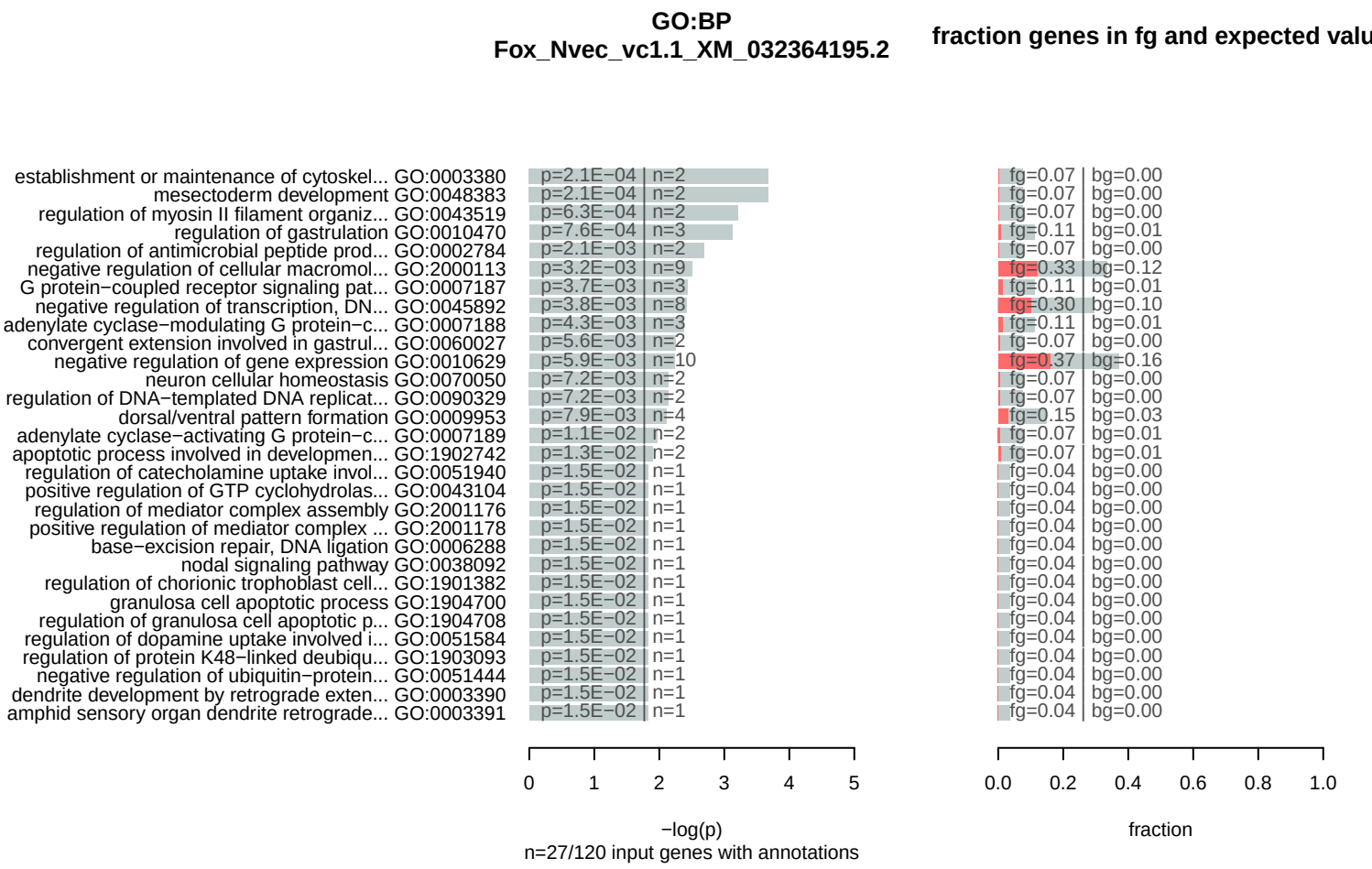
GO:BP
Fox_Nvec_vc1.1_XM_032364195.2
fraction genes in fg and expected valu
establishment or maintenance of cytoskel... GO:0003380 p=2.1E−04 n=2 fg=0.07 bg=0.00
mesectoderm development GO:0048383 p=2.1E−04 n=2 fg=0.07 bg=0.00
regulation of myosin II filament organiz... GO:0043519 p=6.3E−04 n=2 fg=0.07 bg=0.00
regulation of gastrulation GO:0010470 p=7.6E−04 n=3 fg=0.11 bg=0.01
regulation of antimicrobial peptide prod... GO:0002784 p=2.1E−03 n=2 fg=0.07 bg=0.00
negative regulation of cellular macromol... GO:2000113 p=3.2E−03 n=9 fg=0.33 bg=0.12
G protein−coupled receptor signaling pat... GO:0007187 p=3.7E−03 n=3 fg=0.11 bg=0.01
negative regulation of transcription, DN... GO:0045892 p=3.8E−03 n=8 fg=0.30 bg=0.10
adenylate cyclase−modulating G protein−c... GO:0007188 p=4.3E−03 n=3 fg=0.11 bg=0.01
convergent extension involved in gastrul... GO:0060027 p=5.6E−03 n=2 fg=0.07 bg=0.00
negative regulation of gene expression GO:0010629 p=5.9E−03 n=10 fg=0.37 bg=0.16
neuron cellular homeostasis GO:0070050 p=7.2E−03 n=2 fg=0.07 bg=0.00
regulation of DNA−templated DNA replicat... GO:0090329 p=7.2E−03 n=2 fg=0.07 bg=0.00
dorsal/ventral pattern formation GO:0009953 p=7.9E−03 n=4 fg=0.15 bg=0.03
adenylate cyclase−activating G protein−c... GO:0007189 p=1.1E−02 n=2 fg=0.07 bg=0.01
apoptotic process involved in developmen... GO:1902742 p=1.3E−02 n=2 fg=0.07 bg=0.01
regulation of catecholamine uptake invol... GO:0051940 p=1.5E−02 n=1 fg=0.04 bg=0.00
positive regulation of GTP cyclohydrolas... GO:0043104 p=1.5E−02 n=1 fg=0.04 bg=0.00
regulation of mediator complex assembly GO:2001176 p=1.5E−02 n=1 fg=0.04 bg=0.00
positive regulation of mediator complex ... GO:2001178 p=1.5E−02 n=1 fg=0.04 bg=0.00
base−excision repair, DNA ligation GO:0006288 p=1.5E−02 n=1 fg=0.04 bg=0.00
nodal signaling pathway GO:0038092 p=1.5E−02 n=1 fg=0.04 bg=0.00
regulation of chorionic trophoblast cell... GO:1901382 p=1.5E−02 n=1 fg=0.04 bg=0.00
granulosa cell apoptotic process GO:1904700 p=1.5E−02 n=1 fg=0.04 bg=0.00
regulation of granulosa cell apoptotic p... GO:1904708 p=1.5E−02 n=1 fg=0.04 bg=0.00
regulation of dopamine uptake involved i... GO:0051584 p=1.5E−02 n=1 fg=0.04 bg=0.00
regulation of protein K48−linked deubiqu... GO:1903093 p=1.5E−02 n=1 fg=0.04 bg=0.00
negative regulation of ubiquitin−protein... GO:0051444 p=1.5E−02 n=1 fg=0.04 bg=0.00
dendrite development by retrograde exten... GO:0003390 p=1.5E−02 n=1 fg=0.04 bg=0.00
amphid sensory organ dendrite retrograde... GO:0003391 p=1.5E−02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=27/120 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032364195.2
fraction genes in fg and expected valu
ubiquitin ligase inhibitor activity GO:1990948 p=1.6E−02 n=1 fg=0.04 bg=0.00
5S rDNA binding GO:0080084 p=1.6E−02 n=1 fg=0.04 bg=0.00
ATPase−coupled intramembrane lipid trans... GO:0140326 p=1.6E−02 n=1 fg=0.04 bg=0.00
flippase activity GO:0140327 p=1.6E−02 n=1 fg=0.04 bg=0.00
ubiquitin−like modifier activating enzym... GO:0008641 p=1.6E−02 n=1 fg=0.04 bg=0.00
UFM1 activating enzyme activity GO:0071566 p=1.6E−02 n=1 fg=0.04 bg=0.00
RNA polymerase III core binding GO:0000994 p=1.6E−02 n=1 fg=0.04 bg=0.00
RNA polymerase III transcription regulat... GO:0001016 p=1.6E−02 n=1 fg=0.04 bg=0.00
GABA receptor binding GO:0050811 p=1.6E−02 n=1 fg=0.04 bg=0.00
aminophospholipid flippase activity GO:0015247 p=1.6E−02 n=1 fg=0.04 bg=0.00
alkylglycerophosphoethanolamine phosphod... GO:0047391 p=1.6E−02 n=1 fg=0.04 bg=0.00
D5 dopamine receptor binding GO:0031752 p=1.6E−02 n=1 fg=0.04 bg=0.00
ubiquitin−protein transferase inhibitor ... GO:0055105 p=1.6E−02 n=1 fg=0.04 bg=0.00
phosphatidylglycerol binding GO:1901611 p=1.6E−02 n=1 fg=0.04 bg=0.00
cardiolipin binding GO:1901612 p=1.6E−02 n=1 fg=0.04 bg=0.00
dynein light intermediate chain binding GO:0051959 p=1.6E−02 n=1 fg=0.04 bg=0.00
DNA ligase activity GO:0003909 p=3.1E−02 n=1 fg=0.04 bg=0.00
transcription corepressor binding GO:0001222 p=3.1E−02 n=1 fg=0.04 bg=0.00
peroxisome proliferator activated recept... GO:0042975 p=3.1E−02 n=1 fg=0.04 bg=0.00
nuclear retinoid X receptor binding GO:0046965 p=3.1E−02 n=1 fg=0.04 bg=0.00
DNA ligase (ATP) activity GO:0003910 p=3.1E−02 n=1 fg=0.04 bg=0.00
co−SMAD binding GO:0070410 p=3.1E−02 n=1 fg=0.04 bg=0.00
5S rRNA binding GO:0008097 p=3.1E−02 n=1 fg=0.04 bg=0.00
signaling receptor binding GO:0005102 p=3.8E−02 n=6 fg=0.24 bg=0.10
cytoskeletal protein binding GO:0008092 p=4.3E−02 n=5 fg=0.20 bg=0.08
ankyrin binding GO:0030506 p=4.6E−02 n=1 fg=0.04 bg=0.00
rDNA binding GO:0000182 p=4.6E−02 n=1 fg=0.04 bg=0.00
nuclear retinoic acid receptor binding GO:0042974 p=4.6E−02 n=1 fg=0.04 bg=0.00
ligase activity, forming phosphoric este... GO:0016886 p=4.6E−02 n=1 fg=0.04 bg=0.00
ubiquitin−protein transferase regulator ... GO:0055106 p=4.6E−02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=25/120 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032364195.2
fraction genes in fg and expected valu
sensory dendrite GO:0071683 p=2.1E−03 n=2 fg=0.07 bg=0.00
heterotrimeric G−protein complex GO:0005834 p=3.1E−03 n=2 fg=0.07 bg=0.00
spectrosome GO:0045170 p=1.5E−02 n=1 fg=0.04 bg=0.00
spectrin GO:0008091 p=1.5E−02 n=1 fg=0.04 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=1.5E−02 n=1 fg=0.04 bg=0.00
endocytic patch GO:0061645 p=1.5E−02 n=1 fg=0.04 bg=0.00
DNA ligase III−XRCC1 complex GO:0070421 p=1.5E−02 n=1 fg=0.04 bg=0.00
actin cortical patch GO:0030479 p=1.5E−02 n=1 fg=0.04 bg=0.00
molybdopterin synthase complex GO:0019008 p=1.5E−02 n=1 fg=0.04 bg=0.00
brush border membrane GO:0031526 p=1.5E−02 n=2 fg=0.07 bg=0.01
cortical actin cytoskeleton GO:0030864 p=1.5E−02 n=2 fg=0.07 bg=0.01
cell projection membrane GO:0031253 p=1.6E−02 n=4 fg=0.15 bg=0.04
cortical cytoskeleton GO:0030863 p=2.0E−02 n=2 fg=0.07 bg=0.01
ciliary membrane GO:0060170 p=2.3E−02 n=2 fg=0.07 bg=0.01
extrinsic component of endoplasmic retic... GO:0042406 p=3.0E−02 n=1 fg=0.04 bg=0.00
NELF complex GO:0032021 p=3.0E−02 n=1 fg=0.04 bg=0.00
cytoplasmic side of rough endoplasmic re... GO:0098556 p=3.0E−02 n=1 fg=0.04 bg=0.00
photoreceptor outer segment membrane GO:0042622 p=3.0E−02 n=1 fg=0.04 bg=0.00
RSF complex GO:0031213 p=3.0E−02 n=1 fg=0.04 bg=0.00
cytoplasmic cyclin−dependent protein kin... GO:0000308 p=3.0E−02 n=1 fg=0.04 bg=0.00
cis−Golgi network membrane GO:0033106 p=3.0E−02 n=1 fg=0.04 bg=0.00
photoreceptor disc membrane GO:0097381 p=4.4E−02 n=1 fg=0.04 bg=0.00
inhibitory synapse GO:0060077 p=4.4E−02 n=1 fg=0.04 bg=0.00
aster GO:0005818 p=4.4E−02 n=1 fg=0.04 bg=0.00
polysomal ribosome GO:0042788 p=4.4E−02 n=1 fg=0.04 bg=0.00
spindle pole centrosome GO:0031616 p=4.4E−02 n=1 fg=0.04 bg=0.00
ISWI−type complex GO:0031010 p=4.4E−02 n=1 fg=0.04 bg=0.00
spot adherens junction GO:0005914 p=4.4E−02 n=1 fg=0.04 bg=0.00
spindle pole GO:0000922 p=4.8E−02 n=2 fg=0.07 bg=0.01
brush border GO:0005903 p=4.8E−02 n=2 fg=0.07 bg=0.01
0 1 2 3 4 5
−log(p)
n=27/120 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction