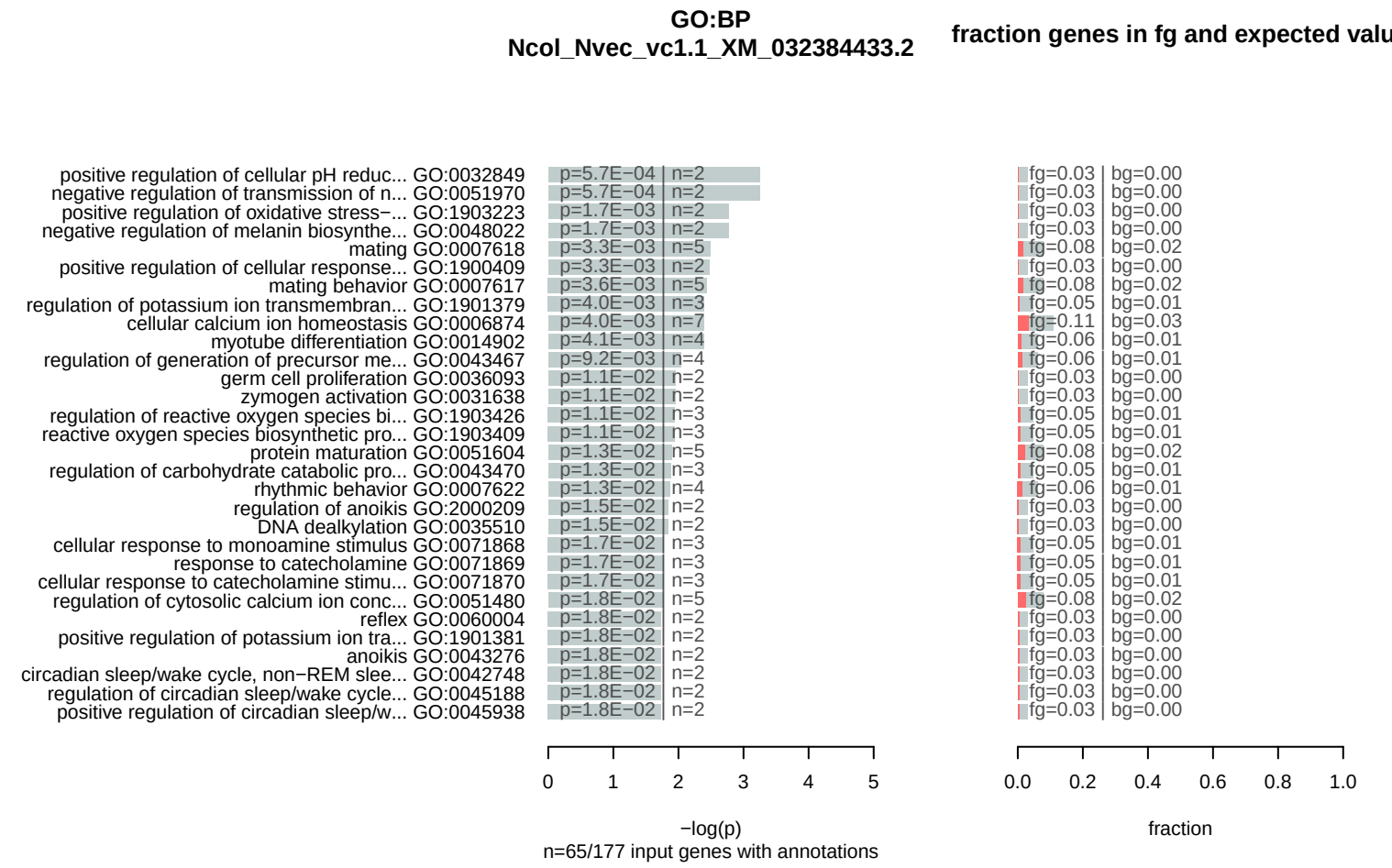
GO:BP
Ncol_Nvec_vc1.1_XM_032384433.2
fraction genes in fg and expected valu
positive regulation of cellular pH reduc... GO:0032849 p=5.7E−04 n=2 fg=0.03 bg=0.00
negative regulation of transmission of n... GO:0051970 p=5.7E−04 n=2 fg=0.03 bg=0.00
positive regulation of oxidative stress−... GO:1903223 p=1.7E−03 n=2 fg=0.03 bg=0.00
negative regulation of melanin biosynthe... GO:0048022 p=1.7E−03 n=2 fg=0.03 bg=0.00
mating GO:0007618 p=3.3E−03 n=5 fg=0.08 bg=0.02
positive regulation of cellular response... GO:1900409 p=3.3E−03 n=2 fg=0.03 bg=0.00
mating behavior GO:0007617 p=3.6E−03 n=5 fg=0.08 bg=0.02
regulation of potassium ion transmembran... GO:1901379 p=4.0E−03 n=3 fg=0.05 bg=0.01
cellular calcium ion homeostasis GO:0006874 p=4.0E−03 n=7 fg=0.11 bg=0.03
myotube differentiation GO:0014902 p=4.1E−03 n=4 fg=0.06 bg=0.01
regulation of generation of precursor me... GO:0043467 p=9.2E−03 n=4 fg=0.06 bg=0.01
germ cell proliferation GO:0036093 p=1.1E−02 n=2 fg=0.03 bg=0.00
zymogen activation GO:0031638 p=1.1E−02 n=2 fg=0.03 bg=0.00
regulation of reactive oxygen species bi... GO:1903426 p=1.1E−02 n=3 fg=0.05 bg=0.01
reactive oxygen species biosynthetic pro... GO:1903409 p=1.1E−02 n=3 fg=0.05 bg=0.01
protein maturation GO:0051604 p=1.3E−02 n=5 fg=0.08 bg=0.02
regulation of carbohydrate catabolic pro... GO:0043470 p=1.3E−02 n=3 fg=0.05 bg=0.01
rhythmic behavior GO:0007622 p=1.3E−02 n=4 fg=0.06 bg=0.01
regulation of anoikis GO:2000209 p=1.5E−02 n=2 fg=0.03 bg=0.00
DNA dealkylation GO:0035510 p=1.5E−02 n=2 fg=0.03 bg=0.00
cellular response to monoamine stimulus GO:0071868 p=1.7E−02 n=3 fg=0.05 bg=0.01
response to catecholamine GO:0071869 p=1.7E−02 n=3 fg=0.05 bg=0.01
cellular response to catecholamine stimu... GO:0071870 p=1.7E−02 n=3 fg=0.05 bg=0.01
regulation of cytosolic calcium ion conc... GO:0051480 p=1.8E−02 n=5 fg=0.08 bg=0.02
reflex GO:0060004 p=1.8E−02 n=2 fg=0.03 bg=0.00
positive regulation of potassium ion tra... GO:1901381 p=1.8E−02 n=2 fg=0.03 bg=0.00
anoikis GO:0043276 p=1.8E−02 n=2 fg=0.03 bg=0.00
circadian sleep/wake cycle, non−REM slee... GO:0042748 p=1.8E−02 n=2 fg=0.03 bg=0.00
regulation of circadian sleep/wake cycle... GO:0045188 p=1.8E−02 n=2 fg=0.03 bg=0.00
positive regulation of circadian sleep/w... GO:0045938 p=1.8E−02 n=2 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=65/177 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032384433.2
fraction genes in fg and expected valu
apolipoprotein binding GO:0034185 p=4.9E−04 n=2 fg=0.04 bg=0.00
calcium, potassium:sodium antiporter act... GO:0008273 p=4.9E−04 n=2 fg=0.04 bg=0.00
sodium ion binding GO:0031402 p=1.4E−03 n=2 fg=0.04 bg=0.00
potassium ion binding GO:0030955 p=1.4E−03 n=2 fg=0.04 bg=0.00
caspase binding GO:0089720 p=1.4E−03 n=2 fg=0.04 bg=0.00
peptide hormone binding GO:0017046 p=2.9E−03 n=2 fg=0.04 bg=0.00
unfolded protein binding GO:0051082 p=1.0E−02 n=4 fg=0.08 bg=0.02
RNA polymerase II CTD heptapeptide repea... GO:0008353 p=2.2E−02 n=1 fg=0.02 bg=0.00
heparan sulfate binding GO:1904399 p=2.2E−02 n=1 fg=0.02 bg=0.00
misfolded RNA binding GO:0034336 p=2.2E−02 n=1 fg=0.02 bg=0.00
calcitonin family binding GO:0097644 p=2.2E−02 n=1 fg=0.02 bg=0.00
amylin binding GO:0097645 p=2.2E−02 n=1 fg=0.02 bg=0.00
G−protein beta−subunit binding GO:0031681 p=2.2E−02 n=1 fg=0.02 bg=0.00
orotidine−5'−phosphate decarboxylase act... GO:0004590 p=2.2E−02 n=1 fg=0.02 bg=0.00
tRNA 2'−phosphotransferase activity GO:0000215 p=2.2E−02 n=1 fg=0.02 bg=0.00
glycerophosphoinositol glycerophosphodie... GO:0047395 p=2.2E−02 n=1 fg=0.02 bg=0.00
phosphoglycerate kinase activity GO:0004618 p=2.2E−02 n=1 fg=0.02 bg=0.00
melatonin binding GO:1904408 p=2.2E−02 n=1 fg=0.02 bg=0.00
V1A vasopressin receptor binding GO:0031894 p=2.2E−02 n=1 fg=0.02 bg=0.00
acetylcholine receptor regulator activit... GO:0030548 p=2.2E−02 n=1 fg=0.02 bg=0.00
acetylcholine receptor activator activit... GO:0030549 p=2.2E−02 n=1 fg=0.02 bg=0.00
neurotransmitter receptor regulator acti... GO:0099602 p=2.2E−02 n=1 fg=0.02 bg=0.00
orotate phosphoribosyltransferase activi... GO:0004588 p=2.2E−02 n=1 fg=0.02 bg=0.00
non−sequence−specific DNA binding, bendi... GO:0044378 p=2.2E−02 n=1 fg=0.02 bg=0.00
protein O−GlcNAc transferase activity GO:0097363 p=2.2E−02 n=1 fg=0.02 bg=0.00
oxidative DNA demethylase activity GO:0035516 p=2.2E−02 n=1 fg=0.02 bg=0.00
N−acetylglucosamine−1−phosphodiester alp... GO:0003944 p=2.2E−02 n=1 fg=0.02 bg=0.00
glycerophosphodiester phosphodiesterase ... GO:0008889 p=2.2E−02 n=1 fg=0.02 bg=0.00
protein N−acetylglucosaminyltransferase ... GO:0016262 p=2.2E−02 n=1 fg=0.02 bg=0.00
melatonin receptor activity GO:0008502 p=2.2E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=53/177 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032384433.2
fraction genes in fg and expected valu
growth cone filopodium GO:1990812 p=5.4E−04 n=2 fg=0.03 bg=0.00
extrinsic component of endoplasmic retic... GO:0042406 p=1.6E−03 n=2 fg=0.03 bg=0.00
growth cone lamellipodium GO:1990761 p=3.1E−03 n=2 fg=0.03 bg=0.00
ribosome GO:0005840 p=5.2E−03 n=6 fg=0.10 bg=0.03
main axon GO:0044304 p=9.0E−03 n=3 fg=0.05 bg=0.01
integral component of plasma membrane GO:0005887 p=1.7E−02 n=9 fg=0.14 bg=0.06
cytosolic ribosome GO:0022626 p=2.1E−02 n=4 fg=0.06 bg=0.02
endosome to plasma membrane transport ve... GO:0070381 p=2.3E−02 n=1 fg=0.02 bg=0.00
amyloid−beta complex GO:0106003 p=2.3E−02 n=1 fg=0.02 bg=0.00
smooth muscle contractile fiber GO:0030485 p=2.3E−02 n=1 fg=0.02 bg=0.00
intermediate−density lipoprotein particl... GO:0034363 p=2.3E−02 n=1 fg=0.02 bg=0.00
transcription factor TFIIK complex GO:0070985 p=2.3E−02 n=1 fg=0.02 bg=0.00
high−density lipoprotein particle GO:0034364 p=2.3E−02 n=1 fg=0.02 bg=0.00
plasma lipoprotein particle GO:0034358 p=2.3E−02 n=1 fg=0.02 bg=0.00
triglyceride−rich plasma lipoprotein par... GO:0034385 p=2.3E−02 n=1 fg=0.02 bg=0.00
lipoprotein particle GO:1990777 p=2.3E−02 n=1 fg=0.02 bg=0.00
sperm individualization complex GO:0070864 p=2.3E−02 n=1 fg=0.02 bg=0.00
investment cone GO:0070865 p=2.3E−02 n=1 fg=0.02 bg=0.00
NLS−dependent protein nuclear import com... GO:0042564 p=2.3E−02 n=1 fg=0.02 bg=0.00
plus−end kinesin complex GO:0005873 p=2.3E−02 n=1 fg=0.02 bg=0.00
protein−containing complex GO:0032991 p=2.4E−02 n=35 fg=0.56 bg=0.42
cytosolic large ribosomal subunit GO:0022625 p=2.4E−02 n=3 fg=0.05 bg=0.01
intrinsic component of plasma membrane GO:0031226 p=2.7E−02 n=9 fg=0.14 bg=0.07
proteasome regulatory particle GO:0005838 p=3.0E−02 n=2 fg=0.03 bg=0.00
proteasome accessory complex GO:0022624 p=3.0E−02 n=2 fg=0.03 bg=0.00
neuronal cell body GO:0043025 p=3.1E−02 n=8 fg=0.13 bg=0.06
dendritic spine GO:0043197 p=3.2E−02 n=4 fg=0.06 bg=0.02
neuron spine GO:0044309 p=3.2E−02 n=4 fg=0.06 bg=0.02
trans−Golgi network membrane GO:0032588 p=3.7E−02 n=3 fg=0.05 bg=0.01
origin recognition complex GO:0000808 p=4.6E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=63/177 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction