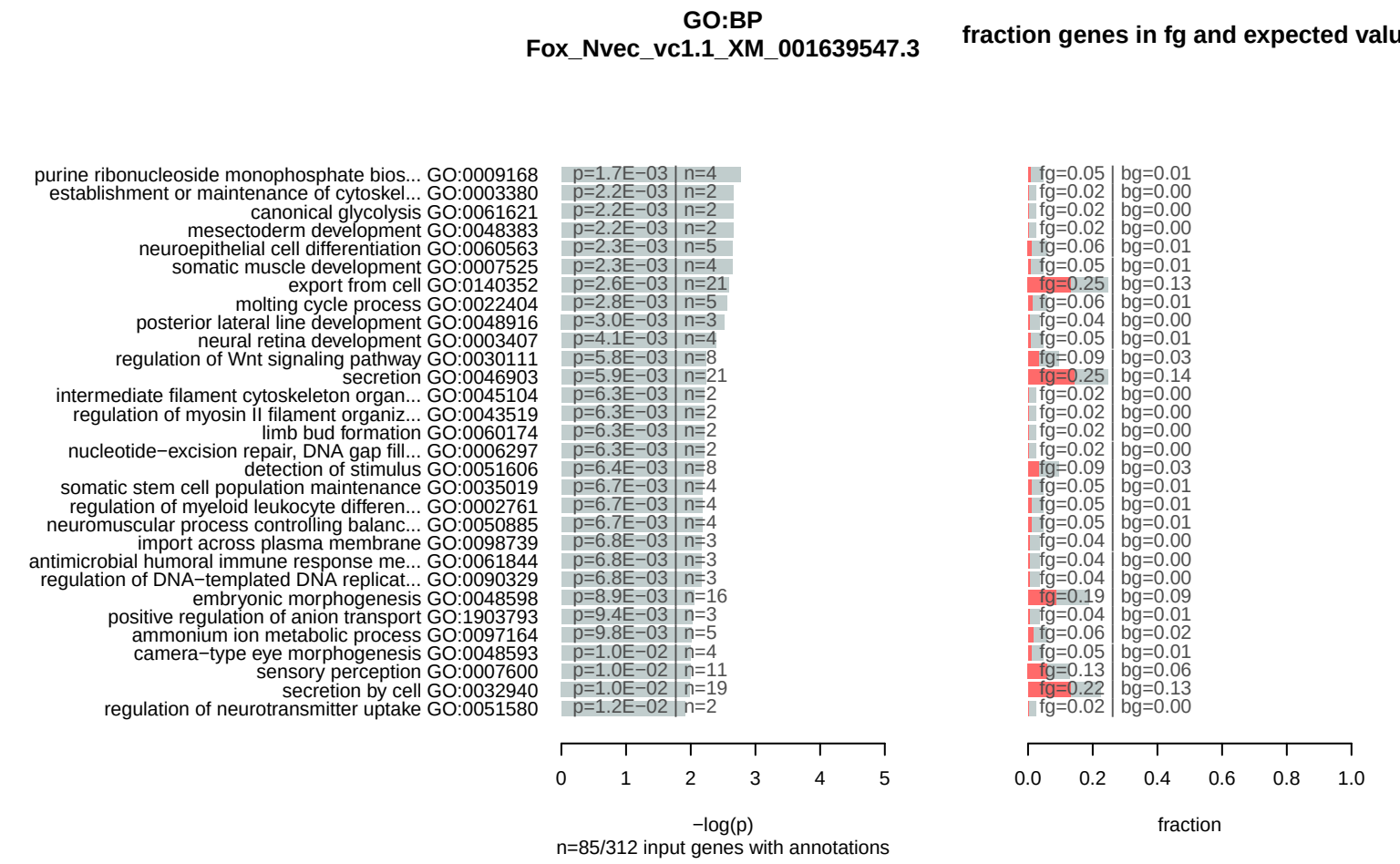
GO:BP
Fox_Nvec_vc1.1_XM_001639547.3
fraction genes in fg and expected valu
purine ribonucleoside monophosphate bios... GO:0009168 p=1.7E−03 n=4 fg=0.05 bg=0.01
establishment or maintenance of cytoskel... GO:0003380 p=2.2E−03 n=2 fg=0.02 bg=0.00
canonical glycolysis GO:0061621 p=2.2E−03 n=2 fg=0.02 bg=0.00
mesectoderm development GO:0048383 p=2.2E−03 n=2 fg=0.02 bg=0.00
neuroepithelial cell differentiation GO:0060563 p=2.3E−03 n=5 fg=0.06 bg=0.01
somatic muscle development GO:0007525 p=2.3E−03 n=4 fg=0.05 bg=0.01
export from cell GO:0140352 p=2.6E−03 n=21 fg=0.25 bg=0.13
molting cycle process GO:0022404 p=2.8E−03 n=5 fg=0.06 bg=0.01
posterior lateral line development GO:0048916 p=3.0E−03 n=3 fg=0.04 bg=0.00
neural retina development GO:0003407 p=4.1E−03 n=4 fg=0.05 bg=0.01
regulation of Wnt signaling pathway GO:0030111 p=5.8E−03 n=8 fg=0.09 bg=0.03
secretion GO:0046903 p=5.9E−03 n=21 fg=0.25 bg=0.14
intermediate filament cytoskeleton organ... GO:0045104 p=6.3E−03 n=2 fg=0.02 bg=0.00
regulation of myosin II filament organiz... GO:0043519 p=6.3E−03 n=2 fg=0.02 bg=0.00
limb bud formation GO:0060174 p=6.3E−03 n=2 fg=0.02 bg=0.00
nucleotide−excision repair, DNA gap fill... GO:0006297 p=6.3E−03 n=2 fg=0.02 bg=0.00
detection of stimulus GO:0051606 p=6.4E−03 n=8 fg=0.09 bg=0.03
somatic stem cell population maintenance GO:0035019 p=6.7E−03 n=4 fg=0.05 bg=0.01
regulation of myeloid leukocyte differen... GO:0002761 p=6.7E−03 n=4 fg=0.05 bg=0.01
neuromuscular process controlling balanc... GO:0050885 p=6.7E−03 n=4 fg=0.05 bg=0.01
import across plasma membrane GO:0098739 p=6.8E−03 n=3 fg=0.04 bg=0.00
antimicrobial humoral immune response me... GO:0061844 p=6.8E−03 n=3 fg=0.04 bg=0.00
regulation of DNA−templated DNA replicat... GO:0090329 p=6.8E−03 n=3 fg=0.04 bg=0.00
embryonic morphogenesis GO:0048598 p=8.9E−03 n=16 fg=0.19 bg=0.09
positive regulation of anion transport GO:1903793 p=9.4E−03 n=3 fg=0.04 bg=0.01
ammonium ion metabolic process GO:0097164 p=9.8E−03 n=5 fg=0.06 bg=0.02
camera−type eye morphogenesis GO:0048593 p=1.0E−02 n=4 fg=0.05 bg=0.01
sensory perception GO:0007600 p=1.0E−02 n=11 fg=0.13 bg=0.06
secretion by cell GO:0032940 p=1.0E−02 n=19 fg=0.22 bg=0.13
regulation of neurotransmitter uptake GO:0051580 p=1.2E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=85/312 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_001639547.3
fraction genes in fg and expected valu
phosphoric diester hydrolase activity GO:0008081 p=1.1E−03 n=5 fg=0.07 bg=0.01
LIM domain binding GO:0030274 p=2.2E−03 n=2 fg=0.03 bg=0.00
phospholipase C activity GO:0004629 p=1.2E−02 n=2 fg=0.03 bg=0.00
ATPase−coupled cation transmembrane tran... GO:0019829 p=1.6E−02 n=3 fg=0.04 bg=0.01
G−protein beta/gamma−subunit complex bin... GO:0031683 p=2.0E−02 n=2 fg=0.03 bg=0.00
ATPase−coupled ion transmembrane transpo... GO:0042625 p=2.0E−02 n=3 fg=0.04 bg=0.01
core promoter sequence−specific DNA bind... GO:0001046 p=3.6E−02 n=3 fg=0.04 bg=0.01
glyceraldehyde−3−phosphate dehydrogenase... GO:0043891 p=4.7E−02 n=1 fg=0.01 bg=0.00
L−proline transmembrane transporter acti... GO:0015193 p=4.7E−02 n=1 fg=0.01 bg=0.00
L−tryptophan transmembrane transporter a... GO:0015196 p=4.7E−02 n=1 fg=0.01 bg=0.00
amino acid:cation symporter activity GO:0005416 p=4.7E−02 n=1 fg=0.01 bg=0.00
RNA strand annealing activity GO:0033592 p=4.7E−02 n=1 fg=0.01 bg=0.00
ubiquitin−protein transferase inhibitor ... GO:0055105 p=4.7E−02 n=1 fg=0.01 bg=0.00
propionyl−CoA carboxylase activity GO:0004658 p=4.7E−02 n=1 fg=0.01 bg=0.00
aminophospholipid flippase activity GO:0015247 p=4.7E−02 n=1 fg=0.01 bg=0.00
glycine transmembrane transporter activi... GO:0015187 p=4.7E−02 n=1 fg=0.01 bg=0.00
alkylglycerophosphoethanolamine phosphod... GO:0047391 p=4.7E−02 n=1 fg=0.01 bg=0.00
phosphoglycerate kinase activity GO:0004618 p=4.7E−02 n=1 fg=0.01 bg=0.00
amino acid:proton symporter activity GO:0005280 p=4.7E−02 n=1 fg=0.01 bg=0.00
calmodulin−activated 3',5'−cyclic−GMP ph... GO:0048101 p=4.7E−02 n=1 fg=0.01 bg=0.00
DNA binding, bending GO:0008301 p=4.7E−02 n=1 fg=0.01 bg=0.00
leptin receptor binding GO:1990460 p=4.7E−02 n=1 fg=0.01 bg=0.00
ubiquitin ligase inhibitor activity GO:1990948 p=4.7E−02 n=1 fg=0.01 bg=0.00
ubiquitin−like modifier activating enzym... GO:0008641 p=4.7E−02 n=1 fg=0.01 bg=0.00
ATPase−coupled intramembrane lipid trans... GO:0140326 p=4.7E−02 n=1 fg=0.01 bg=0.00
flippase activity GO:0140327 p=4.7E−02 n=1 fg=0.01 bg=0.00
transferrin receptor binding GO:1990459 p=4.7E−02 n=1 fg=0.01 bg=0.00
non−sequence−specific DNA binding, bendi... GO:0044378 p=4.7E−02 n=1 fg=0.01 bg=0.00
RNA strand−exchange activity GO:0034057 p=4.7E−02 n=1 fg=0.01 bg=0.00
CoA carboxylase activity GO:0016421 p=4.7E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=75/312 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001639547.3
fraction genes in fg and expected valu
tertiary granule GO:0070820 p=7.4E−03 n=4 fg=0.05 bg=0.01
cell−substrate junction GO:0030055 p=7.4E−03 n=4 fg=0.05 bg=0.01
lipid droplet GO:0005811 p=9.0E−03 n=4 fg=0.05 bg=0.01
cell projection membrane GO:0031253 p=9.3E−03 n=8 fg=0.10 bg=0.04
9+2 motile cilium GO:0097729 p=1.3E−02 n=4 fg=0.05 bg=0.01
brush border membrane GO:0031526 p=1.8E−02 n=3 fg=0.04 bg=0.01
sperm principal piece GO:0097228 p=1.9E−02 n=2 fg=0.02 bg=0.00
sperm fibrous sheath GO:0035686 p=1.9E−02 n=2 fg=0.02 bg=0.00
vacuolar membrane GO:0005774 p=2.0E−02 n=7 fg=0.09 bg=0.03
motile cilium GO:0031514 p=2.1E−02 n=5 fg=0.06 bg=0.02
specific granule membrane GO:0035579 p=2.3E−02 n=3 fg=0.04 bg=0.01
tertiary granule membrane GO:0070821 p=2.7E−02 n=2 fg=0.02 bg=0.00
heterotrimeric G−protein complex GO:0005834 p=2.7E−02 n=2 fg=0.02 bg=0.00
acrosomal vesicle GO:0001669 p=2.7E−02 n=2 fg=0.02 bg=0.00
GTPase complex GO:1905360 p=2.7E−02 n=2 fg=0.02 bg=0.00
adherens junction GO:0005912 p=3.2E−02 n=5 fg=0.06 bg=0.02
early endosome membrane GO:0031901 p=3.3E−02 n=3 fg=0.04 bg=0.01
dynein complex GO:0030286 p=3.7E−02 n=2 fg=0.02 bg=0.00
extrinsic component of membrane GO:0019898 p=3.8E−02 n=5 fg=0.06 bg=0.02
lysosomal membrane GO:0005765 p=4.2E−02 n=5 fg=0.06 bg=0.02
eukaryotic translation initiation factor... GO:0016281 p=4.5E−02 n=1 fg=0.01 bg=0.00
molybdopterin synthase complex GO:0019008 p=4.5E−02 n=1 fg=0.01 bg=0.00
DNA ligase III−XRCC1 complex GO:0070421 p=4.5E−02 n=1 fg=0.01 bg=0.00
synaptic cleft GO:0043083 p=4.5E−02 n=1 fg=0.01 bg=0.00
DNA replication factor C complex GO:0005663 p=4.5E−02 n=1 fg=0.01 bg=0.00
Swi5−Swi2 complex GO:0034974 p=4.5E−02 n=1 fg=0.01 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=4.5E−02 n=1 fg=0.01 bg=0.00
DNA recombinase mediator complex GO:0033061 p=4.5E−02 n=1 fg=0.01 bg=0.00
Swi5−Sfr1 complex GO:0032798 p=4.5E−02 n=1 fg=0.01 bg=0.00
Ctf18 RFC−like complex GO:0031390 p=4.5E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=82/312 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction