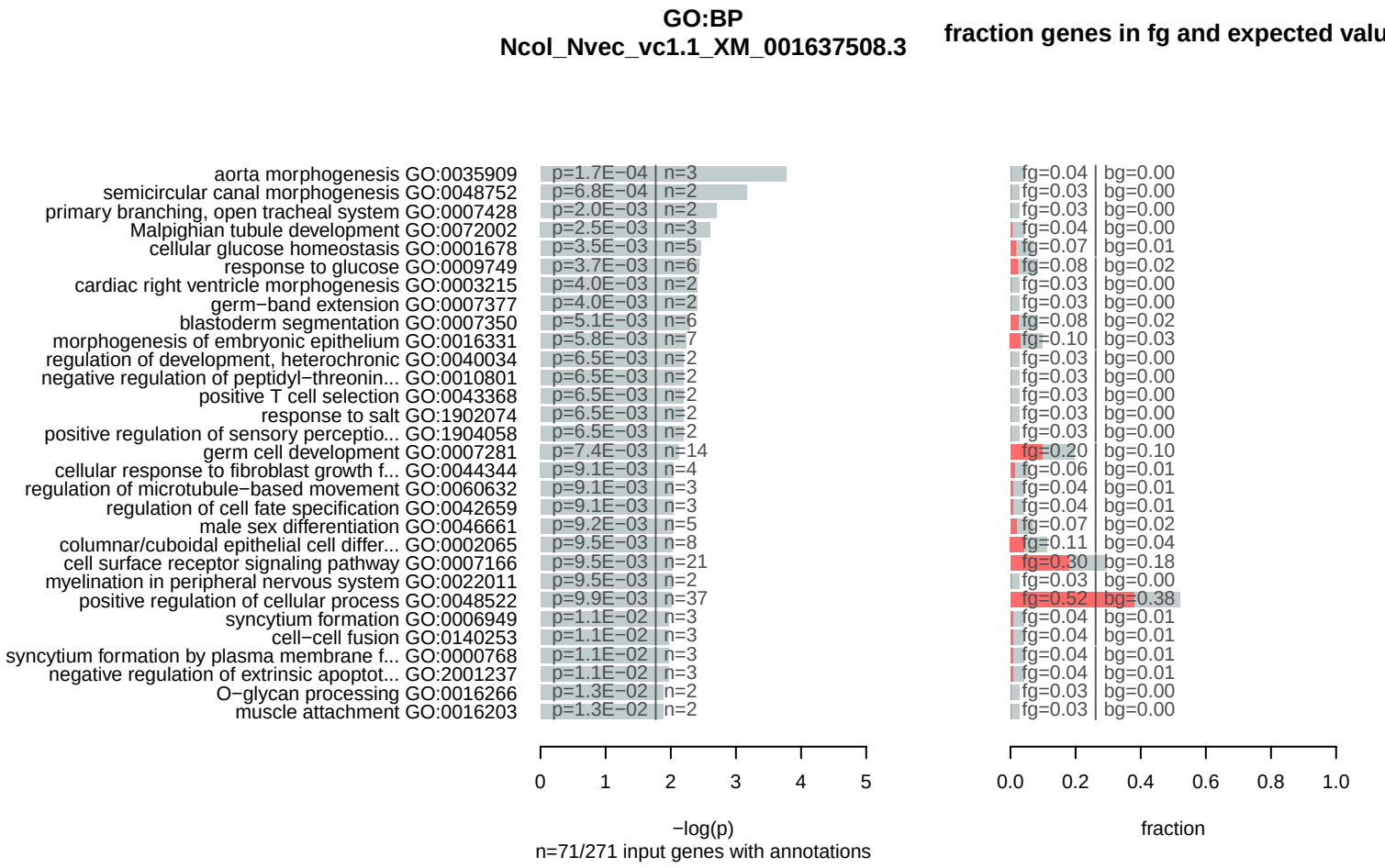
GO:BP
Ncol_Nvec_vc1.1_XM_001637508.3
fraction genes in fg and expected valu
aorta morphogenesis GO:0035909 p=1.7E−04 n=3 fg=0.04 bg=0.00
semicircular canal morphogenesis GO:0048752 p=6.8E−04 n=2 fg=0.03 bg=0.00
primary branching, open tracheal system GO:0007428 p=2.0E−03 n=2 fg=0.03 bg=0.00
Malpighian tubule development GO:0072002 p=2.5E−03 n=3 fg=0.04 bg=0.00
cellular glucose homeostasis GO:0001678 p=3.5E−03 n=5 fg=0.07 bg=0.01
response to glucose GO:0009749 p=3.7E−03 n=6 fg=0.08 bg=0.02
cardiac right ventricle morphogenesis GO:0003215 p=4.0E−03 n=2 fg=0.03 bg=0.00
germ−band extension GO:0007377 p=4.0E−03 n=2 fg=0.03 bg=0.00
blastoderm segmentation GO:0007350 p=5.1E−03 n=6 fg=0.08 bg=0.02
morphogenesis of embryonic epithelium GO:0016331 p=5.8E−03 n=7 fg=0.10 bg=0.03
regulation of development, heterochronic GO:0040034 p=6.5E−03 n=2 fg=0.03 bg=0.00
negative regulation of peptidyl−threonin... GO:0010801 p=6.5E−03 n=2 fg=0.03 bg=0.00
positive T cell selection GO:0043368 p=6.5E−03 n=2 fg=0.03 bg=0.00
response to salt GO:1902074 p=6.5E−03 n=2 fg=0.03 bg=0.00
positive regulation of sensory perceptio... GO:1904058 p=6.5E−03 n=2 fg=0.03 bg=0.00
germ cell development GO:0007281 p=7.4E−03 n=14 fg=0.20 bg=0.10
cellular response to fibroblast growth f... GO:0044344 p=9.1E−03 n=4 fg=0.06 bg=0.01
regulation of microtubule−based movement GO:0060632 p=9.1E−03 n=3 fg=0.04 bg=0.01
regulation of cell fate specification GO:0042659 p=9.1E−03 n=3 fg=0.04 bg=0.01
male sex differentiation GO:0046661 p=9.2E−03 n=5 fg=0.07 bg=0.02
columnar/cuboidal epithelial cell differ... GO:0002065 p=9.5E−03 n=8 fg=0.11 bg=0.04
cell surface receptor signaling pathway GO:0007166 p=9.5E−03 n=21 fg=0.30 bg=0.18
myelination in peripheral nervous system GO:0022011 p=9.5E−03 n=2 fg=0.03 bg=0.00
positive regulation of cellular process GO:0048522 p=9.9E−03 n=37 fg=0.52 bg=0.38
syncytium formation GO:0006949 p=1.1E−02 n=3 fg=0.04 bg=0.01
cell−cell fusion GO:0140253 p=1.1E−02 n=3 fg=0.04 bg=0.01
syncytium formation by plasma membrane f... GO:0000768 p=1.1E−02 n=3 fg=0.04 bg=0.01
negative regulation of extrinsic apoptot... GO:2001237 p=1.1E−02 n=3 fg=0.04 bg=0.01
O−glycan processing GO:0016266 p=1.3E−02 n=2 fg=0.03 bg=0.00
muscle attachment GO:0016203 p=1.3E−02 n=2 fg=0.03 bg=0.00
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−log(p)
n=71/271 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001637508.3
fraction genes in fg and expected valu
poly(A) binding GO:0008143 p=6.8E−03 n=2 fg=0.03 bg=0.00
histone binding GO:0042393 p=2.1E−02 n=4 fg=0.06 bg=0.02
poly(U) RNA binding GO:0008266 p=2.3E−02 n=2 fg=0.03 bg=0.00
inhibin binding GO:0034711 p=2.7E−02 n=1 fg=0.02 bg=0.00
T cell receptor binding GO:0042608 p=2.7E−02 n=1 fg=0.02 bg=0.00
adenylate cyclase activator activity GO:0010856 p=2.7E−02 n=1 fg=0.02 bg=0.00
rhodopsin kinase activity GO:0050254 p=2.7E−02 n=1 fg=0.02 bg=0.00
G protein−coupled receptor kinase activi... GO:0004703 p=2.7E−02 n=1 fg=0.02 bg=0.00
histone kinase activity (H3−T3 specific) GO:0072354 p=2.7E−02 n=1 fg=0.02 bg=0.00
glutamate−cysteine ligase catalytic subu... GO:0035226 p=2.7E−02 n=1 fg=0.02 bg=0.00
6−phosphogluconolactonase activity GO:0017057 p=2.7E−02 n=1 fg=0.02 bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946 p=2.7E−02 n=1 fg=0.02 bg=0.00
phorbol ester receptor activity GO:0001565 p=2.7E−02 n=1 fg=0.02 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=2.7E−02 n=1 fg=0.02 bg=0.00
beta−adrenergic receptor kinase activity GO:0047696 p=2.7E−02 n=1 fg=0.02 bg=0.00
delta−type opioid receptor binding GO:0031850 p=2.7E−02 n=1 fg=0.02 bg=0.00
kappa−type opioid receptor binding GO:0031851 p=2.7E−02 n=1 fg=0.02 bg=0.00
methionine−tRNA ligase activity GO:0004825 p=2.7E−02 n=1 fg=0.02 bg=0.00
endothelial differentiation G protein−co... GO:0031753 p=2.7E−02 n=1 fg=0.02 bg=0.00
Edg−2 lysophosphatidic acid receptor bin... GO:0031755 p=2.7E−02 n=1 fg=0.02 bg=0.00
beta−1,3−galactosyl−O−glycosyl−glycoprot... GO:0047223 p=2.7E−02 n=1 fg=0.02 bg=0.00
isocitrate dehydrogenase (NAD+) activity GO:0004449 p=2.7E−02 n=1 fg=0.02 bg=0.00
nucleosome binding GO:0031491 p=2.8E−02 n=2 fg=0.03 bg=0.00
poly−pyrimidine tract binding GO:0008187 p=2.8E−02 n=2 fg=0.03 bg=0.00
ribonuclease activity GO:0004540 p=3.5E−02 n=3 fg=0.05 bg=0.01
methylation−dependent protein binding GO:0140034 p=4.0E−02 n=2 fg=0.03 bg=0.01
methylated histone binding GO:0035064 p=4.0E−02 n=2 fg=0.03 bg=0.01
modification−dependent protein binding GO:0140030 p=4.2E−02 n=3 fg=0.05 bg=0.01
nuclear androgen receptor binding GO:0050681 p=4.6E−02 n=2 fg=0.03 bg=0.01
catalytic activity, acting on RNA GO:0140098 p=5.0E−02 n=6 fg=0.09 bg=0.04
0 1 2 3 4 5
−log(p)
n=64/271 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001637508.3
fraction genes in fg and expected valu
dendrite terminus GO:0044292 p=9.0E−03 n=2 fg=0.03 bg=0.00
peptidase complex GO:1905368 p=9.1E−03 n=4 fg=0.06 bg=0.01
apicolateral plasma membrane GO:0016327 p=1.2E−02 n=2 fg=0.03 bg=0.00
plasma membrane protein complex GO:0098797 p=1.3E−02 n=6 fg=0.09 bg=0.03
P−body GO:0000932 p=1.5E−02 n=3 fg=0.04 bg=0.01
potassium channel complex GO:0034705 p=2.5E−02 n=2 fg=0.03 bg=0.00
voltage−gated potassium channel complex GO:0008076 p=2.5E−02 n=2 fg=0.03 bg=0.00
internode region of axon GO:0033269 p=2.6E−02 n=1 fg=0.01 bg=0.00
isocitrate dehydrogenase complex (NAD+) GO:0045242 p=2.6E−02 n=1 fg=0.01 bg=0.00
inhibin−betaglycan−ActRII complex GO:0034673 p=2.6E−02 n=1 fg=0.01 bg=0.00
BAT3 complex GO:0071818 p=2.6E−02 n=1 fg=0.01 bg=0.00
ER membrane insertion complex GO:0072379 p=2.6E−02 n=1 fg=0.01 bg=0.00
mitochondrial isocitrate dehydrogenase c... GO:0005962 p=2.6E−02 n=1 fg=0.01 bg=0.00
Grb2−Sos complex GO:0070618 p=2.6E−02 n=1 fg=0.01 bg=0.00
Schmidt−Lanterman incisure GO:0043220 p=2.6E−02 n=1 fg=0.01 bg=0.00
FACT complex GO:0035101 p=2.6E−02 n=1 fg=0.01 bg=0.00
compact myelin GO:0043218 p=2.6E−02 n=1 fg=0.01 bg=0.00
anterior cell cortex GO:0061802 p=2.6E−02 n=1 fg=0.01 bg=0.00
kinesin complex GO:0005871 p=3.6E−02 n=2 fg=0.03 bg=0.00
histone deacetylase complex GO:0000118 p=4.2E−02 n=2 fg=0.03 bg=0.00
fibrillar center GO:0001650 p=5.1E−02 n=3 fg=0.04 bg=0.01
nuclear stress granule GO:0097165 p=5.1E−02 n=1 fg=0.01 bg=0.00
activin receptor complex GO:0048179 p=5.1E−02 n=1 fg=0.01 bg=0.00
signal peptidase complex GO:0005787 p=5.1E−02 n=1 fg=0.01 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000220 p=5.1E−02 n=1 fg=0.01 bg=0.00
exoribonuclease complex GO:1905354 p=5.1E−02 n=1 fg=0.01 bg=0.00
proton−transporting V−type ATPase, V0 do... GO:0033179 p=5.1E−02 n=1 fg=0.01 bg=0.00
exosome (RNase complex) GO:0000178 p=5.1E−02 n=1 fg=0.01 bg=0.00
t−UTP complex GO:0034455 p=5.1E−02 n=1 fg=0.01 bg=0.00
glutamate−cysteine ligase complex GO:0017109 p=5.1E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=69/271 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction