

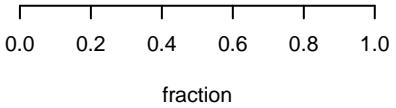
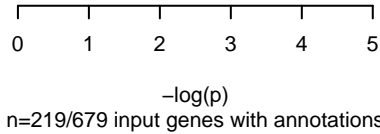
GO:BP
Fox_Nvec_vc1.1_XM_001640853.3

fraction genes in fg and expected value

negative regulation of smoothened signal...	GO:1901621
negative regulation of embryonic develop...	GO:0045992
organic substance catabolic process	GO:1901575
protein targeting to membrane	GO:0006612
amide transport	GO:0042886
cellular catabolic process	GO:0044248
nuclear export	GO:0051168
photoreactive repair	GO:0000719
nephric duct formation	GO:0072179
negative regulation of viral transcripti...	GO:0032897
phosphatidylcholine catabolic process	GO:0034638
negative regulation of fat cell prolifer...	GO:0070345
organelle disassembly	GO:1903008
regulation of organelle assembly	GO:1902115
peptide transport	GO:0015833
protein K48-linked ubiquitination	GO:0070936
secretory granule organization	GO:0033363
protein K11-linked ubiquitination	GO:0070979
leukocyte migration	GO:0050900
microtubule cytoskeleton organization in...	GO:1902850
centrosome separation	GO:0051299
cellular macromolecule localization	GO:0070727
cellular protein localization	GO:0034613
small molecule catabolic process	GO:0044282
neuron remodeling	GO:0016322
neuron maturation	GO:0042551
type 2 immune response	GO:0042092
regulation of nephron tubule epithelial ...	GO:0072182
negative regulation of interleukin-2 pro...	GO:0032703
regulation of type 2 immune response	GO:0002828

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p=3.7E-03	n=5
p=4.4E-03	n=56
p=5.7E-03	n=10
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p=6.3E-03	n=59
p=6.5E-03	n=12
p=6.6E-03	n=2
p=6.6E-03	n=2
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p=6.6E-03	n=2
p=6.6E-03	n=2
p=7.0E-03	n=7
p=8.6E-03	n=11
p=1.1E-02	n=46
p=1.2E-02	n=5
p=1.2E-02	n=4
p=1.2E-02	n=4
p=1.3E-02	n=8
p=1.4E-02	n=11
p=1.7E-02	n=4
p=1.7E-02	n=55
p=1.7E-02	n=54
p=1.8E-02	n=14
p=1.8E-02	n=6
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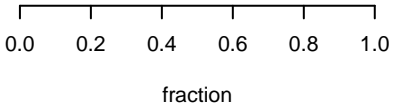
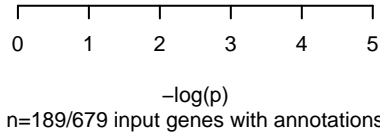
GO:MF
Fox_Nvec_vc1.1_XM_001640853.3

fraction genes in fg and expected value

GTPase activity	GO:0003924
steroid dehydrogenase activity	GO:0016229
calcium-independent phospholipase A2 act...	GO:0047499
lipid phosphatase activity	GO:0042577
ubiquitin-like protein binding	GO:0032182
protein-macromolecule adaptor activity	GO:0030674
GTPase binding	GO:0051020
deoxyribodipyrimidine photo-lyase activi...	GO:0003904
DNA photolyase activity	GO:0003913
small GTPase binding	GO:0031267
C2H2 zinc finger domain binding	GO:0070742
4 iron, 4 sulfur cluster binding	GO:0051539
poly-pyrimidine tract binding	GO:0008187
GTPase activating protein binding	GO:0032794
ubiquitin binding	GO:0043130
general transcription initiation factor ...	GO:0140296
JUN kinase binding	GO:0008432
G-protein beta/gamma-subunit complex bin...	GO:0031683
protein kinase A regulatory subunit bind...	GO:0034237
G protein-coupled peptide receptor activ...	GO:0008528
structural constituent of cytoskeleton	GO:0005200
amide transmembrane transporter activity	GO:0042887
ligase activity, forming carbon-oxygen b...	GO:0016875
peptide receptor activity	GO:0001653
aminoacyl-tRNA ligase activity	GO:0004812
nuclear receptor coactivator activity	GO:0030374
tRNA binding	GO:0000049
phosphatidylinositol bisphosphate bindin...	GO:1902936
nucleotide transmembrane transporter act...	GO:0015215
gamma-tubulin binding	GO:0043015

p=3.7E-03	n=10
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p=7.6E-03	n=6
p=8.5E-03	n=11
p=1.2E-02	n=18
p=1.8E-02	n=2
p=1.8E-02	n=2
p=1.9E-02	n=15
p=3.4E-02	n=2
p=3.4E-02	n=2
p=3.9E-02	n=3
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p=7.7E-02	n=2

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GO:CC
Fox_Nvec_vc1.1_XM_001640853.3

fraction genes in fg and expected value

Golgi medial cisterna	GO:0005797
gamma-tubulin complex	GO:0000930
mitotic spindle midzone	GO:1990023
spindle pole	GO:0000922
cis-Golgi network	GO:0005801
Golgi-associated vesicle membrane	GO:0030660
Golgi-associated vesicle	GO:0005798
SAGA-type complex	GO:0070461
COPII-coated ER to Golgi transport vesic...	GO:0030134
nuclear pore	GO:0005643
subapical complex	GO:0035003
SAGA complex	GO:0000124
COPI-coated vesicle membrane	GO:0030663
nuclear envelope	GO:0005635
cytoplasm	GO:0005737
fibrillar center	GO:0001650
Golgi membrane	GO:0000139
cytosol	GO:0005829
mitotic spindle pole	GO:0097431
neuron projection cytoplasm	GO:0120111
guanyl-nucleotide exchange factor comple...	GO:0032045
nuclear proteasome complex	GO:0031595
phagophore assembly site	GO:0000407
Golgi cis cisterna	GO:0000137
cytoplasmic side of apical plasma membra...	GO:0098592
intrinsic component of mitochondrial mem...	GO:0098573
polytene chromosome puff	GO:0005703
integral component of mitochondrial memb...	GO:0032592
Golgi trans cisterna	GO:0000138
perinuclear region of cytoplasm	GO:0048471

p=5.2E-03	n=5
p=6.6E-03	n=2
p=8.9E-03	n=3
p=1.3E-02	n=8
p=1.5E-02	n=5
p=1.5E-02	n=5
p=1.5E-02	n=8
p=2.2E-02	n=3
p=2.9E-02	n=4
p=2.9E-02	n=5
p=3.5E-02	n=2
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p=3.9E-02	n=16
p=4.0E-02	n=186
p=4.7E-02	n=6
p=5.0E-02	n=17
p=5.4E-02	n=100
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