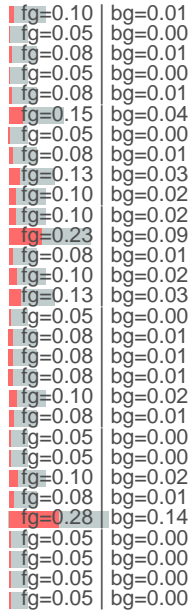
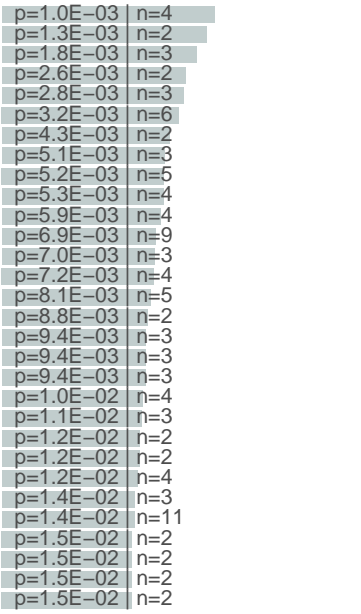


GO:BP  
Fox\_Nvec\_vc1.1\_XM\_032372025.2

fraction genes in fg and expected value

hematopoietic progenitor cell differenti... GO:0002244  
limb bud formation GO:0060174  
regulation of steroid biosynthetic proce... GO:0050810  
negative regulation of necrotic cell dea... GO:0060547  
cardiac ventricle morphogenesis GO:0003208  
protein polyubiquitination GO:0000209  
forebrain ventricular zone progenitor ce... GO:0021869  
somatic stem cell population maintenance GO:0035019  
gonad development GO:0008406  
limbic system development GO:0021761  
chemosensory behavior GO:0007635  
positive regulation of transport GO:0051050  
glial cell development GO:0021782  
spermatid development GO:0007286  
kidney development GO:0001822  
astrocyte differentiation GO:0048708  
neuroepithelial cell differentiation GO:0060563  
positive regulation of canonical Wnt sig... GO:0090263  
activation of GTPase activity GO:0090630  
negative regulation of mitotic cell cycl... GO:0045930  
determination of heart left/right asymme... GO:0061371  
regulation of cholesterol biosynthetic p... GO:0045540  
regulation of sterol biosynthetic proces... GO:0106118  
cell fate specification GO:0001708  
secondary alcohol metabolic process GO:1902652  
cell cycle process GO:0022402  
prostate gland development GO:0030850  
regulation of alcohol biosynthetic proce... GO:1902930  
negative regulation of blood pressure GO:0045776  
negative regulation of systemic arterial... GO:0003085



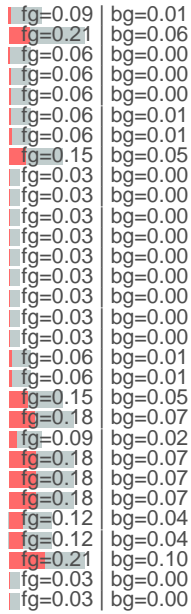
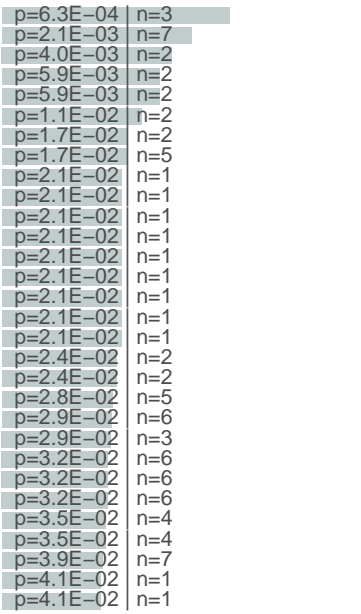
-log(p)  
n=39/186 input genes with annotations

fraction

GO:MF  
Fox\_Nvec\_vc1.1\_XM\_032372025.2

fraction genes in fg and expected value

E-box binding GO:0070888  
protein heterodimerization activity GO:0046982  
ubiquitin-ubiquitin ligase activity GO:0034450  
potassium channel inhibitor activity GO:0019870  
HMG box domain binding GO:0071837  
microtubule motor activity GO:0003777  
ubiquitin conjugating enzyme binding GO:0031624  
GTPase regulator activity GO:0030695  
non-sequence-specific DNA binding, bendi... GO:0044378  
DNA binding, bending GO:0008301  
methylmalonyl-CoA mutase activity GO:0004494  
mevalonate kinase activity GO:0004496  
cobalamin binding GO:0031419  
3'-5' RNA helicase activity GO:0034458  
ABC-type sterol transporter activity GO:0034041  
N6-methyladenosine-containing RNA bindin... GO:1990247  
platelet-derived growth factor receptor ... GO:0005161  
cytoskeletal motor activity GO:0003774  
ubiquitin-like protein conjugating enzym... GO:0044390  
nucleoside-triphosphatase regulator acti... GO:0060589  
nucleoside-triphosphatase activity GO:0017111  
guanyl-nucleotide exchange factor activi... GO:0005085  
hydrolase activity, acting on acid anhyd... GO:0016817  
hydrolase activity, acting on acid anhyd... GO:0016818  
pyrophosphatase activity GO:0016462  
DNA-binding transcription activator acti... GO:0001228  
DNA-binding transcription activator acti... GO:0001216  
protein homodimerization activity GO:0042803  
1-acylglycerophosphocholine O-acyltransf... GO:0047184  
2-acylglycerol-3-phosphate O-acyltransfe... GO:0047144



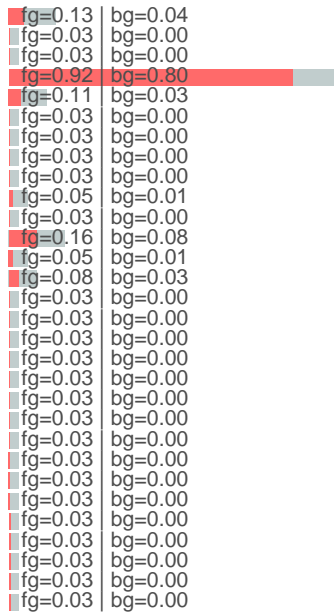
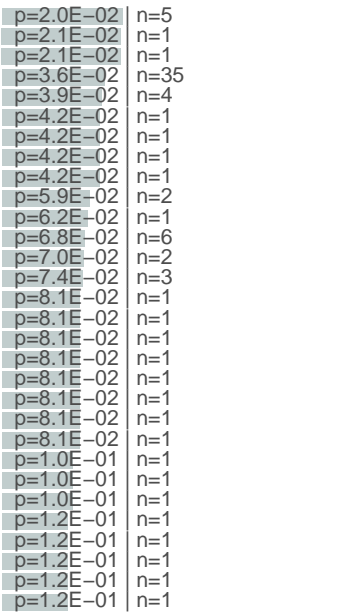
-log(p)  
n=33/186 input genes with annotations

fraction

GO:CC  
Fox\_Nvec\_vc1.1\_XM\_032372025.2

fraction genes in fg and expected value

transcription regulator complex GO:0005667  
plus-end kinesin complex GO:0005873  
axonemal microtubule GO:0005879  
cytoplasm GO:0005737  
ubiquitin ligase complex GO:0000151  
cytosolic aryl hydrocarbon receptor comp... GO:0034752  
BBSome GO:0034464  
Lewy body GO:0097413  
cis-Golgi network membrane GO:0033106  
lipid droplet GO:0005811  
nuclear aryl hydrocarbon receptor comple... GO:0034753  
supramolecular complex GO:0099080  
centriole GO:0005814  
ribonucleoprotein granule GO:0035770  
ER ubiquitin ligase complex GO:0000835  
Hrd1p ubiquitin ligase complex GO:0000836  
chromatoid body GO:0033391  
aryl hydrocarbon receptor complex GO:0034751  
pericentriolar material GO:0000242  
pi-body GO:0071546  
endoplasmic reticulum quality control co... GO:0044322  
intrinsic component of the cytoplasmic s... GO:0031235  
cytochrome complex GO:0070069  
juxtaparanode region of axon GO:0044224  
intracellular canalliculus GO:0046691  
excitatory synapse GO:0060076  
centriolar satellite GO:0034451  
cytoplasmic ubiquitin ligase complex GO:0000153  
Derlin-1 retrotranslocation complex GO:0036513  
tertiary granule lumen GO:1904724



-log(p)  
n=38/186 input genes with annotations

fraction