

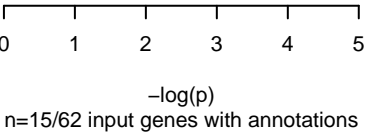
GO:BP  
Fox\_Nvec\_vc1.1\_XM\_001636971.3

fraction genes in fg and expected value

purine-containing compound salvage	GO:0043101
AMP catabolic process	GO:0006196
positive regulation of transcription by ...	GO:0045945
negative regulation of nuclear-transcrib...	GO:2000623
fasciculation of sensory neuron axon	GO:0097155
right ventricular compact myocardium mor...	GO:0003226
prepulse inhibition	GO:0060134
negative regulation of fibroblast apopto...	GO:2000270
positive regulation of retinoic acid rec...	GO:0048386
positive regulation of chemotaxis	GO:0050921
embryonic organ morphogenesis	GO:0048562
embryonic limb morphogenesis	GO:0030326
embryonic appendage morphogenesis	GO:0035113
positive regulation of receptor localiza...	GO:1902685
semicircular canal morphogenesis	GO:0048752
heart trabecula morphogenesis	GO:0061384
epiboly involved in gastrulation with mo...	GO:0055113
ventricular trabecula myocardium morphog...	GO:0003222
determination of digestive tract left/ri...	GO:0071907
protein lipoylation	GO:0009249
atrioventricular canal development	GO:0036302
positive regulation of myoblast differen...	GO:0045663
liquid clearance, open tracheal system	GO:0035002
inner ear morphogenesis	GO:0042472
limb morphogenesis	GO:0035108
steroid hormone mediated signaling pathw...	GO:0043401
ear morphogenesis	GO:0042471
protein localization to non-motile ciliu...	GO:0097499
regulation of receptor localization to s...	GO:1902683
enteric nervous system development	GO:0048484

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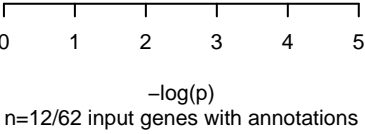
GO:MF  
Fox\_Nvec\_vc1.1\_XM\_001636971.3

fraction genes in fg and expected value

AMP deaminase activity	GO:0003876
deUFMyase activity	GO:0071567
nuclear steroid receptor activity	GO:0003707
armadillo repeat domain binding	GO:0070016
dynein heavy chain binding	GO:0045504
CoA-ligase activity	GO:0016405
RNA polymerase II transcription regulato...	GO:0000977
transcription cis-regulatory region bind...	GO:0000976
nuclear receptor activity	GO:0004879
acid-thiol ligase activity	GO:0016878
ligand-activated transcription factor ac...	GO:0098531
sequence-specific double-stranded DNA bi...	GO:1990837
transcription regulatory region nucleic ...	GO:0001067
ligase activity, forming carbon-sulfur b...	GO:0016877
G-protein beta/gamma-subunit complex bin...	GO:0031683
double-stranded DNA binding	GO:0003690
G-protein alpha-subunit binding	GO:0001965
beta-catenin binding	GO:0008013
sequence-specific DNA binding	GO:0043565
methylation-dependent protein binding	GO:0140034
methyalted histone binding	GO:0035064
promoter-specific chromatin binding	GO:1990841
RNA polymerase II cis-regulatory region ...	GO:0000978
cis-regulatory region sequence-specific ...	GO:0000987
ubiquitin conjugating enzyme activity	GO:0061631
DNA helicase activity	GO:0003678
thiolester hydrolase activity	GO:0016790
ubiquitin-like protein conjugating enzym...	GO:0061650
ATP-dependent activity, acting on DNA	GO:0008094
p53 binding	GO:0002039

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GO:CC  
Fox\_Nvec\_vc1.1\_XM\_001636971.3

fraction genes in fg and expected value

Dsl1/NZR complex	GO:0070939
inner dynein arm	GO:0036156
nucleolus	GO:0005730
nuclear lamina	GO:0005652
axonemal dynein complex	GO:0005858
MLL1 complex	GO:0071339
heterotrimeric G-protein complex	GO:0005834
GTPase complex	GO:1905360
cytosolic small ribosomal subunit	GO:0022627
dynein complex	GO:0030286
MLL1/2 complex	GO:0044665
PML body	GO:0016605
small ribosomal subunit	GO:0015935
cytosolic ribosome	GO:0022626
extrinsic component of cytoplasmic side ...	GO:0031234
mitochondrial matrix	GO:0005759
histone methyltransferase complex	GO:0035097
filopodium	GO:0030175
ciliary plasm	GO:0097014
axoneme	GO:0005930
ribosomal subunit	GO:0044391
intracellular organelle lumen	GO:0070013
organelle lumen	GO:0043233
membrane-enclosed lumen	GO:0031974
methyltransferase complex	GO:0034708
ficolin-1-rich granule lumen	GO:1904813
extrinsic component of plasma membrane	GO:0019897
9+2 motile cilium	GO:0097729
plasma membrane bounded cell projection ...	GO:0032838
ribosome	GO:0005840

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