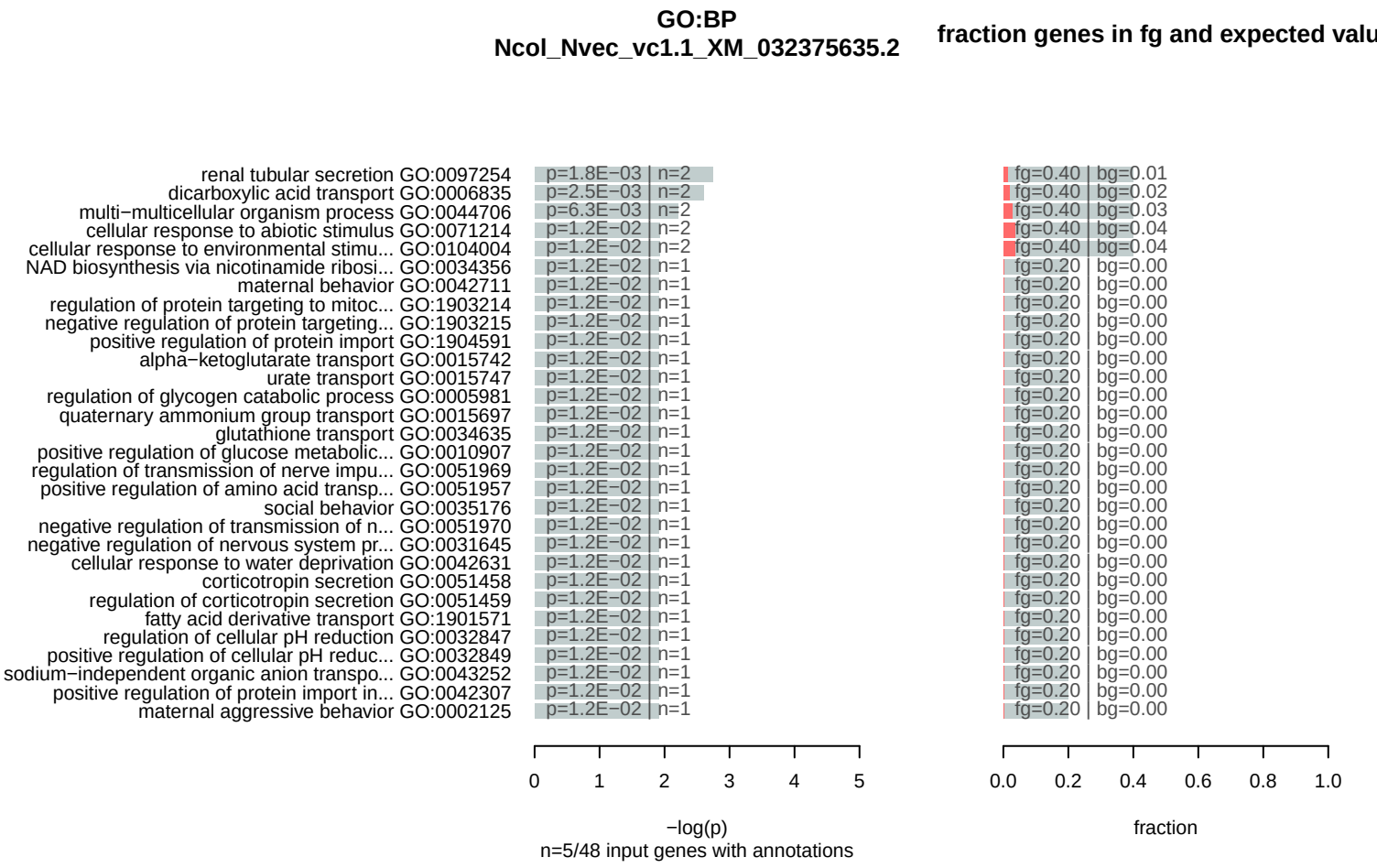
GO:BP
Ncol_Nvec_vc1.1_XM_032375635.2
fraction genes in fg and expected valu
renal tubular secretion GO:0097254 p=1.8E−03 n=2 fg=0.40 bg=0.01
dicarboxylic acid transport GO:0006835 p=2.5E−03 n=2 fg=0.40 bg=0.02
multi−multicellular organism process GO:0044706 p=6.3E−03 n=2 fg=0.40 bg=0.03
cellular response to abiotic stimulus GO:0071214 p=1.2E−02 n=2 fg=0.40 bg=0.04
cellular response to environmental stimu... GO:0104004 p=1.2E−02 n=2 fg=0.40 bg=0.04
NAD biosynthesis via nicotinamide ribosi... GO:0034356 p=1.2E−02 n=1 fg=0.20 bg=0.00
maternal behavior GO:0042711 p=1.2E−02 n=1 fg=0.20 bg=0.00
regulation of protein targeting to mitoc... GO:1903214 p=1.2E−02 n=1 fg=0.20 bg=0.00
negative regulation of protein targeting... GO:1903215 p=1.2E−02 n=1 fg=0.20 bg=0.00
positive regulation of protein import GO:1904591 p=1.2E−02 n=1 fg=0.20 bg=0.00
alpha−ketoglutarate transport GO:0015742 p=1.2E−02 n=1 fg=0.20 bg=0.00
urate transport GO:0015747 p=1.2E−02 n=1 fg=0.20 bg=0.00
regulation of glycogen catabolic process GO:0005981 p=1.2E−02 n=1 fg=0.20 bg=0.00
quaternary ammonium group transport GO:0015697 p=1.2E−02 n=1 fg=0.20 bg=0.00
glutathione transport GO:0034635 p=1.2E−02 n=1 fg=0.20 bg=0.00
positive regulation of glucose metabolic... GO:0010907 p=1.2E−02 n=1 fg=0.20 bg=0.00
regulation of transmission of nerve impu... GO:0051969 p=1.2E−02 n=1 fg=0.20 bg=0.00
positive regulation of amino acid transp... GO:0051957 p=1.2E−02 n=1 fg=0.20 bg=0.00
social behavior GO:0035176 p=1.2E−02 n=1 fg=0.20 bg=0.00
negative regulation of transmission of n... GO:0051970 p=1.2E−02 n=1 fg=0.20 bg=0.00
negative regulation of nervous system pr... GO:0031645 p=1.2E−02 n=1 fg=0.20 bg=0.00
cellular response to water deprivation GO:0042631 p=1.2E−02 n=1 fg=0.20 bg=0.00
corticotropin secretion GO:0051458 p=1.2E−02 n=1 fg=0.20 bg=0.00
regulation of corticotropin secretion GO:0051459 p=1.2E−02 n=1 fg=0.20 bg=0.00
fatty acid derivative transport GO:1901571 p=1.2E−02 n=1 fg=0.20 bg=0.00
regulation of cellular pH reduction GO:0032847 p=1.2E−02 n=1 fg=0.20 bg=0.00
positive regulation of cellular pH reduc... GO:0032849 p=1.2E−02 n=1 fg=0.20 bg=0.00
sodium−independent organic anion transpo... GO:0043252 p=1.2E−02 n=1 fg=0.20 bg=0.00
positive regulation of protein import in... GO:0042307 p=1.2E−02 n=1 fg=0.20 bg=0.00
maternal aggressive behavior GO:0002125 p=1.2E−02 n=1 fg=0.20 bg=0.00
0 1 2 3 4 5
−log(p)
n=5/48 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032375635.2
fraction genes in fg and expected valu
protein kinase C binding GO:0005080 p=1.3E−03 n=2 fg=0.33 bg=0.01
peptide hormone binding GO:0017046 p=1.7E−02 n=1 fg=0.17 bg=0.00
salt transmembrane transporter activity GO:1901702 p=1.7E−02 n=1 fg=0.17 bg=0.00
AMP binding GO:0016208 p=1.7E−02 n=1 fg=0.17 bg=0.00
adenyl−nucleotide exchange factor activi... GO:0000774 p=1.7E−02 n=1 fg=0.17 bg=0.00
nicotinate transmembrane transporter act... GO:0090416 p=1.7E−02 n=1 fg=0.17 bg=0.00
sodium−independent organic anion transme... GO:0015347 p=1.7E−02 n=1 fg=0.17 bg=0.00
carboxypeptidase activity GO:0004180 p=1.7E−02 n=1 fg=0.17 bg=0.00
organic cation transmembrane transporter... GO:0015101 p=1.7E−02 n=1 fg=0.17 bg=0.00
quaternary ammonium group transmembrane ... GO:0015651 p=1.7E−02 n=1 fg=0.17 bg=0.00
ammonium transmembrane transporter activ... GO:0008519 p=1.7E−02 n=1 fg=0.17 bg=0.00
dipeptidase activity GO:0016805 p=1.7E−02 n=1 fg=0.17 bg=0.00
icosanoid receptor activity GO:0004953 p=1.7E−02 n=1 fg=0.17 bg=0.00
prostanoid receptor activity GO:0004954 p=1.7E−02 n=1 fg=0.17 bg=0.00
prostaglandin receptor activity GO:0004955 p=1.7E−02 n=1 fg=0.17 bg=0.00
vitamin transmembrane transporter activi... GO:0090482 p=1.7E−02 n=1 fg=0.17 bg=0.00
urate transmembrane transporter activity GO:0015143 p=1.7E−02 n=1 fg=0.17 bg=0.00
short−chain fatty acid transmembrane tra... GO:0015636 p=1.7E−02 n=1 fg=0.17 bg=0.00
chloride ion binding GO:0031404 p=1.7E−02 n=1 fg=0.17 bg=0.00
V1A vasopressin receptor binding GO:0031894 p=1.7E−02 n=1 fg=0.17 bg=0.00
fatty acid transmembrane transporter act... GO:0015245 p=1.7E−02 n=1 fg=0.17 bg=0.00
inorganic anion exchanger activity GO:0005452 p=3.3E−02 n=1 fg=0.17 bg=0.01
anion:anion antiporter activity GO:0015301 p=3.3E−02 n=1 fg=0.17 bg=0.01
vasopressin receptor activity GO:0005000 p=3.3E−02 n=1 fg=0.17 bg=0.01
toxin transmembrane transporter activity GO:0019534 p=3.3E−02 n=1 fg=0.17 bg=0.01
vasopressin receptor binding GO:0031893 p=3.3E−02 n=1 fg=0.17 bg=0.01
solute:anion antiporter activity GO:0140323 p=3.3E−02 n=1 fg=0.17 bg=0.01
G protein−coupled receptor activity GO:0004930 p=3.4E−02 n=2 fg=0.33 bg=0.05
adenyl nucleotide binding GO:0030554 p=3.8E−02 n=2 fg=0.33 bg=0.06
hormone binding GO:0042562 p=4.9E−02 n=1 fg=0.17 bg=0.01
0 1 2 3 4 5
−log(p)
n=6/48 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032375635.2
fraction genes in fg and expected valu
brush border membrane GO:0031526 p=4.9E−02 n=1 fg=0.20 bg=0.01
external side of plasma membrane GO:0009897 p=4.9E−02 n=1 fg=0.20 bg=0.01
brush border GO:0005903 p=7.3E−02 n=1 fg=0.20 bg=0.01
plasma membrane GO:0005886 p=8.2E−02 n=4 fg=0.80 bg=0.40
caveola GO:0005901 p=8.4E−02 n=1 fg=0.20 bg=0.02
cluster of actin−based cell projections GO:0098862 p=8.4E−02 n=1 fg=0.20 bg=0.02
cell periphery GO:0071944 p=1.0E−01 n=4 fg=0.80 bg=0.42
plasma membrane raft GO:0044853 p=1.2E−01 n=1 fg=0.20 bg=0.02
Z disc GO:0030018 p=1.3E−01 n=1 fg=0.20 bg=0.03
I band GO:0031674 p=1.4E−01 n=1 fg=0.20 bg=0.03
integral component of plasma membrane GO:0005887 p=1.6E−01 n=2 fg=0.40 bg=0.15
sarcomere GO:0030017 p=1.6E−01 n=1 fg=0.20 bg=0.03
myofibril GO:0030016 p=1.7E−01 n=1 fg=0.20 bg=0.04
intrinsic component of plasma membrane GO:0031226 p=1.8E−01 n=2 fg=0.40 bg=0.16
side of membrane GO:0098552 p=2.0E−01 n=1 fg=0.20 bg=0.04
cell cortex GO:0005938 p=2.0E−01 n=1 fg=0.20 bg=0.04
basolateral plasma membrane GO:0016323 p=2.0E−01 n=1 fg=0.20 bg=0.04
basal plasma membrane GO:0009925 p=2.0E−01 n=1 fg=0.20 bg=0.04
cytoplasmic region GO:0099568 p=2.1E−01 n=1 fg=0.20 bg=0.04
contractile fiber GO:0043292 p=2.2E−01 n=1 fg=0.20 bg=0.05
cell surface GO:0009986 p=2.2E−01 n=1 fg=0.20 bg=0.05
basal part of cell GO:0045178 p=2.3E−01 n=1 fg=0.20 bg=0.05
membrane raft GO:0045121 p=2.5E−01 n=1 fg=0.20 bg=0.05
membrane microdomain GO:0098857 p=2.5E−01 n=1 fg=0.20 bg=0.05
membrane GO:0016020 p=2.5E−01 n=4 fg=0.80 bg=0.55
apical plasma membrane GO:0016324 p=2.7E−01 n=1 fg=0.20 bg=0.06
cell projection membrane GO:0031253 p=2.8E−01 n=1 fg=0.20 bg=0.06
apical part of cell GO:0045177 p=2.9E−01 n=1 fg=0.20 bg=0.07
supramolecular polymer GO:0099081 p=3.1E−01 n=1 fg=0.20 bg=0.07
supramolecular fiber GO:0099512 p=3.1E−01 n=1 fg=0.20 bg=0.07
0 1 2 3 4 5
−log(p)
n=5/48 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction