

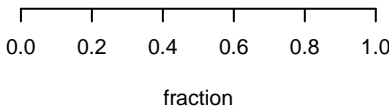
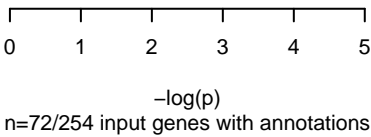
GO:BP
Fox_Nvec_vc1.1_XM_001629694.3

fraction genes in fg and expected value

response to morphine	GO:0043278
embryo development ending in birth or eg...	GO:0009792
nematode larval development	GO:0002119
response to acid chemical	GO:0001101
cellular response to epidermal growth fa...	GO:0071364
regulation of cellular macromolecule bio...	GO:2000112
aging	GO:0007568
calcium-mediated signaling	GO:0019722
cellular response to catecholamine stimu...	GO:0071870
positive regulation of chemotaxis	GO:0050921
response to nutrient	GO:0007584
cellular response to ketone	GO:1901655
positive regulation of T cell anergy	GO:0002669
negative regulation of alpha-beta T cell...	GO:0046642
regulation of cell population proliferat...	GO:0042127
body morphogenesis	GO:0010171
regulation of presynapse organization	GO:0099174
indole-containing compound metabolic pro...	GO:0042430
cellular response to alcohol	GO:0097306
G1/S transition of mitotic cell cycle	GO:0000082
response to bacterium	GO:0009617
response to antibiotic	GO:0046677
response to xenobiotic stimulus	GO:0009410
polyol metabolic process	GO:0019751
regulation of anatomical structure size	GO:0090066
metal ion transport	GO:0030001
cAMP-mediated signaling	GO:0019933
somatic stem cell population maintenance	GO:0035019
neuromuscular process controlling balanc...	GO:0050885
imaginal disc-derived wing morphogenesis	GO:0007476

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p=3.4E-04	n=18
p=3.4E-04	n=10
p=4.9E-04	n=9
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p=5.8E-04	n=33
p=6.6E-04	n=13
p=7.5E-04	n=7
p=8.3E-04	n=5
p=1.1E-03	n=5
p=1.3E-03	n=8
p=1.3E-03	n=5
p=1.5E-03	n=2
p=1.5E-03	n=2
p=1.6E-03	n=19
p=1.6E-03	n=5
p=1.9E-03	n=3
p=1.9E-03	n=3
p=2.0E-03	n=5
p=2.4E-03	n=6
p=2.7E-03	n=9
p=2.7E-03	n=9
p=2.8E-03	n=8
p=2.9E-03	n=4
p=3.1E-03	n=12
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p=3.7E-03	n=4
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fg=0.06	bg=0.01
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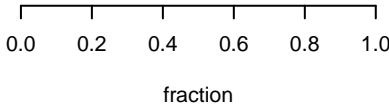
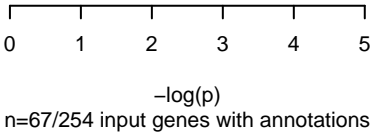
GO:MF
Fox_Nvec_vc1.1_XM_001629694.3

fraction genes in fg and expected value

glutamate receptor binding	GO:0035254
dopamine receptor binding	GO:0050780
sodium:bicarbonate symporter activity	GO:0008510
DNA-binding transcription factor activit...	GO:0003700
phosphotyrosine residue binding	GO:0001784
scaffold protein binding	GO:0097110
protein domain specific binding	GO:0019904
acetylcholine receptor binding	GO:0033130
nitric-oxide synthase binding	GO:0050998
anion:anion antiporter activity	GO:0015301
inorganic anion exchanger activity	GO:0005452
translation repressor activity	GO:0030371
ephrin receptor binding	GO:0046875
monosaccharide binding	GO:0048029
DNA binding	GO:0003677
ribonucleoprotein complex binding	GO:0043021
SMAD binding	GO:0046332
insulin receptor binding	GO:0005158
protein kinase binding	GO:0019901
double-stranded DNA binding	GO:0003690
protein phosphatase binding	GO:0019903
kinase binding	GO:0019900
nucleic acid binding	GO:0003676
sequence-specific DNA binding	GO:0043565
P-type transmembrane transporter activit...	GO:0140358
P-type ion transporter activity	GO:0015662
sequence-specific double-stranded DNA bi...	GO:1990837
beta-adrenergic receptor kinase activity	GO:0047696
insulin-like growth factor II binding	GO:0031995
delta-type opioid receptor binding	GO:0031850

p=7.6E-04	n=4
p=1.3E-03	n=3
p=1.8E-03	n=2
p=2.2E-03	n=13
p=3.4E-03	n=3
p=3.6E-03	n=4
p=8.1E-03	n=13
p=9.9E-03	n=2
p=9.9E-03	n=2
p=9.9E-03	n=2
p=9.9E-03	n=2
p=9.9E-03	n=2
p=1.6E-02	n=2
p=1.6E-02	n=2
p=1.8E-02	n=14
p=1.9E-02	n=4
p=1.9E-02	n=3
p=2.3E-02	n=2
p=2.5E-02	n=10
p=3.0E-02	n=9
p=3.1E-02	n=4
p=3.4E-02	n=10
p=3.9E-02	n=19
p=4.1E-02	n=9
p=4.1E-02	n=2
p=4.1E-02	n=2
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p=4.2E-02	n=1
p=4.2E-02	n=1

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GO:CC
Fox_Nvec_vc1.1_XM_001629694.3

fraction genes in fg and expected value

microvillus membrane	GO:0031528
membrane raft	GO:0045121
Z disc	GO:0030018
dendritic spine membrane	GO:0032591
growth cone lamellipodium	GO:1990761
dendritic shaft	GO:0043198
perinuclear region of cytoplasm	GO:0048471
basolateral plasma membrane	GO:0016323
apical part of cell	GO:0045177
brush border membrane	GO:0031526
intercalated disc	GO:0014704
anchoring junction	GO:0070161
cell-cell junction	GO:0005911
messenger ribonucleoprotein complex	GO:1990124
nuclear envelope lumen	GO:0005641
apical plasma membrane	GO:0016324
nucleus	GO:0005634
caveola	GO:0005901
cell-cell contact zone	GO:0044291
intrinsic component of plasma membrane	GO:0031226
nuclear speck	GO:0016607
cell-substrate junction	GO:0030055
lamellipodium	GO:0030027
U2-type spliceosomal complex	GO:0005684
euchromatin	GO:0000791
TSC1-TSC2 complex	GO:0033596
beta-catenin-TCF7L2 complex	GO:0070369
amyloid-beta complex	GO:0106003
endosome to plasma membrane transport ve...	GO:0070381
post-mRNA release spliceosomal complex	GO:0071014

p=2.4E-04	n=3
p=8.9E-04	n=8
p=2.5E-03	n=5
p=4.6E-03	n=2
p=4.6E-03	n=2
p=4.6E-03	n=4
p=4.7E-03	n=12
p=9.5E-03	n=6
p=1.3E-02	n=9
p=1.3E-02	n=3
p=1.3E-02	n=3
p=1.4E-02	n=8
p=1.4E-02	n=8
p=1.4E-02	n=2
p=1.4E-02	n=2
p=2.1E-02	n=2
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p=2.3E-02	n=43
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