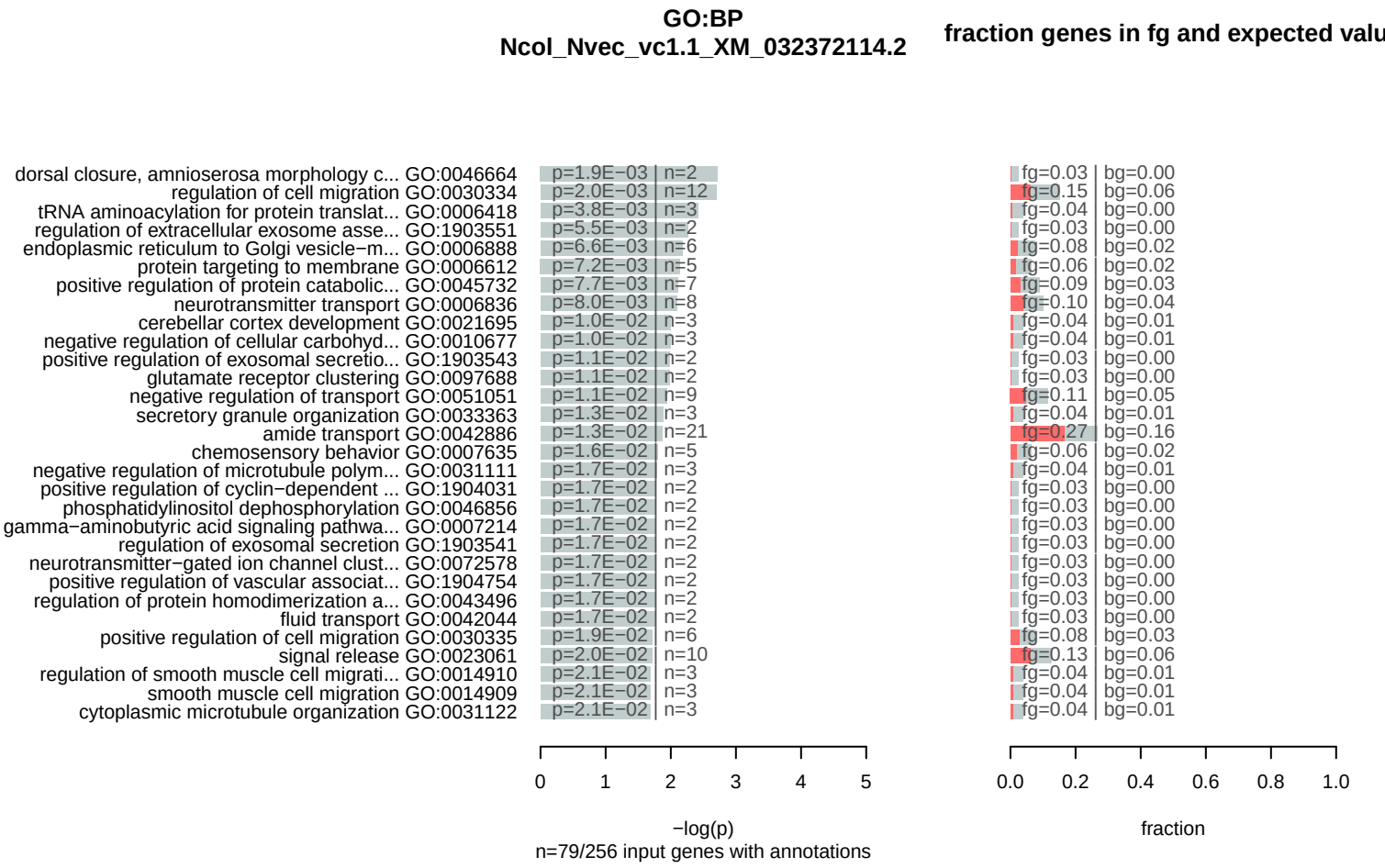
GO:BP
Ncol_Nvec_vc1.1_XM_032372114.2
fraction genes in fg and expected valu
dorsal closure, amnioserosa morphology c... GO:0046664 p=1.9E−03 n=2 fg=0.03 bg=0.00
regulation of cell migration GO:0030334 p=2.0E−03 n=12 fg=0.15 bg=0.06
tRNA aminoacylation for protein translat... GO:0006418 p=3.8E−03 n=3 fg=0.04 bg=0.00
regulation of extracellular exosome asse... GO:1903551 p=5.5E−03 n=2 fg=0.03 bg=0.00
endoplasmic reticulum to Golgi vesicle−m... GO:0006888 p=6.6E−03 n=6 fg=0.08 bg=0.02
protein targeting to membrane GO:0006612 p=7.2E−03 n=5 fg=0.06 bg=0.02
positive regulation of protein catabolic... GO:0045732 p=7.7E−03 n=7 fg=0.09 bg=0.03
neurotransmitter transport GO:0006836 p=8.0E−03 n=8 fg=0.10 bg=0.04
cerebellar cortex development GO:0021695 p=1.0E−02 n=3 fg=0.04 bg=0.01
negative regulation of cellular carbohyd... GO:0010677 p=1.0E−02 n=3 fg=0.04 bg=0.01
positive regulation of exosomal secretio... GO:1903543 p=1.1E−02 n=2 fg=0.03 bg=0.00
glutamate receptor clustering GO:0097688 p=1.1E−02 n=2 fg=0.03 bg=0.00
negative regulation of transport GO:0051051 p=1.1E−02 n=9 fg=0.11 bg=0.05
secretory granule organization GO:0033363 p=1.3E−02 n=3 fg=0.04 bg=0.01
amide transport GO:0042886 p=1.3E−02 n=21 fg=0.27 bg=0.16
chemosensory behavior GO:0007635 p=1.6E−02 n=5 fg=0.06 bg=0.02
negative regulation of microtubule polym... GO:0031111 p=1.7E−02 n=3 fg=0.04 bg=0.01
positive regulation of cyclin−dependent ... GO:1904031 p=1.7E−02 n=2 fg=0.03 bg=0.00
phosphatidylinositol dephosphorylation GO:0046856 p=1.7E−02 n=2 fg=0.03 bg=0.00
gamma−aminobutyric acid signaling pathwa... GO:0007214 p=1.7E−02 n=2 fg=0.03 bg=0.00
regulation of exosomal secretion GO:1903541 p=1.7E−02 n=2 fg=0.03 bg=0.00
neurotransmitter−gated ion channel clust... GO:0072578 p=1.7E−02 n=2 fg=0.03 bg=0.00
positive regulation of vascular associat... GO:1904754 p=1.7E−02 n=2 fg=0.03 bg=0.00
regulation of protein homodimerization a... GO:0043496 p=1.7E−02 n=2 fg=0.03 bg=0.00
fluid transport GO:0042044 p=1.7E−02 n=2 fg=0.03 bg=0.00
positive regulation of cell migration GO:0030335 p=1.9E−02 n=6 fg=0.08 bg=0.03
signal release GO:0023061 p=2.0E−02 n=10 fg=0.13 bg=0.06
regulation of smooth muscle cell migrati... GO:0014910 p=2.1E−02 n=3 fg=0.04 bg=0.01
smooth muscle cell migration GO:0014909 p=2.1E−02 n=3 fg=0.04 bg=0.01
cytoplasmic microtubule organization GO:0031122 p=2.1E−02 n=3 fg=0.04 bg=0.01
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fraction
GO:MF
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fraction genes in fg and expected valu
aminoacyl−tRNA ligase activity GO:0004812 p=4.1E−03 n=3 fg=0.04 bg=0.01
amide transmembrane transporter activity GO:0042887 p=5.9E−03 n=3 fg=0.04 bg=0.01
ubiquitin−like protein binding GO:0032182 p=1.1E−02 n=3 fg=0.04 bg=0.01
phosphatidylinositol bisphosphate phosph... GO:0034593 p=1.1E−02 n=2 fg=0.03 bg=0.00
microtubule plus−end binding GO:0051010 p=1.1E−02 n=2 fg=0.03 bg=0.00
molecular adaptor activity GO:0060090 p=1.9E−02 n=6 fg=0.08 bg=0.03
protein−macromolecule adaptor activity GO:0030674 p=1.9E−02 n=6 fg=0.08 bg=0.03
kinesin binding GO:0019894 p=2.2E−02 n=3 fg=0.04 bg=0.01
structural constituent of cytoskeleton GO:0005200 p=2.6E−02 n=2 fg=0.03 bg=0.00
phosphatidylinositol phosphate phosphata... GO:0052866 p=2.6E−02 n=2 fg=0.03 bg=0.00
ion transmembrane transporter activity GO:0015075 p=2.9E−02 n=10 fg=0.14 bg=0.07
peptide transmembrane transporter activi... GO:1904680 p=3.6E−02 n=2 fg=0.03 bg=0.00
carboxylic ester hydrolase activity GO:0052689 p=3.7E−02 n=3 fg=0.04 bg=0.01
cation transmembrane transporter activit... GO:0008324 p=3.8E−02 n=8 fg=0.11 bg=0.06
voltage−gated cation channel activity GO:0022843 p=4.3E−02 n=3 fg=0.04 bg=0.01
4−hydroxy−2−oxoglutarate aldolase activi... GO:0008700 p=4.5E−02 n=1 fg=0.01 bg=0.00
3'−phosphoadenosine 5'−phosphosulfate tr... GO:0046964 p=4.5E−02 n=1 fg=0.01 bg=0.00
ABC−type vitamin B12 transporter activit... GO:0015420 p=4.5E−02 n=1 fg=0.01 bg=0.00
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myosin VI binding GO:0070853 p=4.5E−02 n=1 fg=0.01 bg=0.00
myosin VI heavy chain binding GO:0070854 p=4.5E−02 n=1 fg=0.01 bg=0.00
neurotrophin binding GO:0043121 p=4.5E−02 n=1 fg=0.01 bg=0.00
testosterone 17−beta−dehydrogenase (NADP... GO:0047045 p=4.5E−02 n=1 fg=0.01 bg=0.00
3−hydroxyisobutyryl−CoA hydrolase activi... GO:0003860 p=4.5E−02 n=1 fg=0.01 bg=0.00
manganese ion transmembrane transporter ... GO:0005384 p=4.5E−02 n=1 fg=0.01 bg=0.00
nickel cation transmembrane transporter ... GO:0015099 p=4.5E−02 n=1 fg=0.01 bg=0.00
calcium−independent phospholipase A2 act... GO:0047499 p=4.5E−02 n=1 fg=0.01 bg=0.00
steroid dehydrogenase activity GO:0016229 p=4.5E−02 n=1 fg=0.01 bg=0.00
bis(5'−nucleosyl)−tetraphosphatase (asym... GO:0004081 p=4.5E−02 n=1 fg=0.01 bg=0.00
6−phosphofructo−2−kinase activity GO:0003873 p=4.5E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=71/256 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032372114.2
fraction genes in fg and expected valu
secretory granule GO:0030141 p=3.1E−03 n=11 fg=0.14 bg=0.05
Golgi membrane GO:0000139 p=7.7E−03 n=11 fg=0.14 bg=0.06
nuclear outer membrane−endoplasmic retic... GO:0042175 p=8.2E−03 n=13 fg=0.16 bg=0.08
Golgi stack GO:0005795 p=8.6E−03 n=6 fg=0.07 bg=0.02
synaptic vesicle membrane GO:0030672 p=8.6E−03 n=4 fg=0.05 bg=0.01
endoplasmic reticulum GO:0005783 p=8.9E−03 n=20 fg=0.25 bg=0.14
integral component of organelle membrane GO:0031301 p=1.8E−02 n=8 fg=0.10 bg=0.04
endoplasmic reticulum membrane GO:0005789 p=1.8E−02 n=12 fg=0.15 bg=0.08
azurophil granule GO:0042582 p=2.0E−02 n=4 fg=0.05 bg=0.01
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Golgi−associated vesicle GO:0005798 p=2.0E−02 n=5 fg=0.06 bg=0.02
intrinsic component of organelle membran... GO:0031300 p=2.1E−02 n=8 fg=0.10 bg=0.04
coated vesicle GO:0030135 p=2.2E−02 n=6 fg=0.07 bg=0.03
neuronal cell body membrane GO:0032809 p=2.2E−02 n=3 fg=0.04 bg=0.01
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Golgi−associated vesicle membrane GO:0030660 p=2.2E−02 n=3 fg=0.04 bg=0.01
leading edge membrane GO:0031256 p=2.3E−02 n=4 fg=0.05 bg=0.01
endoplasmic reticulum subcompartment GO:0098827 p=2.4E−02 n=12 fg=0.15 bg=0.08
acrosomal vesicle GO:0001669 p=2.6E−02 n=2 fg=0.02 bg=0.00
neuron projection membrane GO:0032589 p=2.7E−02 n=3 fg=0.04 bg=0.01
cell body membrane GO:0044298 p=2.7E−02 n=3 fg=0.04 bg=0.01
cytosol GO:0005829 p=3.2E−02 n=40 fg=0.49 bg=0.39
intrinsic component of endoplasmic retic... GO:0031227 p=3.4E−02 n=5 fg=0.06 bg=0.02
integral component of endoplasmic reticu... GO:0030176 p=3.4E−02 n=5 fg=0.06 bg=0.02
microtubule associated complex GO:0005875 p=4.2E−02 n=4 fg=0.05 bg=0.02
polar microtubule GO:0005827 p=4.5E−02 n=1 fg=0.01 bg=0.00
transcription export complex 2 GO:0070390 p=4.5E−02 n=1 fg=0.01 bg=0.00
AMPA glutamate receptor complex GO:0032281 p=4.5E−02 n=1 fg=0.01 bg=0.00
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=4.5E−02 n=1 fg=0.01 bg=0.00
ESCRT−0 complex GO:0033565 p=4.5E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=81/256 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction