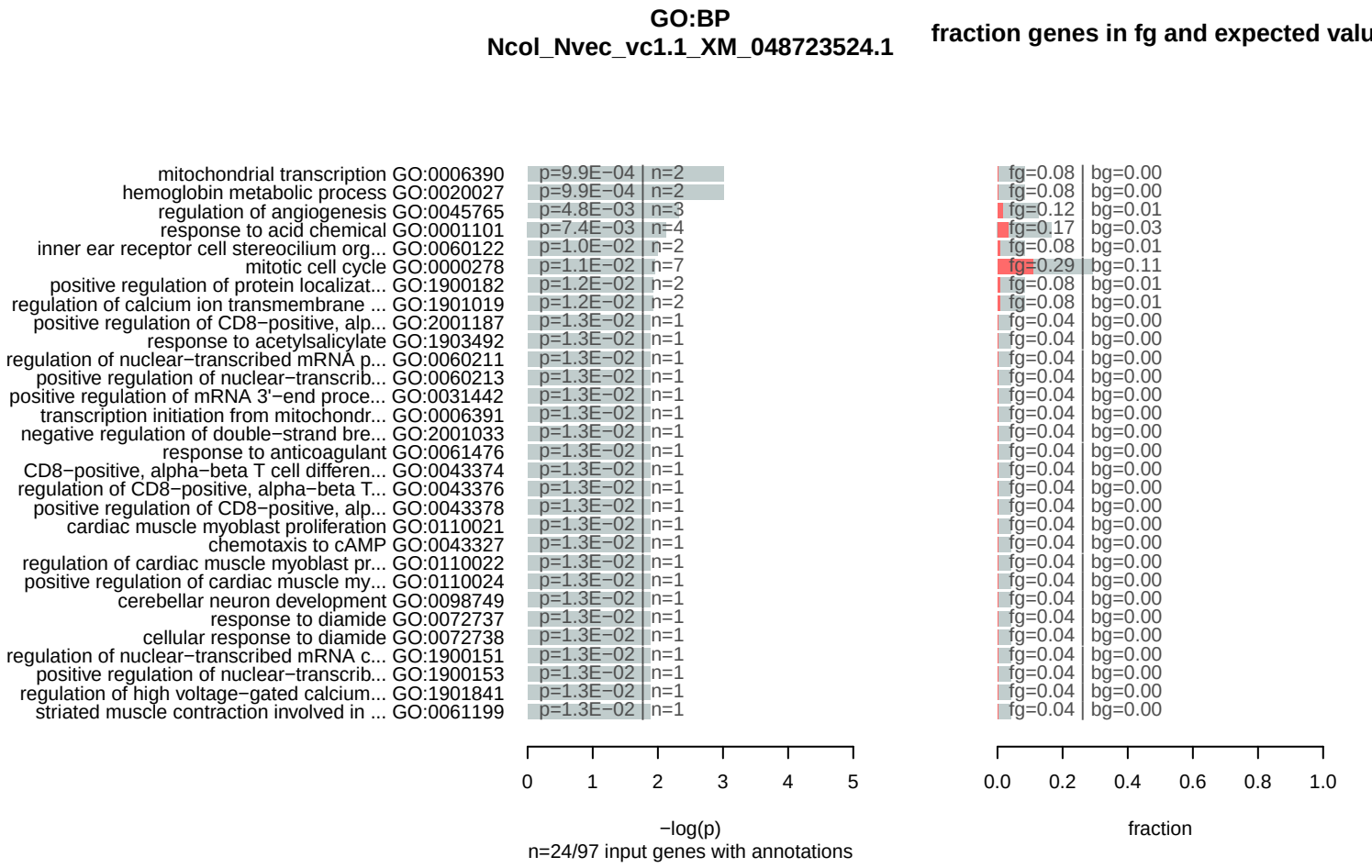
GO:BP
Ncol_Nvec_vc1.1_XM_048723524.1
fraction genes in fg and expected valu
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hemoglobin metabolic process GO:0020027 p=9.9E−04 n=2 fg=0.08 bg=0.00
regulation of angiogenesis GO:0045765 p=4.8E−03 n=3 fg=0.12 bg=0.01
response to acid chemical GO:0001101 p=7.4E−03 n=4 fg=0.17 bg=0.03
inner ear receptor cell stereocilium org... GO:0060122 p=1.0E−02 n=2 fg=0.08 bg=0.01
mitotic cell cycle GO:0000278 p=1.1E−02 n=7 fg=0.29 bg=0.11
positive regulation of protein localizat... GO:1900182 p=1.2E−02 n=2 fg=0.08 bg=0.01
regulation of calcium ion transmembrane ... GO:1901019 p=1.2E−02 n=2 fg=0.08 bg=0.01
positive regulation of CD8−positive, alp... GO:2001187 p=1.3E−02 n=1 fg=0.04 bg=0.00
response to acetylsalicylate GO:1903492 p=1.3E−02 n=1 fg=0.04 bg=0.00
regulation of nuclear−transcribed mRNA p... GO:0060211 p=1.3E−02 n=1 fg=0.04 bg=0.00
positive regulation of nuclear−transcrib... GO:0060213 p=1.3E−02 n=1 fg=0.04 bg=0.00
positive regulation of mRNA 3'−end proce... GO:0031442 p=1.3E−02 n=1 fg=0.04 bg=0.00
transcription initiation from mitochondr... GO:0006391 p=1.3E−02 n=1 fg=0.04 bg=0.00
negative regulation of double−strand bre... GO:2001033 p=1.3E−02 n=1 fg=0.04 bg=0.00
response to anticoagulant GO:0061476 p=1.3E−02 n=1 fg=0.04 bg=0.00
CD8−positive, alpha−beta T cell differen... GO:0043374 p=1.3E−02 n=1 fg=0.04 bg=0.00
regulation of CD8−positive, alpha−beta T... GO:0043376 p=1.3E−02 n=1 fg=0.04 bg=0.00
positive regulation of CD8−positive, alp... GO:0043378 p=1.3E−02 n=1 fg=0.04 bg=0.00
cardiac muscle myoblast proliferation GO:0110021 p=1.3E−02 n=1 fg=0.04 bg=0.00
chemotaxis to cAMP GO:0043327 p=1.3E−02 n=1 fg=0.04 bg=0.00
regulation of cardiac muscle myoblast pr... GO:0110022 p=1.3E−02 n=1 fg=0.04 bg=0.00
positive regulation of cardiac muscle my... GO:0110024 p=1.3E−02 n=1 fg=0.04 bg=0.00
cerebellar neuron development GO:0098749 p=1.3E−02 n=1 fg=0.04 bg=0.00
response to diamide GO:0072737 p=1.3E−02 n=1 fg=0.04 bg=0.00
cellular response to diamide GO:0072738 p=1.3E−02 n=1 fg=0.04 bg=0.00
regulation of nuclear−transcribed mRNA c... GO:1900151 p=1.3E−02 n=1 fg=0.04 bg=0.00
positive regulation of nuclear−transcrib... GO:1900153 p=1.3E−02 n=1 fg=0.04 bg=0.00
regulation of high voltage−gated calcium... GO:1901841 p=1.3E−02 n=1 fg=0.04 bg=0.00
striated muscle contraction involved in ... GO:0061199 p=1.3E−02 n=1 fg=0.04 bg=0.00
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−log(p)
n=24/97 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_048723524.1
fraction genes in fg and expected valu
UDP−glucosyltransferase activity GO:0035251 p=6.5E−04 n=2 fg=0.08 bg=0.00
protein kinase binding GO:0019901 p=7.0E−03 n=6 fg=0.25 bg=0.08
carbohydrate binding GO:0030246 p=1.3E−02 n=2 fg=0.08 bg=0.01
ferrochelatase activity GO:0004325 p=1.5E−02 n=1 fg=0.04 bg=0.00
translation elongation factor binding GO:0061770 p=1.5E−02 n=1 fg=0.04 bg=0.00
transmembrane receptor protein phosphata... GO:0019198 p=1.5E−02 n=1 fg=0.04 bg=0.00
iron−responsive element binding GO:0030350 p=1.5E−02 n=1 fg=0.04 bg=0.00
transmembrane receptor protein tyrosine ... GO:0005001 p=1.5E−02 n=1 fg=0.04 bg=0.00
dolichyl−phosphate beta−glucosyltransfer... GO:0004581 p=1.5E−02 n=1 fg=0.04 bg=0.00
protein phosphatase 5 binding GO:1990634 p=1.5E−02 n=1 fg=0.04 bg=0.00
glycogenin glucosyltransferase activity GO:0008466 p=1.5E−02 n=1 fg=0.04 bg=0.00
DNA−binding transcription factor binding GO:0140297 p=2.2E−02 n=3 fg=0.12 bg=0.03
protein dimerization activity GO:0046983 p=2.7E−02 n=7 fg=0.29 bg=0.13
STAT family protein binding GO:0097677 p=3.0E−02 n=1 fg=0.04 bg=0.00
cAMP response element binding protein bi... GO:0008140 p=3.0E−02 n=1 fg=0.04 bg=0.00
glutathione peroxidase activity GO:0004602 p=3.0E−02 n=1 fg=0.04 bg=0.00
D3 dopamine receptor binding GO:0031750 p=3.0E−02 n=1 fg=0.04 bg=0.00
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sequence−specific single stranded DNA bi... GO:0098847 p=3.0E−02 n=1 fg=0.04 bg=0.00
oligosaccharyl transferase activity GO:0004576 p=3.0E−02 n=1 fg=0.04 bg=0.00
high voltage−gated calcium channel activ... GO:0008331 p=3.0E−02 n=1 fg=0.04 bg=0.00
phosphoprotein binding GO:0051219 p=3.2E−02 n=2 fg=0.08 bg=0.01
identical protein binding GO:0042802 p=3.6E−02 n=8 fg=0.33 bg=0.17
cAMP response element binding GO:0035497 p=4.5E−02 n=1 fg=0.04 bg=0.00
DNA−directed 5'−3' RNA polymerase activi... GO:0003899 p=4.5E−02 n=1 fg=0.04 bg=0.00
beta−glucuronidase activity GO:0004566 p=4.5E−02 n=1 fg=0.04 bg=0.00
peroxidase activity GO:0004601 p=4.5E−02 n=1 fg=0.04 bg=0.00
RNA polymerase II intronic transcription... GO:0001162 p=4.5E−02 n=1 fg=0.04 bg=0.00
pyrimidine nucleotide transmembrane tran... GO:0015218 p=4.5E−02 n=1 fg=0.04 bg=0.00
mRNA regulatory element binding translat... GO:0000900 p=4.5E−02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=24/97 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_048723524.1
fraction genes in fg and expected valu
ficolin−1−rich granule GO:0101002 p=5.5E−03 n=3 fg=0.12 bg=0.01
spindle microtubule GO:0005876 p=7.7E−03 n=2 fg=0.08 bg=0.01
lysosome GO:0005764 p=8.6E−03 n=5 fg=0.20 bg=0.05
phagolysosome membrane GO:0061474 p=1.4E−02 n=1 fg=0.04 bg=0.00
mitochondrial DNA−directed RNA polymeras... GO:0034245 p=1.4E−02 n=1 fg=0.04 bg=0.00
phagolysosome GO:0032010 p=1.4E−02 n=1 fg=0.04 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=1.4E−02 n=1 fg=0.04 bg=0.00
core−binding factor complex GO:0016513 p=1.4E−02 n=1 fg=0.04 bg=0.00
septin collar GO:0032173 p=1.4E−02 n=1 fg=0.04 bg=0.00
alveolar lamellar body GO:0097208 p=1.4E−02 n=1 fg=0.04 bg=0.00
lysosomal lumen GO:0043202 p=2.5E−02 n=2 fg=0.08 bg=0.01
synaptic vesicle GO:0008021 p=2.7E−02 n=3 fg=0.12 bg=0.03
nuclear stress granule GO:0097165 p=2.8E−02 n=1 fg=0.04 bg=0.00
perinuclear region of cytoplasm GO:0048471 p=3.1E−02 n=5 fg=0.20 bg=0.07
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sarcolemma GO:0042383 p=3.3E−02 n=2 fg=0.08 bg=0.01
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midbody GO:0030496 p=3.9E−02 n=2 fg=0.08 bg=0.01
actin cytoskeleton GO:0015629 p=4.0E−02 n=3 fg=0.12 bg=0.03
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sperm annulus GO:0097227 p=4.1E−02 n=1 fg=0.04 bg=0.00
muscle cell projection GO:0036194 p=4.1E−02 n=1 fg=0.04 bg=0.00
muscle cell projection membrane GO:0036195 p=4.1E−02 n=1 fg=0.04 bg=0.00
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septin complex GO:0031105 p=4.1E−02 n=1 fg=0.04 bg=0.00
lamellar body GO:0042599 p=4.1E−02 n=1 fg=0.04 bg=0.00
cytolytic granule GO:0044194 p=4.1E−02 n=1 fg=0.04 bg=0.00
septin ring GO:0005940 p=4.1E−02 n=1 fg=0.04 bg=0.00
azurophil granule GO:0042582 p=4.2E−02 n=2 fg=0.08 bg=0.01
0 1 2 3 4 5
−log(p)
n=25/97 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction