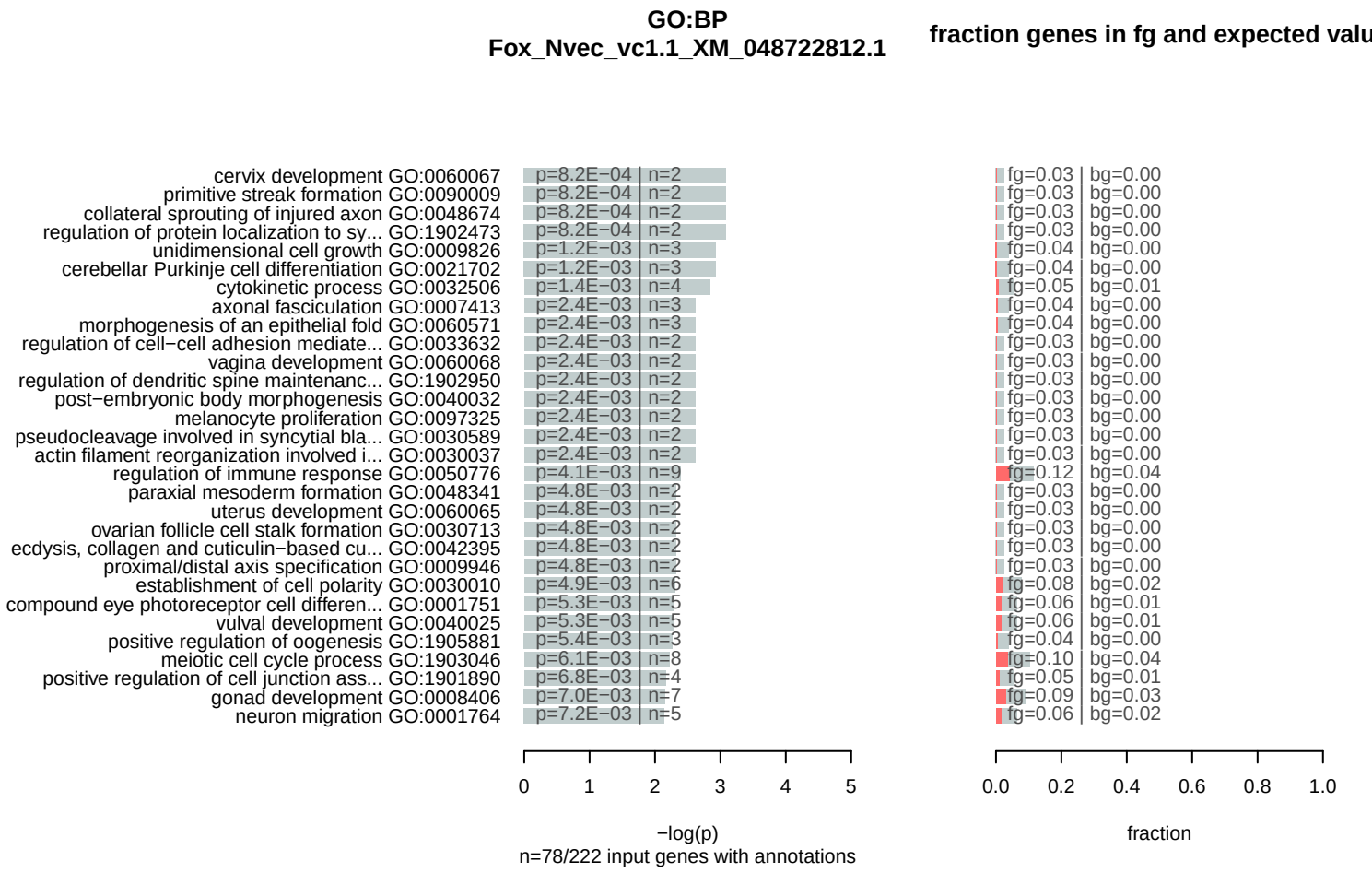
GO:BP
Fox_Nvec_vc1.1_XM_048722812.1
fraction genes in fg and expected valu
cervix development GO:0060067 p=8.2E−04 n=2 fg=0.03 bg=0.00
primitive streak formation GO:0090009 p=8.2E−04 n=2 fg=0.03 bg=0.00
collateral sprouting of injured axon GO:0048674 p=8.2E−04 n=2 fg=0.03 bg=0.00
regulation of protein localization to sy... GO:1902473 p=8.2E−04 n=2 fg=0.03 bg=0.00
unidimensional cell growth GO:0009826 p=1.2E−03 n=3 fg=0.04 bg=0.00
cerebellar Purkinje cell differentiation GO:0021702 p=1.2E−03 n=3 fg=0.04 bg=0.00
cytokinetic process GO:0032506 p=1.4E−03 n=4 fg=0.05 bg=0.01
axonal fasciculation GO:0007413 p=2.4E−03 n=3 fg=0.04 bg=0.00
morphogenesis of an epithelial fold GO:0060571 p=2.4E−03 n=3 fg=0.04 bg=0.00
regulation of cell−cell adhesion mediate... GO:0033632 p=2.4E−03 n=2 fg=0.03 bg=0.00
vagina development GO:0060068 p=2.4E−03 n=2 fg=0.03 bg=0.00
regulation of dendritic spine maintenanc... GO:1902950 p=2.4E−03 n=2 fg=0.03 bg=0.00
post−embryonic body morphogenesis GO:0040032 p=2.4E−03 n=2 fg=0.03 bg=0.00
melanocyte proliferation GO:0097325 p=2.4E−03 n=2 fg=0.03 bg=0.00
pseudocleavage involved in syncytial bla... GO:0030589 p=2.4E−03 n=2 fg=0.03 bg=0.00
actin filament reorganization involved i... GO:0030037 p=2.4E−03 n=2 fg=0.03 bg=0.00
regulation of immune response GO:0050776 p=4.1E−03 n=9 fg=0.12 bg=0.04
paraxial mesoderm formation GO:0048341 p=4.8E−03 n=2 fg=0.03 bg=0.00
uterus development GO:0060065 p=4.8E−03 n=2 fg=0.03 bg=0.00
ovarian follicle cell stalk formation GO:0030713 p=4.8E−03 n=2 fg=0.03 bg=0.00
ecdysis, collagen and cuticulin−based cu... GO:0042395 p=4.8E−03 n=2 fg=0.03 bg=0.00
proximal/distal axis specification GO:0009946 p=4.8E−03 n=2 fg=0.03 bg=0.00
establishment of cell polarity GO:0030010 p=4.9E−03 n=6 fg=0.08 bg=0.02
compound eye photoreceptor cell differen... GO:0001751 p=5.3E−03 n=5 fg=0.06 bg=0.01
vulval development GO:0040025 p=5.3E−03 n=5 fg=0.06 bg=0.01
positive regulation of oogenesis GO:1905881 p=5.4E−03 n=3 fg=0.04 bg=0.00
meiotic cell cycle process GO:1903046 p=6.1E−03 n=8 fg=0.10 bg=0.04
positive regulation of cell junction ass... GO:1901890 p=6.8E−03 n=4 fg=0.05 bg=0.01
gonad development GO:0008406 p=7.0E−03 n=7 fg=0.09 bg=0.03
neuron migration GO:0001764 p=7.2E−03 n=5 fg=0.06 bg=0.02
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−log(p)
n=78/222 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_048722812.1
fraction genes in fg and expected valu
NAD+ ADP−ribosyltransferase activity GO:0003950 p=7.5E−03 n=2 fg=0.03 bg=0.00
epidermal growth factor receptor binding GO:0005154 p=1.1E−02 n=2 fg=0.03 bg=0.00
MAP kinase activity GO:0004707 p=1.5E−02 n=2 fg=0.03 bg=0.00
N−methyltransferase activity GO:0008170 p=2.3E−02 n=3 fg=0.04 bg=0.01
enzyme binding GO:0019899 p=2.7E−02 n=22 fg=0.33 bg=0.22
juvenile hormone epoxide hydrolase activ... GO:0008096 p=2.8E−02 n=1 fg=0.01 bg=0.00
NAD+ synthase (glutamine−hydrolyzing) ac... GO:0003952 p=2.8E−02 n=1 fg=0.01 bg=0.00
phosphopentomutase activity GO:0008973 p=2.8E−02 n=1 fg=0.01 bg=0.00
glucose−1,6−bisphosphate synthase activi... GO:0047933 p=2.8E−02 n=1 fg=0.01 bg=0.00
leucine−tRNA ligase activity GO:0004823 p=2.8E−02 n=1 fg=0.01 bg=0.00
glutamine−tRNA ligase activity GO:0004819 p=2.8E−02 n=1 fg=0.01 bg=0.00
chemoattractant activity involved in axo... GO:1902379 p=2.8E−02 n=1 fg=0.01 bg=0.00
class II DNA−(apurinic or apyrimidinic s... GO:0052720 p=2.8E−02 n=1 fg=0.01 bg=0.00
cis−stilbene−oxide hydrolase activity GO:0033961 p=2.8E−02 n=1 fg=0.01 bg=0.00
phosphatidylserine decarboxylase activit... GO:0004609 p=2.8E−02 n=1 fg=0.01 bg=0.00
valine−tRNA ligase activity GO:0004832 p=2.8E−02 n=1 fg=0.01 bg=0.00
lipoprotein lipase activity GO:0004465 p=2.8E−02 n=1 fg=0.01 bg=0.00
DNA topoisomerase type II (double strand... GO:0003918 p=2.8E−02 n=1 fg=0.01 bg=0.00
NAD+ synthase activity GO:0008795 p=2.8E−02 n=1 fg=0.01 bg=0.00
amidinotransferase activity GO:0015067 p=2.8E−02 n=1 fg=0.01 bg=0.00
glycine amidinotransferase activity GO:0015068 p=2.8E−02 n=1 fg=0.01 bg=0.00
glutaminase activity GO:0004359 p=2.8E−02 n=1 fg=0.01 bg=0.00
JUN kinase activity GO:0004705 p=2.8E−02 n=1 fg=0.01 bg=0.00
NAD+−protein ADP−ribosyltransferase acti... GO:1990404 p=2.8E−02 n=1 fg=0.01 bg=0.00
oxidative DNA demethylase activity GO:0035516 p=2.8E−02 n=1 fg=0.01 bg=0.00
mono−olein transacylation activity GO:0051264 p=2.8E−02 n=1 fg=0.01 bg=0.00
diolein transacylation activity GO:0051265 p=2.8E−02 n=1 fg=0.01 bg=0.00
histone deacetylase regulator activity GO:0035033 p=2.8E−02 n=1 fg=0.01 bg=0.00
3 iron, 4 sulfur cluster binding GO:0051538 p=2.8E−02 n=1 fg=0.01 bg=0.00
aconitate hydratase activity GO:0003994 p=2.8E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=67/222 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_048722812.1
fraction genes in fg and expected valu
collagen and cuticulin−based cuticle ext... GO:0060102 p=8.7E−04 n=2 fg=0.03 bg=0.00
cell−cell junction GO:0005911 p=4.8E−03 n=9 fg=0.11 bg=0.04
striated muscle thin filament GO:0005865 p=5.0E−03 n=2 fg=0.03 bg=0.00
actin filament GO:0005884 p=7.2E−03 n=3 fg=0.04 bg=0.01
preribosome GO:0030684 p=9.7E−03 n=4 fg=0.05 bg=0.01
cytoplasmic region GO:0099568 p=1.8E−02 n=9 fg=0.11 bg=0.05
cell cortex GO:0005938 p=2.0E−02 n=7 fg=0.09 bg=0.03
cortical actin cytoskeleton GO:0030864 p=2.0E−02 n=3 fg=0.04 bg=0.01
contractile ring GO:0070938 p=2.2E−02 n=2 fg=0.03 bg=0.00
adherens junction GO:0005912 p=2.7E−02 n=5 fg=0.06 bg=0.02
cortical cytoskeleton GO:0030863 p=2.9E−02 n=3 fg=0.04 bg=0.01
actin rod GO:0031002 p=3.0E−02 n=1 fg=0.01 bg=0.00
plasmodesma GO:0009506 p=3.0E−02 n=1 fg=0.01 bg=0.00
chloroplast GO:0009507 p=3.0E−02 n=1 fg=0.01 bg=0.00
piP−body GO:0071547 p=3.0E−02 n=1 fg=0.01 bg=0.00
keratin filament GO:0045095 p=3.0E−02 n=1 fg=0.01 bg=0.00
intrinsic component of omegasome membran... GO:0097630 p=3.0E−02 n=1 fg=0.01 bg=0.00
integral component of omegasome membrane GO:0097631 p=3.0E−02 n=1 fg=0.01 bg=0.00
symplast GO:0055044 p=3.0E−02 n=1 fg=0.01 bg=0.00
Mon1−Ccz1 complex GO:0035658 p=3.0E−02 n=1 fg=0.01 bg=0.00
omegasome GO:1990462 p=3.0E−02 n=1 fg=0.01 bg=0.00
DNA topoisomerase type II (double strand... GO:0009330 p=3.0E−02 n=1 fg=0.01 bg=0.00
desmosome GO:0030057 p=3.0E−02 n=1 fg=0.01 bg=0.00
omegasome membrane GO:1903349 p=3.0E−02 n=1 fg=0.01 bg=0.00
apoplast GO:0048046 p=3.0E−02 n=1 fg=0.01 bg=0.00
cofilin−actin rod GO:0090732 p=3.0E−02 n=1 fg=0.01 bg=0.00
plastid GO:0009536 p=3.0E−02 n=1 fg=0.01 bg=0.00
neuron projection cytoplasm GO:0120111 p=4.0E−02 n=2 fg=0.03 bg=0.00
cell−substrate junction GO:0030055 p=4.4E−02 n=3 fg=0.04 bg=0.01
actomyosin contractile ring GO:0005826 p=5.8E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=80/222 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction