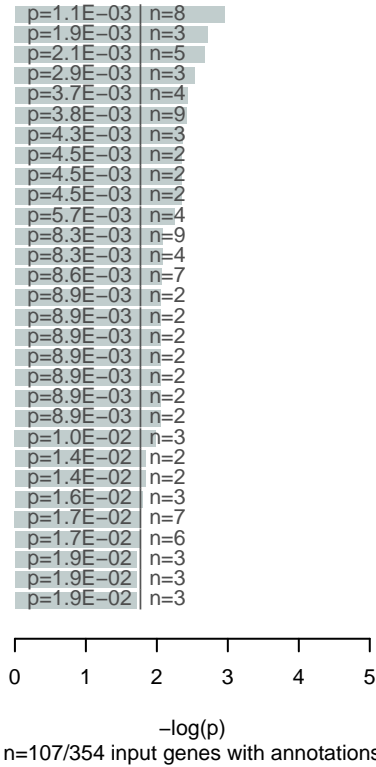


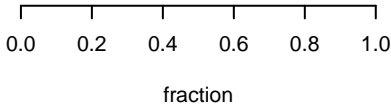
GO:BP
Fox_Nvec_vc1.1_XM_032378941.2

protein autophosphorylation	GO:0046777
negative regulation of hippo signaling	GO:0035331
negative regulation of protein–containin...	GO:0031333
fucosylation	GO:0036065
positive regulation of actin filament bu...	GO:0032233
positive regulation of cell cycle proces...	GO:0090068
branching involved in open tracheal syst...	GO:0060446
positive regulation of DNA–directed DNA ...	GO:1900264
leading strand elongation	GO:0006272
compartment pattern specification	GO:0007386
lymph gland development	GO:0048542
mitotic nuclear division	GO:0140014
somatic stem cell population maintenance	GO:0035019
cell fate specification	GO:0001708
sperm DNA decondensation	GO:0035041
positive regulation of epithelial cell p...	GO:0060501
establishment of centrosome localization	GO:0051660
N–terminal protein amino acid acetylatio...	GO:0006474
limb bud formation	GO:0060174
queuosine biosynthetic process	GO:0008616
regulation of mitotic cell cycle DNA rep...	GO:1903463
positive regulation of DNA replication	GO:0045740
establishment of epithelial cell apical/...	GO:0045198
regulation of respiratory gaseous exchan...	GO:0043576
negative regulation of embryonic develop...	GO:0045992
regulation of neuron apoptotic process	GO:0043523
regulation of mitotic nuclear division	GO:0007088
larval lymph gland hemopoiesis	GO:0035167
positive regulation of stress fiber asse...	GO:0051496
cardiac ventricle morphogenesis	GO:0003208



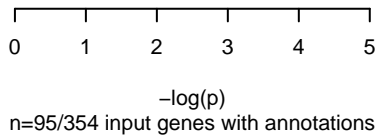
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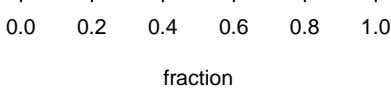
GO:MF
Fox_Nvec_vc1.1_XM_032378941.2

caspase binding	GO:0089720
protein serine/threonine kinase activity	GO:0004674
alpha–(1–>3)–fucosyltransferase activity	GO:0046920
fucosyltransferase activity	GO:0008417
polynucleotide adenyllyltransferase activ...	GO:0004652
NAD(P)+ transhydrogenase (AB–specific) a...	GO:0008750
Rho GDP–dissociation inhibitor binding	GO:0051022
apolipoprotein receptor binding	GO:0034190
apolipoprotein A–I receptor binding	GO:0034191
G–protein beta–subunit binding	GO:0031681
ribokinase activity	GO:0004747
RNA uridylyltransferase activity	GO:0050265
adenylate cyclase activator activity	GO:0010856
5–phosphoribosyl 1–pyrophosphate pyropho...	GO:0043135
DNA clamp loader activity	GO:0003689
inorganic phosphate transmembrane transp...	GO:0005315
high–affinity inorganic phosphate:sodium...	GO:0005316
S–adenosyl–L–methionine transmembrane tr...	GO:0000095
NAD(P)+ transhydrogenase (B–specific) ac...	GO:0003957
short–branched–chain–acyl–CoA dehydrogen...	GO:0016937
ribonuclease P RNA binding	GO:0033204
[3–methyl–2–oxobutanoate dehydrogenase (...	GO:0047323
3–hydroxyacyl–CoA dehydrogenase activity	GO:0003857
acid–sensing ion channel activity	GO:0044736
O–fucosylpeptide 3–beta–N–acetylglucosam...	GO:0033829
GBD domain binding	GO:0032427
MDM2/MDM4 family protein binding	GO:0097371
SMC family protein binding	GO:0043221
sodium:inorganic phosphate symporter act...	GO:0015319
kinase binding	GO:0019900



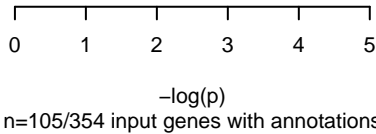
fraction genes in fg and expected value

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GO:CC
Fox_Nvec_vc1.1_XM_032378941.2

Elg1 RFC–like complex	GO:0031391
DNA replication factor C complex	GO:0005663
FAR/SIN/STRIPAK complex	GO:0090443
Ctf18 RFC–like complex	GO:0031390
endocytic vesicle	GO:0030139
pseudopodium	GO:0031143
spindle midzone	GO:0051233
ATPase complex	GO:1904949
mitotic spindle midzone	GO:1990023
Golgi apparatus	GO:0005794
preribosome	GO:0030684
preribosome, small subunit precursor	GO:0030688
vesicle coat	GO:0030120
bleb	GO:0032059
sperm individualization complex	GO:0070864
investment cone	GO:0070865
XPC complex	GO:0071942
microspike	GO:0044393
Schwann cell microvillus	GO:0097454
nucleotide–excision repair complex	GO:0000109
NatB complex	GO:0031416
Sec61 translocon complex	GO:0005784
ACF complex	GO:0016590
translocon complex	GO:0071256
nuclear speck	GO:0016607
Golgi cisterna membrane	GO:0032580
nuclear body	GO:0016604
filopodium	GO:0030175
intracellular membrane–bounded organelle	GO:0043231
mitotic spindle	GO:0072686



fraction genes in fg and expected value

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