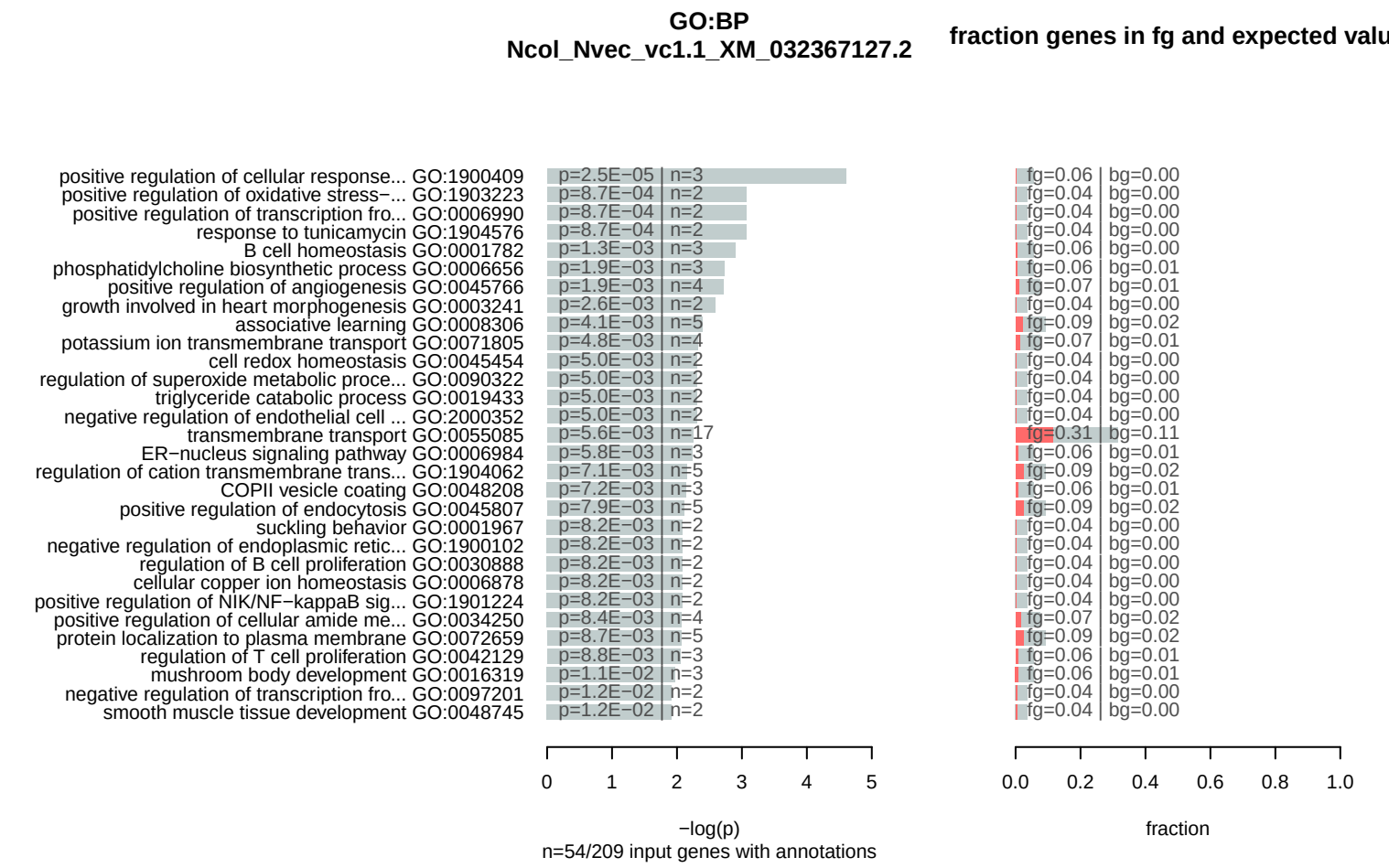
GO:BP
Ncol_Nvec_vc1.1_XM_032367127.2
fraction genes in fg and expected valu
positive regulation of cellular response... GO:1900409 p=2.5E−05 n=3 fg=0.06 bg=0.00
positive regulation of oxidative stress−... GO:1903223 p=8.7E−04 n=2 fg=0.04 bg=0.00
positive regulation of transcription fro... GO:0006990 p=8.7E−04 n=2 fg=0.04 bg=0.00
response to tunicamycin GO:1904576 p=8.7E−04 n=2 fg=0.04 bg=0.00
B cell homeostasis GO:0001782 p=1.3E−03 n=3 fg=0.06 bg=0.00
phosphatidylcholine biosynthetic process GO:0006656 p=1.9E−03 n=3 fg=0.06 bg=0.01
positive regulation of angiogenesis GO:0045766 p=1.9E−03 n=4 fg=0.07 bg=0.01
growth involved in heart morphogenesis GO:0003241 p=2.6E−03 n=2 fg=0.04 bg=0.00
associative learning GO:0008306 p=4.1E−03 n=5 fg=0.09 bg=0.02
potassium ion transmembrane transport GO:0071805 p=4.8E−03 n=4 fg=0.07 bg=0.01
cell redox homeostasis GO:0045454 p=5.0E−03 n=2 fg=0.04 bg=0.00
regulation of superoxide metabolic proce... GO:0090322 p=5.0E−03 n=2 fg=0.04 bg=0.00
triglyceride catabolic process GO:0019433 p=5.0E−03 n=2 fg=0.04 bg=0.00
negative regulation of endothelial cell ... GO:2000352 p=5.0E−03 n=2 fg=0.04 bg=0.00
transmembrane transport GO:0055085 p=5.6E−03 n=17 fg=0.31 bg=0.11
ER−nucleus signaling pathway GO:0006984 p=5.8E−03 n=3 fg=0.06 bg=0.01
regulation of cation transmembrane trans... GO:1904062 p=7.1E−03 n=5 fg=0.09 bg=0.02
COPII vesicle coating GO:0048208 p=7.2E−03 n=3 fg=0.06 bg=0.01
positive regulation of endocytosis GO:0045807 p=7.9E−03 n=5 fg=0.09 bg=0.02
suckling behavior GO:0001967 p=8.2E−03 n=2 fg=0.04 bg=0.00
negative regulation of endoplasmic retic... GO:1900102 p=8.2E−03 n=2 fg=0.04 bg=0.00
regulation of B cell proliferation GO:0030888 p=8.2E−03 n=2 fg=0.04 bg=0.00
cellular copper ion homeostasis GO:0006878 p=8.2E−03 n=2 fg=0.04 bg=0.00
positive regulation of NIK/NF−kappaB sig... GO:1901224 p=8.2E−03 n=2 fg=0.04 bg=0.00
positive regulation of cellular amide me... GO:0034250 p=8.4E−03 n=4 fg=0.07 bg=0.02
protein localization to plasma membrane GO:0072659 p=8.7E−03 n=5 fg=0.09 bg=0.02
regulation of T cell proliferation GO:0042129 p=8.8E−03 n=3 fg=0.06 bg=0.01
mushroom body development GO:0016319 p=1.1E−02 n=3 fg=0.06 bg=0.01
negative regulation of transcription fro... GO:0097201 p=1.2E−02 n=2 fg=0.04 bg=0.00
smooth muscle tissue development GO:0048745 p=1.2E−02 n=2 fg=0.04 bg=0.00
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−log(p)
n=54/209 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032367127.2
fraction genes in fg and expected valu
ion gated channel activity GO:0022839 p=1.3E−04 n=7 fg=0.15 bg=0.03
triglyceride lipase activity GO:0004806 p=2.4E−03 n=2 fg=0.04 bg=0.00
ion channel regulator activity GO:0099106 p=4.3E−03 n=4 fg=0.09 bg=0.01
calcium−release channel activity GO:0015278 p=7.7E−03 n=2 fg=0.04 bg=0.00
ephrin receptor binding GO:0046875 p=7.7E−03 n=2 fg=0.04 bg=0.00
signaling receptor activator activity GO:0030546 p=1.1E−02 n=2 fg=0.04 bg=0.00
receptor ligand activity GO:0048018 p=1.1E−02 n=2 fg=0.04 bg=0.00
insulin receptor binding GO:0005158 p=1.1E−02 n=2 fg=0.04 bg=0.00
voltage−gated cation channel activity GO:0022843 p=1.4E−02 n=3 fg=0.07 bg=0.01
signaling receptor regulator activity GO:0030545 p=1.6E−02 n=2 fg=0.04 bg=0.00
ion channel activity GO:0005216 p=1.6E−02 n=7 fg=0.15 bg=0.04
inorganic molecular entity transmembrane... GO:0015318 p=2.5E−02 n=9 fg=0.20 bg=0.07
transcription coregulator binding GO:0001221 p=2.6E−02 n=2 fg=0.04 bg=0.01
NAD−dependent histone deacetylase activi... GO:0046969 p=2.9E−02 n=1 fg=0.02 bg=0.00
heparan sulfate binding GO:1904399 p=2.9E−02 n=1 fg=0.02 bg=0.00
signal recognition particle binding GO:0005047 p=2.9E−02 n=1 fg=0.02 bg=0.00
lysophosphatidic acid binding GO:0035727 p=2.9E−02 n=1 fg=0.02 bg=0.00
CCR5 chemokine receptor binding GO:0031730 p=2.9E−02 n=1 fg=0.02 bg=0.00
calcitonin family binding GO:0097644 p=2.9E−02 n=1 fg=0.02 bg=0.00
amylin binding GO:0097645 p=2.9E−02 n=1 fg=0.02 bg=0.00
S100 protein binding GO:0044548 p=2.9E−02 n=1 fg=0.02 bg=0.00
7S RNA binding GO:0008312 p=2.9E−02 n=1 fg=0.02 bg=0.00
phospholipase D activator activity GO:1990583 p=2.9E−02 n=1 fg=0.02 bg=0.00
mono−olein transacylation activity GO:0051264 p=2.9E−02 n=1 fg=0.02 bg=0.00
diolein transacylation activity GO:0051265 p=2.9E−02 n=1 fg=0.02 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=2.9E−02 n=1 fg=0.02 bg=0.00
mannosyl−oligosaccharide mannosidase act... GO:0015924 p=2.9E−02 n=1 fg=0.02 bg=0.00
NAD+ binding GO:0070403 p=2.9E−02 n=1 fg=0.02 bg=0.00
NAD−dependent protein deacetylase activi... GO:0034979 p=2.9E−02 n=1 fg=0.02 bg=0.00
CCR chemokine receptor binding GO:0048020 p=2.9E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=46/209 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032367127.2
fraction genes in fg and expected valu
COPII−coated ER to Golgi transport vesic... GO:0030134 p=6.7E−04 n=4 fg=0.07 bg=0.01
endoplasmic reticulum lumen GO:0005788 p=2.7E−03 n=5 fg=0.08 bg=0.02
membrane GO:0016020 p=3.7E−03 n=39 fg=0.64 bg=0.46
endoplasmic reticulum−Golgi intermediate... GO:0005793 p=3.8E−03 n=4 fg=0.07 bg=0.01
platelet alpha granule lumen GO:0031093 p=6.4E−03 n=2 fg=0.03 bg=0.00
endoplasmic reticulum GO:0005783 p=1.0E−02 n=19 fg=0.31 bg=0.14
immunological synapse GO:0001772 p=1.0E−02 n=2 fg=0.03 bg=0.00
microtubule GO:0005874 p=2.1E−02 n=4 fg=0.07 bg=0.02
Golgi lumen GO:0005796 p=2.7E−02 n=2 fg=0.03 bg=0.00
cytoplasmic microtubule GO:0005881 p=2.7E−02 n=2 fg=0.03 bg=0.00
Golgi−associated vesicle GO:0005798 p=3.1E−02 n=4 fg=0.07 bg=0.02
lipoprotein particle GO:1990777 p=3.4E−02 n=1 fg=0.02 bg=0.00
signal recognition particle GO:0048500 p=3.4E−02 n=1 fg=0.02 bg=0.00
apical cytoplasm GO:0090651 p=3.4E−02 n=1 fg=0.02 bg=0.00
amyloid−beta complex GO:0106003 p=3.4E−02 n=1 fg=0.02 bg=0.00
Sec61 translocon complex GO:0005784 p=3.4E−02 n=1 fg=0.02 bg=0.00
signal recognition particle, endoplasmic... GO:0005786 p=3.4E−02 n=1 fg=0.02 bg=0.00
intermediate−density lipoprotein particl... GO:0034363 p=3.4E−02 n=1 fg=0.02 bg=0.00
endosome to plasma membrane transport ve... GO:0070381 p=3.4E−02 n=1 fg=0.02 bg=0.00
high−density lipoprotein particle GO:0034364 p=3.4E−02 n=1 fg=0.02 bg=0.00
translocon complex GO:0071256 p=3.4E−02 n=1 fg=0.02 bg=0.00
plasma lipoprotein particle GO:0034358 p=3.4E−02 n=1 fg=0.02 bg=0.00
triglyceride−rich plasma lipoprotein par... GO:0034385 p=3.4E−02 n=1 fg=0.02 bg=0.00
protein kinase CK2 complex GO:0005956 p=3.4E−02 n=1 fg=0.02 bg=0.00
microtubule cytoskeleton GO:0015630 p=3.4E−02 n=11 fg=0.18 bg=0.10
voltage−gated potassium channel complex GO:0008076 p=3.5E−02 n=2 fg=0.03 bg=0.00
potassium channel complex GO:0034705 p=3.5E−02 n=2 fg=0.03 bg=0.00
integral component of organelle membrane GO:0031301 p=4.0E−02 n=6 fg=0.10 bg=0.04
intrinsic component of organelle membran... GO:0031300 p=4.4E−02 n=6 fg=0.10 bg=0.04
polymeric cytoskeletal fiber GO:0099513 p=4.7E−02 n=4 fg=0.07 bg=0.02
0 1 2 3 4 5
−log(p)
n=61/209 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction