

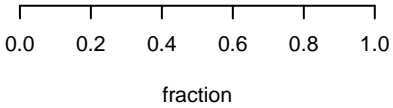
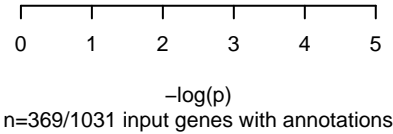
GO:BP
Fox_Nvec_vc1.1_XM_001623131.3

fraction genes in fg and expected value

mitochondrial translational termination	GO:0070126
mitochondrial translational elongation	GO:0070125
negative regulation of protein export fr...	GO:0046826
electron transport chain	GO:0022900
oxidative phosphorylation	GO:0006119
carbohydrate phosphorylation	GO:0046835
negative regulation of hippo signaling	GO:0035331
peripheral nervous system neuron develop...	GO:0048935
mitral valve morphogenesis	GO:0003183
larval midgut histolysis	GO:0035069
eIF2alpha phosphorylation in response to...	GO:0036492
snRNA metabolic process	GO:0016073
snRNA processing	GO:0016180
intra-Golgi vesicle-mediated transport	GO:0006891
mRNA metabolic process	GO:0016071
ATP synthesis coupled electron transport	GO:0042773
mitochondrial ATP synthesis coupled elec...	GO:0042775
mitochondrial electron transport, NADH t...	GO:0006120
snRNA 3'-end processing	GO:0034472
dauer exit	GO:0043054
snRNA transport	GO:0051030
MDA-5 signaling pathway	GO:0039530
regulation of MDA-5 signaling pathway	GO:0039533
negative regulation of MDA-5 signaling p...	GO:0039534
peptidyl-arginine hydroxylation	GO:0030961
glycophagy	GO:0061723
positive regulation of interferon-beta p...	GO:0032728
regulation of vacuolar transport	GO:1903335
lysosomal membrane organization	GO:0097212
exit from diapause	GO:0071981

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p=2.2E-03	n=8
p=2.5E-03	n=3
p=2.8E-03	n=13
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p=6.5E-03	n=5
p=8.6E-03	n=4
p=8.6E-03	n=4
p=9.1E-03	n=3
p=9.1E-03	n=3
p=9.1E-03	n=3
p=9.5E-03	n=9
p=1.1E-02	n=5
p=1.1E-02	n=5
p=1.4E-02	n=37
p=1.5E-02	n=8
p=1.5E-02	n=8
p=1.5E-02	n=6
p=1.5E-02	n=4
p=1.9E-02	n=2
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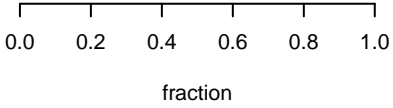
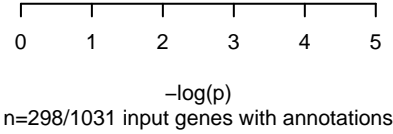
GO:MF
Fox_Nvec_vc1.1_XM_001623131.3

fraction genes in fg and expected value

structural constituent of ribosome	GO:0003735
electron transfer activity	GO:0009055
mRNA binding	GO:0003729
eukaryotic translation initiation factor...	GO:0004694
NADPH binding	GO:0070402
eukaryotic initiation factor eIF2 bindin...	GO:0071074
NADH dehydrogenase activity	GO:0003954
oxidoreductase activity, acting on NAD(P...	GO:0016655
GTPase activating protein binding	GO:0032794
oxidoreductase activity, acting on NAD(P...	GO:0016651
proton transmembrane transporter activit...	GO:0015078
protein tyrosine kinase binding	GO:1990782
primary active transmembrane transporter...	GO:0015399
phosphotransferase activity, alcohol gro...	GO:0016773
protein serine/threonine kinase activato...	GO:0043539
proton channel activity	GO:0015252
ribosomal small subunit binding	GO:0043024
carbohydrate kinase activity	GO:0019200
oxidoreduction-driven active transmembra...	GO:0015453
NADH dehydrogenase (quinone) activity	GO:0050136
NAD(P)H dehydrogenase (quinone) activity	GO:0003955
NADH dehydrogenase (ubiquinone) activity	GO:0008137
protein serine/threonine kinase activity	GO:0004674
phosphotyrosine residue binding	GO:0001784
G-protein alpha-subunit binding	GO:0001965
receptor tyrosine kinase binding	GO:0030971
Lys63-specific deubiquitinase activity	GO:0061578
phosphatidylinositol phosphate 4-phospha...	GO:0034596
palmitoyl-(protein) hydrolase activity	GO:0008474
bHLH transcription factor binding	GO:0043425

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p=9.0E-03	n=9
p=9.7E-03	n=17
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p=1.6E-02	n=3
p=1.7E-02	n=5
p=2.3E-02	n=5
p=2.8E-02	n=4
p=3.3E-02	n=8
p=4.0E-02	n=6
p=4.1E-02	n=5
p=4.2E-02	n=10
p=4.3E-02	n=26
p=4.3E-02	n=2
p=4.3E-02	n=2
p=4.7E-02	n=3
p=4.7E-02	n=3
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p=5.9E-02	n=18
p=6.8E-02	n=3
p=6.8E-02	n=3
p=7.0E-02	n=4
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GO:CC
Fox_Nvec_vc1.1_XM_001623131.3

fraction genes in fg and expected value

catalytic complex	GO:1902494
proton-transporting two-sector ATPase co...	GO:0016469
U2 snRNP	GO:0005686
mitochondrial inner membrane	GO:0005743
mitochondrial large ribosomal subunit	GO:0005762
small ribosomal subunit	GO:0015935
spliceosomal complex	GO:0005681
NADH dehydrogenase complex	GO:0030964
mitochondrial respiratory chain complex ...	GO:0005747
respiratory chain complex I	GO:0045271
protein serine/threonine phosphatase com...	GO:0008287
organellar ribosome	GO:0000313
mitochondrial ribosome	GO:0005761
organellar small ribosomal subunit	GO:0000314
mitochondrial small ribosomal subunit	GO:0005763
U12-type spliceosomal complex	GO:0005689
mitochondrial protein-containing complex	GO:0098798
Atg12-Atg5-Atg16 complex	GO:0034274
mitochondrial proton-transporting ATP sy...	GO:0000275
mitochondrial proton-transporting ATP sy...	GO:0005753
proton-transporting ATP synthase complex...	GO:0045261
proton-transporting ATP synthase complex	GO:0045259
nuclear DNA-directed RNA polymerase comp...	GO:0055029
proton-transporting two-sector ATPase co...	GO:0033178
ribosome	GO:0005840
DNA-directed RNA polymerase complex	GO:0000428
MKS complex	GO:0036038
RNA polymerase II, holoenzyme	GO:0016591
phosphatase complex	GO:1903293
RNA polymerase complex	GO:0030880

p=2.4E-03	n=70
p=6.0E-03	n=5
p=8.1E-03	n=4
p=9.2E-03	n=24
p=9.9E-03	n=5
p=1.0E-02	n=8
p=1.1E-02	n=12
p=1.4E-02	n=6
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p=1.4E-02	n=6
p=1.4E-02	n=9
p=1.4E-02	n=9
p=1.4E-02	n=4
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p=1.4E-02	n=4
p=1.6E-02	n=4
p=1.8E-02	n=18
p=1.8E-02	n=2
p=1.8E-02	n=2
p=1.8E-02	n=2
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p=1.8E-02	n=12
p=2.0E-02	n=3
p=2.0E-02	n=19
p=2.2E-02	n=12
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p=2.5E-02	n=10
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