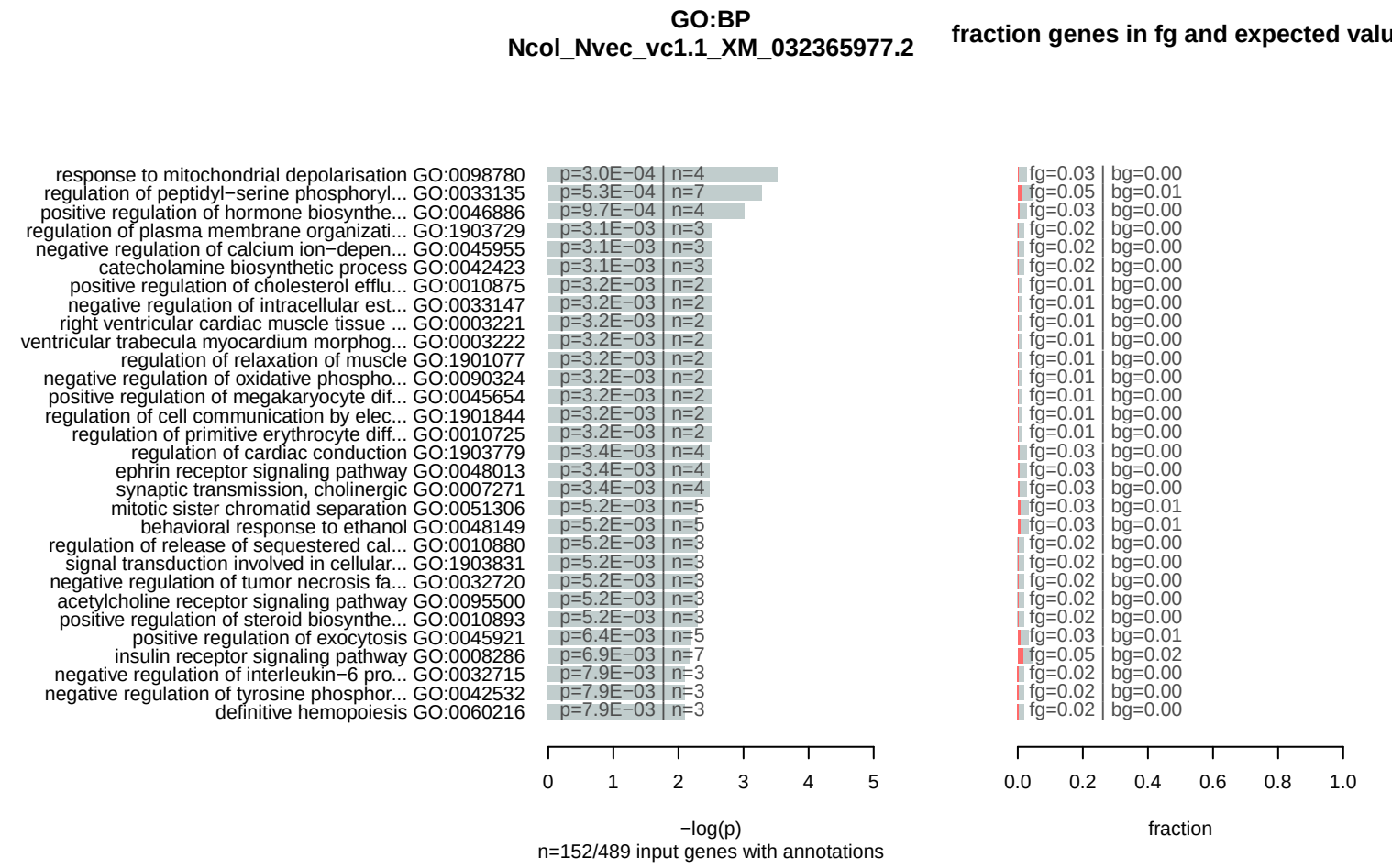
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fraction genes in fg and expected valu
response to mitochondrial depolarisation GO:0098780 p=3.0E−04 n=4 fg=0.03 bg=0.00
regulation of peptidyl−serine phosphoryl... GO:0033135 p=5.3E−04 n=7 fg=0.05 bg=0.01
positive regulation of hormone biosynthe... GO:0046886 p=9.7E−04 n=4 fg=0.03 bg=0.00
regulation of plasma membrane organizati... GO:1903729 p=3.1E−03 n=3 fg=0.02 bg=0.00
negative regulation of calcium ion−depen... GO:0045955 p=3.1E−03 n=3 fg=0.02 bg=0.00
catecholamine biosynthetic process GO:0042423 p=3.1E−03 n=3 fg=0.02 bg=0.00
positive regulation of cholesterol efflu... GO:0010875 p=3.2E−03 n=2 fg=0.01 bg=0.00
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right ventricular cardiac muscle tissue ... GO:0003221 p=3.2E−03 n=2 fg=0.01 bg=0.00
ventricular trabecula myocardium morphog... GO:0003222 p=3.2E−03 n=2 fg=0.01 bg=0.00
regulation of relaxation of muscle GO:1901077 p=3.2E−03 n=2 fg=0.01 bg=0.00
negative regulation of oxidative phospho... GO:0090324 p=3.2E−03 n=2 fg=0.01 bg=0.00
positive regulation of megakaryocyte dif... GO:0045654 p=3.2E−03 n=2 fg=0.01 bg=0.00
regulation of cell communication by elec... GO:1901844 p=3.2E−03 n=2 fg=0.01 bg=0.00
regulation of primitive erythrocyte diff... GO:0010725 p=3.2E−03 n=2 fg=0.01 bg=0.00
regulation of cardiac conduction GO:1903779 p=3.4E−03 n=4 fg=0.03 bg=0.00
ephrin receptor signaling pathway GO:0048013 p=3.4E−03 n=4 fg=0.03 bg=0.00
synaptic transmission, cholinergic GO:0007271 p=3.4E−03 n=4 fg=0.03 bg=0.00
mitotic sister chromatid separation GO:0051306 p=5.2E−03 n=5 fg=0.03 bg=0.01
behavioral response to ethanol GO:0048149 p=5.2E−03 n=5 fg=0.03 bg=0.01
regulation of release of sequestered cal... GO:0010880 p=5.2E−03 n=3 fg=0.02 bg=0.00
signal transduction involved in cellular... GO:1903831 p=5.2E−03 n=3 fg=0.02 bg=0.00
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acetylcholine receptor signaling pathway GO:0095500 p=5.2E−03 n=3 fg=0.02 bg=0.00
positive regulation of steroid biosynthe... GO:0010893 p=5.2E−03 n=3 fg=0.02 bg=0.00
positive regulation of exocytosis GO:0045921 p=6.4E−03 n=5 fg=0.03 bg=0.01
insulin receptor signaling pathway GO:0008286 p=6.9E−03 n=7 fg=0.05 bg=0.02
negative regulation of interleukin−6 pro... GO:0032715 p=7.9E−03 n=3 fg=0.02 bg=0.00
negative regulation of tyrosine phosphor... GO:0042532 p=7.9E−03 n=3 fg=0.02 bg=0.00
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n=152/489 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032365977.2
fraction genes in fg and expected valu
cysteine−type endopeptidase activity GO:0004197 p=7.4E−04 n=5 fg=0.04 bg=0.01
calcium−dependent phospholipid binding GO:0005544 p=1.7E−03 n=3 fg=0.02 bg=0.00
armadillo repeat domain binding GO:0070016 p=3.2E−03 n=2 fg=0.01 bg=0.00
ammonium ion binding GO:0070405 p=4.8E−03 n=4 fg=0.03 bg=0.01
phosphatidylinositol binding GO:0035091 p=9.1E−03 n=9 fg=0.07 bg=0.03
ATPase−coupled transmembrane transporter... GO:0042626 p=9.3E−03 n=7 fg=0.05 bg=0.01
acetylcholine−gated cation−selective cha... GO:0022848 p=9.3E−03 n=2 fg=0.01 bg=0.00
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S100 protein binding GO:0044548 p=9.3E−03 n=2 fg=0.01 bg=0.00
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acetylcholine receptor activity GO:0015464 p=9.3E−03 n=2 fg=0.01 bg=0.00
hydrolase activity GO:0016787 p=9.5E−03 n=42 fg=0.31 bg=0.19
translation initiation factor activity GO:0003743 p=1.1E−02 n=4 fg=0.03 bg=0.01
ATPase−coupled ion transmembrane transpo... GO:0042625 p=1.1E−02 n=4 fg=0.03 bg=0.01
exoribonuclease activity, producing 5'−p... GO:0016896 p=1.2E−02 n=3 fg=0.02 bg=0.00
3'−5'−exoribonuclease activity GO:0000175 p=1.2E−02 n=3 fg=0.02 bg=0.00
P−type ion transporter activity GO:0015662 p=1.6E−02 n=3 fg=0.02 bg=0.00
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phosphatidylinositol−3,4,5−trisphosphate... GO:0005547 p=1.7E−02 n=4 fg=0.03 bg=0.01
transmembrane transporter binding GO:0044325 p=1.7E−02 n=4 fg=0.03 bg=0.01
calcium−dependent cysteine−type endopept... GO:0004198 p=1.8E−02 n=2 fg=0.01 bg=0.00
phosphatidylinositol phosphate 4−phospha... GO:0034596 p=1.8E−02 n=2 fg=0.01 bg=0.00
phosphatidylethanolamine binding GO:0008429 p=1.8E−02 n=2 fg=0.01 bg=0.00
translation factor activity, RNA binding GO:0008135 p=1.9E−02 n=5 fg=0.04 bg=0.01
ATP hydrolysis activity GO:0016887 p=1.9E−02 n=12 fg=0.09 bg=0.05
active ion transmembrane transporter act... GO:0022853 p=2.1E−02 n=7 fg=0.05 bg=0.02
0 1 2 3 4 5
−log(p)
n=135/489 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032365977.2
fraction genes in fg and expected valu
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CA3 pyramidal cell dendrite GO:0097442 p=3.2E−03 n=2 fg=0.01 bg=0.00
dendrite GO:0030425 p=8.2E−03 n=19 fg=0.12 bg=0.06
presynapse GO:0098793 p=8.4E−03 n=14 fg=0.09 bg=0.05
exocytic vesicle GO:0070382 p=8.4E−03 n=9 fg=0.06 bg=0.02
acetylcholine−gated channel complex GO:0005892 p=9.3E−03 n=2 fg=0.01 bg=0.00
fusome GO:0045169 p=1.2E−02 n=3 fg=0.02 bg=0.00
sarcoplasmic reticulum GO:0016529 p=1.6E−02 n=3 fg=0.02 bg=0.00
sarcoplasm GO:0016528 p=2.1E−02 n=3 fg=0.02 bg=0.00
intrinsic component of plasma membrane GO:0031226 p=2.6E−02 n=19 fg=0.12 bg=0.07
extrinsic component of cytoplasmic side ... GO:0031234 p=2.9E−02 n=4 fg=0.03 bg=0.01
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telomerase holoenzyme complex GO:0005697 p=2.9E−02 n=2 fg=0.01 bg=0.00
eukaryotic translation initiation factor... GO:0005851 p=2.9E−02 n=2 fg=0.01 bg=0.00
intercellular canaliculus GO:0046581 p=2.9E−02 n=2 fg=0.01 bg=0.00
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presynaptic membrane GO:0042734 p=3.7E−02 n=5 fg=0.03 bg=0.01
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organelle membrane contact site GO:0044232 p=4.2E−02 n=2 fg=0.01 bg=0.00
sarcoplasmic reticulum membrane GO:0033017 p=4.2E−02 n=2 fg=0.01 bg=0.00
integral component of plasma membrane GO:0005887 p=5.2E−02 n=17 fg=0.11 bg=0.06
axolemma GO:0030673 p=5.6E−02 n=2 fg=0.01 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0016471 p=5.6E−02 n=2 fg=0.01 bg=0.00
nuclear pore cytoplasmic filaments GO:0044614 p=5.7E−02 n=1 fg=0.01 bg=0.00
cytoplasmic periphery of the nuclear por... GO:1990723 p=5.7E−02 n=1 fg=0.01 bg=0.00
microvesicle GO:1990742 p=5.7E−02 n=1 fg=0.01 bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061200 p=5.7E−02 n=1 fg=0.01 bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061202 p=5.7E−02 n=1 fg=0.01 bg=0.00
ribbon synapse GO:0097470 p=5.7E−02 n=1 fg=0.01 bg=0.00
interleukin−5 receptor complex GO:0005895 p=5.7E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=154/489 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction