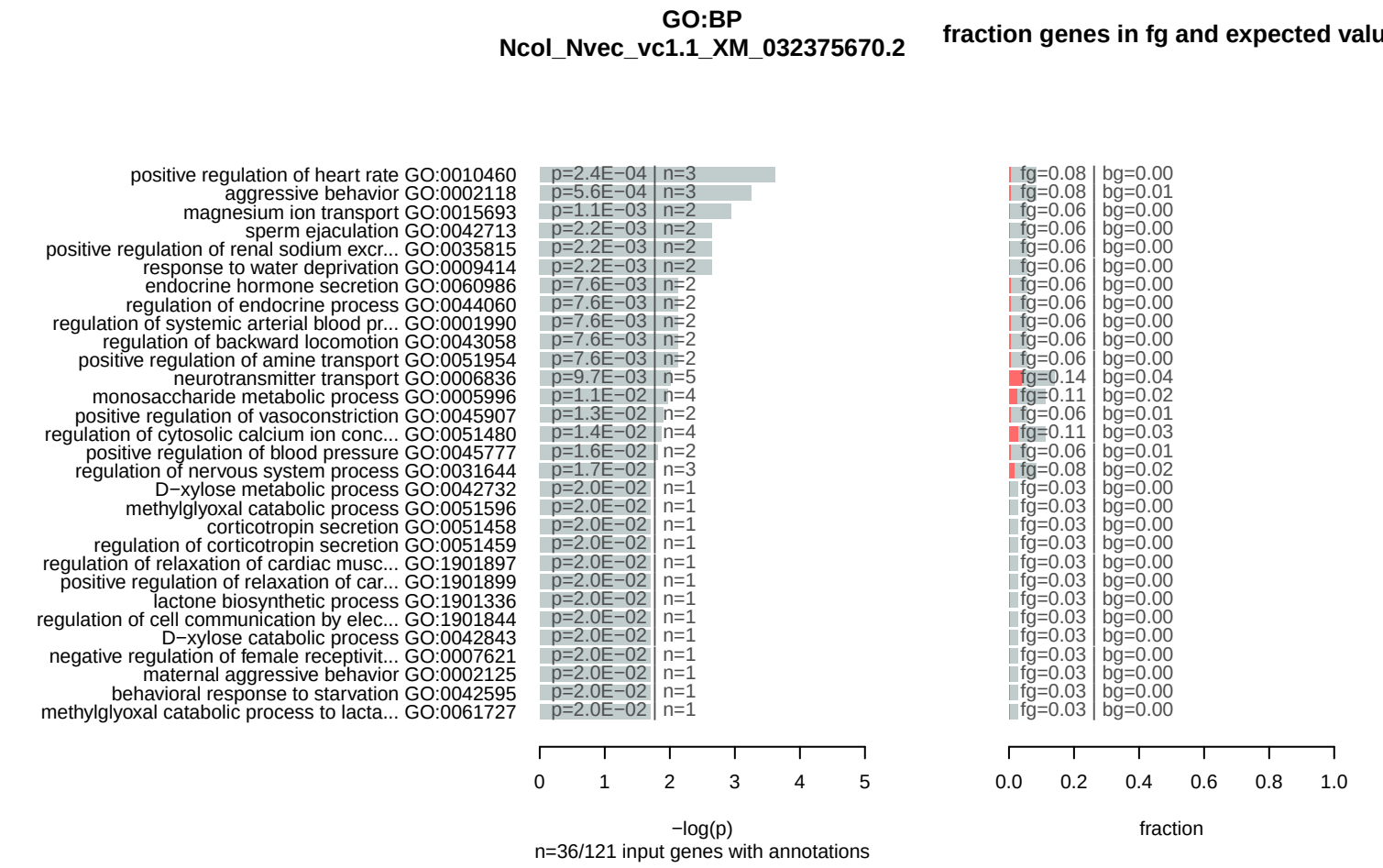
GO:BP
Ncol_Nvec_vc1.1_XM_032375670.2
fraction genes in fg and expected valu
positive regulation of heart rate GO:0010460 p=2.4E−04 n=3 fg=0.08 bg=0.00
aggressive behavior GO:0002118 p=5.6E−04 n=3 fg=0.08 bg=0.01
magnesium ion transport GO:0015693 p=1.1E−03 n=2 fg=0.06 bg=0.00
sperm ejaculation GO:0042713 p=2.2E−03 n=2 fg=0.06 bg=0.00
positive regulation of renal sodium excr... GO:0035815 p=2.2E−03 n=2 fg=0.06 bg=0.00
response to water deprivation GO:0009414 p=2.2E−03 n=2 fg=0.06 bg=0.00
endocrine hormone secretion GO:0060986 p=7.6E−03 n=2 fg=0.06 bg=0.00
regulation of endocrine process GO:0044060 p=7.6E−03 n=2 fg=0.06 bg=0.00
regulation of systemic arterial blood pr... GO:0001990 p=7.6E−03 n=2 fg=0.06 bg=0.00
regulation of backward locomotion GO:0043058 p=7.6E−03 n=2 fg=0.06 bg=0.00
positive regulation of amine transport GO:0051954 p=7.6E−03 n=2 fg=0.06 bg=0.00
neurotransmitter transport GO:0006836 p=9.7E−03 n=5 fg=0.14 bg=0.04
monosaccharide metabolic process GO:0005996 p=1.1E−02 n=4 fg=0.11 bg=0.02
positive regulation of vasoconstriction GO:0045907 p=1.3E−02 n=2 fg=0.06 bg=0.01
regulation of cytosolic calcium ion conc... GO:0051480 p=1.4E−02 n=4 fg=0.11 bg=0.03
positive regulation of blood pressure GO:0045777 p=1.6E−02 n=2 fg=0.06 bg=0.01
regulation of nervous system process GO:0031644 p=1.7E−02 n=3 fg=0.08 bg=0.02
D−xylose metabolic process GO:0042732 p=2.0E−02 n=1 fg=0.03 bg=0.00
methylglyoxal catabolic process GO:0051596 p=2.0E−02 n=1 fg=0.03 bg=0.00
corticotropin secretion GO:0051458 p=2.0E−02 n=1 fg=0.03 bg=0.00
regulation of corticotropin secretion GO:0051459 p=2.0E−02 n=1 fg=0.03 bg=0.00
regulation of relaxation of cardiac musc... GO:1901897 p=2.0E−02 n=1 fg=0.03 bg=0.00
positive regulation of relaxation of car... GO:1901899 p=2.0E−02 n=1 fg=0.03 bg=0.00
lactone biosynthetic process GO:1901336 p=2.0E−02 n=1 fg=0.03 bg=0.00
regulation of cell communication by elec... GO:1901844 p=2.0E−02 n=1 fg=0.03 bg=0.00
D−xylose catabolic process GO:0042843 p=2.0E−02 n=1 fg=0.03 bg=0.00
negative regulation of female receptivit... GO:0007621 p=2.0E−02 n=1 fg=0.03 bg=0.00
maternal aggressive behavior GO:0002125 p=2.0E−02 n=1 fg=0.03 bg=0.00
behavioral response to starvation GO:0042595 p=2.0E−02 n=1 fg=0.03 bg=0.00
methylglyoxal catabolic process to lacta... GO:0061727 p=2.0E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=36/121 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032375670.2
fraction genes in fg and expected valu
peptide receptor activity GO:0001653 p=1.6E−02 n=2 fg=0.06 bg=0.01
G protein−coupled peptide receptor activ... GO:0008528 p=1.6E−02 n=2 fg=0.06 bg=0.01
hydrolase activity, acting on ester bond... GO:0016788 p=1.9E−02 n=6 fg=0.19 bg=0.07
thiolester hydrolase activity GO:0016790 p=1.9E−02 n=2 fg=0.06 bg=0.01
oxidoreductase activity, acting on NAD(P... GO:0016652 p=2.0E−02 n=1 fg=0.03 bg=0.00
NAD(P)+ transhydrogenase activity GO:0008746 p=2.0E−02 n=1 fg=0.03 bg=0.00
gamma−glutamylaminecyclotransferase acti... GO:0061929 p=2.0E−02 n=1 fg=0.03 bg=0.00
nickel cation transmembrane transporter ... GO:0015099 p=2.0E−02 n=1 fg=0.03 bg=0.00
hydroxyacylglutathione hydrolase activit... GO:0004416 p=2.0E−02 n=1 fg=0.03 bg=0.00
D−xylose 1−dehydrogenase (NADP+) activit... GO:0047837 p=2.0E−02 n=1 fg=0.03 bg=0.00
V1A vasopressin receptor binding GO:0031894 p=2.0E−02 n=1 fg=0.03 bg=0.00
cysteine−tRNA ligase activity GO:0004817 p=2.0E−02 n=1 fg=0.03 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=2.0E−02 n=1 fg=0.03 bg=0.00
N−acylneuraminate−9−phosphatase activity GO:0050124 p=2.0E−02 n=1 fg=0.03 bg=0.00
S100 protein binding GO:0044548 p=2.0E−02 n=1 fg=0.03 bg=0.00
cobalt ion transmembrane transporter act... GO:0015087 p=2.0E−02 n=1 fg=0.03 bg=0.00
manganese ion transmembrane transporter ... GO:0005384 p=2.0E−02 n=1 fg=0.03 bg=0.00
DNA end binding GO:0045027 p=2.0E−02 n=1 fg=0.03 bg=0.00
acetyltransferase activity GO:0016407 p=2.7E−02 n=2 fg=0.06 bg=0.01
phospholipase activity GO:0004620 p=3.9E−02 n=2 fg=0.06 bg=0.01
dipeptidase activity GO:0016805 p=4.0E−02 n=1 fg=0.03 bg=0.00
ferrous iron transmembrane transporter a... GO:0015093 p=4.0E−02 n=1 fg=0.03 bg=0.00
magnesium ion transmembrane transporter ... GO:0015095 p=4.0E−02 n=1 fg=0.03 bg=0.00
platelet−activating factor acetyltransfe... GO:0047179 p=4.0E−02 n=1 fg=0.03 bg=0.00
cAMP response element binding protein bi... GO:0008140 p=4.0E−02 n=1 fg=0.03 bg=0.00
vasopressin receptor binding GO:0031893 p=4.0E−02 n=1 fg=0.03 bg=0.00
vasopressin receptor activity GO:0005000 p=4.0E−02 n=1 fg=0.03 bg=0.00
eukaryotic initiation factor 4E binding GO:0008190 p=4.0E−02 n=1 fg=0.03 bg=0.00
copper ion transmembrane transporter act... GO:0005375 p=4.0E−02 n=1 fg=0.03 bg=0.00
neurotransmitter:sodium symporter activi... GO:0005328 p=4.0E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=32/121 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032375670.2
fraction genes in fg and expected valu
endoplasmic reticulum protein−containing... GO:0140534 p=1.3E−02 n=3 fg=0.08 bg=0.01
nuclear SCF ubiquitin ligase complex GO:0043224 p=2.0E−02 n=1 fg=0.03 bg=0.00
sarcoplasmic reticulum lumen GO:0033018 p=2.0E−02 n=1 fg=0.03 bg=0.00
Cul5−RING ubiquitin ligase complex GO:0031466 p=2.0E−02 n=1 fg=0.03 bg=0.00
Cul7−RING ubiquitin ligase complex GO:0031467 p=2.0E−02 n=1 fg=0.03 bg=0.00
Dsl1/NZR complex GO:0070939 p=2.0E−02 n=1 fg=0.03 bg=0.00
9+2 non−motile cilium GO:0097732 p=2.0E−02 n=1 fg=0.03 bg=0.00
kinocilium GO:0060091 p=2.0E−02 n=1 fg=0.03 bg=0.00
neuronal cell body membrane GO:0032809 p=3.2E−02 n=2 fg=0.05 bg=0.01
cell body membrane GO:0044298 p=3.6E−02 n=2 fg=0.05 bg=0.01
neuron projection membrane GO:0032589 p=3.6E−02 n=2 fg=0.05 bg=0.01
anchored component of plasma membrane GO:0046658 p=4.0E−02 n=1 fg=0.03 bg=0.00
endoplasmic reticulum chaperone complex GO:0034663 p=4.0E−02 n=1 fg=0.03 bg=0.00
presynaptic cytoskeleton GO:0099569 p=4.0E−02 n=1 fg=0.03 bg=0.00
VCB complex GO:0030891 p=4.0E−02 n=1 fg=0.03 bg=0.00
Cul4B−RING E3 ubiquitin ligase complex GO:0031465 p=4.0E−02 n=1 fg=0.03 bg=0.00
Cul4A−RING E3 ubiquitin ligase complex GO:0031464 p=6.0E−02 n=1 fg=0.03 bg=0.00
Ino80 complex GO:0031011 p=6.0E−02 n=1 fg=0.03 bg=0.00
muscle cell projection GO:0036194 p=6.0E−02 n=1 fg=0.03 bg=0.00
muscle cell projection membrane GO:0036195 p=6.0E−02 n=1 fg=0.03 bg=0.00
sperm flagellum GO:0036126 p=6.1E−02 n=2 fg=0.05 bg=0.01
9+2 motile cilium GO:0097729 p=6.7E−02 n=2 fg=0.05 bg=0.01
mitochondrial matrix GO:0005759 p=6.9E−02 n=4 fg=0.11 bg=0.04
intrinsic component of plasma membrane GO:0031226 p=7.2E−02 n=6 fg=0.16 bg=0.08
synaptic vesicle GO:0008021 p=7.3E−02 n=3 fg=0.08 bg=0.03
DNA helicase complex GO:0033202 p=7.9E−02 n=1 fg=0.03 bg=0.00
Cul2−RING ubiquitin ligase complex GO:0031462 p=7.9E−02 n=1 fg=0.03 bg=0.00
INO80−type complex GO:0097346 p=7.9E−02 n=1 fg=0.03 bg=0.00
sperm head GO:0061827 p=7.9E−02 n=1 fg=0.03 bg=0.00
anaphase−promoting complex GO:0005680 p=7.9E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=37/121 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction