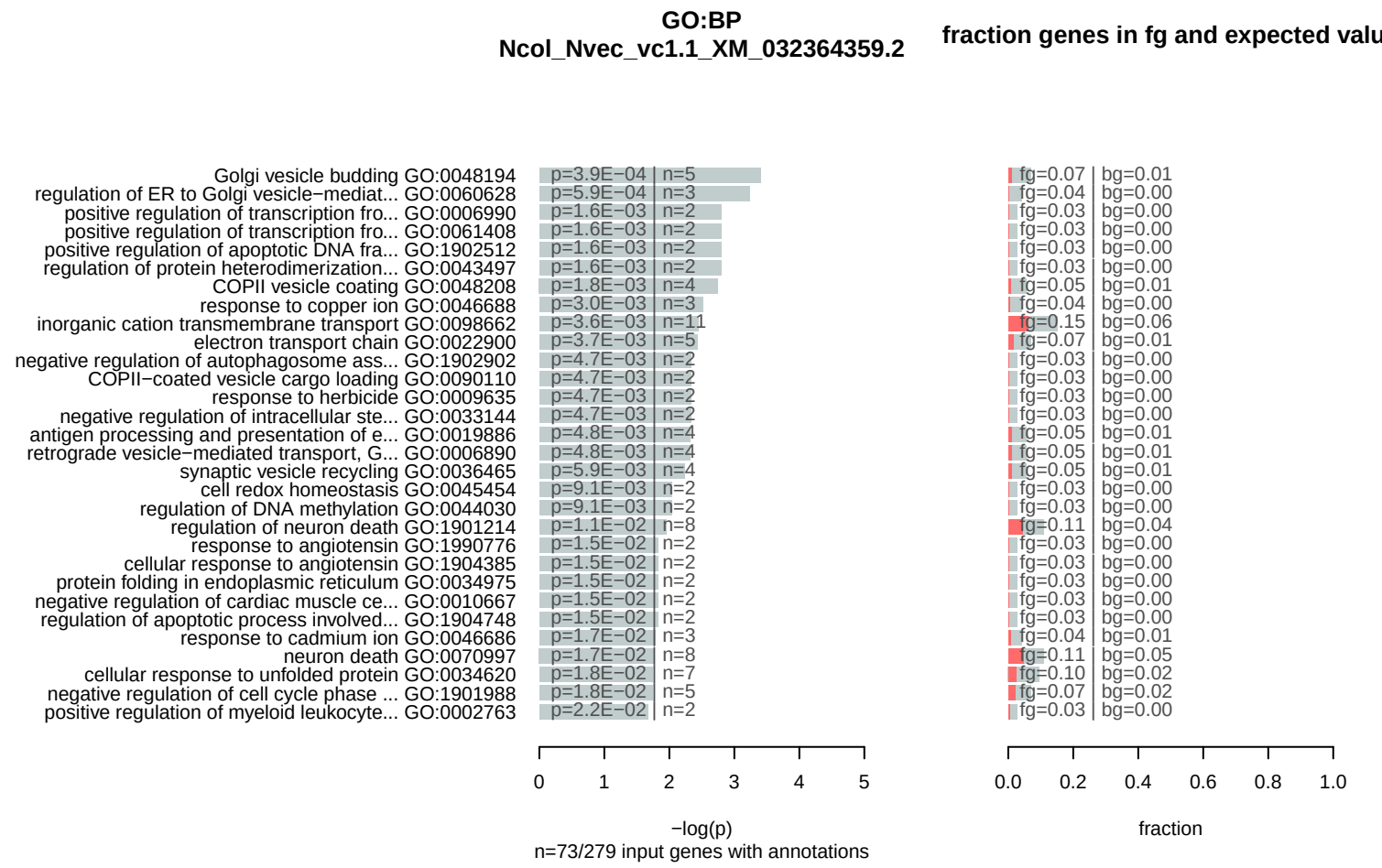
GO:BP
Ncol_Nvec_vc1.1_XM_032364359.2
fraction genes in fg and expected valu
Golgi vesicle budding GO:0048194 p=3.9E−04 n=5 fg=0.07 bg=0.01
regulation of ER to Golgi vesicle−mediat... GO:0060628 p=5.9E−04 n=3 fg=0.04 bg=0.00
positive regulation of transcription fro... GO:0006990 p=1.6E−03 n=2 fg=0.03 bg=0.00
positive regulation of transcription fro... GO:0061408 p=1.6E−03 n=2 fg=0.03 bg=0.00
positive regulation of apoptotic DNA fra... GO:1902512 p=1.6E−03 n=2 fg=0.03 bg=0.00
regulation of protein heterodimerization... GO:0043497 p=1.6E−03 n=2 fg=0.03 bg=0.00
COPII vesicle coating GO:0048208 p=1.8E−03 n=4 fg=0.05 bg=0.01
response to copper ion GO:0046688 p=3.0E−03 n=3 fg=0.04 bg=0.00
inorganic cation transmembrane transport GO:0098662 p=3.6E−03 n=11 fg=0.15 bg=0.06
electron transport chain GO:0022900 p=3.7E−03 n=5 fg=0.07 bg=0.01
negative regulation of autophagosome ass... GO:1902902 p=4.7E−03 n=2 fg=0.03 bg=0.00
COPII−coated vesicle cargo loading GO:0090110 p=4.7E−03 n=2 fg=0.03 bg=0.00
response to herbicide GO:0009635 p=4.7E−03 n=2 fg=0.03 bg=0.00
negative regulation of intracellular ste... GO:0033144 p=4.7E−03 n=2 fg=0.03 bg=0.00
antigen processing and presentation of e... GO:0019886 p=4.8E−03 n=4 fg=0.05 bg=0.01
retrograde vesicle−mediated transport, G... GO:0006890 p=4.8E−03 n=4 fg=0.05 bg=0.01
synaptic vesicle recycling GO:0036465 p=5.9E−03 n=4 fg=0.05 bg=0.01
cell redox homeostasis GO:0045454 p=9.1E−03 n=2 fg=0.03 bg=0.00
regulation of DNA methylation GO:0044030 p=9.1E−03 n=2 fg=0.03 bg=0.00
regulation of neuron death GO:1901214 p=1.1E−02 n=8 fg=0.11 bg=0.04
response to angiotensin GO:1990776 p=1.5E−02 n=2 fg=0.03 bg=0.00
cellular response to angiotensin GO:1904385 p=1.5E−02 n=2 fg=0.03 bg=0.00
protein folding in endoplasmic reticulum GO:0034975 p=1.5E−02 n=2 fg=0.03 bg=0.00
negative regulation of cardiac muscle ce... GO:0010667 p=1.5E−02 n=2 fg=0.03 bg=0.00
regulation of apoptotic process involved... GO:1904748 p=1.5E−02 n=2 fg=0.03 bg=0.00
response to cadmium ion GO:0046686 p=1.7E−02 n=3 fg=0.04 bg=0.01
neuron death GO:0070997 p=1.7E−02 n=8 fg=0.11 bg=0.05
cellular response to unfolded protein GO:0034620 p=1.8E−02 n=7 fg=0.10 bg=0.02
negative regulation of cell cycle phase ... GO:1901988 p=1.8E−02 n=5 fg=0.07 bg=0.02
positive regulation of myeloid leukocyte... GO:0002763 p=2.2E−02 n=2 fg=0.03 bg=0.00
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−log(p)
n=73/279 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032364359.2
fraction genes in fg and expected valu
chromatin DNA binding GO:0031490 p=1.9E−03 n=4 fg=0.06 bg=0.01
acyl−CoA dehydrogenase activity GO:0003995 p=2.0E−03 n=2 fg=0.03 bg=0.00
voltage−gated cation channel activity GO:0022843 p=6.9E−03 n=4 fg=0.06 bg=0.01
cysteine−type endopeptidase activity GO:0004197 p=1.1E−02 n=3 fg=0.04 bg=0.01
cis−regulatory region sequence−specific ... GO:0000987 p=1.1E−02 n=7 fg=0.10 bg=0.04
RNA polymerase II cis−regulatory region ... GO:0000978 p=1.1E−02 n=7 fg=0.10 bg=0.04
electron transfer activity GO:0009055 p=1.2E−02 n=4 fg=0.06 bg=0.01
DNA−binding transcription factor activit... GO:0000981 p=1.8E−02 n=10 fg=0.14 bg=0.07
flavin adenine dinucleotide binding GO:0050660 p=1.8E−02 n=2 fg=0.03 bg=0.00
intronic transcription regulatory region... GO:0001161 p=1.8E−02 n=2 fg=0.03 bg=0.00
RNA polymerase II transcription regulato... GO:0000977 p=2.1E−02 n=8 fg=0.11 bg=0.05
core promoter sequence−specific DNA bind... GO:0001046 p=3.1E−02 n=3 fg=0.04 bg=0.01
heparin binding GO:0008201 p=3.6E−02 n=2 fg=0.03 bg=0.00
ion gated channel activity GO:0022839 p=3.6E−02 n=5 fg=0.07 bg=0.03
transcription cis−regulatory region bind... GO:0000976 p=4.1E−02 n=8 fg=0.11 bg=0.06
SNARE binding GO:0000149 p=4.1E−02 n=4 fg=0.06 bg=0.02
sulfur compound binding GO:1901681 p=4.3E−02 n=3 fg=0.04 bg=0.01
L−leucine transmembrane transporter acti... GO:0015190 p=4.5E−02 n=1 fg=0.01 bg=0.00
L−methionine transmembrane transporter a... GO:0015191 p=4.5E−02 n=1 fg=0.01 bg=0.00
glucuronosyl−N−acetylgalactosaminyl−prot... GO:0047238 p=4.5E−02 n=1 fg=0.01 bg=0.00
acyl−CoA desaturase activity GO:0016215 p=4.5E−02 n=1 fg=0.01 bg=0.00
manganese ion transmembrane transporter ... GO:0005384 p=4.5E−02 n=1 fg=0.01 bg=0.00
methionine transmembrane transporter act... GO:0043865 p=4.5E−02 n=1 fg=0.01 bg=0.00
L−asparagine transmembrane transporter a... GO:0015182 p=4.5E−02 n=1 fg=0.01 bg=0.00
L−aspartate transmembrane transporter ac... GO:0015183 p=4.5E−02 n=1 fg=0.01 bg=0.00
NAD(P)+ transhydrogenase activity GO:0008746 p=4.5E−02 n=1 fg=0.01 bg=0.00
L−glutamine transmembrane transporter ac... GO:0015186 p=4.5E−02 n=1 fg=0.01 bg=0.00
L−glutamate transmembrane transporter ac... GO:0005313 p=4.5E−02 n=1 fg=0.01 bg=0.00
phospholipase D activator activity GO:1990583 p=4.5E−02 n=1 fg=0.01 bg=0.00
nickel cation transmembrane transporter ... GO:0015099 p=4.5E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=71/279 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032364359.2
fraction genes in fg and expected valu
COPII vesicle coat GO:0030127 p=1.8E−03 n=2 fg=0.03 bg=0.00
Golgi−associated vesicle GO:0005798 p=3.4E−03 n=6 fg=0.08 bg=0.02
euchromatin GO:0000791 p=3.6E−03 n=3 fg=0.04 bg=0.00
protein−DNA complex GO:0032993 p=3.7E−03 n=4 fg=0.05 bg=0.01
Golgi apparatus GO:0005794 p=4.1E−03 n=19 fg=0.25 bg=0.13
integral component of endoplasmic reticu... GO:0030176 p=6.7E−03 n=6 fg=0.08 bg=0.02
EMC complex GO:0072546 p=1.7E−02 n=2 fg=0.03 bg=0.00
voltage−gated calcium channel complex GO:0005891 p=1.7E−02 n=2 fg=0.03 bg=0.00
Golgi−associated vesicle membrane GO:0030660 p=1.9E−02 n=3 fg=0.04 bg=0.01
endoplasmic reticulum protein−containing... GO:0140534 p=1.9E−02 n=4 fg=0.05 bg=0.01
transmembrane transporter complex GO:1902495 p=2.1E−02 n=5 fg=0.06 bg=0.02
membrane protein complex GO:0098796 p=2.2E−02 n=14 fg=0.18 bg=0.09
vacuolar lumen GO:0005775 p=2.2E−02 n=4 fg=0.05 bg=0.01
tertiary granule lumen GO:1904724 p=2.4E−02 n=2 fg=0.03 bg=0.00
transporter complex GO:1990351 p=2.5E−02 n=5 fg=0.06 bg=0.02
Golgi stack GO:0005795 p=2.8E−02 n=5 fg=0.06 bg=0.02
kinetochore GO:0000776 p=2.8E−02 n=3 fg=0.04 bg=0.01
calcium channel complex GO:0034704 p=3.3E−02 n=2 fg=0.03 bg=0.00
endoplasmic reticulum membrane GO:0005789 p=3.9E−02 n=14 fg=0.18 bg=0.08
condensed chromosome GO:0000793 p=4.0E−02 n=4 fg=0.05 bg=0.02
Dsl1/NZR complex GO:0070939 p=4.3E−02 n=1 fg=0.01 bg=0.00
dendritic growth cone GO:0044294 p=4.3E−02 n=1 fg=0.01 bg=0.00
axonemal microtubule GO:0005879 p=4.3E−02 n=1 fg=0.01 bg=0.00
BAX complex GO:0097144 p=4.3E−02 n=1 fg=0.01 bg=0.00
peripheral region of growth cone GO:0090725 p=4.3E−02 n=1 fg=0.01 bg=0.00
CCR4−NOT complex GO:0030014 p=4.3E−02 n=1 fg=0.01 bg=0.00
CCR4−NOT core complex GO:0030015 p=4.3E−02 n=1 fg=0.01 bg=0.00
nuclear outer membrane−endoplasmic retic... GO:0042175 p=4.3E−02 n=14 fg=0.18 bg=0.08
clathrin−coated vesicle GO:0030136 p=4.4E−02 n=4 fg=0.05 bg=0.02
organelle subcompartment GO:0031984 p=4.6E−02 n=20 fg=0.26 bg=0.14
0 1 2 3 4 5
−log(p)
n=77/279 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction