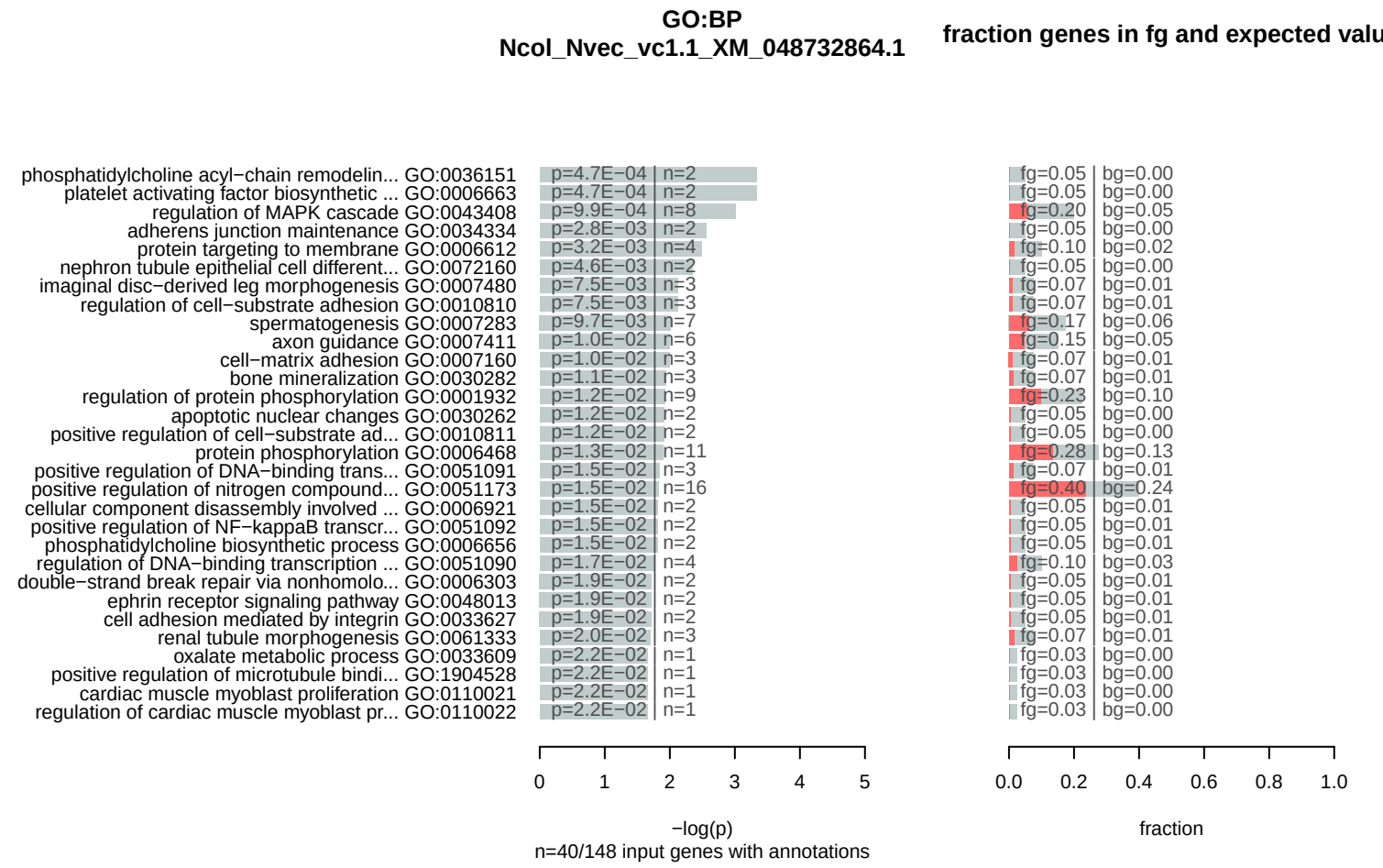
GO:BP
Ncol_Nvec_vc1.1_XM_048732864.1
fraction genes in fg and expected valu
phosphatidylcholine acyl−chain remodelin... GO:0036151 p=4.7E−04 n=2 fg=0.05 bg=0.00
platelet activating factor biosynthetic ... GO:0006663 p=4.7E−04 n=2 fg=0.05 bg=0.00
regulation of MAPK cascade GO:0043408 p=9.9E−04 n=8 fg=0.20 bg=0.05
adherens junction maintenance GO:0034334 p=2.8E−03 n=2 fg=0.05 bg=0.00
protein targeting to membrane GO:0006612 p=3.2E−03 n=4 fg=0.10 bg=0.02
nephron tubule epithelial cell different... GO:0072160 p=4.6E−03 n=2 fg=0.05 bg=0.00
imaginal disc−derived leg morphogenesis GO:0007480 p=7.5E−03 n=3 fg=0.07 bg=0.01
regulation of cell−substrate adhesion GO:0010810 p=7.5E−03 n=3 fg=0.07 bg=0.01
spermatogenesis GO:0007283 p=9.7E−03 n=7 fg=0.17 bg=0.06
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cell−matrix adhesion GO:0007160 p=1.0E−02 n=3 fg=0.07 bg=0.01
bone mineralization GO:0030282 p=1.1E−02 n=3 fg=0.07 bg=0.01
regulation of protein phosphorylation GO:0001932 p=1.2E−02 n=9 fg=0.23 bg=0.10
apoptotic nuclear changes GO:0030262 p=1.2E−02 n=2 fg=0.05 bg=0.00
positive regulation of cell−substrate ad... GO:0010811 p=1.2E−02 n=2 fg=0.05 bg=0.00
protein phosphorylation GO:0006468 p=1.3E−02 n=11 fg=0.28 bg=0.13
positive regulation of DNA−binding trans... GO:0051091 p=1.5E−02 n=3 fg=0.07 bg=0.01
positive regulation of nitrogen compound... GO:0051173 p=1.5E−02 n=16 fg=0.40 bg=0.24
cellular component disassembly involved ... GO:0006921 p=1.5E−02 n=2 fg=0.05 bg=0.01
positive regulation of NF−kappaB transcr... GO:0051092 p=1.5E−02 n=2 fg=0.05 bg=0.01
phosphatidylcholine biosynthetic process GO:0006656 p=1.5E−02 n=2 fg=0.05 bg=0.01
regulation of DNA−binding transcription ... GO:0051090 p=1.7E−02 n=4 fg=0.10 bg=0.03
double−strand break repair via nonhomolo... GO:0006303 p=1.9E−02 n=2 fg=0.05 bg=0.01
ephrin receptor signaling pathway GO:0048013 p=1.9E−02 n=2 fg=0.05 bg=0.01
cell adhesion mediated by integrin GO:0033627 p=1.9E−02 n=2 fg=0.05 bg=0.01
renal tubule morphogenesis GO:0061333 p=2.0E−02 n=3 fg=0.07 bg=0.01
oxalate metabolic process GO:0033609 p=2.2E−02 n=1 fg=0.03 bg=0.00
positive regulation of microtubule bindi... GO:1904528 p=2.2E−02 n=1 fg=0.03 bg=0.00
cardiac muscle myoblast proliferation GO:0110021 p=2.2E−02 n=1 fg=0.03 bg=0.00
regulation of cardiac muscle myoblast pr... GO:0110022 p=2.2E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=40/148 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_048732864.1
fraction genes in fg and expected valu
1−acylglycerophosphocholine O−acyltransf... GO:0047184 p=5.0E−04 n=2 fg=0.06 bg=0.00
2−acylglycerol−3−phosphate O−acyltransfe... GO:0047144 p=5.0E−04 n=2 fg=0.06 bg=0.00
1−alkylglycerophosphocholine O−acetyltra... GO:0047192 p=5.0E−04 n=2 fg=0.06 bg=0.00
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=1.5E−03 n=2 fg=0.06 bg=0.00
protein kinase binding GO:0019901 p=4.1E−03 n=8 fg=0.22 bg=0.08
DNA−binding transcription factor binding GO:0140297 p=1.2E−02 n=4 fg=0.11 bg=0.03
mitogen−activated protein kinase binding GO:0051019 p=2.0E−02 n=2 fg=0.06 bg=0.01
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=2.3E−02 n=1 fg=0.03 bg=0.00
platelet−derived growth factor receptor ... GO:0005161 p=2.3E−02 n=1 fg=0.03 bg=0.00
signal recognition particle binding GO:0005047 p=2.3E−02 n=1 fg=0.03 bg=0.00
translation elongation factor binding GO:0061770 p=2.3E−02 n=1 fg=0.03 bg=0.00
4−hydroxy−2−oxoglutarate aldolase activi... GO:0008700 p=2.3E−02 n=1 fg=0.03 bg=0.00
MDM2/MDM4 family protein binding GO:0097371 p=2.3E−02 n=1 fg=0.03 bg=0.00
cysteine−tRNA ligase activity GO:0004817 p=2.3E−02 n=1 fg=0.03 bg=0.00
phorbol ester receptor activity GO:0001565 p=2.3E−02 n=1 fg=0.03 bg=0.00
7S RNA binding GO:0008312 p=2.3E−02 n=1 fg=0.03 bg=0.00
1−alkylglycerophosphocholine O−acyltrans... GO:0047191 p=2.3E−02 n=1 fg=0.03 bg=0.00
protein−membrane adaptor activity GO:0043495 p=2.3E−02 n=1 fg=0.03 bg=0.00
aldehyde−lyase activity GO:0016832 p=2.3E−02 n=1 fg=0.03 bg=0.00
protein dimerization activity GO:0046983 p=3.5E−02 n=9 fg=0.25 bg=0.13
actin filament binding GO:0051015 p=4.3E−02 n=2 fg=0.06 bg=0.01
transmembrane transporter binding GO:0044325 p=4.3E−02 n=2 fg=0.06 bg=0.01
calcium−dependent protein kinase inhibit... GO:0008427 p=4.5E−02 n=1 fg=0.03 bg=0.00
calcium−dependent protein kinase regulat... GO:0010858 p=4.5E−02 n=1 fg=0.03 bg=0.00
STAT family protein binding GO:0097677 p=4.5E−02 n=1 fg=0.03 bg=0.00
cAMP response element binding protein bi... GO:0008140 p=4.5E−02 n=1 fg=0.03 bg=0.00
protein kinase B binding GO:0043422 p=4.5E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol−3−phosphatase activ... GO:0004438 p=4.5E−02 n=1 fg=0.03 bg=0.00
sequence−specific single stranded DNA bi... GO:0098847 p=4.5E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol−4−phosphate phospha... GO:0043812 p=4.5E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=36/148 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_048732864.1
fraction genes in fg and expected valu
intrinsic component of the cytoplasmic s... GO:0031235 p=3.1E−03 n=2 fg=0.05 bg=0.00
site of DNA damage GO:0090734 p=1.3E−02 n=2 fg=0.05 bg=0.00
site of double−strand break GO:0035861 p=1.3E−02 n=2 fg=0.05 bg=0.00
signal recognition particle GO:0048500 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
AMPA glutamate receptor complex GO:0032281 p=2.3E−02 n=1 fg=0.02 bg=0.00
signal recognition particle, endoplasmic... GO:0005786 p=2.3E−02 n=1 fg=0.02 bg=0.00
endoplasmic reticulum membrane GO:0005789 p=3.8E−02 n=7 fg=0.17 bg=0.08
nuclear outer membrane−endoplasmic retic... GO:0042175 p=4.0E−02 n=7 fg=0.17 bg=0.08
cell periphery GO:0071944 p=4.4E−02 n=19 fg=0.45 bg=0.29
endoplasmic reticulum subcompartment GO:0098827 p=4.4E−02 n=7 fg=0.17 bg=0.08
anchored component of plasma membrane GO:0046658 p=4.6E−02 n=1 fg=0.02 bg=0.00
neurotransmitter receptor complex GO:0098878 p=4.6E−02 n=1 fg=0.02 bg=0.00
protein−lipid complex GO:0032994 p=4.6E−02 n=1 fg=0.02 bg=0.00
nuclear stress granule GO:0097165 p=4.6E−02 n=1 fg=0.02 bg=0.00
ionotropic glutamate receptor complex GO:0008328 p=4.6E−02 n=1 fg=0.02 bg=0.00
filopodium GO:0030175 p=5.1E−02 n=2 fg=0.05 bg=0.01
secretory granule membrane GO:0030667 p=5.6E−02 n=3 fg=0.07 bg=0.02
ruffle GO:0001726 p=6.4E−02 n=2 fg=0.05 bg=0.01
Hrd1p ubiquitin ligase ERAD−L complex GO:0000839 p=6.8E−02 n=1 fg=0.02 bg=0.00
phagophore assembly site GO:0000407 p=6.8E−02 n=1 fg=0.02 bg=0.00
lipid droplet GO:0005811 p=7.0E−02 n=2 fg=0.05 bg=0.01
endoplasmic reticulum GO:0005783 p=7.1E−02 n=10 fg=0.24 bg=0.14
ER ubiquitin ligase complex GO:0000835 p=9.0E−02 n=1 fg=0.02 bg=0.00
integral component of peroxisomal membra... GO:0005779 p=9.0E−02 n=1 fg=0.02 bg=0.00
Hrd1p ubiquitin ligase complex GO:0000836 p=9.0E−02 n=1 fg=0.02 bg=0.00
chromatoid body GO:0033391 p=9.0E−02 n=1 fg=0.02 bg=0.00
intrinsic component of peroxisomal membr... GO:0031231 p=9.0E−02 n=1 fg=0.02 bg=0.00
plasma membrane GO:0005886 p=9.5E−02 n=17 fg=0.40 bg=0.27
autophagosome GO:0005776 p=9.8E−02 n=2 fg=0.05 bg=0.01
0 1 2 3 4 5
−log(p)
n=42/148 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction