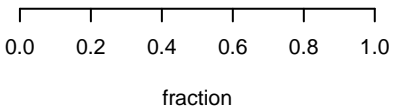
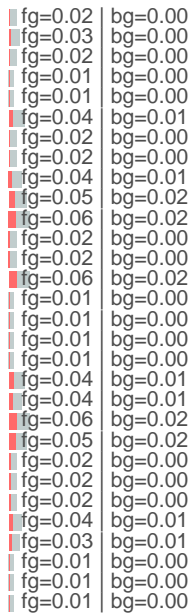
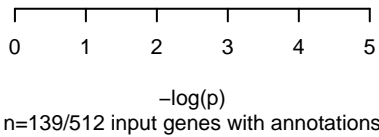
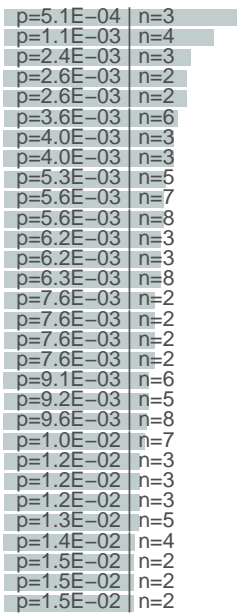


GO:BP  
Fox\_Nvec\_vc1.1\_XM\_032375228.2

fraction genes in fg and expected value

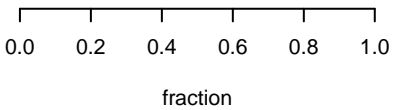
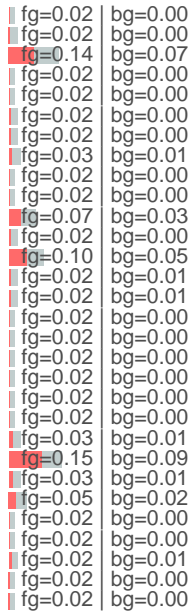
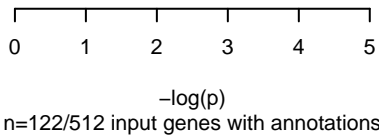
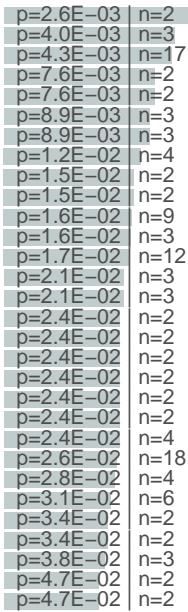
dorsal/ventral axis specification, ovari... GO:0008069  
negative regulation of protein tyrosine ... GO:0061099  
negative regulation of transcription fro... GO:0097201  
positive regulation of cholesterol efflu... GO:0010875  
positive regulation of transcription fro... GO:0061408  
SRP-dependent cotranslational protein ta... GO:0006614  
negative regulation of signaling recepto... GO:2000272  
cellular response to angiotensin GO:1904385  
organophosphate ester transport GO:0015748  
epidermal growth factor receptor signali... GO:0007173  
cellular response to topologically incor... GO:0035967  
cellular response to fluid shear stress GO:0071498  
regulation of antigen receptor-mediated ... GO:0050854  
response to unfolded protein GO:0006986  
chondroitin sulfate proteoglycan biosynt... GO:0050650  
response to herbicide GO:0009635  
positive regulation of natural killer ce... GO:0032816  
positive regulation of natural killer ce... GO:0045954  
response to hydrogen peroxide GO:0042542  
negative regulation of intrinsic apoptot... GO:2001243  
cellular response to inorganic substance GO:0071241  
cellular response to unfolded protein GO:0034620  
positive regulation of epidermal growth ... GO:0045742  
positive regulation of execution phase o... GO:1900119  
positive regulation of ERBB signaling pa... GO:1901186  
negative regulation of autophagy GO:0010507  
hormone biosynthetic process GO:0042446  
regulation of apoptotic DNA fragmentatio... GO:1902510  
epithalamus development GO:0021538  
regulation of DNA catabolic process GO:1903624



GO:MF  
Fox\_Nvec\_vc1.1\_XM\_032375228.2

fraction genes in fg and expected value

electron-transferring-flavoprotein dehyd... GO:0004174  
cholesterol binding GO:0015485  
DNA-binding transcription factor activit... GO:0003700  
organic hydroxy compound transmembrane t... GO:1901618  
ATPase-coupled lipid transmembrane trans... GO:0034040  
organophosphate ester transmembrane tran... GO:0015605  
ATPase activator activity GO:0001671  
potassium channel activity GO:0005267  
sterol transporter activity GO:0015248  
cAMP binding GO:0030552  
transcription coactivator activity GO:0003713  
voltage-gated potassium channel activity GO:0005249  
transcription coregulator activity GO:0003712  
flavin adenine dinucleotide binding GO:0050660  
nuclear receptor coactivator activity GO:0030374  
cyclic nucleotide binding GO:0030551  
sequence-specific single stranded DNA bi... GO:0098847  
ABC-type transporter activity GO:0140359  
leak channel activity GO:0022840  
potassium ion leak channel activity GO:0022841  
narrow pore channel activity GO:0022842  
voltage-gated cation channel activity GO:0022843  
enzyme regulator activity GO:0030234  
potassium ion transmembrane transporter ... GO:0015079  
heat shock protein binding GO:0031072  
epidermal growth factor receptor binding GO:0005154  
glucuronosyltransferase activity GO:0015020  
ATPase regulator activity GO:0060590  
metal cluster binding GO:0051540  
iron-sulfur cluster binding GO:0051536



GO:CC  
Fox\_Nvec\_vc1.1\_XM\_032375228.2

fraction genes in fg and expected value

centrosome GO:0005813  
bounding membrane of organelle GO:0098588  
ER ubiquitin ligase complex GO:0000835  
Hrd1p ubiquitin ligase complex GO:0000836  
endoplasmic reticulum quality control co... GO:0044322  
intrinsic component of plasma membrane GO:0031226  
intrinsic component of membrane GO:0031224  
recycling endosome GO:0055037  
integral component of plasma membrane GO:0005887  
Derlin-1 retrotranslocation complex GO:0036513  
cation channel complex GO:0034703  
integral component of membrane GO:0016021  
cytoplasmic ubiquitin ligase complex GO:0000153  
endoplasmic reticulum membrane GO:0005789  
AP-1 adaptor complex GO:0030121  
NF-kappaB complex GO:0071159  
clathrin coat of trans-Golgi network ves... GO:0030130  
cyclin E1-CDK2 complex GO:0097134  
cyclin E2-CDK2 complex GO:0097135  
actin cortical patch GO:0030479  
electron transfer flavoprotein complex GO:0045251  
mitochondrial electron transfer flavopro... GO:0017133  
endocytic patch GO:0061645  
nuclear outer membrane-endoplasmic retic... GO:0042175  
endoplasmic reticulum subcompartment GO:0098827  
U12-type spliceosomal complex GO:0005689  
ruffle GO:0001726  
transcription repressor complex GO:0017053  
motile cilium GO:0031514  
perinuclear region of cytoplasm GO:0048471

