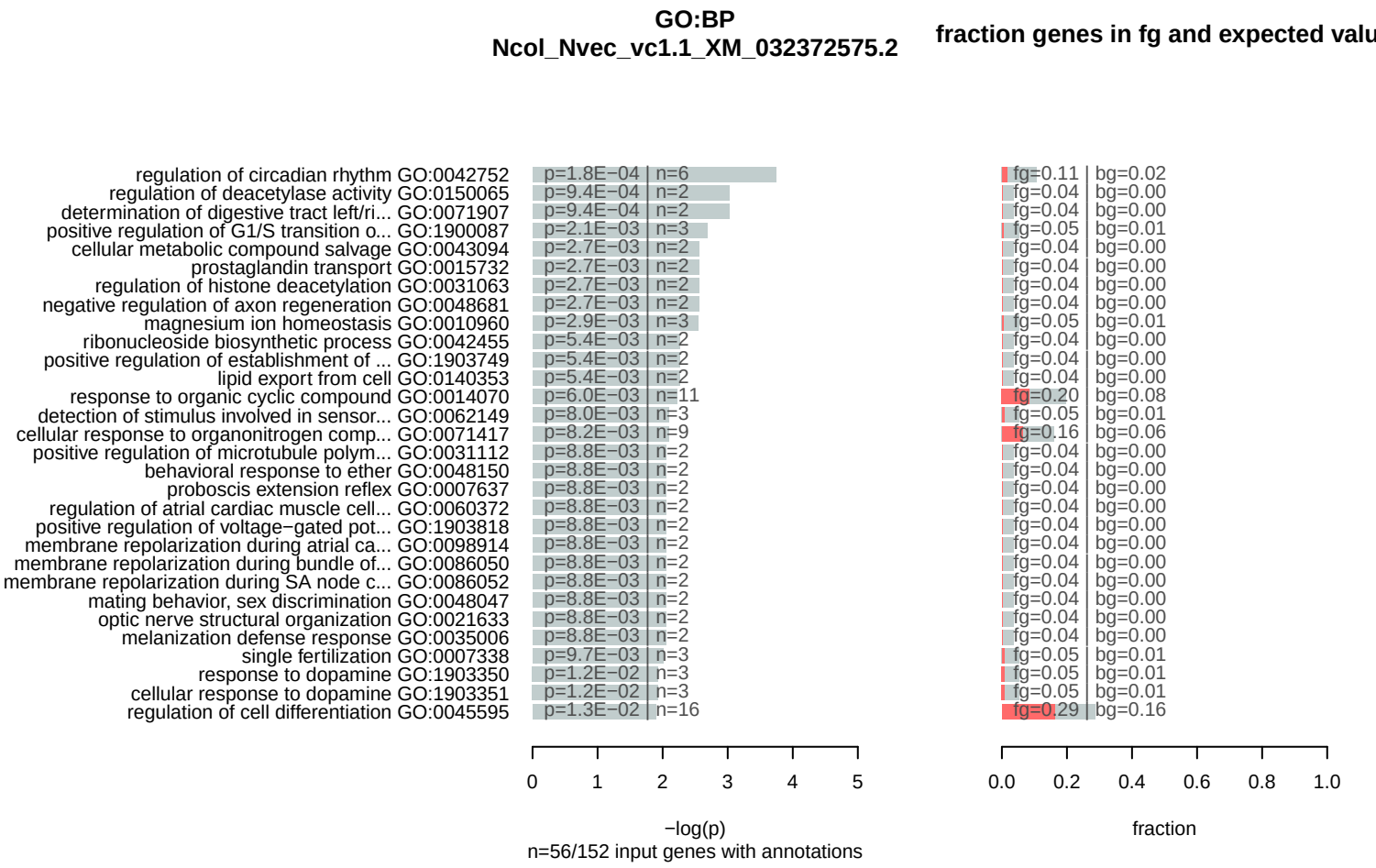
GO:BP
Ncol_Nvec_vc1.1_XM_032372575.2
fraction genes in fg and expected valu
regulation of circadian rhythm GO:0042752 p=1.8E−04 n=6 fg=0.11 bg=0.02
regulation of deacetylase activity GO:0150065 p=9.4E−04 n=2 fg=0.04 bg=0.00
determination of digestive tract left/ri... GO:0071907 p=9.4E−04 n=2 fg=0.04 bg=0.00
positive regulation of G1/S transition o... GO:1900087 p=2.1E−03 n=3 fg=0.05 bg=0.01
cellular metabolic compound salvage GO:0043094 p=2.7E−03 n=2 fg=0.04 bg=0.00
prostaglandin transport GO:0015732 p=2.7E−03 n=2 fg=0.04 bg=0.00
regulation of histone deacetylation GO:0031063 p=2.7E−03 n=2 fg=0.04 bg=0.00
negative regulation of axon regeneration GO:0048681 p=2.7E−03 n=2 fg=0.04 bg=0.00
magnesium ion homeostasis GO:0010960 p=2.9E−03 n=3 fg=0.05 bg=0.01
ribonucleoside biosynthetic process GO:0042455 p=5.4E−03 n=2 fg=0.04 bg=0.00
positive regulation of establishment of ... GO:1903749 p=5.4E−03 n=2 fg=0.04 bg=0.00
lipid export from cell GO:0140353 p=5.4E−03 n=2 fg=0.04 bg=0.00
response to organic cyclic compound GO:0014070 p=6.0E−03 n=11 fg=0.20 bg=0.08
detection of stimulus involved in sensor... GO:0062149 p=8.0E−03 n=3 fg=0.05 bg=0.01
cellular response to organonitrogen comp... GO:0071417 p=8.2E−03 n=9 fg=0.16 bg=0.06
positive regulation of microtubule polym... GO:0031112 p=8.8E−03 n=2 fg=0.04 bg=0.00
behavioral response to ether GO:0048150 p=8.8E−03 n=2 fg=0.04 bg=0.00
proboscis extension reflex GO:0007637 p=8.8E−03 n=2 fg=0.04 bg=0.00
regulation of atrial cardiac muscle cell... GO:0060372 p=8.8E−03 n=2 fg=0.04 bg=0.00
positive regulation of voltage−gated pot... GO:1903818 p=8.8E−03 n=2 fg=0.04 bg=0.00
membrane repolarization during atrial ca... GO:0098914 p=8.8E−03 n=2 fg=0.04 bg=0.00
membrane repolarization during bundle of... GO:0086050 p=8.8E−03 n=2 fg=0.04 bg=0.00
membrane repolarization during SA node c... GO:0086052 p=8.8E−03 n=2 fg=0.04 bg=0.00
mating behavior, sex discrimination GO:0048047 p=8.8E−03 n=2 fg=0.04 bg=0.00
optic nerve structural organization GO:0021633 p=8.8E−03 n=2 fg=0.04 bg=0.00
melanization defense response GO:0035006 p=8.8E−03 n=2 fg=0.04 bg=0.00
single fertilization GO:0007338 p=9.7E−03 n=3 fg=0.05 bg=0.01
response to dopamine GO:1903350 p=1.2E−02 n=3 fg=0.05 bg=0.01
cellular response to dopamine GO:1903351 p=1.2E−02 n=3 fg=0.05 bg=0.01
regulation of cell differentiation GO:0045595 p=1.3E−02 n=16 fg=0.29 bg=0.16
0 1 2 3 4 5
−log(p)
n=56/152 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032372575.2
fraction genes in fg and expected valu
protein disulfide isomerase activity GO:0003756 p=2.6E−04 n=3 fg=0.06 bg=0.00
mitogen−activated protein kinase binding GO:0051019 p=2.8E−03 n=3 fg=0.06 bg=0.01
kinesin binding GO:0019894 p=7.9E−03 n=3 fg=0.06 bg=0.01
voltage−gated potassium channel activity... GO:0086087 p=8.8E−03 n=2 fg=0.04 bg=0.00
voltage−gated potassium channel activity... GO:0086089 p=8.8E−03 n=2 fg=0.04 bg=0.00
delayed rectifier potassium channel acti... GO:0005251 p=8.8E−03 n=2 fg=0.04 bg=0.00
intracellular cyclic nucleotide activate... GO:0005221 p=8.8E−03 n=2 fg=0.04 bg=0.00
voltage−gated potassium channel activity... GO:0086090 p=8.8E−03 n=2 fg=0.04 bg=0.00
oxidoreductase activity, acting on a sul... GO:0016667 p=9.6E−03 n=3 fg=0.06 bg=0.01
potassium channel inhibitor activity GO:0019870 p=1.3E−02 n=2 fg=0.04 bg=0.00
outward rectifier potassium channel acti... GO:0015271 p=1.8E−02 n=2 fg=0.04 bg=0.00
actinin binding GO:0042805 p=2.3E−02 n=2 fg=0.04 bg=0.01
alpha−actinin binding GO:0051393 p=2.3E−02 n=2 fg=0.04 bg=0.01
ion channel inhibitor activity GO:0008200 p=2.9E−02 n=2 fg=0.04 bg=0.01
disordered domain specific binding GO:0097718 p=2.9E−02 n=2 fg=0.04 bg=0.01
phosphatase activity GO:0016791 p=2.9E−02 n=4 fg=0.08 bg=0.02
tRNA (guanine−N1−)−methyltransferase act... GO:0009019 p=3.1E−02 n=1 fg=0.02 bg=0.00
adenosylmethionine decarboxylase activit... GO:0004014 p=3.1E−02 n=1 fg=0.02 bg=0.00
chloride ion binding GO:0031404 p=3.1E−02 n=1 fg=0.02 bg=0.00
nicotinate transmembrane transporter act... GO:0090416 p=3.1E−02 n=1 fg=0.02 bg=0.00
biotin−protein ligase activity GO:0018271 p=3.1E−02 n=1 fg=0.02 bg=0.00
fatty acid transmembrane transporter act... GO:0015245 p=3.1E−02 n=1 fg=0.02 bg=0.00
adenosine−phosphate deaminase activity GO:0047623 p=3.1E−02 n=1 fg=0.02 bg=0.00
urate transmembrane transporter activity GO:0015143 p=3.1E−02 n=1 fg=0.02 bg=0.00
[phosphorylase] phosphatase activity GO:0050196 p=3.1E−02 n=1 fg=0.02 bg=0.00
hydrolase activity, acting on carbon−nit... GO:0016812 p=3.1E−02 n=1 fg=0.02 bg=0.00
histone H3−tri/di/monomethyl−lysine−4 de... GO:0034647 p=3.1E−02 n=1 fg=0.02 bg=0.00
transmembrane receptor protein phosphata... GO:0019198 p=3.1E−02 n=1 fg=0.02 bg=0.00
putrescine binding GO:0019810 p=3.1E−02 n=1 fg=0.02 bg=0.00
TFIIF−class transcription factor complex... GO:0001096 p=3.1E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=49/152 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032372575.2
fraction genes in fg and expected valu
perikaryon GO:0043204 p=3.3E−03 n=4 fg=0.07 bg=0.01
intracellular canaliculus GO:0046691 p=8.9E−03 n=2 fg=0.04 bg=0.00
juxtaparanode region of axon GO:0044224 p=8.9E−03 n=2 fg=0.04 bg=0.00
cell surface GO:0009986 p=1.5E−02 n=6 fg=0.11 bg=0.04
paranode region of axon GO:0033270 p=1.8E−02 n=2 fg=0.04 bg=0.00
intrinsic component of postsynaptic memb... GO:0098936 p=1.8E−02 n=2 fg=0.04 bg=0.00
intrinsic component of synaptic membrane GO:0099240 p=1.8E−02 n=2 fg=0.04 bg=0.00
integral component of synaptic membrane GO:0099699 p=1.8E−02 n=2 fg=0.04 bg=0.00
intrinsic component of presynaptic membr... GO:0098889 p=1.8E−02 n=2 fg=0.04 bg=0.00
integral component of postsynaptic membr... GO:0099055 p=1.8E−02 n=2 fg=0.04 bg=0.00
integral component of presynaptic membra... GO:0099056 p=1.8E−02 n=2 fg=0.04 bg=0.00
cation channel complex GO:0034703 p=2.5E−02 n=3 fg=0.05 bg=0.01
transmembrane transporter complex GO:1902495 p=2.8E−02 n=4 fg=0.07 bg=0.02
voltage−gated potassium channel complex GO:0008076 p=2.9E−02 n=2 fg=0.04 bg=0.01
potassium channel complex GO:0034705 p=2.9E−02 n=2 fg=0.04 bg=0.01
katanin complex GO:0008352 p=3.1E−02 n=1 fg=0.02 bg=0.00
core−binding factor complex GO:0016513 p=3.1E−02 n=1 fg=0.02 bg=0.00
ion channel complex GO:0034702 p=3.2E−02 n=3 fg=0.05 bg=0.01
midbody GO:0030496 p=3.2E−02 n=3 fg=0.05 bg=0.01
transporter complex GO:1990351 p=3.3E−02 n=4 fg=0.07 bg=0.02
membrane protein complex GO:0098796 p=4.6E−02 n=9 fg=0.16 bg=0.09
intracellular membrane−bounded organelle GO:0043231 p=5.0E−02 n=49 fg=0.88 bg=0.78
intercalated disc GO:0014704 p=5.9E−02 n=2 fg=0.04 bg=0.01
endoplasmic reticulum chaperone complex GO:0034663 p=6.1E−02 n=1 fg=0.02 bg=0.00
COPII vesicle coat GO:0030127 p=6.1E−02 n=1 fg=0.02 bg=0.00
Gtr1−Gtr2 GTPase complex GO:1990131 p=6.1E−02 n=1 fg=0.02 bg=0.00
mitochondrial permeability transition po... GO:0005757 p=6.1E−02 n=1 fg=0.02 bg=0.00
HOPS complex GO:0030897 p=6.1E−02 n=1 fg=0.02 bg=0.00
platelet alpha granule membrane GO:0031092 p=6.1E−02 n=1 fg=0.02 bg=0.00
pore complex GO:0046930 p=6.1E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=56/152 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction