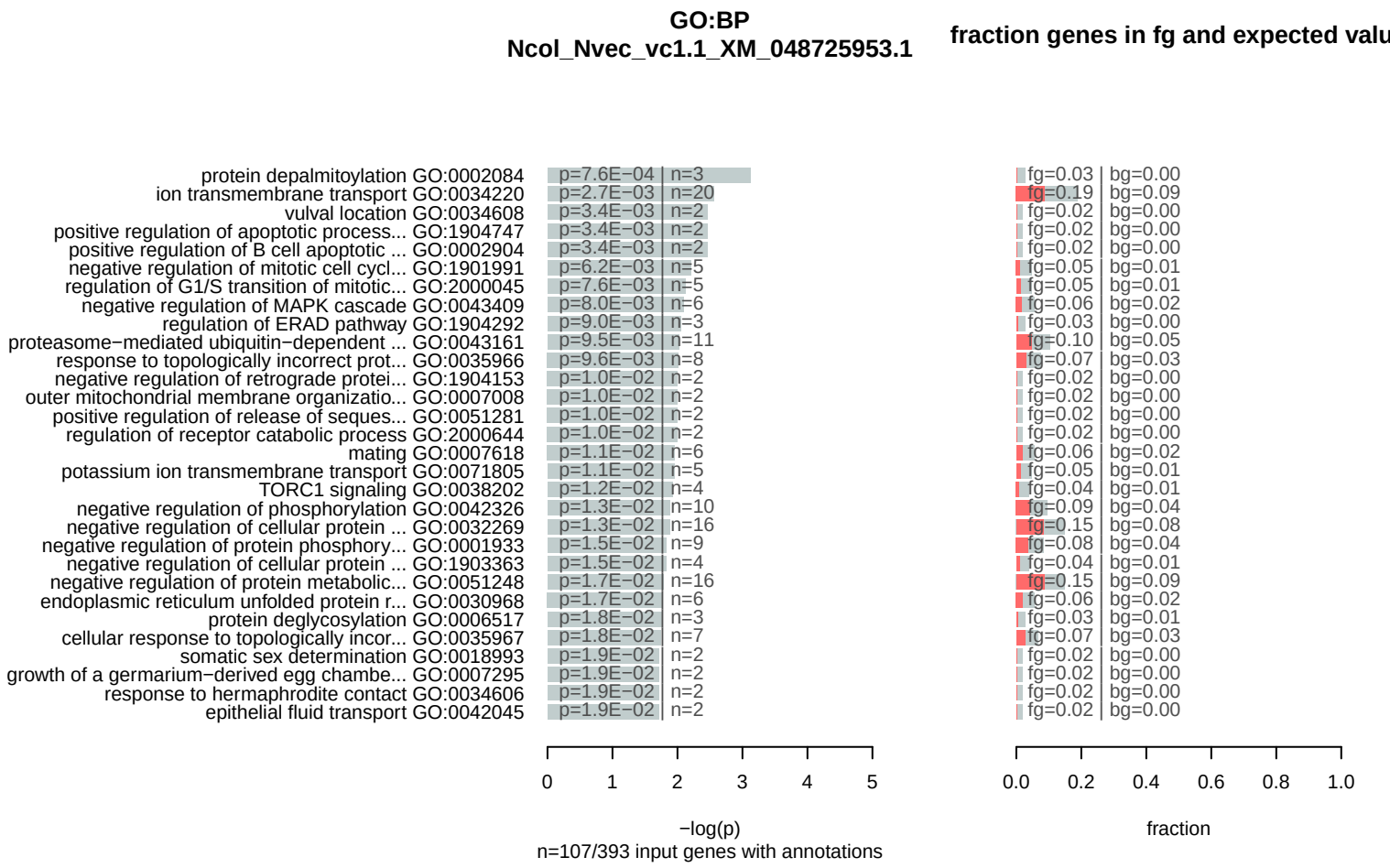
GO:BP
Ncol_Nvec_vc1.1_XM_048725953.1
fraction genes in fg and expected valu
protein depalmitoylation GO:0002084 p=7.6E−04 n=3 fg=0.03 bg=0.00
ion transmembrane transport GO:0034220 p=2.7E−03 n=20 fg=0.19 bg=0.09
vulval location GO:0034608 p=3.4E−03 n=2 fg=0.02 bg=0.00
positive regulation of apoptotic process... GO:1904747 p=3.4E−03 n=2 fg=0.02 bg=0.00
positive regulation of B cell apoptotic ... GO:0002904 p=3.4E−03 n=2 fg=0.02 bg=0.00
negative regulation of mitotic cell cycl... GO:1901991 p=6.2E−03 n=5 fg=0.05 bg=0.01
regulation of G1/S transition of mitotic... GO:2000045 p=7.6E−03 n=5 fg=0.05 bg=0.01
negative regulation of MAPK cascade GO:0043409 p=8.0E−03 n=6 fg=0.06 bg=0.02
regulation of ERAD pathway GO:1904292 p=9.0E−03 n=3 fg=0.03 bg=0.00
proteasome−mediated ubiquitin−dependent ... GO:0043161 p=9.5E−03 n=11 fg=0.10 bg=0.05
response to topologically incorrect prot... GO:0035966 p=9.6E−03 n=8 fg=0.07 bg=0.03
negative regulation of retrograde protei... GO:1904153 p=1.0E−02 n=2 fg=0.02 bg=0.00
outer mitochondrial membrane organizatio... GO:0007008 p=1.0E−02 n=2 fg=0.02 bg=0.00
positive regulation of release of seques... GO:0051281 p=1.0E−02 n=2 fg=0.02 bg=0.00
regulation of receptor catabolic process GO:2000644 p=1.0E−02 n=2 fg=0.02 bg=0.00
mating GO:0007618 p=1.1E−02 n=6 fg=0.06 bg=0.02
potassium ion transmembrane transport GO:0071805 p=1.1E−02 n=5 fg=0.05 bg=0.01
TORC1 signaling GO:0038202 p=1.2E−02 n=4 fg=0.04 bg=0.01
negative regulation of phosphorylation GO:0042326 p=1.3E−02 n=10 fg=0.09 bg=0.04
negative regulation of cellular protein ... GO:0032269 p=1.3E−02 n=16 fg=0.15 bg=0.08
negative regulation of protein phosphory... GO:0001933 p=1.5E−02 n=9 fg=0.08 bg=0.04
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negative regulation of protein metabolic... GO:0051248 p=1.7E−02 n=16 fg=0.15 bg=0.09
endoplasmic reticulum unfolded protein r... GO:0030968 p=1.7E−02 n=6 fg=0.06 bg=0.02
protein deglycosylation GO:0006517 p=1.8E−02 n=3 fg=0.03 bg=0.01
cellular response to topologically incor... GO:0035967 p=1.8E−02 n=7 fg=0.07 bg=0.03
somatic sex determination GO:0018993 p=1.9E−02 n=2 fg=0.02 bg=0.00
growth of a germarium−derived egg chambe... GO:0007295 p=1.9E−02 n=2 fg=0.02 bg=0.00
response to hermaphrodite contact GO:0034606 p=1.9E−02 n=2 fg=0.02 bg=0.00
epithelial fluid transport GO:0042045 p=1.9E−02 n=2 fg=0.02 bg=0.00
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−log(p)
n=107/393 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_048725953.1
fraction genes in fg and expected valu
ion gated channel activity GO:0022839 p=7.7E−04 n=9 fg=0.09 bg=0.03
palmitoyl−(protein) hydrolase activity GO:0008474 p=8.9E−04 n=3 fg=0.03 bg=0.00
voltage−gated cation channel activity GO:0022843 p=3.0E−03 n=7 fg=0.07 bg=0.01
BH3 domain binding GO:0051434 p=3.8E−03 n=2 fg=0.02 bg=0.00
transferase activity, transferring alkyl... GO:0016765 p=4.1E−03 n=3 fg=0.03 bg=0.00
outward rectifier potassium channel acti... GO:0015271 p=6.8E−03 n=3 fg=0.03 bg=0.00
voltage−gated calcium channel activity GO:0005245 p=1.0E−02 n=3 fg=0.03 bg=0.01
calcium−activated potassium channel acti... GO:0015269 p=1.1E−02 n=2 fg=0.02 bg=0.00
voltage−gated sodium channel activity GO:0005248 p=2.1E−02 n=2 fg=0.02 bg=0.00
phosphatidylinositol phosphate 4−phospha... GO:0034596 p=2.1E−02 n=2 fg=0.02 bg=0.00
metal ion transmembrane transporter acti... GO:0046873 p=3.1E−02 n=10 fg=0.10 bg=0.04
sodium channel activity GO:0005272 p=3.4E−02 n=2 fg=0.02 bg=0.00
transmitter−gated ion channel activity GO:0022824 p=3.4E−02 n=2 fg=0.02 bg=0.00
transmitter−gated channel activity GO:0022835 p=3.4E−02 n=2 fg=0.02 bg=0.00
peptide antigen binding GO:0042605 p=3.4E−02 n=2 fg=0.02 bg=0.00
L−cystine transmembrane transporter acti... GO:0015184 p=3.4E−02 n=2 fg=0.02 bg=0.00
sulfur amino acid transmembrane transpor... GO:0000099 p=4.9E−02 n=2 fg=0.02 bg=0.00
modified amino acid transmembrane transp... GO:0072349 p=4.9E−02 n=2 fg=0.02 bg=0.00
phosphatidylinositol phosphate phosphata... GO:0052866 p=4.9E−02 n=2 fg=0.02 bg=0.00
structural constituent of muscle GO:0008307 p=4.9E−02 n=2 fg=0.02 bg=0.00
calcium channel activity GO:0005262 p=5.0E−02 n=4 fg=0.04 bg=0.01
ligand−gated ion channel activity GO:0015276 p=5.0E−02 n=4 fg=0.04 bg=0.01
ligand−gated channel activity GO:0022834 p=5.0E−02 n=4 fg=0.04 bg=0.01
ligand−gated cation channel activity GO:0099094 p=6.1E−02 n=3 fg=0.03 bg=0.01
sodium ion transmembrane transporter act... GO:0015081 p=6.1E−02 n=3 fg=0.03 bg=0.01
sodium:phosphate symporter activity GO:0005436 p=6.2E−02 n=1 fg=0.01 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=6.2E−02 n=1 fg=0.01 bg=0.00
MDM2/MDM4 family protein binding GO:0097371 p=6.2E−02 n=1 fg=0.01 bg=0.00
phosphate ion binding GO:0042301 p=6.2E−02 n=1 fg=0.01 bg=0.00
neurotrophin binding GO:0043121 p=6.2E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=99/393 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_048725953.1
fraction genes in fg and expected valu
neuronal cell body GO:0043025 p=3.2E−03 n=16 fg=0.15 bg=0.07
dendrite GO:0030425 p=4.1E−03 n=16 fg=0.15 bg=0.07
cation channel complex GO:0034703 p=7.0E−03 n=5 fg=0.05 bg=0.01
axon GO:0030424 p=9.1E−03 n=16 fg=0.15 bg=0.08
Bcl−2 family protein complex GO:0097136 p=1.1E−02 n=2 fg=0.02 bg=0.00
potassium channel complex GO:0034705 p=1.4E−02 n=3 fg=0.03 bg=0.01
voltage−gated potassium channel complex GO:0008076 p=1.4E−02 n=3 fg=0.03 bg=0.01
Cul2−RING ubiquitin ligase complex GO:0031462 p=2.0E−02 n=2 fg=0.02 bg=0.00
cluster of actin−based cell projections GO:0098862 p=2.4E−02 n=5 fg=0.05 bg=0.02
intracellular vesicle GO:0097708 p=2.8E−02 n=28 fg=0.25 bg=0.18
cytoplasmic vesicle GO:0031410 p=2.8E−02 n=28 fg=0.25 bg=0.18
sensory dendrite GO:0071683 p=3.3E−02 n=2 fg=0.02 bg=0.00
membrane raft GO:0045121 p=3.8E−02 n=7 fg=0.06 bg=0.03
membrane microdomain GO:0098857 p=3.8E−02 n=7 fg=0.06 bg=0.03
brush border membrane GO:0031526 p=4.0E−02 n=3 fg=0.03 bg=0.01
extracellular space GO:0005615 p=4.6E−02 n=7 fg=0.06 bg=0.03
cell projection membrane GO:0031253 p=4.7E−02 n=8 fg=0.07 bg=0.04
vesicle GO:0031982 p=5.3E−02 n=28 fg=0.25 bg=0.19
brush border GO:0005903 p=5.4E−02 n=4 fg=0.04 bg=0.01
kinocilium GO:0060091 p=6.1E−02 n=1 fg=0.01 bg=0.00
Sin3 complex GO:0016580 p=6.1E−02 n=1 fg=0.01 bg=0.00
BAX complex GO:0097144 p=6.1E−02 n=1 fg=0.01 bg=0.00
septin collar GO:0032173 p=6.1E−02 n=1 fg=0.01 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=6.1E−02 n=1 fg=0.01 bg=0.00
protein farnesyltransferase complex GO:0005965 p=6.1E−02 n=1 fg=0.01 bg=0.00
protein kinase CK2 complex GO:0005956 p=6.1E−02 n=1 fg=0.01 bg=0.00
endocytic vesicle lumen GO:0071682 p=6.1E−02 n=1 fg=0.01 bg=0.00
neuronal ribonucleoprotein granule GO:0071598 p=6.1E−02 n=1 fg=0.01 bg=0.00
polycystin complex GO:0002133 p=6.1E−02 n=1 fg=0.01 bg=0.00
9+2 non−motile cilium GO:0097732 p=6.1E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=110/393 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction