

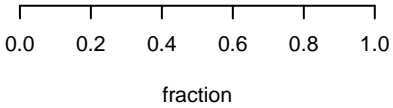
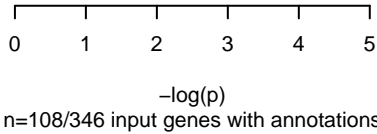
GO:BP
Fox_Nvec_vc1.1_XM_001627049.3

fraction genes in fg and expected value

developmental process involved in reprod...	GO:0003006
negative regulation of cellular macromol...	GO:2000113
gamete generation	GO:0007276
negative regulation of gene expression	GO:0010629
regulation of mitochondrial membrane pot...	GO:0051881
negative regulation of transcription, DN...	GO:0045892
liver morphogenesis	GO:0072576
negative regulation by host of viral gen...	GO:0044828
positive regulation of cellular componen...	GO:0051130
osteoclast differentiation	GO:0030316
regulation of R7 cell differentiation	GO:0045676
cardiac ventricle morphogenesis	GO:0003208
positive regulation of neuron differenti...	GO:0045666
multi-organism reproductive process	GO:0044703
negative regulation of T cell proliferat...	GO:0042130
imaginal disc growth	GO:0007446
cellular response to organonitrogen comp...	GO:0071417
cellular process involved in reproductio...	GO:0022412
regulation of protein catabolic process	GO:0042176
regulation of retina development in came...	GO:1902866
regulation of neural retina development	GO:0061074
modulation by virus of host cellular pro...	GO:0019054
deoxynucleotide transport	GO:0030302
pyrimidine nucleotide import into mitoch...	GO:1990519
negative regulation of protein modificat...	GO:0031400
neuron projection development	GO:0031175
response to gravity	GO:0009629
transmembrane receptor protein tyrosine ...	GO:0007169
positive regulation of neurogenesis	GO:0050769
nematode larval development	GO:0002119

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p=1.6E-03	n=2
p=1.6E-03	n=2
p=1.8E-03	n=23
p=1.8E-03	n=5
p=1.9E-03	n=3
p=2.4E-03	n=4
p=2.9E-03	n=11
p=3.0E-03	n=29
p=3.0E-03	n=3
p=3.0E-03	n=3
p=3.1E-03	n=14
p=3.6E-03	n=22
p=4.1E-03	n=11
p=4.6E-03	n=2
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p=4.6E-03	n=2
p=4.6E-03	n=2
p=4.6E-03	n=2
p=4.7E-03	n=13
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p=6.7E-03	n=12
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fg=0.09	bg=0.04



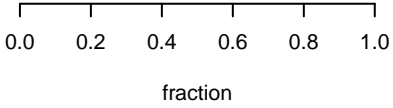
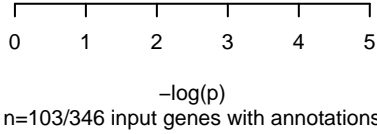
GO:MF
Fox_Nvec_vc1.1_XM_001627049.3

fraction genes in fg and expected value

DNA-binding transcription repressor acti...	GO:0001227
single-stranded DNA binding	GO:0003697
DNA replication origin binding	GO:0003688
phosphotyrosine residue binding	GO:0001784
channel regulator activity	GO:0016247
RNA polymerase II cis-regulatory region ...	GO:0000978
myosin binding	GO:0017022
pyrimidine nucleotide transmembrane tran...	GO:0015218
DNA-binding transcription factor activit...	GO:0003700
DNA-binding transcription activator acti...	GO:0001228
DNA-binding transcription activator acti...	GO:0001216
ion channel regulator activity	GO:0099106
potassium channel regulator activity	GO:0015459
chromatin binding	GO:0003682
sodium channel regulator activity	GO:0017080
transcription factor binding	GO:0008134
protein phosphatase regulator activity	GO:0019888
aryl hydrocarbon receptor binding	GO:0017162
mRNA 5'-UTR binding	GO:0048027
cyclase activity	GO:0009975
RNA polymerase II-specific DNA-binding t...	GO:0061629
mRNA 3'-UTR binding	GO:0003730
DNA helicase activity	GO:0003678
ligand-activated transcription factor ac...	GO:0098531
chloride channel regulator activity	GO:0017081
nuclear receptor activity	GO:0004879
adenylate cyclase binding	GO:0008179
ubiquitin-specific protease binding	GO:1990381
enzyme binding	GO:0019899
DNA-binding transcription factor binding	GO:0140297

p=1.0E-04	n=7
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p=3.8E-03	n=3
p=3.9E-03	n=6
p=4.5E-03	n=9
p=4.5E-03	n=5
p=5.5E-03	n=2
p=1.0E-02	n=19
p=1.3E-02	n=8
p=1.3E-02	n=8
p=1.4E-02	n=5
p=1.7E-02	n=3
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p=2.5E-02	n=2
p=2.5E-02	n=6
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p=3.0E-02	n=3
p=3.4E-02	n=2
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GO:CC
Fox_Nvec_vc1.1_XM_001627049.3

fraction genes in fg and expected value

Lewy body	GO:0097413
immunological synapse	GO:0001772
nucleus	GO:0005634
postsynaptic density	GO:0014069
myelin sheath abaxonal region	GO:0035748
chromatin	GO:0000785
transcription regulator complex	GO:0005667
lysosome	GO:0005764
microvillus	GO:0005902
nuclear lumen	GO:0031981
lysosomal membrane	GO:0005765
nuclear chromosome	GO:0000228
supramolecular complex	GO:0099080
intrinsic component of the cytoplasmic s...	GO:0031235
dendrite	GO:0030425
dendritic tree	GO:0097447
lytic vacuole membrane	GO:0098852
cytoplasmic side of plasma membrane	GO:0009898
spindle pole centrosome	GO:0031616
somatodendritic compartment	GO:0036477
excitatory synapse	GO:0060076
neuron projection	GO:0043005
cytoplasmic side of membrane	GO:0098562
sperm connecting piece	GO:0097224
junctional membrane complex	GO:0030314
apicomedial cortex	GO:0106037
junctional sarcoplasmic reticulum membra...	GO:0014701
microvesicle	GO:1990742
AP-4 adaptor complex	GO:0030124
dense core granule membrane	GO:0032127

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p=4.0E-03	n=7
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p=5.8E-03	n=12
p=7.5E-03	n=10
p=9.2E-03	n=11
p=9.7E-03	n=4
p=1.3E-02	n=50
p=1.3E-02	n=6
p=1.4E-02	n=11
p=1.5E-02	n=16
p=1.6E-02	n=2
p=1.6E-02	n=13
p=1.7E-02	n=13
p=2.1E-02	n=6
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p=2.3E-02	n=2
p=2.6E-02	n=16
p=3.1E-02	n=2
p=3.7E-02	n=20
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p=4.2E-02	n=1
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