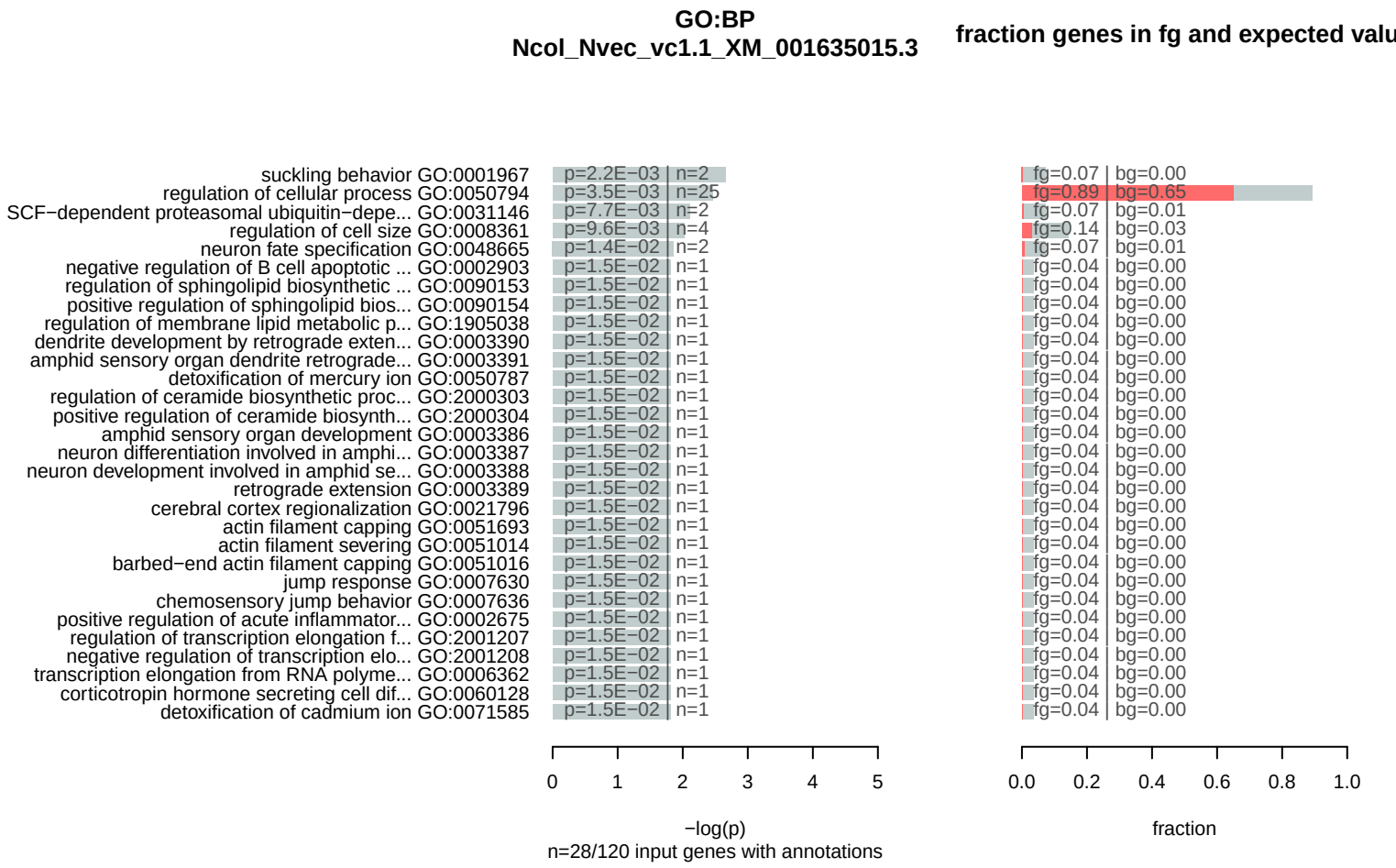
GO:BP
Ncol_Nvec_vc1.1_XM_001635015.3
fraction genes in fg and expected valu
suckling behavior GO:0001967 p=2.2E−03 n=2 fg=0.07 bg=0.00
regulation of cellular process GO:0050794 p=3.5E−03 n=25 fg=0.89 bg=0.65
SCF−dependent proteasomal ubiquitin−depe... GO:0031146 p=7.7E−03 n=2 fg=0.07 bg=0.01
regulation of cell size GO:0008361 p=9.6E−03 n=4 fg=0.14 bg=0.03
neuron fate specification GO:0048665 p=1.4E−02 n=2 fg=0.07 bg=0.01
negative regulation of B cell apoptotic ... GO:0002903 p=1.5E−02 n=1 fg=0.04 bg=0.00
regulation of sphingolipid biosynthetic ... GO:0090153 p=1.5E−02 n=1 fg=0.04 bg=0.00
positive regulation of sphingolipid bios... GO:0090154 p=1.5E−02 n=1 fg=0.04 bg=0.00
regulation of membrane lipid metabolic p... GO:1905038 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
detoxification of mercury ion GO:0050787 p=1.5E−02 n=1 fg=0.04 bg=0.00
regulation of ceramide biosynthetic proc... GO:2000303 p=1.5E−02 n=1 fg=0.04 bg=0.00
positive regulation of ceramide biosynth... GO:2000304 p=1.5E−02 n=1 fg=0.04 bg=0.00
amphid sensory organ development GO:0003386 p=1.5E−02 n=1 fg=0.04 bg=0.00
neuron differentiation involved in amphi... GO:0003387 p=1.5E−02 n=1 fg=0.04 bg=0.00
neuron development involved in amphid se... GO:0003388 p=1.5E−02 n=1 fg=0.04 bg=0.00
retrograde extension GO:0003389 p=1.5E−02 n=1 fg=0.04 bg=0.00
cerebral cortex regionalization GO:0021796 p=1.5E−02 n=1 fg=0.04 bg=0.00
actin filament capping GO:0051693 p=1.5E−02 n=1 fg=0.04 bg=0.00
actin filament severing GO:0051014 p=1.5E−02 n=1 fg=0.04 bg=0.00
barbed−end actin filament capping GO:0051016 p=1.5E−02 n=1 fg=0.04 bg=0.00
jump response GO:0007630 p=1.5E−02 n=1 fg=0.04 bg=0.00
chemosensory jump behavior GO:0007636 p=1.5E−02 n=1 fg=0.04 bg=0.00
positive regulation of acute inflammator... GO:0002675 p=1.5E−02 n=1 fg=0.04 bg=0.00
regulation of transcription elongation f... GO:2001207 p=1.5E−02 n=1 fg=0.04 bg=0.00
negative regulation of transcription elo... GO:2001208 p=1.5E−02 n=1 fg=0.04 bg=0.00
transcription elongation from RNA polyme... GO:0006362 p=1.5E−02 n=1 fg=0.04 bg=0.00
corticotropin hormone secreting cell dif... GO:0060128 p=1.5E−02 n=1 fg=0.04 bg=0.00
detoxification of cadmium ion GO:0071585 p=1.5E−02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=28/120 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001635015.3
fraction genes in fg and expected valu
DNA−binding transcription factor activit... GO:0000981 p=7.4E−03 n=6 fg=0.22 bg=0.07
aminoacyltransferase activity GO:0016755 p=1.7E−02 n=1 fg=0.04 bg=0.00
glutathione gamma−glutamylcysteinyltrans... GO:0016756 p=1.7E−02 n=1 fg=0.04 bg=0.00
glycerophosphoinositol glycerophosphodie... GO:0047395 p=1.7E−02 n=1 fg=0.04 bg=0.00
dynein light intermediate chain binding GO:0051959 p=1.7E−02 n=1 fg=0.04 bg=0.00
glycerophosphodiester phosphodiesterase ... GO:0008889 p=1.7E−02 n=1 fg=0.04 bg=0.00
cadmium ion binding GO:0046870 p=1.7E−02 n=1 fg=0.04 bg=0.00
regulatory region RNA binding GO:0001069 p=1.7E−02 n=1 fg=0.04 bg=0.00
passive transmembrane transporter activi... GO:0022803 p=1.9E−02 n=4 fg=0.15 bg=0.04
channel activity GO:0015267 p=1.9E−02 n=4 fg=0.15 bg=0.04
actin filament binding GO:0051015 p=2.5E−02 n=2 fg=0.07 bg=0.01
phosphatidylinositol−4,5−bisphosphate bi... GO:0005546 p=2.9E−02 n=2 fg=0.07 bg=0.01
transmembrane transporter activity GO:0022857 p=3.1E−02 n=6 fg=0.22 bg=0.09
ion gated channel activity GO:0022839 p=3.2E−02 n=3 fg=0.11 bg=0.03
phosphatidylinositol 3−kinase regulatory... GO:0036312 p=3.4E−02 n=1 fg=0.04 bg=0.00
arylsulfatase activity GO:0004065 p=3.4E−02 n=1 fg=0.04 bg=0.00
caspase binding GO:0089720 p=3.4E−02 n=1 fg=0.04 bg=0.00
N−acetylgalactosamine−4−sulfatase activi... GO:0003943 p=3.4E−02 n=1 fg=0.04 bg=0.00
BH3 domain binding GO:0051434 p=3.4E−02 n=1 fg=0.04 bg=0.00
sulfuric ester hydrolase activity GO:0008484 p=3.4E−02 n=1 fg=0.04 bg=0.00
voltage−gated cation channel activity GO:0022843 p=3.6E−02 n=2 fg=0.07 bg=0.01
gated channel activity GO:0022836 p=3.6E−02 n=3 fg=0.11 bg=0.03
phosphatidylinositol binding GO:0035091 p=4.1E−02 n=3 fg=0.11 bg=0.03
phosphatidylinositol bisphosphate bindin... GO:1902936 p=4.4E−02 n=2 fg=0.07 bg=0.01
lipid binding GO:0008289 p=4.8E−02 n=4 fg=0.15 bg=0.05
benzodiazepine receptor activity GO:0008503 p=5.0E−02 n=1 fg=0.04 bg=0.00
GABA−gated chloride ion channel activity GO:0022851 p=5.0E−02 n=1 fg=0.04 bg=0.00
protein transmembrane transporter activi... GO:0008320 p=5.0E−02 n=1 fg=0.04 bg=0.00
macromolecule transmembrane transporter ... GO:0022884 p=5.0E−02 n=1 fg=0.04 bg=0.00
GABA receptor activity GO:0016917 p=5.0E−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:CC
Ncol_Nvec_vc1.1_XM_001635015.3
fraction genes in fg and expected valu
voltage−gated potassium channel complex GO:0008076 p=6.2E−03 n=2 fg=0.08 bg=0.00
SCF ubiquitin ligase complex GO:0019005 p=9.3E−03 n=2 fg=0.08 bg=0.01
H zone GO:0031673 p=1.4E−02 n=1 fg=0.04 bg=0.00
protein−lipid complex GO:0032994 p=2.8E−02 n=1 fg=0.04 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000221 p=4.1E−02 n=1 fg=0.04 bg=0.00
proton−transporting V−type ATPase, V1 do... GO:0033180 p=4.1E−02 n=1 fg=0.04 bg=0.00
Bcl−2 family protein complex GO:0097136 p=4.1E−02 n=1 fg=0.04 bg=0.00
proton−transporting two−sector ATPase co... GO:0033178 p=4.1E−02 n=1 fg=0.04 bg=0.00
spot adherens junction GO:0005914 p=4.1E−02 n=1 fg=0.04 bg=0.00
neuron projection GO:0043005 p=4.9E−02 n=7 fg=0.28 bg=0.14
integral component of peroxisomal membra... GO:0005779 p=5.4E−02 n=1 fg=0.04 bg=0.00
intrinsic component of peroxisomal membr... GO:0031231 p=5.4E−02 n=1 fg=0.04 bg=0.00
zonula adherens GO:0005915 p=5.4E−02 n=1 fg=0.04 bg=0.00
sensory dendrite GO:0071683 p=6.7E−02 n=1 fg=0.04 bg=0.00
microbody membrane GO:0031903 p=8.0E−02 n=1 fg=0.04 bg=0.00
peroxisomal membrane GO:0005778 p=8.0E−02 n=1 fg=0.04 bg=0.00
tertiary granule membrane GO:0070821 p=8.0E−02 n=1 fg=0.04 bg=0.00
plasma membrane proton−transporting V−ty... GO:0033181 p=8.0E−02 n=1 fg=0.04 bg=0.00
integral component of organelle membrane GO:0031301 p=8.5E−02 n=3 fg=0.12 bg=0.04
postsynapse GO:0098794 p=8.7E−02 n=3 fg=0.12 bg=0.04
intrinsic component of organelle membran... GO:0031300 p=9.0E−02 n=3 fg=0.12 bg=0.04
vacuolar proton−transporting V−type ATPa... GO:0016471 p=9.3E−02 n=1 fg=0.04 bg=0.00
somatodendritic compartment GO:0036477 p=9.5E−02 n=5 fg=0.20 bg=0.10
plasma membrane bounded cell projection GO:0120025 p=9.9E−02 n=8 fg=0.32 bg=0.20
dendrite GO:0030425 p=9.9E−02 n=4 fg=0.16 bg=0.07
dendritic tree GO:0097447 p=9.9E−02 n=4 fg=0.16 bg=0.07
cell projection GO:0042995 p=1.0E−01 n=8 fg=0.32 bg=0.20
proton−transporting two−sector ATPase co... GO:0016469 p=1.1E−01 n=1 fg=0.04 bg=0.00
proton−transporting V−type ATPase comple... GO:0033176 p=1.1E−01 n=1 fg=0.04 bg=0.00
myofibril GO:0030016 p=1.1E−01 n=2 fg=0.08 bg=0.02
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