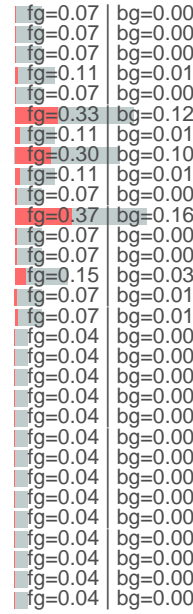
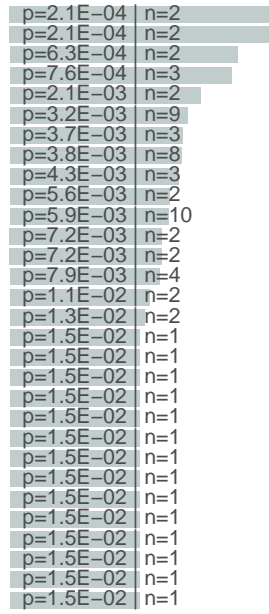


GO:BP
Fox_Nvec_vc1.1_XM_032373800.2

fraction genes in fg and expected value

establishment or maintenance of cytoskel...	GO:0003380
mesectoderm development	GO:0048383
regulation of myosin II filament organiz...	GO:0043519
regulation of gastrulation	GO:0010470
regulation of antimicrobial peptide prod...	GO:0002784
negative regulation of cellular macromol...	GO:2000113
G protein-coupled receptor signaling pat...	GO:0007187
negative regulation of transcription, DN...	GO:0045892
adenylate cyclase-modulating G protein-c...	GO:0007188
convergent extension involved in gastrul...	GO:0060027
negative regulation of gene expression	GO:0010629
neuron cellular homeostasis	GO:0070050
regulation of DNA-templated DNA replicat...	GO:0090329
dorsal/ventral pattern formation	GO:0009953
adenylate cyclase-activating G protein-c...	GO:0007189
apoptotic process involved in developmen...	GO:1902742
regulation of catecholamine uptake invol...	GO:0051940
positive regulation of GTP cyclohydrolas...	GO:0043104
regulation of mediator complex assembly	GO:2001176
positive regulation of mediator complex ...	GO:2001178
base-excision repair, DNA ligation	GO:0006288
nodal signaling pathway	GO:0038092
regulation of chorionic trophoblast cell...	GO:1901382
granulosa cell apoptotic process	GO:1904700
regulation of granulosa cell apoptotic p...	GO:1904708
regulation of dopamine uptake involved i...	GO:0051584
regulation of protein K48-linked deubiqu...	GO:1903093
negative regulation of ubiquitin-protein...	GO:0051444
dendrite development by retrograde exten...	GO:0003390
amphid sensory organ dendrite retrograde...	GO:0003391



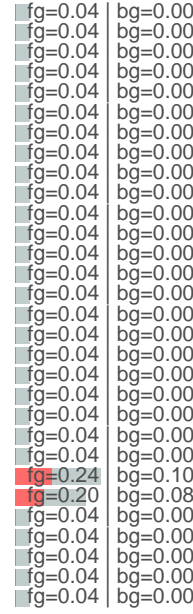
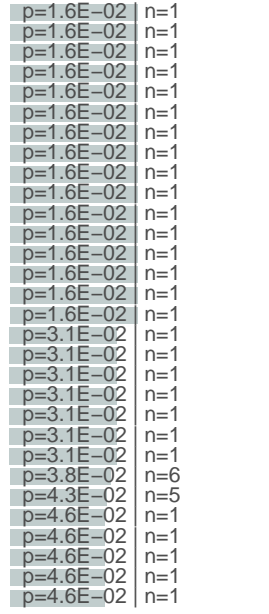
-log(p)
n=27/120 input genes with annotations

fraction

GO:MF
Fox_Nvec_vc1.1_XM_032373800.2

fraction genes in fg and expected value

ubiquitin ligase inhibitor activity	GO:1990948
5S rDNA binding	GO:0080084
ATPase-coupled intramembrane lipid trans...	GO:0140326
flippase activity	GO:0140327
ubiquitin-like modifier activating enzym...	GO:0008641
UFM1 activating enzyme activity	GO:0071566
RNA polymerase III core binding	GO:0000994
RNA polymerase III transcription regulat...	GO:0001016
GABA receptor binding	GO:0050811
aminophospholipid flippase activity	GO:0015247
alkylglycerophosphoethanolamine phosphod...	GO:0047391
D5 dopamine receptor binding	GO:0031752
ubiquitin-protein transferase inhibitor ...	GO:0055105
phosphatidylglycerol binding	GO:1901611
cardiolipin binding	GO:1901612
dynein light intermediate chain binding	GO:0051959
DNA ligase activity	GO:0003909
transcription corepressor binding	GO:0001222
peroxisome proliferator activated recept...	GO:0042975
nuclear retinoid X receptor binding	GO:0046965
DNA ligase (ATP) activity	GO:0003910
co-SMAD binding	GO:0070410
5S rRNA binding	GO:0008097
signaling receptor binding	GO:0005102
cytoskeletal protein binding	GO:0008092
ankyrin binding	GO:0030506
rDNA binding	GO:0000182
nuclear retinoic acid receptor binding	GO:0042974
ligase activity, forming phosphoric este...	GO:0016886
ubiquitin-protein transferase regulator ...	GO:0055106



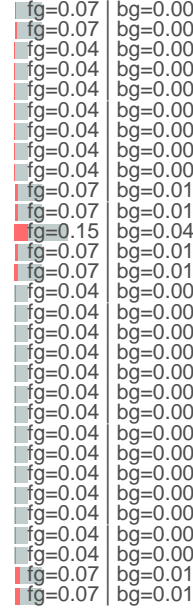
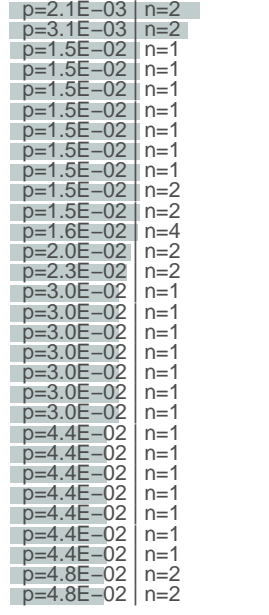
-log(p)
n=25/120 input genes with annotations

fraction

GO:CC
Fox_Nvec_vc1.1_XM_032373800.2

fraction genes in fg and expected value

sensory dendrite	GO:0071683
heterotrimeric G-protein complex	GO:0005834
spectrosome	GO:0045170
spectrin	GO:0008091
collagen and cuticulin-based cuticle ext...	GO:0060102
endocytic patch	GO:0061645
DNA ligase III-XRCC1 complex	GO:0070421
actin cortical patch	GO:0030479
molybdopterin synthase complex	GO:0019008
brush border membrane	GO:0031526
cortical actin cytoskeleton	GO:0030864
cell projection membrane	GO:0031253
cortical cytoskeleton	GO:0030863
ciliary membrane	GO:0060170
extrinsic component of endoplasmic retic...	GO:0042406
NELF complex	GO:0032021
cytoplasmic side of rough endoplasmic re...	GO:0098556
photoreceptor outer segment membrane	GO:0042622
RSF complex	GO:0031213
cytoplasmic cyclin-dependent protein kin...	GO:0000308
cis-Golgi network membrane	GO:0033106
photoreceptor disc membrane	GO:0097381
inhibitory synapse	GO:0060077
aster	GO:0005818
polysomal ribosome	GO:0042788
spindle pole centrosome	GO:0031616
ISWI-type complex	GO:0031010
spot adherens junction	GO:0005914
spindle pole	GO:0000922
brush border	GO:0005903



-log(p)
n=27/120 input genes with annotations

fraction