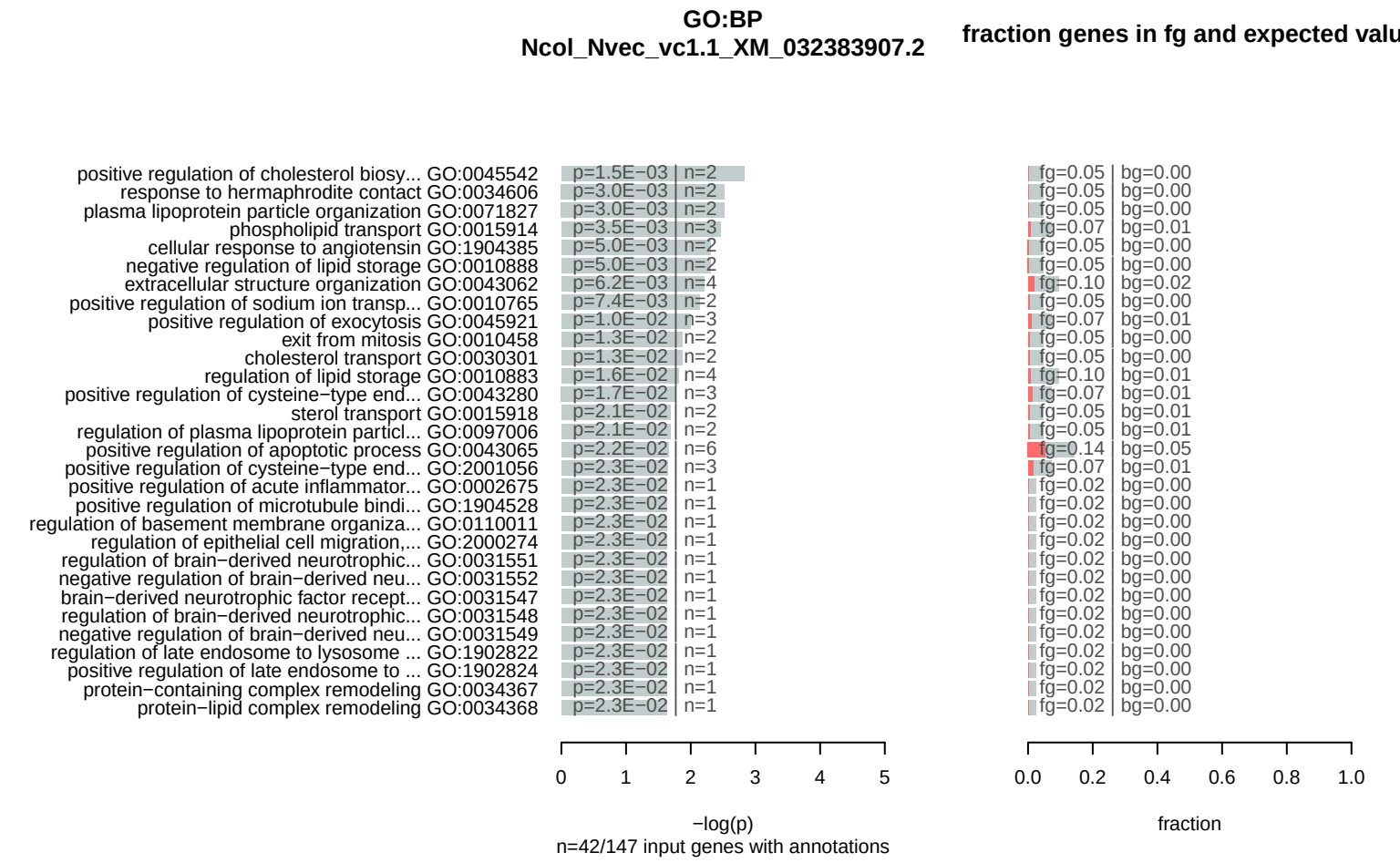
GO:BP
Ncol_Nvec_vc1.1_XM_032383907.2
fraction genes in fg and expected valu
positive regulation of cholesterol biosy... GO:0045542 p=1.5E−03 n=2 fg=0.05 bg=0.00
response to hermaphrodite contact GO:0034606 p=3.0E−03 n=2 fg=0.05 bg=0.00
plasma lipoprotein particle organization GO:0071827 p=3.0E−03 n=2 fg=0.05 bg=0.00
phospholipid transport GO:0015914 p=3.5E−03 n=3 fg=0.07 bg=0.01
cellular response to angiotensin GO:1904385 p=5.0E−03 n=2 fg=0.05 bg=0.00
negative regulation of lipid storage GO:0010888 p=5.0E−03 n=2 fg=0.05 bg=0.00
extracellular structure organization GO:0043062 p=6.2E−03 n=4 fg=0.10 bg=0.02
positive regulation of sodium ion transp... GO:0010765 p=7.4E−03 n=2 fg=0.05 bg=0.00
positive regulation of exocytosis GO:0045921 p=1.0E−02 n=3 fg=0.07 bg=0.01
exit from mitosis GO:0010458 p=1.3E−02 n=2 fg=0.05 bg=0.00
cholesterol transport GO:0030301 p=1.3E−02 n=2 fg=0.05 bg=0.00
regulation of lipid storage GO:0010883 p=1.6E−02 n=4 fg=0.10 bg=0.01
positive regulation of cysteine−type end... GO:0043280 p=1.7E−02 n=3 fg=0.07 bg=0.01
sterol transport GO:0015918 p=2.1E−02 n=2 fg=0.05 bg=0.01
regulation of plasma lipoprotein particl... GO:0097006 p=2.1E−02 n=2 fg=0.05 bg=0.01
positive regulation of apoptotic process GO:0043065 p=2.2E−02 n=6 fg=0.14 bg=0.05
positive regulation of cysteine−type end... GO:2001056 p=2.3E−02 n=3 fg=0.07 bg=0.01
positive regulation of acute inflammator... GO:0002675 p=2.3E−02 n=1 fg=0.02 bg=0.00
positive regulation of microtubule bindi... GO:1904528 p=2.3E−02 n=1 fg=0.02 bg=0.00
regulation of basement membrane organiza... GO:0110011 p=2.3E−02 n=1 fg=0.02 bg=0.00
regulation of epithelial cell migration,... GO:2000274 p=2.3E−02 n=1 fg=0.02 bg=0.00
regulation of brain−derived neurotrophic... GO:0031551 p=2.3E−02 n=1 fg=0.02 bg=0.00
negative regulation of brain−derived neu... GO:0031552 p=2.3E−02 n=1 fg=0.02 bg=0.00
brain−derived neurotrophic factor recept... GO:0031547 p=2.3E−02 n=1 fg=0.02 bg=0.00
regulation of brain−derived neurotrophic... GO:0031548 p=2.3E−02 n=1 fg=0.02 bg=0.00
negative regulation of brain−derived neu... GO:0031549 p=2.3E−02 n=1 fg=0.02 bg=0.00
regulation of late endosome to lysosome ... GO:1902822 p=2.3E−02 n=1 fg=0.02 bg=0.00
positive regulation of late endosome to ... GO:1902824 p=2.3E−02 n=1 fg=0.02 bg=0.00
protein−containing complex remodeling GO:0034367 p=2.3E−02 n=1 fg=0.02 bg=0.00
protein−lipid complex remodeling GO:0034368 p=2.3E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=42/147 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032383907.2
fraction genes in fg and expected valu
phospholipid transporter activity GO:0005548 p=2.8E−03 n=3 fg=0.08 bg=0.01
protein disulfide isomerase activity GO:0003756 p=5.0E−03 n=2 fg=0.05 bg=0.00
cholesterol binding GO:0015485 p=7.4E−03 n=2 fg=0.05 bg=0.00
RNA polymerase II−specific DNA−binding t... GO:0061629 p=1.0E−02 n=4 fg=0.11 bg=0.02
DNA−binding transcription factor binding GO:0140297 p=1.3E−02 n=4 fg=0.11 bg=0.03
phospholipid binding GO:0005543 p=1.6E−02 n=5 fg=0.14 bg=0.04
protein heterodimerization activity GO:0046982 p=1.7E−02 n=6 fg=0.16 bg=0.06
dystroglycan binding GO:0002162 p=2.3E−02 n=1 fg=0.03 bg=0.00
steroid dehydrogenase activity GO:0016229 p=2.3E−02 n=1 fg=0.03 bg=0.00
TFIIF−class transcription factor complex... GO:0001096 p=2.3E−02 n=1 fg=0.03 bg=0.00
translation elongation factor binding GO:0061770 p=2.3E−02 n=1 fg=0.03 bg=0.00
N−acylneuraminate−9−phosphatase activity GO:0050124 p=2.3E−02 n=1 fg=0.03 bg=0.00
lysine N−acetyltransferase activity, act... GO:0004468 p=2.3E−02 n=1 fg=0.03 bg=0.00
kinetochore binding GO:0043515 p=2.3E−02 n=1 fg=0.03 bg=0.00
steroid dehydrogenase activity, acting o... GO:0033764 p=2.3E−02 n=1 fg=0.03 bg=0.00
glycerophosphoinositol glycerophosphodie... GO:0047395 p=2.3E−02 n=1 fg=0.03 bg=0.00
phospholipase D activator activity GO:1990583 p=2.3E−02 n=1 fg=0.03 bg=0.00
ABC−type sterol transporter activity GO:0034041 p=2.3E−02 n=1 fg=0.03 bg=0.00
estradiol 17−beta−dehydrogenase activity GO:0004303 p=2.3E−02 n=1 fg=0.03 bg=0.00
testosterone 17−beta−dehydrogenase (NADP... GO:0047045 p=2.3E−02 n=1 fg=0.03 bg=0.00
glycerophosphodiester phosphodiesterase ... GO:0008889 p=2.3E−02 n=1 fg=0.03 bg=0.00
RNA polymerase II transcription regulato... GO:0000977 p=3.3E−02 n=5 fg=0.14 bg=0.05
identical protein binding GO:0042802 p=3.5E−02 n=11 fg=0.30 bg=0.17
cis−regulatory region sequence−specific ... GO:0000987 p=4.1E−02 n=4 fg=0.11 bg=0.04
RNA polymerase II cis−regulatory region ... GO:0000978 p=4.1E−02 n=4 fg=0.11 bg=0.04
BH3 domain binding GO:0051434 p=4.6E−02 n=1 fg=0.03 bg=0.00
Tat protein binding GO:0030957 p=4.6E−02 n=1 fg=0.03 bg=0.00
nuclear retinoid X receptor binding GO:0046965 p=4.6E−02 n=1 fg=0.03 bg=0.00
STAT family protein binding GO:0097677 p=4.6E−02 n=1 fg=0.03 bg=0.00
toxin transmembrane transporter activity GO:0019534 p=4.6E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=37/147 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032383907.2
fraction genes in fg and expected valu
centrosomal corona GO:0031592 p=2.4E−02 n=1 fg=0.02 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=2.4E−02 n=1 fg=0.02 bg=0.00
cortical microtubule cytoskeleton GO:0030981 p=2.4E−02 n=1 fg=0.02 bg=0.00
MutLalpha complex GO:0032389 p=2.4E−02 n=1 fg=0.02 bg=0.00
neuronal ribonucleoprotein granule GO:0071598 p=2.4E−02 n=1 fg=0.02 bg=0.00
cytoplasmic microtubule plus−end GO:1904511 p=2.4E−02 n=1 fg=0.02 bg=0.00
protein kinase CK2 complex GO:0005956 p=2.4E−02 n=1 fg=0.02 bg=0.00
cortical microtubule GO:0055028 p=2.4E−02 n=1 fg=0.02 bg=0.00
ESCRT−0 complex GO:0033565 p=2.4E−02 n=1 fg=0.02 bg=0.00
cortical microtubule plus−end GO:1903754 p=2.4E−02 n=1 fg=0.02 bg=0.00
chromosome, centromeric region GO:0000775 p=2.7E−02 n=3 fg=0.07 bg=0.02
myosin V complex GO:0031475 p=4.7E−02 n=1 fg=0.02 bg=0.00
muscle myosin complex GO:0005859 p=4.7E−02 n=1 fg=0.02 bg=0.00
Seh1−associated complex GO:0035859 p=4.7E−02 n=1 fg=0.02 bg=0.00
myosin II complex GO:0016460 p=4.7E−02 n=1 fg=0.02 bg=0.00
mismatch repair complex GO:0032300 p=4.7E−02 n=1 fg=0.02 bg=0.00
COPI vesicle coat GO:0030126 p=4.7E−02 n=1 fg=0.02 bg=0.00
nuclear stress granule GO:0097165 p=4.7E−02 n=1 fg=0.02 bg=0.00
GATOR2 complex GO:0061700 p=4.7E−02 n=1 fg=0.02 bg=0.00
U2AF complex GO:0089701 p=4.7E−02 n=1 fg=0.02 bg=0.00
COPI−coated vesicle membrane GO:0030663 p=4.7E−02 n=1 fg=0.02 bg=0.00
kinetochore GO:0000776 p=5.4E−02 n=2 fg=0.05 bg=0.01
heterochromatin GO:0000792 p=6.0E−02 n=2 fg=0.05 bg=0.01
myosin VI complex GO:0031476 p=7.0E−02 n=1 fg=0.02 bg=0.00
myosin VII complex GO:0031477 p=7.0E−02 n=1 fg=0.02 bg=0.00
microtubule plus−end GO:0035371 p=7.0E−02 n=1 fg=0.02 bg=0.00
Bcl−2 family protein complex GO:0097136 p=7.0E−02 n=1 fg=0.02 bg=0.00
kinetochore microtubule GO:0005828 p=7.0E−02 n=1 fg=0.02 bg=0.00
U2−type prespliceosome GO:0071004 p=7.0E−02 n=1 fg=0.02 bg=0.00
commitment complex GO:0000243 p=7.0E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=43/147 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction