

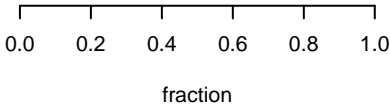
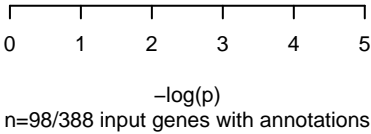
GO:BP  
Fox\_Nvec\_vc1.1\_XM\_001623084.3

fraction genes in fg and expected value

regulation of cellular macromolecule bio...	GO:2000112
positive regulation of transcription by ...	GO:0045944
antibiotic catabolic process	GO:0017001
cellular response to cAMP	GO:0071320
aorta morphogenesis	GO:0035909
intestinal absorption	GO:0050892
positive regulation of gene expression	GO:0010628
cellular response to corticosteroid stim...	GO:0071384
liver development	GO:0001889
cellular response to toxic substance	GO:0097237
regulation of calcium ion import	GO:0090279
branching involved in ureteric bud morph...	GO:0001658
detection of endogenous stimulus	GO:0009726
semicircular canal morphogenesis	GO:0048752
cytoplasmic sequestering of transcriptio...	GO:0042994
right ventricular cardiac muscle tissue ...	GO:0003221
ventricular trabecula myocardium morphog...	GO:0003222
neural tube formation	GO:0001841
regulation of Wnt signaling pathway	GO:0030111
response to estradiol	GO:0032355
cellular response to glucose stimulus	GO:0071333
regulation of phosphatase activity	GO:0010921
cellular response to glucagon stimulus	GO:0071377
negative regulation of cell population p...	GO:0008285
mesenchyme development	GO:0060485
canonical Wnt signaling pathway	GO:0060070
signal transduction	GO:0007165
protein heterooligomerization	GO:0051291
positive regulation of reactive oxygen s...	GO:1903428
neuroblast fate commitment	GO:0014017

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p=1.9E-03	n=27
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p=2.0E-03	n=6
p=2.5E-03	n=6
p=2.7E-03	n=3
p=2.8E-03	n=4
p=2.9E-03	n=2
p=2.9E-03	n=2
p=2.9E-03	n=2
p=2.9E-03	n=2
p=2.9E-03	n=2
p=3.7E-03	n=6
p=4.0E-03	n=9
p=4.2E-03	n=5
p=4.4E-03	n=6
p=4.4E-03	n=6
p=4.6E-03	n=3
p=5.2E-03	n=12
p=5.2E-03	n=6
p=5.7E-03	n=8
p=5.7E-03	n=53
p=6.9E-03	n=4
p=7.0E-03	n=3
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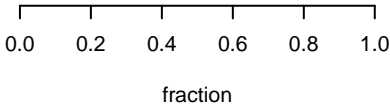
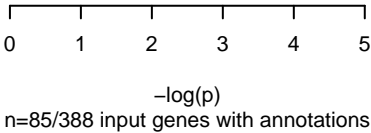
GO:MF  
Fox\_Nvec\_vc1.1\_XM\_001623084.3

fraction genes in fg and expected value

DNA-binding transcription activator acti...	GO:0001228
epinephrine binding	GO:0051379
cadherin binding	GO:0045296
ligand-gated calcium channel activity	GO:0099604
RNA polymerase II transcription regulato...	GO:0000977
DNA-binding transcription factor activit...	GO:0000981
transmembrane transporter binding	GO:0044325
actin filament binding	GO:0051015
small molecule binding	GO:0036094
oxidoreductase activity, acting on the C...	GO:0016899
inosine kinase activity	GO:0008906
lactate dehydrogenase activity	GO:0004457
phosphoenolpyruvate carboxykinase (GTP) ...	GO:0004613
DNA binding domain binding	GO:0050692
RNA polymerase II cis-regulatory region ...	GO:0000978
nucleobase-containing compound kinase ac...	GO:0019205
histone deacetylase binding	GO:0042826
anion binding	GO:0043168
nucleoside diphosphate kinase activity	GO:0004550
ligand-activated transcription factor ac...	GO:0098531
gamma-tubulin binding	GO:0043015
regulatory RNA binding	GO:0061980
nuclear receptor activity	GO:0004879
actin monomer binding	GO:0003785
phosphoprotein binding	GO:0051219
signaling receptor activity	GO:0038023
molecular transducer activity	GO:0060089
protein heterodimerization activity	GO:0046982
protein kinase binding	GO:0019901
DNA-binding transcription repressor acti...	GO:0001227

p=1.1E-03	n=10
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p=1.9E-03	n=4
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p=5.9E-03	n=17
p=6.6E-03	n=4
p=6.6E-03	n=4
p=7.3E-03	n=16
p=8.2E-03	n=2
p=8.2E-03	n=2
p=8.2E-03	n=2
p=8.2E-03	n=2
p=9.1E-03	n=8
p=9.8E-03	n=3
p=1.3E-02	n=4
p=1.5E-02	n=18
p=1.6E-02	n=2
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p=2.2E-02	n=12
p=2.3E-02	n=4

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GO:CC  
Fox\_Nvec\_vc1.1\_XM\_001623084.3

fraction genes in fg and expected value

integral component of plasma membrane	GO:0005887
beta-catenin-TCF complex	GO:1990907
side of membrane	GO:0098552
cytoplasmic side of membrane	GO:0098562
intrinsic component of the cytoplasmic s...	GO:0031235
adherens junction	GO:0005912
cytoplasmic side of plasma membrane	GO:0009898
protein phosphatase type 1 complex	GO:0000164
transcription regulator complex	GO:0005667
protein serine/threonine phosphatase com...	GO:0008287
protein-DNA complex	GO:0032993
beta-catenin-TCF7L2 complex	GO:0070369
beta-catenin destruction complex	GO:0030877
dendritic spine neck	GO:0044326
catenin-TCF7L2 complex	GO:0071664
dendritic spine head	GO:0044327
polycystin complex	GO:0002133
fascia adherens	GO:0005916
cytoplasmic side of dendritic spine plas...	GO:1990780
Scrib-APC-beta-catenin complex	GO:0034750
catenin complex	GO:0016342
phosphatase complex	GO:1903293
MKS complex	GO:0036038
euchromatin	GO:0000791
RNA polymerase II transcription regulato...	GO:0090575
intrinsic component of plasma membrane	GO:0031226
plasma membrane region	GO:0098590
extrinsic component of plasma membrane	GO:0019897
apical junction complex	GO:0043296
intrinsic component of nuclear inner mem...	GO:0031229

p=6.2E-03	n=15
p=8.8E-03	n=2
p=8.9E-03	n=9
p=1.3E-02	n=7
p=1.7E-02	n=2
p=2.0E-02	n=6
p=2.5E-02	n=6
p=2.7E-02	n=2
p=4.3E-02	n=10
p=4.6E-02	n=3
p=5.4E-02	n=3
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p=9.9E-02	n=14
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