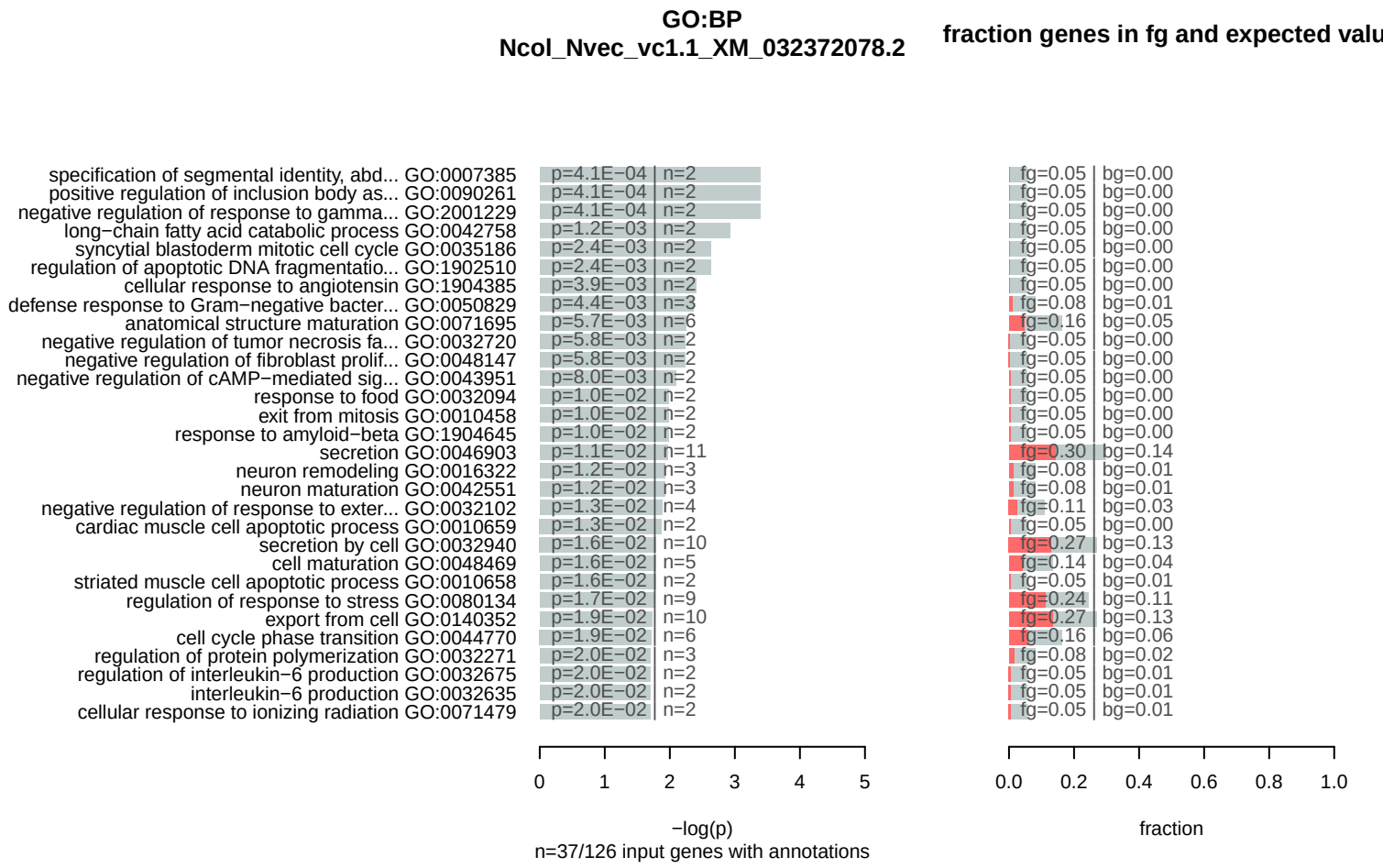
GO:BP
Ncol_Nvec_vc1.1_XM_032372078.2
fraction genes in fg and expected valu
specification of segmental identity, abd... GO:0007385 p=4.1E−04 n=2 fg=0.05 bg=0.00
positive regulation of inclusion body as... GO:0090261 p=4.1E−04 n=2 fg=0.05 bg=0.00
negative regulation of response to gamma... GO:2001229 p=4.1E−04 n=2 fg=0.05 bg=0.00
long−chain fatty acid catabolic process GO:0042758 p=1.2E−03 n=2 fg=0.05 bg=0.00
syncytial blastoderm mitotic cell cycle GO:0035186 p=2.4E−03 n=2 fg=0.05 bg=0.00
regulation of apoptotic DNA fragmentatio... GO:1902510 p=2.4E−03 n=2 fg=0.05 bg=0.00
cellular response to angiotensin GO:1904385 p=3.9E−03 n=2 fg=0.05 bg=0.00
defense response to Gram−negative bacter... GO:0050829 p=4.4E−03 n=3 fg=0.08 bg=0.01
anatomical structure maturation GO:0071695 p=5.7E−03 n=6 fg=0.16 bg=0.05
negative regulation of tumor necrosis fa... GO:0032720 p=5.8E−03 n=2 fg=0.05 bg=0.00
negative regulation of fibroblast prolif... GO:0048147 p=5.8E−03 n=2 fg=0.05 bg=0.00
negative regulation of cAMP−mediated sig... GO:0043951 p=8.0E−03 n=2 fg=0.05 bg=0.00
response to food GO:0032094 p=1.0E−02 n=2 fg=0.05 bg=0.00
exit from mitosis GO:0010458 p=1.0E−02 n=2 fg=0.05 bg=0.00
response to amyloid−beta GO:1904645 p=1.0E−02 n=2 fg=0.05 bg=0.00
secretion GO:0046903 p=1.1E−02 n=11 fg=0.30 bg=0.14
neuron remodeling GO:0016322 p=1.2E−02 n=3 fg=0.08 bg=0.01
neuron maturation GO:0042551 p=1.2E−02 n=3 fg=0.08 bg=0.01
negative regulation of response to exter... GO:0032102 p=1.3E−02 n=4 fg=0.11 bg=0.03
cardiac muscle cell apoptotic process GO:0010659 p=1.3E−02 n=2 fg=0.05 bg=0.00
secretion by cell GO:0032940 p=1.6E−02 n=10 fg=0.27 bg=0.13
cell maturation GO:0048469 p=1.6E−02 n=5 fg=0.14 bg=0.04
striated muscle cell apoptotic process GO:0010658 p=1.6E−02 n=2 fg=0.05 bg=0.01
regulation of response to stress GO:0080134 p=1.7E−02 n=9 fg=0.24 bg=0.11
export from cell GO:0140352 p=1.9E−02 n=10 fg=0.27 bg=0.13
cell cycle phase transition GO:0044770 p=1.9E−02 n=6 fg=0.16 bg=0.06
regulation of protein polymerization GO:0032271 p=2.0E−02 n=3 fg=0.08 bg=0.02
regulation of interleukin−6 production GO:0032675 p=2.0E−02 n=2 fg=0.05 bg=0.01
interleukin−6 production GO:0032635 p=2.0E−02 n=2 fg=0.05 bg=0.01
cellular response to ionizing radiation GO:0071479 p=2.0E−02 n=2 fg=0.05 bg=0.01
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n=37/126 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032372078.2
fraction genes in fg and expected valu
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actin filament binding GO:0051015 p=3.1E−03 n=3 fg=0.09 bg=0.01
phosphatidylcholine binding GO:0031210 p=8.2E−03 n=2 fg=0.06 bg=0.00
protein kinase binding GO:0019901 p=9.5E−03 n=7 fg=0.21 bg=0.08
methylated histone binding GO:0035064 p=1.1E−02 n=2 fg=0.06 bg=0.01
methylation−dependent protein binding GO:0140034 p=1.1E−02 n=2 fg=0.06 bg=0.01
rRNA binding GO:0019843 p=1.1E−02 n=2 fg=0.06 bg=0.01
5−oxoprolinase (ATP−hydrolyzing) activit... GO:0017168 p=2.1E−02 n=1 fg=0.03 bg=0.00
endoribonuclease activity, producing 3'−... GO:0016892 p=2.1E−02 n=1 fg=0.03 bg=0.00
dystroglycan binding GO:0002162 p=2.1E−02 n=1 fg=0.03 bg=0.00
endonuclease activity, active with eithe... GO:0016894 p=2.1E−02 n=1 fg=0.03 bg=0.00
translation elongation factor binding GO:0061770 p=2.1E−02 n=1 fg=0.03 bg=0.00
tRNA−intron endonuclease activity GO:0000213 p=2.1E−02 n=1 fg=0.03 bg=0.00
rRNA primary transcript binding GO:0042134 p=2.1E−02 n=1 fg=0.03 bg=0.00
uridine−diphosphatase activity GO:0045134 p=2.1E−02 n=1 fg=0.03 bg=0.00
hydrolase activity, acting on carbon−nit... GO:0016812 p=2.1E−02 n=1 fg=0.03 bg=0.00
TFIIF−class transcription factor complex... GO:0001096 p=2.1E−02 n=1 fg=0.03 bg=0.00
kinetochore binding GO:0043515 p=2.1E−02 n=1 fg=0.03 bg=0.00
protein serine/threonine phosphatase act... GO:0004722 p=3.7E−02 n=2 fg=0.06 bg=0.01
cytidylyltransferase activity GO:0070567 p=4.1E−02 n=1 fg=0.03 bg=0.00
choline−phosphate cytidylyltransferase a... GO:0004105 p=4.1E−02 n=1 fg=0.03 bg=0.00
Tat protein binding GO:0030957 p=4.1E−02 n=1 fg=0.03 bg=0.00
STAT family protein binding GO:0097677 p=4.1E−02 n=1 fg=0.03 bg=0.00
nucleoside−diphosphatase activity GO:0017110 p=4.1E−02 n=1 fg=0.03 bg=0.00
acetylcholine−gated cation−selective cha... GO:0022848 p=4.1E−02 n=1 fg=0.03 bg=0.00
ubiquitin−protein transferase activator ... GO:0097027 p=4.1E−02 n=1 fg=0.03 bg=0.00
acetylcholine receptor activity GO:0015464 p=4.1E−02 n=1 fg=0.03 bg=0.00
sequence−specific single stranded DNA bi... GO:0098847 p=4.1E−02 n=1 fg=0.03 bg=0.00
neurotransmitter receptor activity invol... GO:0099529 p=4.1E−02 n=1 fg=0.03 bg=0.00
acylglycerol lipase activity GO:0047372 p=4.1E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=33/126 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032372078.2
fraction genes in fg and expected valu
intercalary heterochromatin GO:0005725 p=1.1E−03 n=2 fg=0.06 bg=0.00
PRC1 complex GO:0035102 p=1.1E−03 n=2 fg=0.06 bg=0.00
spindle GO:0005819 p=3.1E−03 n=5 fg=0.14 bg=0.03
PML body GO:0016605 p=7.6E−03 n=2 fg=0.06 bg=0.00
euchromatin GO:0000791 p=1.0E−02 n=2 fg=0.06 bg=0.00
spindle pole GO:0000922 p=1.1E−02 n=3 fg=0.08 bg=0.01
centrosomal corona GO:0031592 p=2.0E−02 n=1 fg=0.03 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=2.0E−02 n=1 fg=0.03 bg=0.00
cortical microtubule cytoskeleton GO:0030981 p=2.0E−02 n=1 fg=0.03 bg=0.00
cytoplasmic microtubule plus−end GO:1904511 p=2.0E−02 n=1 fg=0.03 bg=0.00
intrinsic component of autophagosome mem... GO:0097636 p=2.0E−02 n=1 fg=0.03 bg=0.00
integral component of autophagosome memb... GO:0097637 p=2.0E−02 n=1 fg=0.03 bg=0.00
apoptosome GO:0043293 p=2.0E−02 n=1 fg=0.03 bg=0.00
lumenal side of Golgi membrane GO:0098547 p=2.0E−02 n=1 fg=0.03 bg=0.00
cortical microtubule GO:0055028 p=2.0E−02 n=1 fg=0.03 bg=0.00
tRNA−intron endonuclease complex GO:0000214 p=2.0E−02 n=1 fg=0.03 bg=0.00
nuclear outer membrane GO:0005640 p=2.0E−02 n=1 fg=0.03 bg=0.00
cortical microtubule plus−end GO:1903754 p=2.0E−02 n=1 fg=0.03 bg=0.00
endoplasmic reticulum lumen GO:0005788 p=2.0E−02 n=3 fg=0.08 bg=0.02
polytene chromosome GO:0005700 p=2.2E−02 n=3 fg=0.08 bg=0.02
smooth endoplasmic reticulum GO:0005790 p=2.2E−02 n=2 fg=0.06 bg=0.01
centrosome GO:0005813 p=3.3E−02 n=5 fg=0.14 bg=0.05
Golgi−associated vesicle GO:0005798 p=3.3E−02 n=3 fg=0.08 bg=0.02
kinetochore GO:0000776 p=3.9E−02 n=2 fg=0.06 bg=0.01
endoplasmic reticulum chaperone complex GO:0034663 p=3.9E−02 n=1 fg=0.03 bg=0.00
integral component of vacuolar membrane GO:0031166 p=3.9E−02 n=1 fg=0.03 bg=0.00
mitochondrial crista GO:0030061 p=3.9E−02 n=1 fg=0.03 bg=0.00
intrinsic component of vacuolar membrane GO:0031310 p=3.9E−02 n=1 fg=0.03 bg=0.00
extrinsic component of Golgi membrane GO:0090498 p=3.9E−02 n=1 fg=0.03 bg=0.00
COPI vesicle coat GO:0030126 p=3.9E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=36/126 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction