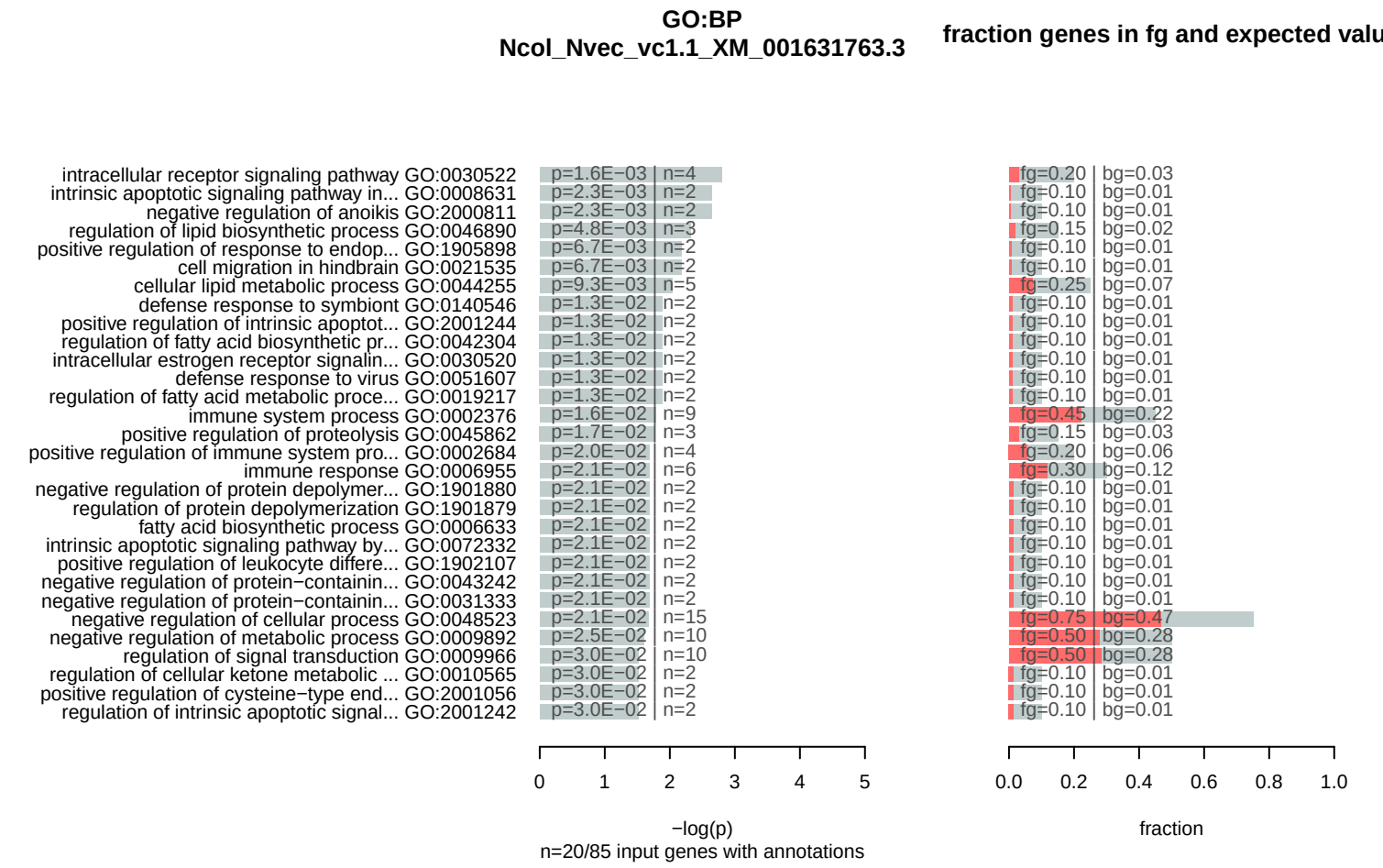
GO:BP
Ncol_Nvec_vc1.1_XM_001631763.3
fraction genes in fg and expected valu
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intrinsic apoptotic signaling pathway in... GO:0008631 p=2.3E−03 n=2 fg=0.10 bg=0.01
negative regulation of anoikis GO:2000811 p=2.3E−03 n=2 fg=0.10 bg=0.01
regulation of lipid biosynthetic process GO:0046890 p=4.8E−03 n=3 fg=0.15 bg=0.02
positive regulation of response to endop... GO:1905898 p=6.7E−03 n=2 fg=0.10 bg=0.01
cell migration in hindbrain GO:0021535 p=6.7E−03 n=2 fg=0.10 bg=0.01
cellular lipid metabolic process GO:0044255 p=9.3E−03 n=5 fg=0.25 bg=0.07
defense response to symbiont GO:0140546 p=1.3E−02 n=2 fg=0.10 bg=0.01
positive regulation of intrinsic apoptot... GO:2001244 p=1.3E−02 n=2 fg=0.10 bg=0.01
regulation of fatty acid biosynthetic pr... GO:0042304 p=1.3E−02 n=2 fg=0.10 bg=0.01
intracellular estrogen receptor signalin... GO:0030520 p=1.3E−02 n=2 fg=0.10 bg=0.01
defense response to virus GO:0051607 p=1.3E−02 n=2 fg=0.10 bg=0.01
regulation of fatty acid metabolic proce... GO:0019217 p=1.3E−02 n=2 fg=0.10 bg=0.01
immune system process GO:0002376 p=1.6E−02 n=9 fg=0.45 bg=0.22
positive regulation of proteolysis GO:0045862 p=1.7E−02 n=3 fg=0.15 bg=0.03
positive regulation of immune system pro... GO:0002684 p=2.0E−02 n=4 fg=0.20 bg=0.06
immune response GO:0006955 p=2.1E−02 n=6 fg=0.30 bg=0.12
negative regulation of protein depolymer... GO:1901880 p=2.1E−02 n=2 fg=0.10 bg=0.01
regulation of protein depolymerization GO:1901879 p=2.1E−02 n=2 fg=0.10 bg=0.01
fatty acid biosynthetic process GO:0006633 p=2.1E−02 n=2 fg=0.10 bg=0.01
intrinsic apoptotic signaling pathway by... GO:0072332 p=2.1E−02 n=2 fg=0.10 bg=0.01
positive regulation of leukocyte differe... GO:1902107 p=2.1E−02 n=2 fg=0.10 bg=0.01
negative regulation of protein−containin... GO:0043242 p=2.1E−02 n=2 fg=0.10 bg=0.01
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negative regulation of cellular process GO:0048523 p=2.1E−02 n=15 fg=0.75 bg=0.47
negative regulation of metabolic process GO:0009892 p=2.5E−02 n=10 fg=0.50 bg=0.28
regulation of signal transduction GO:0009966 p=3.0E−02 n=10 fg=0.50 bg=0.28
regulation of cellular ketone metabolic ... GO:0010565 p=3.0E−02 n=2 fg=0.10 bg=0.01
positive regulation of cysteine−type end... GO:2001056 p=3.0E−02 n=2 fg=0.10 bg=0.01
regulation of intrinsic apoptotic signal... GO:2001242 p=3.0E−02 n=2 fg=0.10 bg=0.01
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−log(p)
n=20/85 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001631763.3
fraction genes in fg and expected valu
caspase binding GO:0089720 p=2.3E−03 n=2 fg=0.11 bg=0.01
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=5.0E−02 n=1 fg=0.06 bg=0.00
peptide hormone binding GO:0017046 p=5.0E−02 n=1 fg=0.06 bg=0.00
O−acyltransferase activity GO:0008374 p=5.0E−02 n=1 fg=0.06 bg=0.00
protein transmembrane transporter activi... GO:0008320 p=5.0E−02 n=1 fg=0.06 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=5.0E−02 n=1 fg=0.06 bg=0.00
amide transmembrane transporter activity GO:0042887 p=5.0E−02 n=1 fg=0.06 bg=0.00
macromolecule transmembrane transporter ... GO:0022884 p=5.0E−02 n=1 fg=0.06 bg=0.00
1−acylglycerophosphocholine O−acyltransf... GO:0047184 p=5.0E−02 n=1 fg=0.06 bg=0.00
serine transmembrane transporter activit... GO:0022889 p=5.0E−02 n=1 fg=0.06 bg=0.00
BH3 domain binding GO:0051434 p=5.0E−02 n=1 fg=0.06 bg=0.00
L−serine transmembrane transporter activ... GO:0015194 p=5.0E−02 n=1 fg=0.06 bg=0.00
histone methyltransferase activity GO:0042054 p=5.0E−02 n=1 fg=0.06 bg=0.00
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death domain binding GO:0070513 p=5.0E−02 n=1 fg=0.06 bg=0.00
peptide transmembrane transporter activi... GO:1904680 p=5.0E−02 n=1 fg=0.06 bg=0.00
protein methyltransferase activity GO:0008276 p=5.0E−02 n=1 fg=0.06 bg=0.00
pyruvate dehydrogenase (acetyl−transferr... GO:0004740 p=5.0E−02 n=1 fg=0.06 bg=0.00
V1A vasopressin receptor binding GO:0031894 p=5.0E−02 n=1 fg=0.06 bg=0.00
1−alkylglycerophosphocholine O−acyltrans... GO:0047191 p=5.0E−02 n=1 fg=0.06 bg=0.00
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2−acylglycerol−3−phosphate O−acyltransfe... GO:0047144 p=5.0E−02 n=1 fg=0.06 bg=0.00
acylglycerol O−acyltransferase activity GO:0016411 p=5.0E−02 n=1 fg=0.06 bg=0.00
O−acetyltransferase activity GO:0016413 p=5.0E−02 n=1 fg=0.06 bg=0.00
protein transporter activity GO:0140318 p=5.0E−02 n=1 fg=0.06 bg=0.00
DNA−binding transcription factor activit... GO:0003700 p=5.3E−02 n=6 fg=0.33 bg=0.16
protein serine/threonine kinase activity GO:0004674 p=6.0E−02 n=3 fg=0.17 bg=0.05
DNA binding GO:0003677 p=8.5E−02 n=5 fg=0.28 bg=0.14
transcription regulator activity GO:0140110 p=9.2E−02 n=6 fg=0.33 bg=0.18
vasopressin receptor activity GO:0005000 p=9.7E−02 n=1 fg=0.06 bg=0.01
0 1 2 3 4 5
−log(p)
n=18/85 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001631763.3
fraction genes in fg and expected valu
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lysosomal membrane GO:0005765 p=2.6E−02 n=2 fg=0.11 bg=0.02
endoplasmic reticulum membrane GO:0005789 p=2.9E−02 n=4 fg=0.22 bg=0.07
nuclear outer membrane−endoplasmic retic... GO:0042175 p=2.9E−02 n=4 fg=0.22 bg=0.07
lysosome GO:0005764 p=2.9E−02 n=3 fg=0.17 bg=0.04
primary lysosome GO:0005766 p=3.5E−02 n=2 fg=0.11 bg=0.02
azurophil granule GO:0042582 p=3.5E−02 n=2 fg=0.11 bg=0.02
endoplasmic reticulum subcompartment GO:0098827 p=4.1E−02 n=4 fg=0.22 bg=0.08
pyruvate dehydrogenase complex GO:0045254 p=4.5E−02 n=1 fg=0.06 bg=0.00
perinuclear endoplasmic reticulum GO:0097038 p=4.5E−02 n=1 fg=0.06 bg=0.00
Bcl−2 family protein complex GO:0097136 p=4.5E−02 n=1 fg=0.06 bg=0.00
mitochondrial pyruvate dehydrogenase com... GO:0005967 p=4.5E−02 n=1 fg=0.06 bg=0.00
GATOR2 complex GO:0061700 p=4.5E−02 n=1 fg=0.06 bg=0.00
preribosome GO:0030684 p=4.5E−02 n=1 fg=0.06 bg=0.00
preribosome, small subunit precursor GO:0030688 p=4.5E−02 n=1 fg=0.06 bg=0.00
Seh1−associated complex GO:0035859 p=4.5E−02 n=1 fg=0.06 bg=0.00
ER to Golgi transport vesicle membrane GO:0012507 p=4.5E−02 n=1 fg=0.06 bg=0.00
core−binding factor complex GO:0016513 p=4.5E−02 n=1 fg=0.06 bg=0.00
oxidoreductase complex GO:1990204 p=4.5E−02 n=1 fg=0.06 bg=0.00
RNA polymerase II transcription regulato... GO:0090575 p=4.5E−02 n=2 fg=0.11 bg=0.02
perinuclear region of cytoplasm GO:0048471 p=4.6E−02 n=4 fg=0.22 bg=0.08
mitochondrial matrix GO:0005759 p=5.7E−02 n=2 fg=0.11 bg=0.02
centriole GO:0005814 p=8.8E−02 n=1 fg=0.06 bg=0.01
azurophil granule membrane GO:0035577 p=8.8E−02 n=1 fg=0.06 bg=0.01
COPII−coated ER to Golgi transport vesic... GO:0030134 p=8.8E−02 n=1 fg=0.06 bg=0.01
Golgi−associated vesicle membrane GO:0030660 p=8.8E−02 n=1 fg=0.06 bg=0.01
endoplasmic reticulum−Golgi intermediate... GO:0033116 p=8.8E−02 n=1 fg=0.06 bg=0.01
mitochondrial protein−containing complex GO:0098798 p=8.8E−02 n=1 fg=0.06 bg=0.01
endoplasmic reticulum−Golgi intermediate... GO:0005793 p=8.8E−02 n=1 fg=0.06 bg=0.01
protein−containing complex GO:0032991 p=1.1E−01 n=9 fg=0.50 bg=0.34
0 1 2 3 4 5
−log(p)
n=18/85 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction