

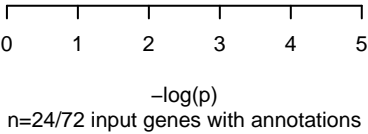
GO:BP
Fox_Nvec_vc1.1_XM_032371461.2

fraction genes in fg and expected value

actin cortical patch localization GO:0051666
lysine transport GO:0015819
late endosome to vacuole transport GO:0045324
establishment of imaginal disc-derived w... GO:0001737
cytoplasmic translation GO:0002181
cellular response to ketone GO:1901655
regulation of cytokinesis GO:0032465
cellular response to glucose starvation GO:0042149
biomineral tissue development GO:0031214
cellular response to glucocorticoid stim... GO:0071385
establishment of ommatidial planar polar... GO:0042067
import into cell GO:0098657
protein localization to membrane GO:0072657
cellular response to interferon-gamma GO:0071346
response to interferon-gamma GO:0034341
monovalent inorganic cation homeostasis GO:0055067
regulation of endothelial cell developme... GO:1901550
regulation of angiotensin-activated sign... GO:0110061
detoxification of zinc ion GO:0010312
nurse cell nucleus anchoring GO:0007302
regulation of establishment of endothe... GO:1903140
maintenance of protein location in cell ... GO:0032065
nuclear axial expansion GO:0035191
positive regulation of connective tissue... GO:0032723
regulation of actomyosin contractile rin... GO:1901648
equator specification GO:0045317
regulation of planar cell polarity pathw... GO:2000040
positive regulation of aspartic-type pep... GO:1905247
pharyngeal gland morphogenesis GO:1905905
female germline ring canal stabilization GO:0008335

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p=5.9E-03	n=3
p=7.1E-03	n=2
p=8.6E-03	n=2
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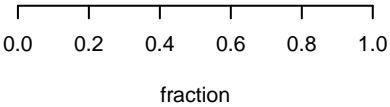
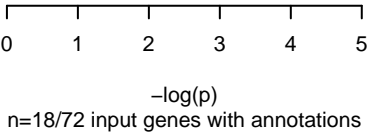
GO:MF
Fox_Nvec_vc1.1_XM_032371461.2

fraction genes in fg and expected value

ubiquitin-like protein binding GO:0032182
taste receptor binding GO:0031883
SUMO binding GO:0032183
Rho-dependent protein serine/threonine k... GO:0072518
proline-tRNA ligase activity GO:0004827
glutamate-tRNA ligase activity GO:0004818
structural constituent of ribosome GO:0003735
nitric-oxide synthase inhibitor activity GO:0036487
G protein-coupled adenosine receptor act... GO:0001609
nitric-oxide synthase regulator activity GO:0030235
calcium-dependent ATPase activity GO:0030899
protein tag GO:0031386
ubiquitin-like protein ligase activity GO:0061659
structural molecule activity GO:0005198
ubiquitin protein ligase activity GO:0061630
GTPase binding GO:0051020
metal ion binding GO:0046872
RNA stem-loop binding GO:0035613
lactate dehydrogenase activity GO:0004457
inosine kinase activity GO:0008906
oxidoreductase activity, acting on the C... GO:0016899
mRNA regulatory element binding translat... GO:0000900
DNA binding domain binding GO:0050692
phosphoenolpyruvate carboxykinase activi... GO:0004611
phosphoenolpyruvate carboxykinase (GTP) ... GO:0004613
zinc ion transmembrane transporter activ... GO:0005385
P-type calcium transporter activity GO:0005388
heterotrimeric G-protein binding GO:0032795
nitric-oxide synthase binding GO:0050998
translation repressor activity GO:0030371

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GO:CC
Fox_Nvec_vc1.1_XM_032371461.2

fraction genes in fg and expected value

cell division site GO:0032153
fungal-type vacuole membrane GO:0000329
cell tip GO:0051286
cytosolic small ribosomal subunit GO:0022627
integral component of organelle membrane GO:0031301
apicomedial cortex GO:0106037
neuron projection membrane GO:0032589
integral component of endoplasmic reticu... GO:0030176
intrinsic component of endoplasmic retic... GO:0031227
microtubule minus-end GO:0036449
GAIT complex GO:0097452
aminoacyl-tRNA synthetase multienzyme co... GO:0017101
basolateral plasma membrane GO:0016323
basal plasma membrane GO:0009925
contractile fiber GO:0043292
supramolecular fiber GO:0099512
supramolecular polymer GO:0099081
Hrd1p ubiquitin ligase ERAD-L complex GO:0000839
phagophore assembly site GO:0000407
postsynaptic specialization membrane GO:0099634
dendritic spine membrane GO:0032591
preribosome, large subunit precursor GO:0030687
postsynaptic density membrane GO:0098839
spindle pole centrosome GO:0031616
basal part of cell GO:0045178
leading edge membrane GO:0031256
ER ubiquitin ligase complex GO:0000835
Hrd1p ubiquitin ligase complex GO:0000836
costamere GO:0043034
endoplasmic reticulum quality control co... GO:0044322

p=1.3E-03	n=3
p=1.4E-03	n=2
p=1.4E-03	n=2
p=4.6E-03	n=2
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p=1.5E-02	n=1
p=2.1E-02	n=2
p=2.4E-02	n=3
p=2.4E-02	n=3
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