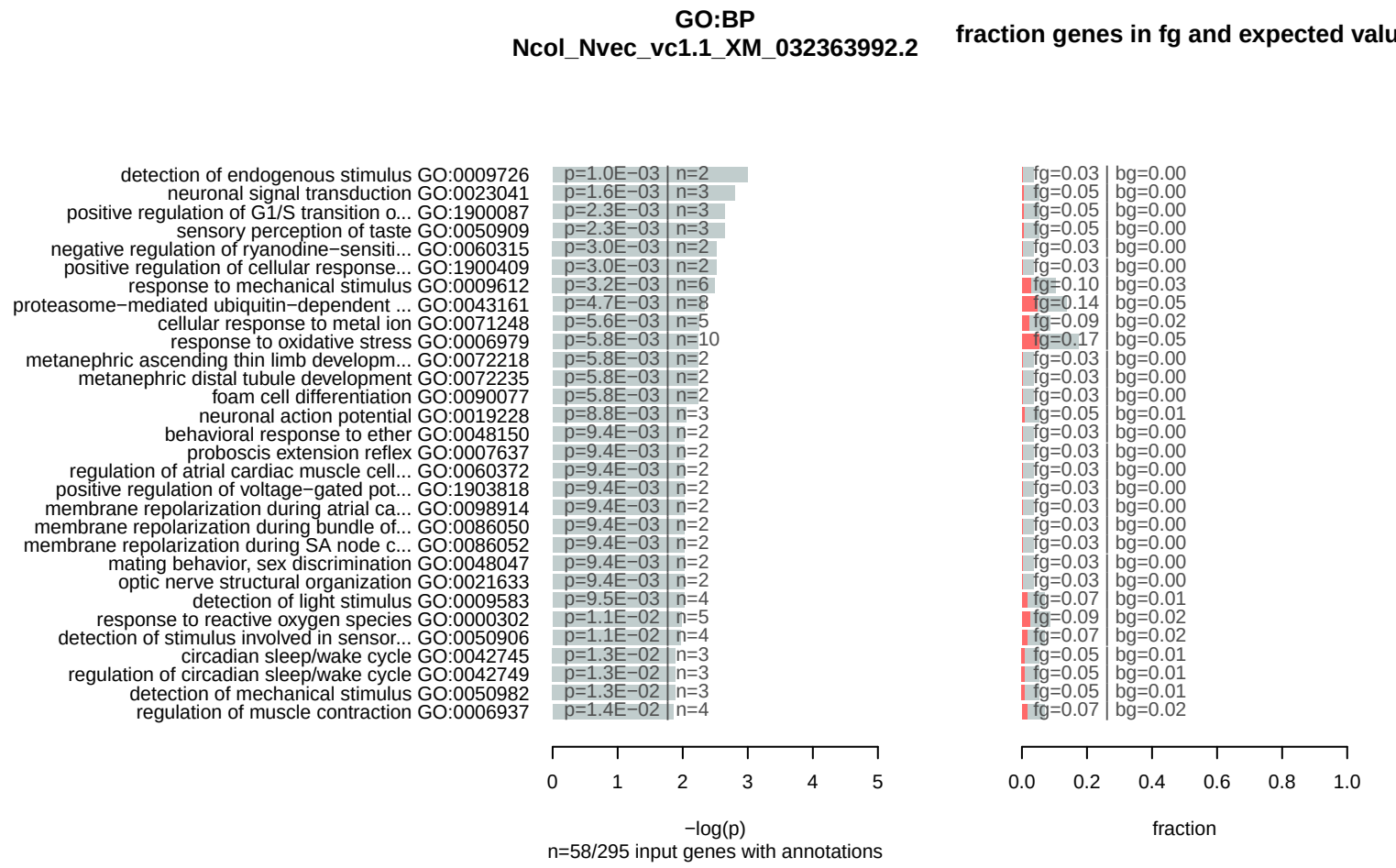
GO:BP
Ncol_Nvec_vc1.1_XM_032363992.2
fraction genes in fg and expected valu
detection of endogenous stimulus GO:0009726 p=1.0E−03 n=2 fg=0.03 bg=0.00
neuronal signal transduction GO:0023041 p=1.6E−03 n=3 fg=0.05 bg=0.00
positive regulation of G1/S transition o... GO:1900087 p=2.3E−03 n=3 fg=0.05 bg=0.00
sensory perception of taste GO:0050909 p=2.3E−03 n=3 fg=0.05 bg=0.00
negative regulation of ryanodine−sensiti... GO:0060315 p=3.0E−03 n=2 fg=0.03 bg=0.00
positive regulation of cellular response... GO:1900409 p=3.0E−03 n=2 fg=0.03 bg=0.00
response to mechanical stimulus GO:0009612 p=3.2E−03 n=6 fg=0.10 bg=0.03
proteasome−mediated ubiquitin−dependent ... GO:0043161 p=4.7E−03 n=8 fg=0.14 bg=0.05
cellular response to metal ion GO:0071248 p=5.6E−03 n=5 fg=0.09 bg=0.02
response to oxidative stress GO:0006979 p=5.8E−03 n=10 fg=0.17 bg=0.05
metanephric ascending thin limb developm... GO:0072218 p=5.8E−03 n=2 fg=0.03 bg=0.00
metanephric distal tubule development GO:0072235 p=5.8E−03 n=2 fg=0.03 bg=0.00
foam cell differentiation GO:0090077 p=5.8E−03 n=2 fg=0.03 bg=0.00
neuronal action potential GO:0019228 p=8.8E−03 n=3 fg=0.05 bg=0.01
behavioral response to ether GO:0048150 p=9.4E−03 n=2 fg=0.03 bg=0.00
proboscis extension reflex GO:0007637 p=9.4E−03 n=2 fg=0.03 bg=0.00
regulation of atrial cardiac muscle cell... GO:0060372 p=9.4E−03 n=2 fg=0.03 bg=0.00
positive regulation of voltage−gated pot... GO:1903818 p=9.4E−03 n=2 fg=0.03 bg=0.00
membrane repolarization during atrial ca... GO:0098914 p=9.4E−03 n=2 fg=0.03 bg=0.00
membrane repolarization during bundle of... GO:0086050 p=9.4E−03 n=2 fg=0.03 bg=0.00
membrane repolarization during SA node c... GO:0086052 p=9.4E−03 n=2 fg=0.03 bg=0.00
mating behavior, sex discrimination GO:0048047 p=9.4E−03 n=2 fg=0.03 bg=0.00
optic nerve structural organization GO:0021633 p=9.4E−03 n=2 fg=0.03 bg=0.00
detection of light stimulus GO:0009583 p=9.5E−03 n=4 fg=0.07 bg=0.01
response to reactive oxygen species GO:0000302 p=1.1E−02 n=5 fg=0.09 bg=0.02
detection of stimulus involved in sensor... GO:0050906 p=1.1E−02 n=4 fg=0.07 bg=0.02
circadian sleep/wake cycle GO:0042745 p=1.3E−02 n=3 fg=0.05 bg=0.01
regulation of circadian sleep/wake cycle GO:0042749 p=1.3E−02 n=3 fg=0.05 bg=0.01
detection of mechanical stimulus GO:0050982 p=1.3E−02 n=3 fg=0.05 bg=0.01
regulation of muscle contraction GO:0006937 p=1.4E−02 n=4 fg=0.07 bg=0.02
0 1 2 3 4 5
−log(p)
n=58/295 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032363992.2
fraction genes in fg and expected valu
ion gated channel activity GO:0022839 p=7.5E−05 n=8 fg=0.14 bg=0.03
outward rectifier potassium channel acti... GO:0015271 p=1.4E−03 n=3 fg=0.05 bg=0.00
calcium ion binding GO:0005509 p=2.1E−03 n=6 fg=0.11 bg=0.02
voltage−gated calcium channel activity GO:0005245 p=2.1E−03 n=3 fg=0.05 bg=0.01
alpha−actinin binding GO:0051393 p=2.1E−03 n=3 fg=0.05 bg=0.01
intracellular ligand−gated ion channel a... GO:0005217 p=4.4E−03 n=3 fg=0.05 bg=0.01
potassium channel regulator activity GO:0015459 p=5.9E−03 n=3 fg=0.05 bg=0.01
voltage−gated sodium channel activity GO:0005248 p=7.2E−03 n=2 fg=0.04 bg=0.00
signaling adaptor activity GO:0035591 p=9.6E−03 n=3 fg=0.05 bg=0.01
voltage−gated potassium channel activity... GO:0086087 p=1.2E−02 n=2 fg=0.04 bg=0.00
voltage−gated potassium channel activity... GO:0086089 p=1.2E−02 n=2 fg=0.04 bg=0.00
BH domain binding GO:0051400 p=1.2E−02 n=2 fg=0.04 bg=0.00
delayed rectifier potassium channel acti... GO:0005251 p=1.2E−02 n=2 fg=0.04 bg=0.00
voltage−gated potassium channel activity... GO:0086008 p=1.2E−02 n=2 fg=0.04 bg=0.00
intracellular cyclic nucleotide activate... GO:0005221 p=1.2E−02 n=2 fg=0.04 bg=0.00
cyclic nucleotide−gated ion channel acti... GO:0043855 p=1.2E−02 n=2 fg=0.04 bg=0.00
voltage−gated potassium channel activity... GO:0086090 p=1.2E−02 n=2 fg=0.04 bg=0.00
kinesin binding GO:0019894 p=1.2E−02 n=3 fg=0.05 bg=0.01
ligand−gated cation channel activity GO:0099094 p=1.5E−02 n=3 fg=0.05 bg=0.01
cholesterol binding GO:0015485 p=1.7E−02 n=2 fg=0.04 bg=0.00
potassium channel inhibitor activity GO:0019870 p=1.7E−02 n=2 fg=0.04 bg=0.00
signaling receptor complex adaptor activ... GO:0030159 p=2.4E−02 n=2 fg=0.04 bg=0.00
sterol binding GO:0032934 p=2.4E−02 n=2 fg=0.04 bg=0.00
lipase activity GO:0016298 p=2.8E−02 n=3 fg=0.05 bg=0.01
steroid binding GO:0005496 p=3.1E−02 n=2 fg=0.04 bg=0.01
mannosyl−oligosaccharide 1,2−alpha−manno... GO:0004571 p=3.6E−02 n=1 fg=0.02 bg=0.00
mitogen−activated protein kinase p38 bin... GO:0048273 p=3.6E−02 n=1 fg=0.02 bg=0.00
rRNA primary transcript binding GO:0042134 p=3.6E−02 n=1 fg=0.02 bg=0.00
HLH domain binding GO:0043398 p=3.6E−02 n=1 fg=0.02 bg=0.00
guanylate cyclase regulator activity GO:0030249 p=3.6E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=57/295 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032363992.2
fraction genes in fg and expected valu
voltage−gated potassium channel complex GO:0008076 p=2.4E−03 n=3 fg=0.05 bg=0.00
presynapse GO:0098793 p=3.9E−03 n=9 fg=0.15 bg=0.05
contractile fiber GO:0043292 p=4.4E−03 n=6 fg=0.10 bg=0.03
lamellipodium GO:0030027 p=4.8E−03 n=5 fg=0.08 bg=0.02
neuronal cell body membrane GO:0032809 p=9.3E−03 n=3 fg=0.05 bg=0.01
intracellular canaliculus GO:0046691 p=9.8E−03 n=2 fg=0.03 bg=0.00
juxtaparanode region of axon GO:0044224 p=9.8E−03 n=2 fg=0.03 bg=0.00
transmembrane transporter complex GO:1902495 p=1.1E−02 n=7 fg=0.12 bg=0.02
ubiquitin ligase complex GO:0000151 p=1.4E−02 n=6 fg=0.10 bg=0.03
transporter complex GO:1990351 p=1.4E−02 n=7 fg=0.12 bg=0.02
postsynaptic membrane GO:0045211 p=1.5E−02 n=4 fg=0.07 bg=0.02
endoplasmic reticulum GO:0005783 p=1.7E−02 n=15 fg=0.25 bg=0.14
paranode region of axon GO:0033270 p=2.0E−02 n=2 fg=0.03 bg=0.00
intrinsic component of postsynaptic memb... GO:0098936 p=2.0E−02 n=2 fg=0.03 bg=0.00
intrinsic component of synaptic membrane GO:0099240 p=2.0E−02 n=2 fg=0.03 bg=0.00
integral component of synaptic membrane GO:0099699 p=2.0E−02 n=2 fg=0.03 bg=0.00
intrinsic component of presynaptic membr... GO:0098889 p=2.0E−02 n=2 fg=0.03 bg=0.00
integral component of postsynaptic membr... GO:0099055 p=2.0E−02 n=2 fg=0.03 bg=0.00
integral component of presynaptic membra... GO:0099056 p=2.0E−02 n=2 fg=0.03 bg=0.00
calcium channel complex GO:0034704 p=2.0E−02 n=2 fg=0.03 bg=0.00
dendrite GO:0030425 p=2.2E−02 n=9 fg=0.15 bg=0.07
dendritic tree GO:0097447 p=2.2E−02 n=9 fg=0.15 bg=0.07
sarcomere GO:0030017 p=2.5E−02 n=4 fg=0.07 bg=0.02
exocytic vesicle membrane GO:0099501 p=2.5E−02 n=3 fg=0.05 bg=0.01
striated muscle dense body GO:0055120 p=2.6E−02 n=2 fg=0.03 bg=0.00
exocytic vesicle GO:0070382 p=3.1E−02 n=5 fg=0.08 bg=0.03
polycystin complex GO:0002133 p=3.3E−02 n=1 fg=0.02 bg=0.00
integral component of organelle membrane GO:0031301 p=3.5E−02 n=6 fg=0.10 bg=0.04
intrinsic component of organelle membran... GO:0031300 p=3.9E−02 n=6 fg=0.10 bg=0.04
brush border GO:0005903 p=4.1E−02 n=3 fg=0.05 bg=0.01
0 1 2 3 4 5
−log(p)
n=59/295 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction