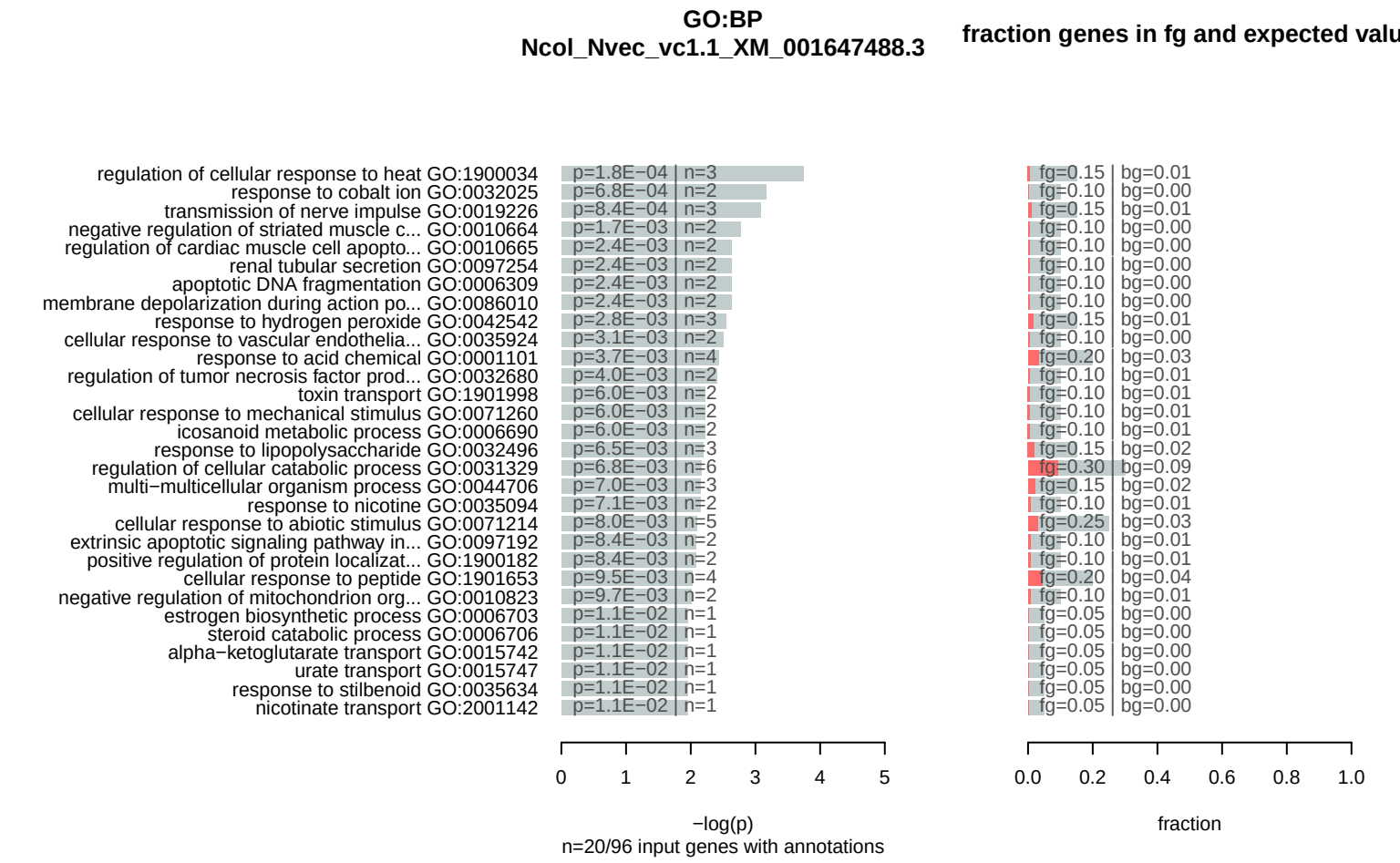
GO:BP
Ncol_Nvec_vc1.1_XM_001647488.3
fraction genes in fg and expected valu
regulation of cellular response to heat GO:1900034 p=1.8E−04 n=3 fg=0.15 bg=0.01
response to cobalt ion GO:0032025 p=6.8E−04 n=2 fg=0.10 bg=0.00
transmission of nerve impulse GO:0019226 p=8.4E−04 n=3 fg=0.15 bg=0.01
negative regulation of striated muscle c... GO:0010664 p=1.7E−03 n=2 fg=0.10 bg=0.00
regulation of cardiac muscle cell apopto... GO:0010665 p=2.4E−03 n=2 fg=0.10 bg=0.00
renal tubular secretion GO:0097254 p=2.4E−03 n=2 fg=0.10 bg=0.00
apoptotic DNA fragmentation GO:0006309 p=2.4E−03 n=2 fg=0.10 bg=0.00
membrane depolarization during action po... GO:0086010 p=2.4E−03 n=2 fg=0.10 bg=0.00
response to hydrogen peroxide GO:0042542 p=2.8E−03 n=3 fg=0.15 bg=0.01
cellular response to vascular endothelia... GO:0035924 p=3.1E−03 n=2 fg=0.10 bg=0.00
response to acid chemical GO:0001101 p=3.7E−03 n=4 fg=0.20 bg=0.03
regulation of tumor necrosis factor prod... GO:0032680 p=4.0E−03 n=2 fg=0.10 bg=0.01
toxin transport GO:1901998 p=6.0E−03 n=2 fg=0.10 bg=0.01
cellular response to mechanical stimulus GO:0071260 p=6.0E−03 n=2 fg=0.10 bg=0.01
icosanoid metabolic process GO:0006690 p=6.0E−03 n=2 fg=0.10 bg=0.01
response to lipopolysaccharide GO:0032496 p=6.5E−03 n=3 fg=0.15 bg=0.02
regulation of cellular catabolic process GO:0031329 p=6.8E−03 n=6 fg=0.30 bg=0.09
multi−multicellular organism process GO:0044706 p=7.0E−03 n=3 fg=0.15 bg=0.02
response to nicotine GO:0035094 p=7.1E−03 n=2 fg=0.10 bg=0.01
cellular response to abiotic stimulus GO:0071214 p=8.0E−03 n=5 fg=0.25 bg=0.03
extrinsic apoptotic signaling pathway in... GO:0097192 p=8.4E−03 n=2 fg=0.10 bg=0.01
positive regulation of protein localizat... GO:1900182 p=8.4E−03 n=2 fg=0.10 bg=0.01
cellular response to peptide GO:1901653 p=9.5E−03 n=4 fg=0.20 bg=0.04
negative regulation of mitochondrion org... GO:0010823 p=9.7E−03 n=2 fg=0.10 bg=0.01
estrogen biosynthetic process GO:0006703 p=1.1E−02 n=1 fg=0.05 bg=0.00
steroid catabolic process GO:0006706 p=1.1E−02 n=1 fg=0.05 bg=0.00
alpha−ketoglutarate transport GO:0015742 p=1.1E−02 n=1 fg=0.05 bg=0.00
urate transport GO:0015747 p=1.1E−02 n=1 fg=0.05 bg=0.00
response to stilbenoid GO:0035634 p=1.1E−02 n=1 fg=0.05 bg=0.00
nicotinate transport GO:2001142 p=1.1E−02 n=1 fg=0.05 bg=0.00
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−log(p)
n=20/96 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001647488.3
fraction genes in fg and expected valu
voltage−gated calcium channel activity GO:0005245 p=4.0E−03 n=2 fg=0.10 bg=0.01
protein kinase C binding GO:0005080 p=5.1E−03 n=2 fg=0.10 bg=0.01
oxidoreductase activity, acting on the C... GO:0016616 p=7.7E−03 n=2 fg=0.10 bg=0.01
oxidoreductase activity, acting on NAD(P... GO:0016652 p=1.3E−02 n=1 fg=0.05 bg=0.00
NAD(P)+ transhydrogenase activity GO:0008746 p=1.3E−02 n=1 fg=0.05 bg=0.00
nicotinate transmembrane transporter act... GO:0090416 p=1.3E−02 n=1 fg=0.05 bg=0.00
testosterone 17−beta−dehydrogenase (NADP... GO:0047045 p=1.3E−02 n=1 fg=0.05 bg=0.00
steroid dehydrogenase activity GO:0016229 p=1.3E−02 n=1 fg=0.05 bg=0.00
translation elongation factor binding GO:0061770 p=1.3E−02 n=1 fg=0.05 bg=0.00
urate transmembrane transporter activity GO:0015143 p=1.3E−02 n=1 fg=0.05 bg=0.00
chloride ion binding GO:0031404 p=1.3E−02 n=1 fg=0.05 bg=0.00
D−xylose 1−dehydrogenase (NADP+) activit... GO:0047837 p=1.3E−02 n=1 fg=0.05 bg=0.00
estradiol 17−beta−dehydrogenase activity GO:0004303 p=1.3E−02 n=1 fg=0.05 bg=0.00
V1A vasopressin receptor binding GO:0031894 p=1.3E−02 n=1 fg=0.05 bg=0.00
salt transmembrane transporter activity GO:1901702 p=1.3E−02 n=1 fg=0.05 bg=0.00
steroid dehydrogenase activity, acting o... GO:0033764 p=1.3E−02 n=1 fg=0.05 bg=0.00
icosanoid receptor activity GO:0004953 p=1.3E−02 n=1 fg=0.05 bg=0.00
prostanoid receptor activity GO:0004954 p=1.3E−02 n=1 fg=0.05 bg=0.00
prostaglandin receptor activity GO:0004955 p=1.3E−02 n=1 fg=0.05 bg=0.00
fatty acid transmembrane transporter act... GO:0015245 p=1.3E−02 n=1 fg=0.05 bg=0.00
sodium−independent organic anion transme... GO:0015347 p=1.3E−02 n=1 fg=0.05 bg=0.00
phospholipase A2 activator activity GO:0016005 p=1.3E−02 n=1 fg=0.05 bg=0.00
short−chain fatty acid transmembrane tra... GO:0015636 p=1.3E−02 n=1 fg=0.05 bg=0.00
ion gated channel activity GO:0022839 p=1.4E−02 n=3 fg=0.15 bg=0.03
cyclin−dependent protein serine/threonin... GO:0004861 p=2.5E−02 n=1 fg=0.05 bg=0.00
dipeptidase activity GO:0016805 p=2.5E−02 n=1 fg=0.05 bg=0.00
lipase activator activity GO:0060229 p=2.5E−02 n=1 fg=0.05 bg=0.00
toxin transmembrane transporter activity GO:0019534 p=2.5E−02 n=1 fg=0.05 bg=0.00
STAT family protein binding GO:0097677 p=2.5E−02 n=1 fg=0.05 bg=0.00
quaternary ammonium group transmembrane ... GO:0015651 p=2.5E−02 n=1 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=20/96 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001647488.3
fraction genes in fg and expected valu
death−inducing signaling complex GO:0031264 p=1.2E−02 n=1 fg=0.05 bg=0.00
Lsm1−7−Pat1 complex GO:1990726 p=1.2E−02 n=1 fg=0.05 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=1.2E−02 n=1 fg=0.05 bg=0.00
mRNA cap binding complex GO:0005845 p=2.3E−02 n=1 fg=0.05 bg=0.00
nuclear stress granule GO:0097165 p=2.3E−02 n=1 fg=0.05 bg=0.00
mitochondrial crista GO:0030061 p=2.3E−02 n=1 fg=0.05 bg=0.00
intrinsic component of mitochondrial out... GO:0031306 p=3.4E−02 n=1 fg=0.05 bg=0.00
integral component of mitochondrial oute... GO:0031307 p=3.4E−02 n=1 fg=0.05 bg=0.00
kinetochore microtubule GO:0005828 p=3.4E−02 n=1 fg=0.05 bg=0.00
RNA cap binding complex GO:0034518 p=3.4E−02 n=1 fg=0.05 bg=0.00
ESCRT III complex GO:0000815 p=4.6E−02 n=1 fg=0.05 bg=0.00
messenger ribonucleoprotein complex GO:1990124 p=5.7E−02 n=1 fg=0.05 bg=0.00
voltage−gated calcium channel complex GO:0005891 p=5.7E−02 n=1 fg=0.05 bg=0.00
mitotic spindle pole GO:0097431 p=5.7E−02 n=1 fg=0.05 bg=0.00
integral component of plasma membrane GO:0005887 p=6.7E−02 n=4 fg=0.19 bg=0.08
sarcoplasm GO:0016528 p=6.8E−02 n=1 fg=0.05 bg=0.00
sarcoplasmic reticulum GO:0016529 p=6.8E−02 n=1 fg=0.05 bg=0.00
pronucleus GO:0045120 p=6.8E−02 n=1 fg=0.05 bg=0.00
supramolecular complex GO:0099080 p=7.3E−02 n=4 fg=0.19 bg=0.08
PML body GO:0016605 p=7.9E−02 n=1 fg=0.05 bg=0.00
calcium channel complex GO:0034704 p=7.9E−02 n=1 fg=0.05 bg=0.00
intrinsic component of plasma membrane GO:0031226 p=8.3E−02 n=4 fg=0.19 bg=0.08
integral component of mitochondrial memb... GO:0032592 p=8.9E−02 n=1 fg=0.05 bg=0.00
euchromatin GO:0000791 p=8.9E−02 n=1 fg=0.05 bg=0.00
intrinsic component of mitochondrial mem... GO:0098573 p=8.9E−02 n=1 fg=0.05 bg=0.00
ribonucleoprotein granule GO:0035770 p=1.0E−01 n=2 fg=0.10 bg=0.03
ESCRT complex GO:0036452 p=1.1E−01 n=1 fg=0.05 bg=0.01
T−tubule GO:0030315 p=1.1E−01 n=1 fg=0.05 bg=0.01
spindle microtubule GO:0005876 p=1.1E−01 n=1 fg=0.05 bg=0.01
spindle GO:0005819 p=1.2E−01 n=2 fg=0.10 bg=0.03
0 1 2 3 4 5
−log(p)
n=21/96 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction