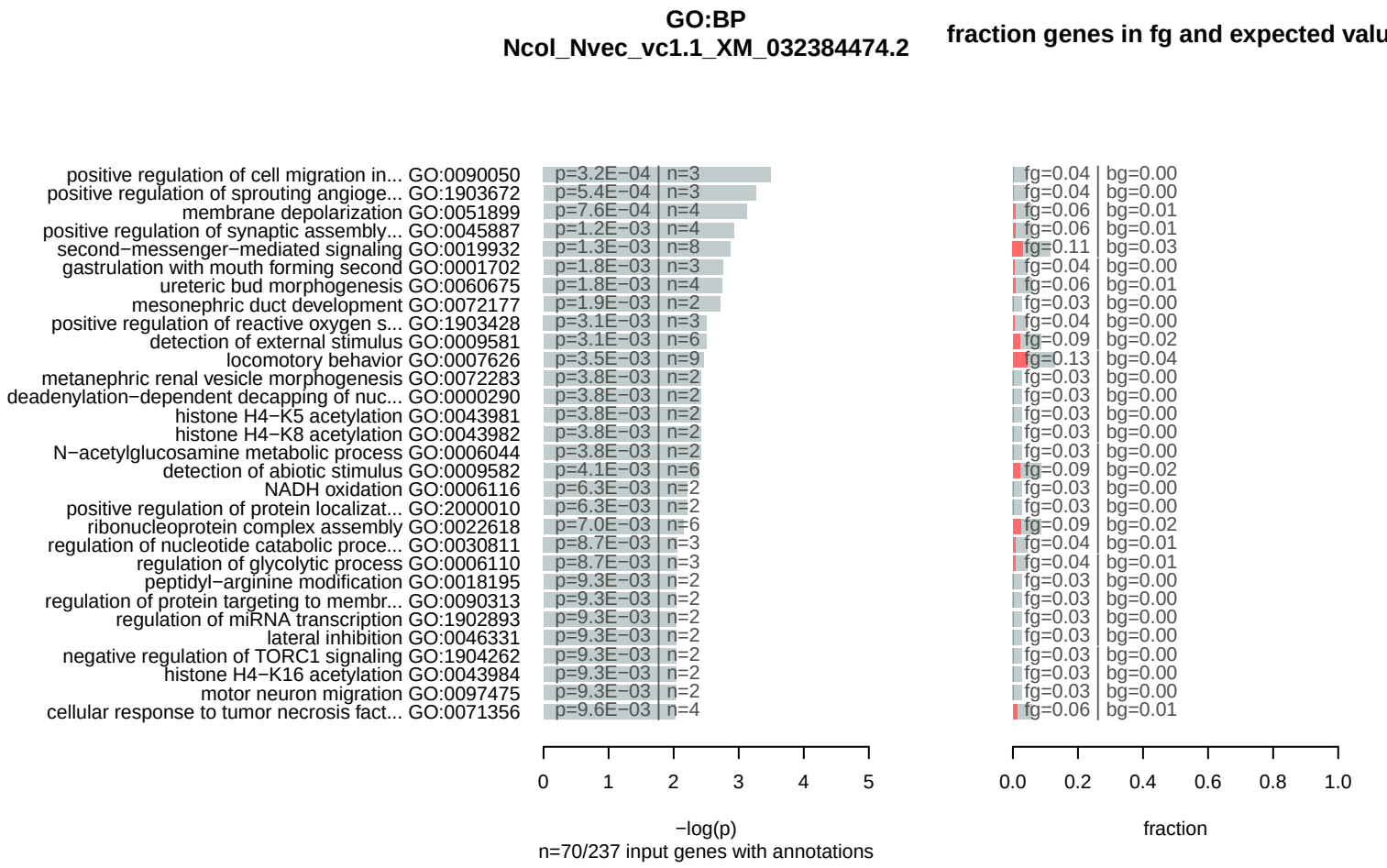
GO:BP
Ncol_Nvec_vc1.1_XM_032384474.2
fraction genes in fg and expected valu
positive regulation of cell migration in... GO:0090050 p=3.2E−04 n=3 fg=0.04 bg=0.00
positive regulation of sprouting angioge... GO:1903672 p=5.4E−04 n=3 fg=0.04 bg=0.00
membrane depolarization GO:0051899 p=7.6E−04 n=4 fg=0.06 bg=0.01
positive regulation of synaptic assembly... GO:0045887 p=1.2E−03 n=4 fg=0.06 bg=0.01
second−messenger−mediated signaling GO:0019932 p=1.3E−03 n=8 fg=0.11 bg=0.03
gastrulation with mouth forming second GO:0001702 p=1.8E−03 n=3 fg=0.04 bg=0.00
ureteric bud morphogenesis GO:0060675 p=1.8E−03 n=4 fg=0.06 bg=0.01
mesonephric duct development GO:0072177 p=1.9E−03 n=2 fg=0.03 bg=0.00
positive regulation of reactive oxygen s... GO:1903428 p=3.1E−03 n=3 fg=0.04 bg=0.00
detection of external stimulus GO:0009581 p=3.1E−03 n=6 fg=0.09 bg=0.02
locomotory behavior GO:0007626 p=3.5E−03 n=9 fg=0.13 bg=0.04
metanephric renal vesicle morphogenesis GO:0072283 p=3.8E−03 n=2 fg=0.03 bg=0.00
deadenylation−dependent decapping of nuc... GO:0000290 p=3.8E−03 n=2 fg=0.03 bg=0.00
histone H4−K5 acetylation GO:0043981 p=3.8E−03 n=2 fg=0.03 bg=0.00
histone H4−K8 acetylation GO:0043982 p=3.8E−03 n=2 fg=0.03 bg=0.00
N−acetylglucosamine metabolic process GO:0006044 p=3.8E−03 n=2 fg=0.03 bg=0.00
detection of abiotic stimulus GO:0009582 p=4.1E−03 n=6 fg=0.09 bg=0.02
NADH oxidation GO:0006116 p=6.3E−03 n=2 fg=0.03 bg=0.00
positive regulation of protein localizat... GO:2000010 p=6.3E−03 n=2 fg=0.03 bg=0.00
ribonucleoprotein complex assembly GO:0022618 p=7.0E−03 n=6 fg=0.09 bg=0.02
regulation of nucleotide catabolic proce... GO:0030811 p=8.7E−03 n=3 fg=0.04 bg=0.01
regulation of glycolytic process GO:0006110 p=8.7E−03 n=3 fg=0.04 bg=0.01
peptidyl−arginine modification GO:0018195 p=9.3E−03 n=2 fg=0.03 bg=0.00
regulation of protein targeting to membr... GO:0090313 p=9.3E−03 n=2 fg=0.03 bg=0.00
regulation of miRNA transcription GO:1902893 p=9.3E−03 n=2 fg=0.03 bg=0.00
lateral inhibition GO:0046331 p=9.3E−03 n=2 fg=0.03 bg=0.00
negative regulation of TORC1 signaling GO:1904262 p=9.3E−03 n=2 fg=0.03 bg=0.00
histone H4−K16 acetylation GO:0043984 p=9.3E−03 n=2 fg=0.03 bg=0.00
motor neuron migration GO:0097475 p=9.3E−03 n=2 fg=0.03 bg=0.00
cellular response to tumor necrosis fact... GO:0071356 p=9.6E−03 n=4 fg=0.06 bg=0.01
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−log(p)
n=70/237 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032384474.2
fraction genes in fg and expected valu
high voltage−gated calcium channel activ... GO:0008331 p=6.1E−04 n=2 fg=0.03 bg=0.00
methyltransferase activity GO:0008168 p=1.1E−03 n=6 fg=0.10 bg=0.02
acetylglucosaminyltransferase activity GO:0008375 p=1.6E−03 n=3 fg=0.05 bg=0.00
S−adenosyl−L−methionine binding GO:1904047 p=5.8E−03 n=2 fg=0.03 bg=0.00
protein serine/threonine phosphatase act... GO:0004722 p=1.1E−02 n=3 fg=0.05 bg=0.01
transcription corepressor activity GO:0003714 p=1.2E−02 n=4 fg=0.07 bg=0.02
manganese ion binding GO:0030145 p=1.4E−02 n=3 fg=0.05 bg=0.01
S−adenosylmethionine−dependent methyltra... GO:0008757 p=1.8E−02 n=4 fg=0.07 bg=0.02
protein kinase regulator activity GO:0019887 p=1.8E−02 n=4 fg=0.07 bg=0.02
RNA methyltransferase activity GO:0008173 p=1.8E−02 n=3 fg=0.05 bg=0.01
histone methyltransferase activity GO:0042054 p=2.0E−02 n=2 fg=0.03 bg=0.00
oxidoreductase activity, acting on CH−OH... GO:0016614 p=2.0E−02 n=3 fg=0.05 bg=0.01
kinase regulator activity GO:0019207 p=2.2E−02 n=4 fg=0.07 bg=0.02
superoxide dismutase activity GO:0004784 p=2.5E−02 n=1 fg=0.02 bg=0.00
vascular endothelial growth factor recep... GO:0043184 p=2.5E−02 n=1 fg=0.02 bg=0.00
protein−membrane adaptor activity GO:0043495 p=2.5E−02 n=1 fg=0.02 bg=0.00
[myelin basic protein]−arginine N−methyl... GO:0016277 p=2.5E−02 n=1 fg=0.02 bg=0.00
histone H3−methyl−arginine−2 demethylase... GO:0033746 p=2.5E−02 n=1 fg=0.02 bg=0.00
histone H3−methyl−arginine−3 demethylase... GO:0033749 p=2.5E−02 n=1 fg=0.02 bg=0.00
peptidyl−lysine 5−dioxygenase activity GO:0070815 p=2.5E−02 n=1 fg=0.02 bg=0.00
histone methyltransferase activity (H3−K... GO:0046976 p=2.5E−02 n=1 fg=0.02 bg=0.00
RNA uridylyltransferase activity GO:0050265 p=2.5E−02 n=1 fg=0.02 bg=0.00
arginine binding GO:0034618 p=2.5E−02 n=1 fg=0.02 bg=0.00
H3 histone acetyltransferase activity GO:0010484 p=2.5E−02 n=1 fg=0.02 bg=0.00
tRNA 2'−phosphotransferase activity GO:0000215 p=2.5E−02 n=1 fg=0.02 bg=0.00
glutamate−cysteine ligase catalytic subu... GO:0035226 p=2.5E−02 n=1 fg=0.02 bg=0.00
glycerophosphoinositol glycerophosphodie... GO:0047395 p=2.5E−02 n=1 fg=0.02 bg=0.00
cadmium ion binding GO:0046870 p=2.5E−02 n=1 fg=0.02 bg=0.00
protein−arginine omega−N symmetric methy... GO:0035243 p=2.5E−02 n=1 fg=0.02 bg=0.00
TFIIF−class transcription factor complex... GO:0001096 p=2.5E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=59/237 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032384474.2
fraction genes in fg and expected valu
histone acetyltransferase complex GO:0000123 p=2.8E−03 n=4 fg=0.06 bg=0.01
voltage−gated calcium channel complex GO:0005891 p=9.8E−03 n=2 fg=0.03 bg=0.00
histone methyltransferase complex GO:0035097 p=1.9E−02 n=3 fg=0.04 bg=0.01
presynaptic active zone GO:0048786 p=2.2E−02 n=3 fg=0.04 bg=0.01
H4 histone acetyltransferase complex GO:1902562 p=2.2E−02 n=2 fg=0.03 bg=0.00
neuromuscular junction GO:0031594 p=2.6E−02 n=4 fg=0.06 bg=0.02
host intracellular part GO:0033646 p=2.7E−02 n=1 fg=0.01 bg=0.00
host intracellular organelle GO:0033647 p=2.7E−02 n=1 fg=0.01 bg=0.00
host intracellular membrane−bounded orga... GO:0033648 p=2.7E−02 n=1 fg=0.01 bg=0.00
autosome GO:0030849 p=2.7E−02 n=1 fg=0.01 bg=0.00
host cellular component GO:0018995 p=2.7E−02 n=1 fg=0.01 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=2.7E−02 n=1 fg=0.01 bg=0.00
host cell nucleus GO:0042025 p=2.7E−02 n=1 fg=0.01 bg=0.00
plus−end kinesin complex GO:0005873 p=2.7E−02 n=1 fg=0.01 bg=0.00
integral component of lysosomal membrane GO:1905103 p=2.7E−02 n=1 fg=0.01 bg=0.00
host intracellular region GO:0043656 p=2.7E−02 n=1 fg=0.01 bg=0.00
host cell GO:0043657 p=2.7E−02 n=1 fg=0.01 bg=0.00
other organism part GO:0044217 p=2.7E−02 n=1 fg=0.01 bg=0.00
host cell nuclear part GO:0044094 p=2.7E−02 n=1 fg=0.01 bg=0.00
host cell PML body GO:0075341 p=2.7E−02 n=1 fg=0.01 bg=0.00
host cell part GO:0033643 p=2.7E−02 n=1 fg=0.01 bg=0.00
Sm−like protein family complex GO:0120114 p=2.8E−02 n=3 fg=0.04 bg=0.01
kinesin complex GO:0005871 p=3.9E−02 n=2 fg=0.03 bg=0.00
extrinsic component of organelle membran... GO:0031312 p=4.5E−02 n=2 fg=0.03 bg=0.00
methyltransferase complex GO:0034708 p=5.2E−02 n=3 fg=0.04 bg=0.01
transcription factor TFIIIC complex GO:0000127 p=5.3E−02 n=1 fg=0.01 bg=0.00
Lsm1−7−Pat1 complex GO:1990726 p=5.3E−02 n=1 fg=0.01 bg=0.00
GATOR2 complex GO:0061700 p=5.3E−02 n=1 fg=0.01 bg=0.00
glutamate−cysteine ligase complex GO:0017109 p=5.3E−02 n=1 fg=0.01 bg=0.00
NSL complex GO:0044545 p=5.3E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=72/237 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction