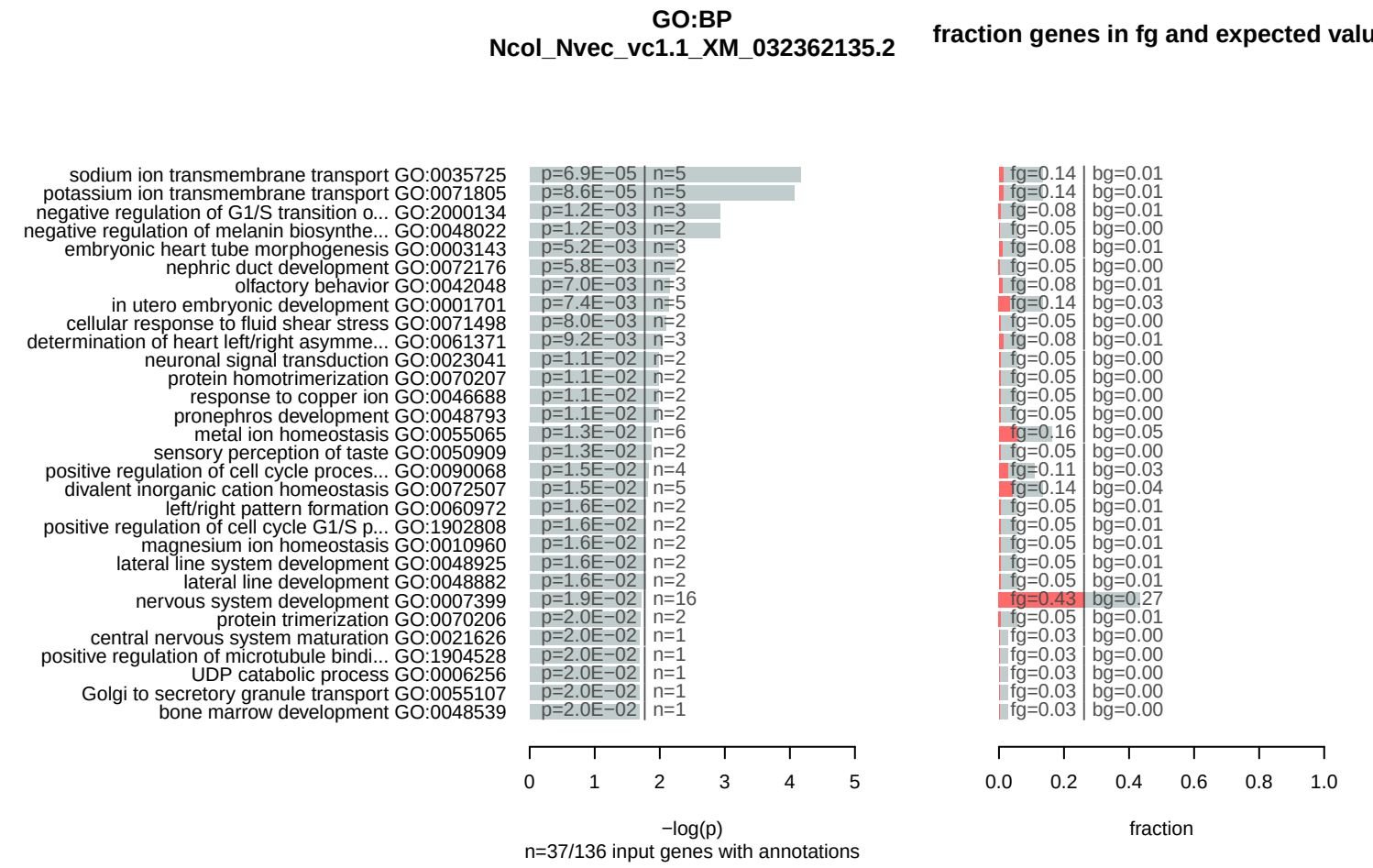
GO:BP
Ncol_Nvec_vc1.1_XM_032362135.2
fraction genes in fg and expected valu
sodium ion transmembrane transport GO:0035725 p=6.9E−05 n=5 fg=0.14 bg=0.01
potassium ion transmembrane transport GO:0071805 p=8.6E−05 n=5 fg=0.14 bg=0.01
negative regulation of G1/S transition o... GO:2000134 p=1.2E−03 n=3 fg=0.08 bg=0.01
negative regulation of melanin biosynthe... GO:0048022 p=1.2E−03 n=2 fg=0.05 bg=0.00
embryonic heart tube morphogenesis GO:0003143 p=5.2E−03 n=3 fg=0.08 bg=0.01
nephric duct development GO:0072176 p=5.8E−03 n=2 fg=0.05 bg=0.00
olfactory behavior GO:0042048 p=7.0E−03 n=3 fg=0.08 bg=0.01
in utero embryonic development GO:0001701 p=7.4E−03 n=5 fg=0.14 bg=0.03
cellular response to fluid shear stress GO:0071498 p=8.0E−03 n=2 fg=0.05 bg=0.00
determination of heart left/right asymme... GO:0061371 p=9.2E−03 n=3 fg=0.08 bg=0.01
neuronal signal transduction GO:0023041 p=1.1E−02 n=2 fg=0.05 bg=0.00
protein homotrimerization GO:0070207 p=1.1E−02 n=2 fg=0.05 bg=0.00
response to copper ion GO:0046688 p=1.1E−02 n=2 fg=0.05 bg=0.00
pronephros development GO:0048793 p=1.1E−02 n=2 fg=0.05 bg=0.00
metal ion homeostasis GO:0055065 p=1.3E−02 n=6 fg=0.16 bg=0.05
sensory perception of taste GO:0050909 p=1.3E−02 n=2 fg=0.05 bg=0.00
positive regulation of cell cycle proces... GO:0090068 p=1.5E−02 n=4 fg=0.11 bg=0.03
divalent inorganic cation homeostasis GO:0072507 p=1.5E−02 n=5 fg=0.14 bg=0.04
left/right pattern formation GO:0060972 p=1.6E−02 n=2 fg=0.05 bg=0.01
positive regulation of cell cycle G1/S p... GO:1902808 p=1.6E−02 n=2 fg=0.05 bg=0.01
magnesium ion homeostasis GO:0010960 p=1.6E−02 n=2 fg=0.05 bg=0.01
lateral line system development GO:0048925 p=1.6E−02 n=2 fg=0.05 bg=0.01
lateral line development GO:0048882 p=1.6E−02 n=2 fg=0.05 bg=0.01
nervous system development GO:0007399 p=1.9E−02 n=16 fg=0.43 bg=0.27
protein trimerization GO:0070206 p=2.0E−02 n=2 fg=0.05 bg=0.01
central nervous system maturation GO:0021626 p=2.0E−02 n=1 fg=0.03 bg=0.00
positive regulation of microtubule bindi... GO:1904528 p=2.0E−02 n=1 fg=0.03 bg=0.00
UDP catabolic process GO:0006256 p=2.0E−02 n=1 fg=0.03 bg=0.00
Golgi to secretory granule transport GO:0055107 p=2.0E−02 n=1 fg=0.03 bg=0.00
bone marrow development GO:0048539 p=2.0E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=37/136 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032362135.2
fraction genes in fg and expected valu
calcium, potassium:sodium antiporter act... GO:0008273 p=4.2E−04 n=2 fg=0.06 bg=0.00
potassium ion binding GO:0030955 p=1.2E−03 n=2 fg=0.06 bg=0.00
sodium ion binding GO:0031402 p=1.2E−03 n=2 fg=0.06 bg=0.00
ion gated channel activity GO:0022839 p=1.4E−03 n=5 fg=0.15 bg=0.03
voltage−gated sodium channel activity GO:0005248 p=2.4E−03 n=2 fg=0.06 bg=0.00
channel activity GO:0015267 p=4.9E−03 n=8 fg=0.24 bg=0.04
inorganic molecular entity transmembrane... GO:0015318 p=6.7E−03 n=11 fg=0.33 bg=0.07
ion transmembrane transporter activity GO:0015075 p=8.1E−03 n=11 fg=0.33 bg=0.07
outward rectifier potassium channel acti... GO:0015271 p=8.2E−03 n=2 fg=0.06 bg=0.00
alpha−actinin binding GO:0051393 p=1.1E−02 n=2 fg=0.06 bg=0.01
actinin binding GO:0042805 p=1.1E−02 n=2 fg=0.06 bg=0.01
calcium channel activity GO:0005262 p=1.1E−02 n=3 fg=0.09 bg=0.01
ligand−gated channel activity GO:0022834 p=1.1E−02 n=3 fg=0.09 bg=0.01
ligand−gated ion channel activity GO:0015276 p=1.1E−02 n=3 fg=0.09 bg=0.01
ion channel activity GO:0005216 p=1.3E−02 n=7 fg=0.21 bg=0.04
intracellular ligand−gated ion channel a... GO:0005217 p=1.7E−02 n=2 fg=0.06 bg=0.01
ubiquitin conjugating enzyme binding GO:0031624 p=1.7E−02 n=2 fg=0.06 bg=0.01
voltage−gated cation channel activity GO:0022843 p=1.8E−02 n=4 fg=0.12 bg=0.01
transmembrane receptor protein tyrosine ... GO:0005001 p=2.1E−02 n=1 fg=0.03 bg=0.00
translation elongation factor binding GO:0061770 p=2.1E−02 n=1 fg=0.03 bg=0.00
transmembrane receptor protein phosphata... GO:0019198 p=2.1E−02 n=1 fg=0.03 bg=0.00
HLH domain binding GO:0043398 p=2.1E−02 n=1 fg=0.03 bg=0.00
ribitol beta−1,4−xylosyltransferase acti... GO:0120053 p=2.1E−02 n=1 fg=0.03 bg=0.00
glycerophosphoinositol glycerophosphodie... GO:0047395 p=2.1E−02 n=1 fg=0.03 bg=0.00
fatty acid alpha−hydroxylase activity GO:0080132 p=2.1E−02 n=1 fg=0.03 bg=0.00
muscle alpha−actinin binding GO:0051371 p=2.1E−02 n=1 fg=0.03 bg=0.00
glycerophosphodiester phosphodiesterase ... GO:0008889 p=2.1E−02 n=1 fg=0.03 bg=0.00
uridine−diphosphatase activity GO:0045134 p=2.1E−02 n=1 fg=0.03 bg=0.00
active transmembrane transporter activit... GO:0022804 p=2.4E−02 n=6 fg=0.18 bg=0.04
ubiquitin−like protein conjugating enzym... GO:0044390 p=2.4E−02 n=2 fg=0.06 bg=0.01
0 1 2 3 4 5
−log(p)
n=33/136 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032362135.2
fraction genes in fg and expected valu
integral component of plasma membrane GO:0005887 p=9.6E−04 n=9 fg=0.25 bg=0.08
cation channel complex GO:0034703 p=7.5E−03 n=3 fg=0.08 bg=0.01
voltage−gated potassium channel complex GO:0008076 p=1.3E−02 n=2 fg=0.06 bg=0.01
potassium channel complex GO:0034705 p=1.3E−02 n=2 fg=0.06 bg=0.01
cell body GO:0044297 p=1.6E−02 n=7 fg=0.19 bg=0.08
axon GO:0030424 p=1.8E−02 n=7 fg=0.19 bg=0.08
UBC13−UEV1A complex GO:0035370 p=2.0E−02 n=1 fg=0.03 bg=0.00
core−binding factor complex GO:0016513 p=2.0E−02 n=1 fg=0.03 bg=0.00
polycystin complex GO:0002133 p=2.0E−02 n=1 fg=0.03 bg=0.00
intrinsic component of autophagosome mem... GO:0097636 p=2.0E−02 n=1 fg=0.03 bg=0.00
integral component of autophagosome memb... GO:0097637 p=2.0E−02 n=1 fg=0.03 bg=0.00
FHF complex GO:0070695 p=2.0E−02 n=1 fg=0.03 bg=0.00
neuronal cell body membrane GO:0032809 p=3.0E−02 n=2 fg=0.06 bg=0.01
ubiquitin ligase complex GO:0000151 p=3.2E−02 n=4 fg=0.11 bg=0.03
cell body membrane GO:0044298 p=3.4E−02 n=2 fg=0.06 bg=0.01
neuronal cell body GO:0043025 p=3.6E−02 n=6 fg=0.17 bg=0.07
cell leading edge GO:0031252 p=3.8E−02 n=4 fg=0.11 bg=0.04
Lewy body GO:0097413 p=3.9E−02 n=1 fg=0.03 bg=0.00
integral component of vacuolar membrane GO:0031166 p=3.9E−02 n=1 fg=0.03 bg=0.00
intrinsic component of vacuolar membrane GO:0031310 p=3.9E−02 n=1 fg=0.03 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000220 p=3.9E−02 n=1 fg=0.03 bg=0.00
proton−transporting two−sector ATPase co... GO:0033177 p=3.9E−02 n=1 fg=0.03 bg=0.00
proton−transporting V−type ATPase, V0 do... GO:0033179 p=3.9E−02 n=1 fg=0.03 bg=0.00
COPI vesicle coat GO:0030126 p=3.9E−02 n=1 fg=0.03 bg=0.00
nuclear stress granule GO:0097165 p=3.9E−02 n=1 fg=0.03 bg=0.00
ESCRT I complex GO:0000813 p=3.9E−02 n=1 fg=0.03 bg=0.00
COPI−coated vesicle membrane GO:0030663 p=3.9E−02 n=1 fg=0.03 bg=0.00
mitotic spindle GO:0072686 p=4.3E−02 n=2 fg=0.06 bg=0.01
bounding membrane of organelle GO:0098588 p=4.4E−02 n=10 fg=0.28 bg=0.16
synaptic membrane GO:0097060 p=5.8E−02 n=3 fg=0.08 bg=0.03
0 1 2 3 4 5
−log(p)
n=36/136 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction