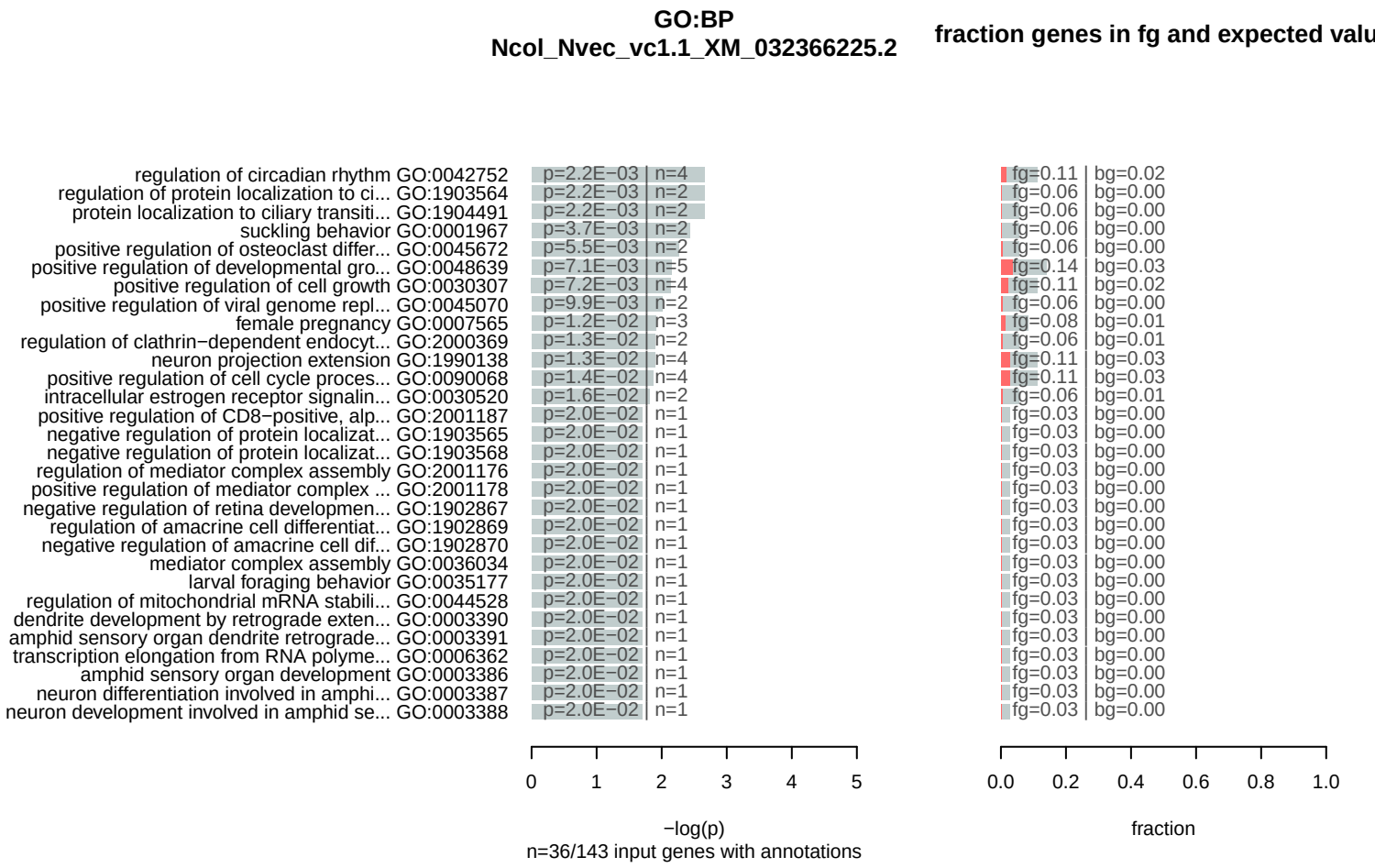
GO:BP
Ncol_Nvec_vc1.1_XM_032366225.2
fraction genes in fg and expected valu
regulation of circadian rhythm GO:0042752 p=2.2E−03 n=4 fg=0.11 bg=0.02
regulation of protein localization to ci... GO:1903564 p=2.2E−03 n=2 fg=0.06 bg=0.00
protein localization to ciliary transiti... GO:1904491 p=2.2E−03 n=2 fg=0.06 bg=0.00
suckling behavior GO:0001967 p=3.7E−03 n=2 fg=0.06 bg=0.00
positive regulation of osteoclast differ... GO:0045672 p=5.5E−03 n=2 fg=0.06 bg=0.00
positive regulation of developmental gro... GO:0048639 p=7.1E−03 n=5 fg=0.14 bg=0.03
positive regulation of cell growth GO:0030307 p=7.2E−03 n=4 fg=0.11 bg=0.02
positive regulation of viral genome repl... GO:0045070 p=9.9E−03 n=2 fg=0.06 bg=0.00
female pregnancy GO:0007565 p=1.2E−02 n=3 fg=0.08 bg=0.01
regulation of clathrin−dependent endocyt... GO:2000369 p=1.3E−02 n=2 fg=0.06 bg=0.01
neuron projection extension GO:1990138 p=1.3E−02 n=4 fg=0.11 bg=0.03
positive regulation of cell cycle proces... GO:0090068 p=1.4E−02 n=4 fg=0.11 bg=0.03
intracellular estrogen receptor signalin... GO:0030520 p=1.6E−02 n=2 fg=0.06 bg=0.01
positive regulation of CD8−positive, alp... GO:2001187 p=2.0E−02 n=1 fg=0.03 bg=0.00
negative regulation of protein localizat... GO:1903565 p=2.0E−02 n=1 fg=0.03 bg=0.00
negative regulation of protein localizat... GO:1903568 p=2.0E−02 n=1 fg=0.03 bg=0.00
regulation of mediator complex assembly GO:2001176 p=2.0E−02 n=1 fg=0.03 bg=0.00
positive regulation of mediator complex ... GO:2001178 p=2.0E−02 n=1 fg=0.03 bg=0.00
negative regulation of retina developmen... GO:1902867 p=2.0E−02 n=1 fg=0.03 bg=0.00
regulation of amacrine cell differentiat... GO:1902869 p=2.0E−02 n=1 fg=0.03 bg=0.00
negative regulation of amacrine cell dif... GO:1902870 p=2.0E−02 n=1 fg=0.03 bg=0.00
mediator complex assembly GO:0036034 p=2.0E−02 n=1 fg=0.03 bg=0.00
larval foraging behavior GO:0035177 p=2.0E−02 n=1 fg=0.03 bg=0.00
regulation of mitochondrial mRNA stabili... GO:0044528 p=2.0E−02 n=1 fg=0.03 bg=0.00
dendrite development by retrograde exten... GO:0003390 p=2.0E−02 n=1 fg=0.03 bg=0.00
amphid sensory organ dendrite retrograde... GO:0003391 p=2.0E−02 n=1 fg=0.03 bg=0.00
transcription elongation from RNA polyme... GO:0006362 p=2.0E−02 n=1 fg=0.03 bg=0.00
amphid sensory organ development GO:0003386 p=2.0E−02 n=1 fg=0.03 bg=0.00
neuron differentiation involved in amphi... GO:0003387 p=2.0E−02 n=1 fg=0.03 bg=0.00
neuron development involved in amphid se... GO:0003388 p=2.0E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=36/143 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032366225.2
fraction genes in fg and expected valu
voltage−gated cation channel activity GO:0022843 p=4.5E−03 n=3 fg=0.10 bg=0.01
voltage−gated potassium channel activity GO:0005249 p=1.5E−02 n=2 fg=0.06 bg=0.01
sequence−specific DNA binding GO:0043565 p=1.8E−02 n=6 fg=0.19 bg=0.07
1−phosphatidylinositol−3−phosphate 4−kin... GO:0052811 p=1.9E−02 n=1 fg=0.03 bg=0.00
branched−chain−amino−acid transaminase a... GO:0004084 p=1.9E−02 n=1 fg=0.03 bg=0.00
hedgehog receptor activity GO:0008158 p=1.9E−02 n=1 fg=0.03 bg=0.00
acid sphingomyelin phosphodiesterase act... GO:0061750 p=1.9E−02 n=1 fg=0.03 bg=0.00
rRNA primary transcript binding GO:0042134 p=1.9E−02 n=1 fg=0.03 bg=0.00
homogentisate 1,2−dioxygenase activity GO:0004411 p=1.9E−02 n=1 fg=0.03 bg=0.00
GABA receptor binding GO:0050811 p=1.9E−02 n=1 fg=0.03 bg=0.00
RNA polymerase III transcription regulat... GO:0001016 p=1.9E−02 n=1 fg=0.03 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=1.9E−02 n=1 fg=0.03 bg=0.00
dynein light intermediate chain binding GO:0051959 p=1.9E−02 n=1 fg=0.03 bg=0.00
S100 protein binding GO:0044548 p=1.9E−02 n=1 fg=0.03 bg=0.00
RNA polymerase III core binding GO:0000994 p=1.9E−02 n=1 fg=0.03 bg=0.00
glycogenin glucosyltransferase activity GO:0008466 p=1.9E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol phosphate kinase ac... GO:0016307 p=1.9E−02 n=1 fg=0.03 bg=0.00
1−phosphatidylinositol−4−phosphate 5−kin... GO:0016308 p=1.9E−02 n=1 fg=0.03 bg=0.00
1−phosphatidylinositol−5−phosphate 4−kin... GO:0016309 p=1.9E−02 n=1 fg=0.03 bg=0.00
oxidoreductase activity, acting on singl... GO:0016702 p=1.9E−02 n=1 fg=0.03 bg=0.00
5S rDNA binding GO:0080084 p=1.9E−02 n=1 fg=0.03 bg=0.00
RNA polymerase binding GO:0070063 p=2.1E−02 n=2 fg=0.06 bg=0.01
potassium channel activity GO:0005267 p=2.9E−02 n=2 fg=0.06 bg=0.01
DNA−binding transcription factor activit... GO:0003700 p=3.5E−02 n=6 fg=0.19 bg=0.08
PTB domain binding GO:0051425 p=3.9E−02 n=1 fg=0.03 bg=0.00
acylglycerol lipase activity GO:0047372 p=3.9E−02 n=1 fg=0.03 bg=0.00
nuclear retinoid X receptor binding GO:0046965 p=3.9E−02 n=1 fg=0.03 bg=0.00
oxidoreductase activity, acting on singl... GO:0016701 p=3.9E−02 n=1 fg=0.03 bg=0.00
sphingomyelin phosphodiesterase activity GO:0004767 p=3.9E−02 n=1 fg=0.03 bg=0.00
potassium ion transmembrane transporter ... GO:0015079 p=4.2E−02 n=2 fg=0.06 bg=0.01
0 1 2 3 4 5
−log(p)
n=31/143 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032366225.2
fraction genes in fg and expected valu
core−binding factor complex GO:0016513 p=2.0E−02 n=1 fg=0.03 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=2.0E−02 n=1 fg=0.03 bg=0.00
endoplasmic reticulum chaperone complex GO:0034663 p=3.9E−02 n=1 fg=0.03 bg=0.00
clathrin complex GO:0071439 p=3.9E−02 n=1 fg=0.03 bg=0.00
lysosomal lumen GO:0043202 p=4.8E−02 n=2 fg=0.06 bg=0.01
pyruvate dehydrogenase complex GO:0045254 p=5.9E+02 n=1 fg=0.03 bg=0.00
inhibitory synapse GO:0060077 p=5.9E+02 n=1 fg=0.03 bg=0.00
CHD−type complex GO:0090545 p=5.9E+02 n=1 fg=0.03 bg=0.00
lamellar body GO:0042599 p=5.9E+02 n=1 fg=0.03 bg=0.00
spindle pole centrosome GO:0031616 p=5.9E+02 n=1 fg=0.03 bg=0.00
NuRD complex GO:0016581 p=5.9E+02 n=1 fg=0.03 bg=0.00
spot adherens junction GO:0005914 p=5.9E+02 n=1 fg=0.03 bg=0.00
muscle cell projection GO:0036194 p=5.9E+02 n=1 fg=0.03 bg=0.00
muscle cell projection membrane GO:0036195 p=5.9E+02 n=1 fg=0.03 bg=0.00
transcription regulator complex GO:0005667 p=6.4E+02 n=4 fg=0.11 bg=0.04
extrinsic component of plasma membrane GO:0019897 p=6.4E+02 n=2 fg=0.06 bg=0.01
autophagosome GO:0005776 p=7.5E−02 n=2 fg=0.06 bg=0.01
zonula adherens GO:0005915 p=7.7E−02 n=1 fg=0.03 bg=0.00
membrane raft GO:0045121 p=8.6E−02 n=3 fg=0.08 bg=0.03
membrane microdomain GO:0098857 p=8.6E−02 n=3 fg=0.08 bg=0.03
vacuolar lumen GO:0005775 p=9.3E−02 n=2 fg=0.06 bg=0.01
extracellular space GO:0005615 p=9.4E−02 n=3 fg=0.08 bg=0.03
sperm fibrous sheath GO:0035686 p=9.6E−02 n=1 fg=0.03 bg=0.00
sperm principal piece GO:0097228 p=9.6E−02 n=1 fg=0.03 bg=0.00
sensory dendrite GO:0071683 p=9.6E−02 n=1 fg=0.03 bg=0.00
juxtaparanode region of axon GO:0044224 p=9.6E−02 n=1 fg=0.03 bg=0.00
intracellular canaliculus GO:0046691 p=9.6E−02 n=1 fg=0.03 bg=0.00
ciliary basal body GO:0036064 p=9.9E−02 n=2 fg=0.06 bg=0.02
extracellular region GO:0005576 p=1.0E−01 n=5 fg=0.14 bg=0.07
dendrite GO:0030425 p=1.1E−01 n=5 fg=0.14 bg=0.07
0 1 2 3 4 5
−log(p)
n=36/143 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction