskeletal protein binding	GO:0008092
5S rRNA binding	GO:0008097
JUN kinase binding	GO:0008432
glucosidase activity	GO:0015926
SH2 domain binding	GO:0042169
pentosyltransferase activity	GO:0016763
GTPase binding	GO:0051020
small GTPase binding	GO:0031267
guanyl-nucleotide exchange factor activi...	GO:0005085
GTPase regulator activity	GO:0030695
nucleoside-triphosphatase regulator acti...	GO:0060589
extracellular matrix binding	GO:0050840
phosphatidylinositol 3-kinase binding	GO:0043548
dynactin binding	GO:0034452
histone acetyltransferase activity	GO:0004402

p=2.5E-03	n=3
p=3.4E-03	n=16
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p=8.1E-03	n=3
p=1.1E-02	n=9
p=1.2E-02	n=3
p=1.2E-02	n=2
p=2.4E-02	n=2
p=2.4E-02	n=2
p=2.4E-02	n=2
p=2.4E-02	n=3
p=2.5E-02	n=47
p=3.1E-02	n=3
p=3.8E-02	n=19
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p=4.0E-02	n=3
p=4.1E-02	n=14
p=4.3E-02	n=12
p=4.4E-02	n=6
p=4.8E-02	n=11
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GO:CC
Fox_Nvec_vc1.1_XM_032377897.2

fraction genes in fg and expected value

cytosolic large ribosomal subunit	GO:0022625
intracellular anatomical structure	GO:0005622
EARP complex	GO:1990745
GARP complex	GO:0000938
filamentous actin	GO:0031941
telomerase holoenzyme complex	GO:0005697
cytoplasmic side of membrane	GO:0098562
extrinsic component of cytoplasmic side ...	GO:0031234
exocytic vesicle	GO:0070382
cytoplasmic side of plasma membrane	GO:0009898
sno(s)RNA-containing ribonucleoprotein c...	GO:0005732
eukaryotic translation initiation factor...	GO:0005852
axon cytoplasm	GO:1904115
dendrite terminus	GO:0044292
plasma membrane proton-transporting V-ty...	GO:0033181
transport vesicle	GO:0030133
actin cytoskeleton	GO:0015629
phagolysosome	GO:0032010
Yb body	GO:0070725
anchored component of synaptic vesicle m...	GO:0098993
smooth septate junction	GO:0005920
kinesin II complex	GO:0016939
FACT complex	GO:0035101
NMDA selective glutamate receptor comple...	GO:0017146
sarcoplasmic reticulum lumen	GO:0033018
bub1-bub3 complex	GO:1990298
signal recognition particle	GO:0048500
synaptic cleft	GO:0043083
synaptobrevin 2-SNAP-25-syntaxin-1a-comp...	GO:0070032
axonemal heterotrimeric kinesin-II compl...	GO:0030993

p=9.8E-04	n=7
p=3.6E-03	n=166
p=1.1E-02	n=2
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p=2.1E-02	n=2
p=3.4E-02	n=2
p=3.6E-02	n=8
p=3.8E-02	n=4
p=3.9E-02	n=8
p=4.7E-02	n=7
p=4.9E-02	n=2
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p=6.0E-02	n=10
p=6.1E-02	n=9
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