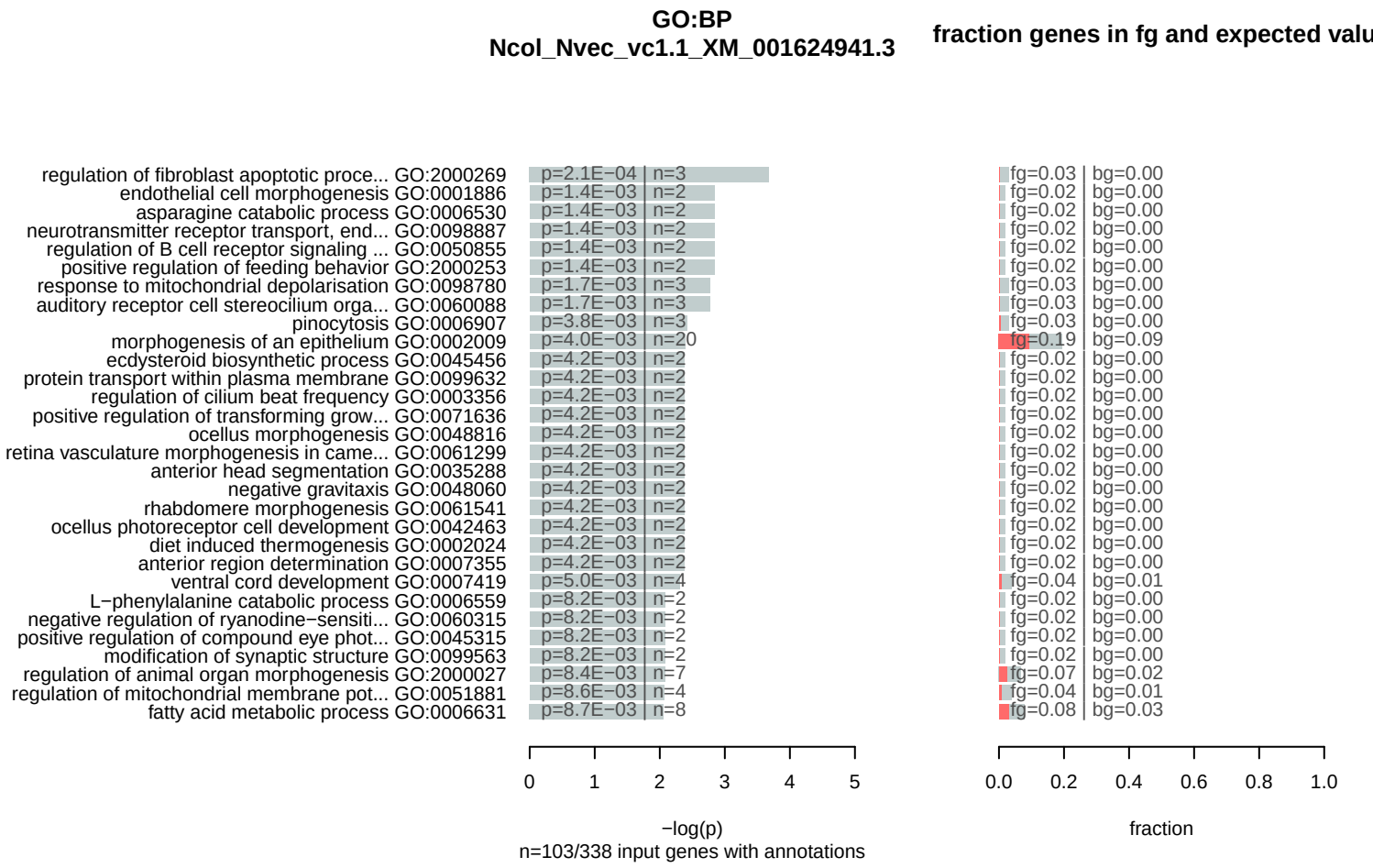
GO:BP
Ncol_Nvec_vc1.1_XM_001624941.3
fraction genes in fg and expected valu
regulation of fibroblast apoptotic proce... GO:2000269 p=2.1E−04 n=3 fg=0.03 bg=0.00
endothelial cell morphogenesis GO:0001886 p=1.4E−03 n=2 fg=0.02 bg=0.00
asparagine catabolic process GO:0006530 p=1.4E−03 n=2 fg=0.02 bg=0.00
neurotransmitter receptor transport, end... GO:0098887 p=1.4E−03 n=2 fg=0.02 bg=0.00
regulation of B cell receptor signaling ... GO:0050855 p=1.4E−03 n=2 fg=0.02 bg=0.00
positive regulation of feeding behavior GO:2000253 p=1.4E−03 n=2 fg=0.02 bg=0.00
response to mitochondrial depolarisation GO:0098780 p=1.7E−03 n=3 fg=0.03 bg=0.00
auditory receptor cell stereocilium orga... GO:0060088 p=1.7E−03 n=3 fg=0.03 bg=0.00
pinocytosis GO:0006907 p=3.8E−03 n=3 fg=0.03 bg=0.00
morphogenesis of an epithelium GO:0002009 p=4.0E−03 n=20 fg=0.19 bg=0.09
ecdysteroid biosynthetic process GO:0045456 p=4.2E−03 n=2 fg=0.02 bg=0.00
protein transport within plasma membrane GO:0099632 p=4.2E−03 n=2 fg=0.02 bg=0.00
regulation of cilium beat frequency GO:0003356 p=4.2E−03 n=2 fg=0.02 bg=0.00
positive regulation of transforming grow... GO:0071636 p=4.2E−03 n=2 fg=0.02 bg=0.00
ocellus morphogenesis GO:0048816 p=4.2E−03 n=2 fg=0.02 bg=0.00
retina vasculature morphogenesis in came... GO:0061299 p=4.2E−03 n=2 fg=0.02 bg=0.00
anterior head segmentation GO:0035288 p=4.2E−03 n=2 fg=0.02 bg=0.00
negative gravitaxis GO:0048060 p=4.2E−03 n=2 fg=0.02 bg=0.00
rhabdomere morphogenesis GO:0061541 p=4.2E−03 n=2 fg=0.02 bg=0.00
ocellus photoreceptor cell development GO:0042463 p=4.2E−03 n=2 fg=0.02 bg=0.00
diet induced thermogenesis GO:0002024 p=4.2E−03 n=2 fg=0.02 bg=0.00
anterior region determination GO:0007355 p=4.2E−03 n=2 fg=0.02 bg=0.00
ventral cord development GO:0007419 p=5.0E−03 n=4 fg=0.04 bg=0.01
L−phenylalanine catabolic process GO:0006559 p=8.2E−03 n=2 fg=0.02 bg=0.00
negative regulation of ryanodine−sensiti... GO:0060315 p=8.2E−03 n=2 fg=0.02 bg=0.00
positive regulation of compound eye phot... GO:0045315 p=8.2E−03 n=2 fg=0.02 bg=0.00
modification of synaptic structure GO:0099563 p=8.2E−03 n=2 fg=0.02 bg=0.00
regulation of animal organ morphogenesis GO:2000027 p=8.4E−03 n=7 fg=0.07 bg=0.02
regulation of mitochondrial membrane pot... GO:0051881 p=8.6E−03 n=4 fg=0.04 bg=0.01
fatty acid metabolic process GO:0006631 p=8.7E−03 n=8 fg=0.08 bg=0.03
0 1 2 3 4 5
−log(p)
n=103/338 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001624941.3
fraction genes in fg and expected valu
phospholipase A2 activity GO:0004623 p=1.0E−03 n=3 fg=0.03 bg=0.00
asparaginase activity GO:0004067 p=1.5E−03 n=2 fg=0.02 bg=0.00
D3 dopamine receptor binding GO:0031750 p=1.5E−03 n=2 fg=0.02 bg=0.00
D4 dopamine receptor binding GO:0031751 p=1.5E−03 n=2 fg=0.02 bg=0.00
D2 dopamine receptor binding GO:0031749 p=4.3E−03 n=2 fg=0.02 bg=0.00
dopamine receptor binding GO:0050780 p=8.0E−03 n=4 fg=0.04 bg=0.00
glutathione peroxidase activity GO:0004602 p=8.3E−03 n=2 fg=0.02 bg=0.00
GTPase regulator activity GO:0030695 p=1.0E−02 n=9 fg=0.10 bg=0.04
protein heterodimerization activity GO:0046982 p=1.3E−02 n=11 fg=0.12 bg=0.06
TFIID−class transcription factor complex... GO:0001094 p=1.3E−02 n=2 fg=0.02 bg=0.00
transcription coactivator binding GO:0001223 p=1.3E−02 n=2 fg=0.02 bg=0.00
GTPase activator activity GO:0005096 p=1.5E−02 n=6 fg=0.07 bg=0.02
exopeptidase activity GO:0008238 p=1.5E−02 n=3 fg=0.03 bg=0.01
DNA−binding transcription repressor acti... GO:0001227 p=1.8E−02 n=4 fg=0.04 bg=0.01
DNA−binding transcription repressor acti... GO:0001217 p=1.8E−02 n=4 fg=0.04 bg=0.01
RNA polymerase II general transcription ... GO:0001091 p=2.0E−02 n=2 fg=0.02 bg=0.00
intramolecular oxidoreductase activity, ... GO:0016864 p=2.0E−02 n=2 fg=0.02 bg=0.00
protein disulfide isomerase activity GO:0003756 p=2.0E−02 n=2 fg=0.02 bg=0.00
amino acid binding GO:0016597 p=2.1E−02 n=3 fg=0.03 bg=0.01
nucleoside−triphosphatase regulator acti... GO:0060589 p=2.3E−02 n=9 fg=0.10 bg=0.05
voltage−gated ion channel activity GO:0005244 p=2.3E−02 n=4 fg=0.04 bg=0.01
voltage−gated channel activity GO:0022832 p=2.3E−02 n=4 fg=0.04 bg=0.01
voltage−gated chloride channel activity GO:0005247 p=2.7E−02 n=2 fg=0.02 bg=0.00
voltage−gated anion channel activity GO:0008308 p=2.7E−02 n=2 fg=0.02 bg=0.00
lysophospholipase activity GO:0004622 p=2.7E−02 n=2 fg=0.02 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=3.8E−02 n=1 fg=0.01 bg=0.00
tRNA 2'−phosphotransferase activity GO:0000215 p=3.8E−02 n=1 fg=0.01 bg=0.00
purine−specific nucleoside:sodium sympor... GO:0015390 p=3.8E−02 n=1 fg=0.01 bg=0.00
nucleobase:cation symporter activity GO:0015391 p=3.8E−02 n=1 fg=0.01 bg=0.00
glutamate−ammonia ligase activity GO:0004356 p=3.8E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=91/338 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001624941.3
fraction genes in fg and expected valu
muscle cell projection membrane GO:0036195 p=5.4E−05 n=3 fg=0.03 bg=0.00
nuclear matrix GO:0016363 p=4.2E−03 n=5 fg=0.05 bg=0.01
striated muscle dense body GO:0055120 p=5.3E−03 n=3 fg=0.03 bg=0.00
nuclear body GO:0016604 p=8.4E−03 n=13 fg=0.13 bg=0.06
nuclear speck GO:0016607 p=1.3E−02 n=8 fg=0.08 bg=0.03
extrinsic component of membrane GO:0019898 p=2.9E−02 n=6 fg=0.06 bg=0.02
polar microtubule GO:0005827 p=3.8E−02 n=1 fg=0.01 bg=0.00
protein phosphatase 4 complex GO:0030289 p=3.8E−02 n=1 fg=0.01 bg=0.00
perichromatin fibrils GO:0005726 p=3.8E−02 n=1 fg=0.01 bg=0.00
ATF4−CREB1 transcription factor complex GO:1990589 p=3.8E−02 n=1 fg=0.01 bg=0.00
gamma−tubulin small complex GO:0008275 p=3.8E−02 n=1 fg=0.01 bg=0.00
core−binding factor complex GO:0016513 p=3.8E−02 n=1 fg=0.01 bg=0.00
equatorial microtubule organizing center GO:0000923 p=3.8E−02 n=1 fg=0.01 bg=0.00
macropinocytic cup GO:0070685 p=3.8E−02 n=1 fg=0.01 bg=0.00
tubular endosome GO:0097422 p=3.8E−02 n=1 fg=0.01 bg=0.00
postsynaptic endosome GO:0098845 p=3.8E−02 n=1 fg=0.01 bg=0.00
postsynaptic recycling endosome GO:0098837 p=3.8E−02 n=1 fg=0.01 bg=0.00
brush border GO:0005903 p=4.2E−02 n=4 fg=0.04 bg=0.01
mitochondrion GO:0005739 p=4.3E−02 n=21 fg=0.20 bg=0.14
Cul4−RING E3 ubiquitin ligase complex GO:0080008 p=5.3E−02 n=2 fg=0.02 bg=0.00
presynaptic active zone GO:0048786 p=5.5E−02 n=3 fg=0.03 bg=0.01
extracellular exosome GO:0070062 p=5.5E−02 n=3 fg=0.03 bg=0.01
apical junction complex GO:0043296 p=6.1E−02 n=3 fg=0.03 bg=0.01
extracellular vesicle GO:1903561 p=6.1E−02 n=3 fg=0.03 bg=0.01
extracellular membrane−bounded organelle GO:0065010 p=6.1E−02 n=3 fg=0.03 bg=0.01
extracellular organelle GO:0043230 p=6.1E−02 n=3 fg=0.03 bg=0.01
integral component of mitochondrial memb... GO:0032592 p=7.4E−02 n=2 fg=0.02 bg=0.00
intrinsic component of mitochondrial mem... GO:0098573 p=7.4E−02 n=2 fg=0.02 bg=0.00
molybdopterin synthase complex GO:0019008 p=7.5E−02 n=1 fg=0.01 bg=0.00
GATOR2 complex GO:0061700 p=7.5E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=103/338 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction