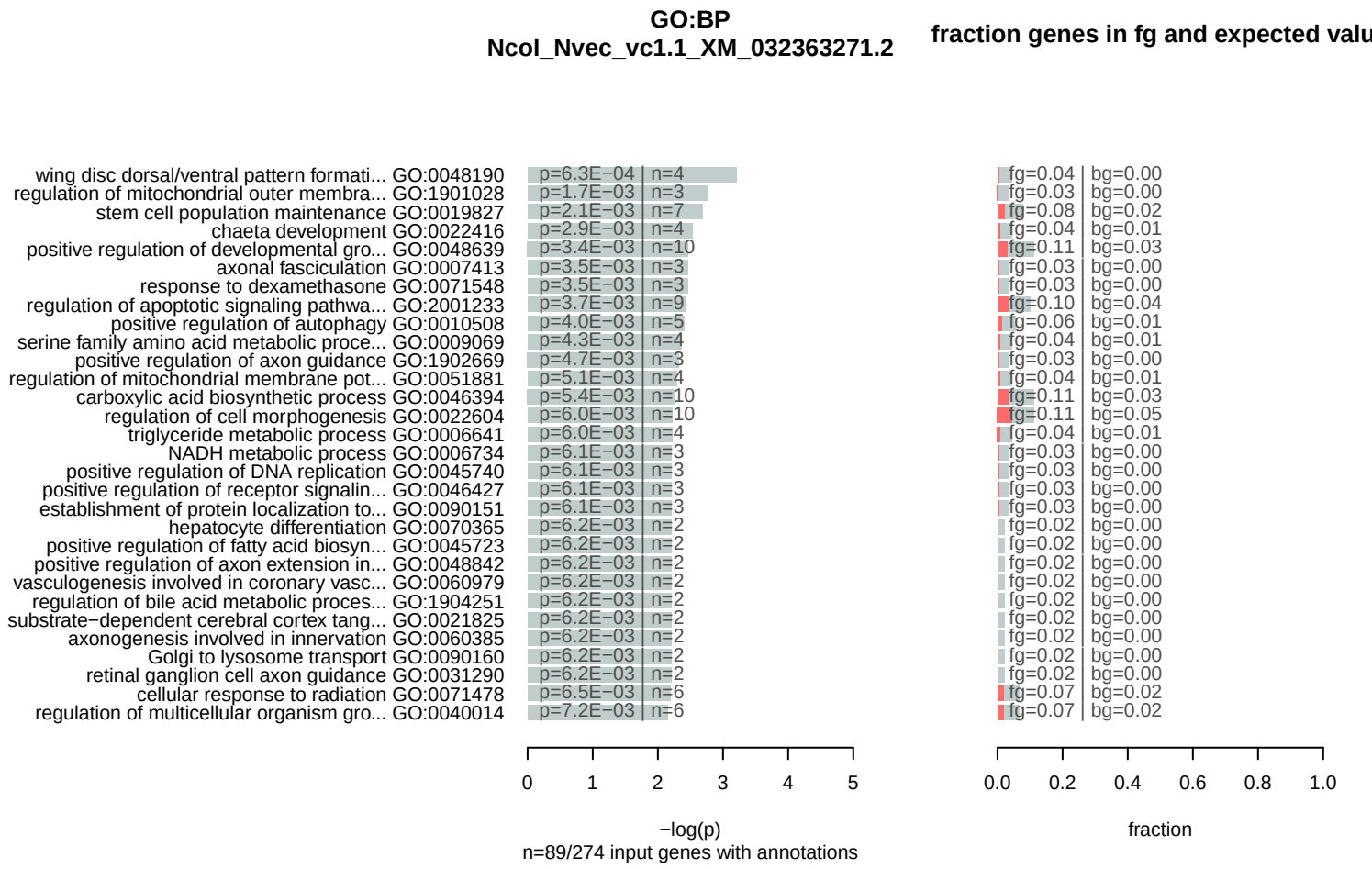
GO:BP
Ncol_Nvec_vc1.1_XM_032363271.2
fraction genes in fg and expected valu
wing disc dorsal/ventral pattern formati... GO:0048190 p=6.3E−04 n=4 fg=0.04 bg=0.00
regulation of mitochondrial outer membra... GO:1901028 p=1.7E−03 n=3 fg=0.03 bg=0.00
stem cell population maintenance GO:0019827 p=2.1E−03 n=7 fg=0.08 bg=0.02
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axonal fasciculation GO:0007413 p=3.5E−03 n=3 fg=0.03 bg=0.00
response to dexamethasone GO:0071548 p=3.5E−03 n=3 fg=0.03 bg=0.00
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positive regulation of autophagy GO:0010508 p=4.0E−03 n=5 fg=0.06 bg=0.01
serine family amino acid metabolic proce... GO:0009069 p=4.3E−03 n=4 fg=0.04 bg=0.01
positive regulation of axon guidance GO:1902669 p=4.7E−03 n=3 fg=0.03 bg=0.00
regulation of mitochondrial membrane pot... GO:0051881 p=5.1E−03 n=4 fg=0.04 bg=0.01
carboxylic acid biosynthetic process GO:0046394 p=5.4E−03 n=10 fg=0.11 bg=0.03
regulation of cell morphogenesis GO:0022604 p=6.0E−03 n=10 fg=0.11 bg=0.05
triglyceride metabolic process GO:0006641 p=6.0E−03 n=4 fg=0.04 bg=0.01
NADH metabolic process GO:0006734 p=6.1E−03 n=3 fg=0.03 bg=0.00
positive regulation of DNA replication GO:0045740 p=6.1E−03 n=3 fg=0.03 bg=0.00
positive regulation of receptor signalin... GO:0046427 p=6.1E−03 n=3 fg=0.03 bg=0.00
establishment of protein localization to... GO:0090151 p=6.1E−03 n=3 fg=0.03 bg=0.00
hepatocyte differentiation GO:0070365 p=6.2E−03 n=2 fg=0.02 bg=0.00
positive regulation of fatty acid biosyn... GO:0045723 p=6.2E−03 n=2 fg=0.02 bg=0.00
positive regulation of axon extension in... GO:0048842 p=6.2E−03 n=2 fg=0.02 bg=0.00
vasculogenesis involved in coronary vasc... GO:0060979 p=6.2E−03 n=2 fg=0.02 bg=0.00
regulation of bile acid metabolic proces... GO:1904251 p=6.2E−03 n=2 fg=0.02 bg=0.00
substrate−dependent cerebral cortex tang... GO:0021825 p=6.2E−03 n=2 fg=0.02 bg=0.00
axonogenesis involved in innervation GO:0060385 p=6.2E−03 n=2 fg=0.02 bg=0.00
Golgi to lysosome transport GO:0090160 p=6.2E−03 n=2 fg=0.02 bg=0.00
retinal ganglion cell axon guidance GO:0031290 p=6.2E−03 n=2 fg=0.02 bg=0.00
cellular response to radiation GO:0071478 p=6.5E−03 n=6 fg=0.07 bg=0.02
regulation of multicellular organism gro... GO:0040014 p=7.2E−03 n=6 fg=0.07 bg=0.02
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n=89/274 input genes with annotations
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fraction
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Ncol_Nvec_vc1.1_XM_032363271.2
fraction genes in fg and expected valu
MAP kinase activity GO:0004707 p=1.3E−03 n=3 fg=0.04 bg=0.00
K63−linked polyubiquitin modification−de... GO:0070530 p=3.5E−03 n=2 fg=0.02 bg=0.00
cation binding GO:0043169 p=6.2E−03 n=17 fg=0.21 bg=0.11
metal ion binding GO:0046872 p=1.3E−02 n=15 fg=0.18 bg=0.10
nuclear localization sequence binding GO:0008139 p=1.6E−02 n=2 fg=0.02 bg=0.00
peptidase activator activity GO:0016504 p=2.2E−02 n=2 fg=0.02 bg=0.00
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carboxy−lyase activity GO:0016831 p=2.9E−02 n=2 fg=0.02 bg=0.00
identical protein binding GO:0042802 p=3.4E−02 n=21 fg=0.26 bg=0.17
peptide binding GO:0042277 p=3.4E−02 n=5 fg=0.06 bg=0.02
histone deacetylase regulator activity GO:0035033 p=3.5E−02 n=1 fg=0.01 bg=0.00
choline binding GO:0033265 p=3.5E−02 n=1 fg=0.01 bg=0.00
misfolded RNA binding GO:0034336 p=3.5E−02 n=1 fg=0.01 bg=0.00
ribosomal protein S6 kinase activity GO:0004711 p=3.5E−02 n=1 fg=0.01 bg=0.00
adiponectin binding GO:0055100 p=3.5E−02 n=1 fg=0.01 bg=0.00
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methylthioribulose 1−phosphate dehydrata... GO:0046570 p=3.5E−02 n=1 fg=0.01 bg=0.00
semaphorin receptor activity GO:0017154 p=3.5E−02 n=1 fg=0.01 bg=0.00
pantothenate kinase activity GO:0004594 p=3.5E−02 n=1 fg=0.01 bg=0.00
acyltransferase activity, acyl groups co... GO:0046912 p=3.5E−02 n=1 fg=0.01 bg=0.00
inorganic phosphate transmembrane transp... GO:0005315 p=3.5E−02 n=1 fg=0.01 bg=0.00
high−affinity inorganic phosphate:sodium... GO:0005316 p=3.5E−02 n=1 fg=0.01 bg=0.00
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JUN kinase activity GO:0004705 p=3.5E−02 n=1 fg=0.01 bg=0.00
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phosphopentomutase activity GO:0008973 p=3.5E−02 n=1 fg=0.01 bg=0.00
phosphatidylserine decarboxylase activit... GO:0004609 p=3.5E−02 n=1 fg=0.01 bg=0.00
uroporphyrinogen−III synthase activity GO:0004852 p=3.5E−02 n=1 fg=0.01 bg=0.00
icosanoid binding GO:0050542 p=3.5E−02 n=1 fg=0.01 bg=0.00
icosatetraenoic acid binding GO:0050543 p=3.5E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=82/274 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032363271.2
fraction genes in fg and expected valu
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AP−type membrane coat adaptor complex GO:0030119 p=2.2E−02 n=2 fg=0.02 bg=0.00
female germ cell nucleus GO:0001674 p=2.9E−02 n=2 fg=0.02 bg=0.00
organelle envelope GO:0031967 p=3.0E−02 n=19 fg=0.20 bg=0.11
envelope GO:0031975 p=3.0E−02 n=19 fg=0.20 bg=0.11
coated membrane GO:0048475 p=3.4E−02 n=3 fg=0.03 bg=0.01
membrane coat GO:0030117 p=3.4E−02 n=3 fg=0.03 bg=0.01
Dsl1/NZR complex GO:0070939 p=3.4E−02 n=1 fg=0.01 bg=0.00
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NMS complex GO:0031617 p=3.4E−02 n=1 fg=0.01 bg=0.00
Shu complex GO:0097196 p=3.4E−02 n=1 fg=0.01 bg=0.00
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Ndc80 complex GO:0031262 p=3.4E−02 n=1 fg=0.01 bg=0.00
clathrin coat of trans−Golgi network ves... GO:0030130 p=3.4E−02 n=1 fg=0.01 bg=0.00
retromer, cargo−selective complex GO:0030906 p=3.4E−02 n=1 fg=0.01 bg=0.00
semaphorin receptor complex GO:0002116 p=3.4E−02 n=1 fg=0.01 bg=0.00
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secretory granule lumen GO:0034774 p=4.7E−02 n=5 fg=0.05 bg=0.02
organellar large ribosomal subunit GO:0000315 p=5.3E−02 n=2 fg=0.02 bg=0.00
mitochondrial large ribosomal subunit GO:0005762 p=5.3E−02 n=2 fg=0.02 bg=0.00
vesicle lumen GO:0031983 p=5.3E−02 n=5 fg=0.05 bg=0.02
cytoplasmic vesicle lumen GO:0060205 p=5.3E−02 n=5 fg=0.05 bg=0.02
extracellular region GO:0005576 p=6.7E−02 n=11 fg=0.12 bg=0.07
Sin3 complex GO:0016580 p=6.8E−02 n=1 fg=0.01 bg=0.00
endosome lumen GO:0031904 p=6.8E−02 n=1 fg=0.01 bg=0.00
GATOR2 complex GO:0061700 p=6.8E−02 n=1 fg=0.01 bg=0.00
Barr body GO:0001740 p=6.8E−02 n=1 fg=0.01 bg=0.00
glutamate−cysteine ligase complex GO:0017109 p=6.8E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=93/274 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction