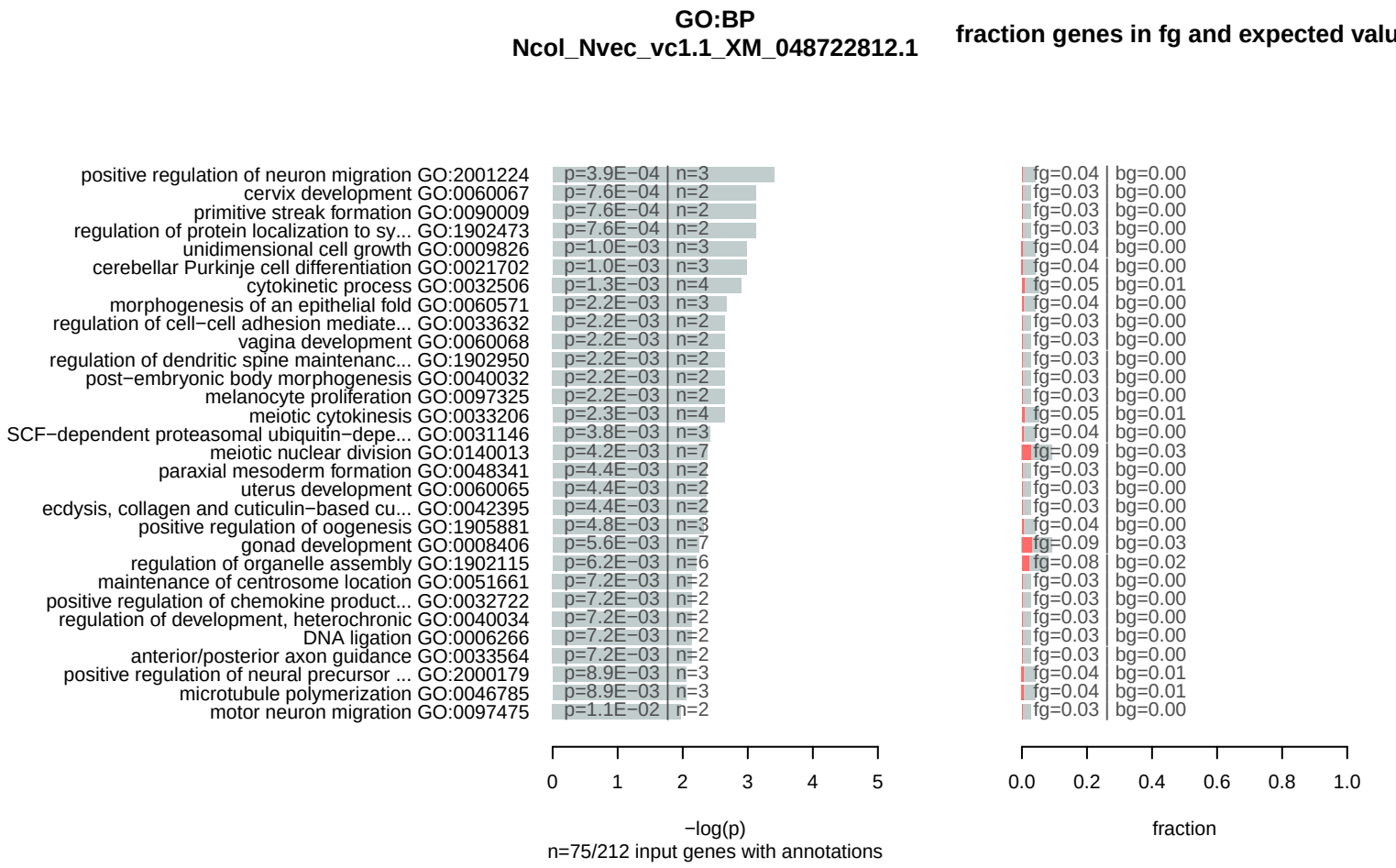
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fraction genes in fg and expected valu
positive regulation of neuron migration GO:2001224 p=3.9E−04 n=3 fg=0.04 bg=0.00
cervix development GO:0060067 p=7.6E−04 n=2 fg=0.03 bg=0.00
primitive streak formation GO:0090009 p=7.6E−04 n=2 fg=0.03 bg=0.00
regulation of protein localization to sy... GO:1902473 p=7.6E−04 n=2 fg=0.03 bg=0.00
unidimensional cell growth GO:0009826 p=1.0E−03 n=3 fg=0.04 bg=0.00
cerebellar Purkinje cell differentiation GO:0021702 p=1.0E−03 n=3 fg=0.04 bg=0.00
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regulation of cell−cell adhesion mediate... GO:0033632 p=2.2E−03 n=2 fg=0.03 bg=0.00
vagina development GO:0060068 p=2.2E−03 n=2 fg=0.03 bg=0.00
regulation of dendritic spine maintenanc... GO:1902950 p=2.2E−03 n=2 fg=0.03 bg=0.00
post−embryonic body morphogenesis GO:0040032 p=2.2E−03 n=2 fg=0.03 bg=0.00
melanocyte proliferation GO:0097325 p=2.2E−03 n=2 fg=0.03 bg=0.00
meiotic cytokinesis GO:0033206 p=2.3E−03 n=4 fg=0.05 bg=0.01
SCF−dependent proteasomal ubiquitin−depe... GO:0031146 p=3.8E−03 n=3 fg=0.04 bg=0.00
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paraxial mesoderm formation GO:0048341 p=4.4E−03 n=2 fg=0.03 bg=0.00
uterus development GO:0060065 p=4.4E−03 n=2 fg=0.03 bg=0.00
ecdysis, collagen and cuticulin−based cu... GO:0042395 p=4.4E−03 n=2 fg=0.03 bg=0.00
positive regulation of oogenesis GO:1905881 p=4.8E−03 n=3 fg=0.04 bg=0.00
gonad development GO:0008406 p=5.6E−03 n=7 fg=0.09 bg=0.03
regulation of organelle assembly GO:1902115 p=6.2E−03 n=6 fg=0.08 bg=0.02
maintenance of centrosome location GO:0051661 p=7.2E−03 n=2 fg=0.03 bg=0.00
positive regulation of chemokine product... GO:0032722 p=7.2E−03 n=2 fg=0.03 bg=0.00
regulation of development, heterochronic GO:0040034 p=7.2E−03 n=2 fg=0.03 bg=0.00
DNA ligation GO:0006266 p=7.2E−03 n=2 fg=0.03 bg=0.00
anterior/posterior axon guidance GO:0033564 p=7.2E−03 n=2 fg=0.03 bg=0.00
positive regulation of neural precursor ... GO:2000179 p=8.9E−03 n=3 fg=0.04 bg=0.01
microtubule polymerization GO:0046785 p=8.9E−03 n=3 fg=0.04 bg=0.01
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fraction
GO:MF
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fraction genes in fg and expected valu
intramolecular transferase activity, pho... GO:0016868 p=7.2E−03 n=2 fg=0.03 bg=0.00
NAD+ ADP−ribosyltransferase activity GO:0003950 p=7.2E−03 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=2.2E−02 n=3 fg=0.05 bg=0.01
phosphoglycerate mutase activity GO:0004619 p=2.8E−02 n=1 fg=0.02 bg=0.00
juvenile hormone epoxide hydrolase activ... GO:0008096 p=2.8E−02 n=1 fg=0.02 bg=0.00
NAD+ synthase (glutamine−hydrolyzing) ac... GO:0003952 p=2.8E−02 n=1 fg=0.02 bg=0.00
phosphopentomutase activity GO:0008973 p=2.8E−02 n=1 fg=0.02 bg=0.00
glucose−1,6−bisphosphate synthase activi... GO:0047933 p=2.8E−02 n=1 fg=0.02 bg=0.00
leucine−tRNA ligase activity GO:0004823 p=2.8E−02 n=1 fg=0.02 bg=0.00
glutamine−tRNA ligase activity GO:0004819 p=2.8E−02 n=1 fg=0.02 bg=0.00
chemoattractant activity involved in axo... GO:1902379 p=2.8E−02 n=1 fg=0.02 bg=0.00
class II DNA−(apurinic or apyrimidinic s... GO:0052720 p=2.8E−02 n=1 fg=0.02 bg=0.00
cis−stilbene−oxide hydrolase activity GO:0033961 p=2.8E−02 n=1 fg=0.02 bg=0.00
valine−tRNA ligase activity GO:0004832 p=2.8E−02 n=1 fg=0.02 bg=0.00
lipoprotein lipase activity GO:0004465 p=2.8E−02 n=1 fg=0.02 bg=0.00
DNA topoisomerase type II (double strand... GO:0003918 p=2.8E−02 n=1 fg=0.02 bg=0.00
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glycine amidinotransferase activity GO:0015068 p=2.8E−02 n=1 fg=0.02 bg=0.00
glutaminase activity GO:0004359 p=2.8E−02 n=1 fg=0.02 bg=0.00
JUN kinase activity GO:0004705 p=2.8E−02 n=1 fg=0.02 bg=0.00
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oxidative DNA demethylase activity GO:0035516 p=2.8E−02 n=1 fg=0.02 bg=0.00
mono−olein transacylation activity GO:0051264 p=2.8E−02 n=1 fg=0.02 bg=0.00
diolein transacylation activity GO:0051265 p=2.8E−02 n=1 fg=0.02 bg=0.00
histone deacetylase regulator activity GO:0035033 p=2.8E−02 n=1 fg=0.02 bg=0.00
3 iron, 4 sulfur cluster binding GO:0051538 p=2.8E−02 n=1 fg=0.02 bg=0.00
aconitate hydratase activity GO:0003994 p=2.8E−02 n=1 fg=0.02 bg=0.00
protein C−terminal methylesterase activi... GO:0051722 p=2.8E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=66/212 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_048722812.1
fraction genes in fg and expected valu
collagen and cuticulin−based cuticle ext... GO:0060102 p=8.5E−04 n=2 fg=0.03 bg=0.00
striated muscle thin filament GO:0005865 p=4.9E−03 n=2 fg=0.03 bg=0.00
actin filament GO:0005884 p=6.9E−03 n=3 fg=0.04 bg=0.01
SCF ubiquitin ligase complex GO:0019005 p=1.0E−02 n=3 fg=0.04 bg=0.01
cortical actin cytoskeleton GO:0030864 p=1.9E−02 n=3 fg=0.04 bg=0.01
contractile ring GO:0070938 p=2.1E−02 n=2 fg=0.03 bg=0.00
cortical cytoskeleton GO:0030863 p=2.8E−02 n=3 fg=0.04 bg=0.01
actin rod GO:0031002 p=2.9E−02 n=1 fg=0.01 bg=0.00
plasmodesma GO:0009506 p=2.9E−02 n=1 fg=0.01 bg=0.00
chloroplast GO:0009507 p=2.9E−02 n=1 fg=0.01 bg=0.00
piP−body GO:0071547 p=2.9E−02 n=1 fg=0.01 bg=0.00
keratin filament GO:0045095 p=2.9E−02 n=1 fg=0.01 bg=0.00
intrinsic component of omegasome membran... GO:0097630 p=2.9E−02 n=1 fg=0.01 bg=0.00
integral component of omegasome membrane GO:0097631 p=2.9E−02 n=1 fg=0.01 bg=0.00
symplast GO:0055044 p=2.9E−02 n=1 fg=0.01 bg=0.00
Mon1−Ccz1 complex GO:0035658 p=2.9E−02 n=1 fg=0.01 bg=0.00
omegasome GO:1990462 p=2.9E−02 n=1 fg=0.01 bg=0.00
DNA topoisomerase type II (double strand... GO:0009330 p=2.9E−02 n=1 fg=0.01 bg=0.00
desmosome GO:0030057 p=2.9E−02 n=1 fg=0.01 bg=0.00
omegasome membrane GO:1903349 p=2.9E−02 n=1 fg=0.01 bg=0.00
apoplast GO:0048046 p=2.9E−02 n=1 fg=0.01 bg=0.00
cofilin−actin rod GO:0090732 p=2.9E−02 n=1 fg=0.01 bg=0.00
plastid GO:0009536 p=2.9E−02 n=1 fg=0.01 bg=0.00
ficolin−1−rich granule GO:0101002 p=3.5E−02 n=4 fg=0.05 bg=0.02
neuron projection cytoplasm GO:0120111 p=3.9E−02 n=2 fg=0.03 bg=0.00
anchoring junction GO:0070161 p=4.1E−02 n=7 fg=0.09 bg=0.04
cell−cell junction GO:0005911 p=4.1E−02 n=7 fg=0.09 bg=0.04
cytoplasmic region GO:0099568 p=4.3E−02 n=8 fg=0.10 bg=0.05
preribosome GO:0030684 p=5.1E−02 n=3 fg=0.04 bg=0.01
cell cortex GO:0005938 p=5.5E−02 n=6 fg=0.08 bg=0.03
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−log(p)
n=79/212 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction