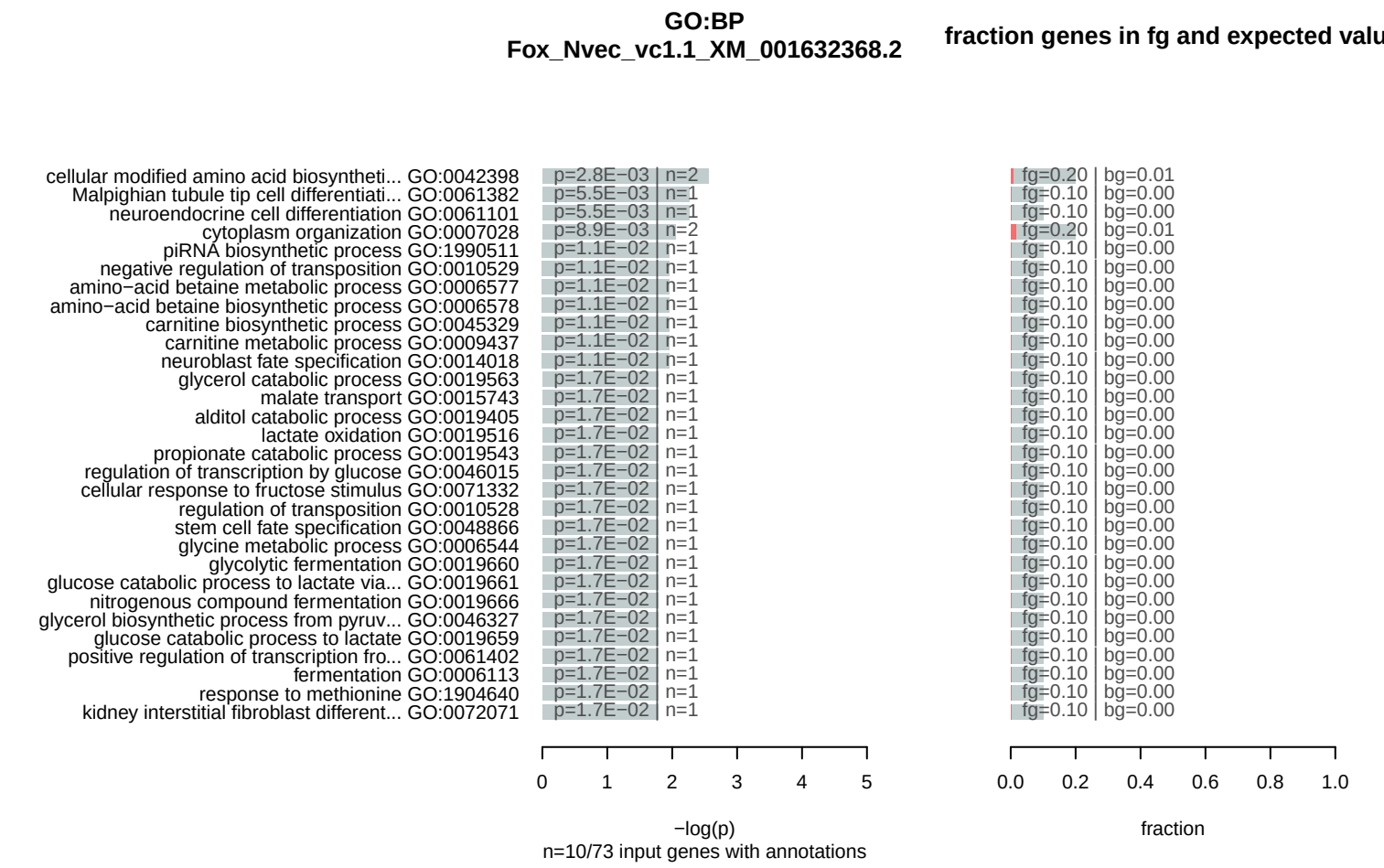
GO:BP
Fox_Nvec_vc1.1_XM_001632368.2
fraction genes in fg and expected valu
cellular modified amino acid biosyntheti... GO:0042398 p=2.8E−03 n=2 fg=0.20 bg=0.01
Malpighian tubule tip cell differentiati... GO:0061382 p=5.5E−03 n=1 fg=0.10 bg=0.00
neuroendocrine cell differentiation GO:0061101 p=5.5E−03 n=1 fg=0.10 bg=0.00
cytoplasm organization GO:0007028 p=8.9E−03 n=2 fg=0.20 bg=0.01
piRNA biosynthetic process GO:1990511 p=1.1E−02 n=1 fg=0.10 bg=0.00
negative regulation of transposition GO:0010529 p=1.1E−02 n=1 fg=0.10 bg=0.00
amino−acid betaine metabolic process GO:0006577 p=1.1E−02 n=1 fg=0.10 bg=0.00
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neuroblast fate specification GO:0014018 p=1.1E−02 n=1 fg=0.10 bg=0.00
glycerol catabolic process GO:0019563 p=1.7E−02 n=1 fg=0.10 bg=0.00
malate transport GO:0015743 p=1.7E−02 n=1 fg=0.10 bg=0.00
alditol catabolic process GO:0019405 p=1.7E−02 n=1 fg=0.10 bg=0.00
lactate oxidation GO:0019516 p=1.7E−02 n=1 fg=0.10 bg=0.00
propionate catabolic process GO:0019543 p=1.7E−02 n=1 fg=0.10 bg=0.00
regulation of transcription by glucose GO:0046015 p=1.7E−02 n=1 fg=0.10 bg=0.00
cellular response to fructose stimulus GO:0071332 p=1.7E−02 n=1 fg=0.10 bg=0.00
regulation of transposition GO:0010528 p=1.7E−02 n=1 fg=0.10 bg=0.00
stem cell fate specification GO:0048866 p=1.7E−02 n=1 fg=0.10 bg=0.00
glycine metabolic process GO:0006544 p=1.7E−02 n=1 fg=0.10 bg=0.00
glycolytic fermentation GO:0019660 p=1.7E−02 n=1 fg=0.10 bg=0.00
glucose catabolic process to lactate via... GO:0019661 p=1.7E−02 n=1 fg=0.10 bg=0.00
nitrogenous compound fermentation GO:0019666 p=1.7E−02 n=1 fg=0.10 bg=0.00
glycerol biosynthetic process from pyruv... GO:0046327 p=1.7E−02 n=1 fg=0.10 bg=0.00
glucose catabolic process to lactate GO:0019659 p=1.7E−02 n=1 fg=0.10 bg=0.00
positive regulation of transcription fro... GO:0061402 p=1.7E−02 n=1 fg=0.10 bg=0.00
fermentation GO:0006113 p=1.7E−02 n=1 fg=0.10 bg=0.00
response to methionine GO:1904640 p=1.7E−02 n=1 fg=0.10 bg=0.00
kidney interstitial fibroblast different... GO:0072071 p=1.7E−02 n=1 fg=0.10 bg=0.00
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−log(p)
n=10/73 input genes with annotations
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fraction
GO:MF
Fox_Nvec_vc1.1_XM_001632368.2
fraction genes in fg and expected valu
ecdysis−triggering hormone receptor acti... GO:0042654 p=4.4E−03 n=1 fg=0.14 bg=0.00
dipeptidase activity GO:0016805 p=8.8E−03 n=1 fg=0.14 bg=0.00
gamma−butyrobetaine dioxygenase activity GO:0008336 p=8.8E−03 n=1 fg=0.14 bg=0.00
protein tag GO:0031386 p=8.8E−03 n=1 fg=0.14 bg=0.00
lactate dehydrogenase activity GO:0004457 p=1.3E−02 n=1 fg=0.14 bg=0.00
oxidoreductase activity, acting on the C... GO:0016899 p=1.3E−02 n=1 fg=0.14 bg=0.00
DNA binding domain binding GO:0050692 p=1.3E−02 n=1 fg=0.14 bg=0.00
inosine kinase activity GO:0008906 p=1.3E−02 n=1 fg=0.14 bg=0.00
phosphoenolpyruvate carboxykinase activi... GO:0004611 p=1.3E−02 n=1 fg=0.14 bg=0.00
phosphoenolpyruvate carboxykinase (GTP) ... GO:0004613 p=1.3E−02 n=1 fg=0.14 bg=0.00
cAMP response element binding GO:0035497 p=1.3E−02 n=1 fg=0.14 bg=0.00
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carboxypeptidase activity GO:0004180 p=1.3E−02 n=1 fg=0.14 bg=0.00
nucleoside diphosphate kinase activity GO:0004550 p=1.8E−02 n=1 fg=0.14 bg=0.00
G protein−coupled amine receptor activit... GO:0008227 p=2.2E−02 n=1 fg=0.14 bg=0.00
epinephrine binding GO:0051379 p=2.2E−02 n=1 fg=0.14 bg=0.00
catecholamine binding GO:1901338 p=2.2E−02 n=1 fg=0.14 bg=0.00
HMG box domain binding GO:0071837 p=2.6E−02 n=1 fg=0.14 bg=0.00
carboxy−lyase activity GO:0016831 p=2.6E−02 n=1 fg=0.14 bg=0.00
oxidoreductase activity, acting on a sul... GO:0016668 p=3.0E−02 n=1 fg=0.14 bg=0.00
protein−disulfide reductase (NAD(P)) act... GO:0047134 p=3.0E−02 n=1 fg=0.14 bg=0.00
phosphotransferase activity, phosphate g... GO:0016776 p=3.0E−02 n=1 fg=0.14 bg=0.00
neuropeptide receptor activity GO:0008188 p=3.5E−02 n=1 fg=0.14 bg=0.01
E−box binding GO:0070888 p=3.9E−02 n=1 fg=0.14 bg=0.01
protein−disulfide reductase activity GO:0015035 p=3.9E−02 n=1 fg=0.14 bg=0.01
nucleobase−containing compound kinase ac... GO:0019205 p=3.9E−02 n=1 fg=0.14 bg=0.01
GDP binding GO:0019003 p=4.3E−02 n=1 fg=0.14 bg=0.01
peptide receptor activity GO:0001653 p=4.3E−02 n=1 fg=0.14 bg=0.01
carbon−carbon lyase activity GO:0016830 p=4.3E−02 n=1 fg=0.14 bg=0.01
G protein−coupled peptide receptor activ... GO:0008528 p=4.3E−02 n=1 fg=0.14 bg=0.01
0 1 2 3 4 5
−log(p)
n=7/73 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001632368.2
fraction genes in fg and expected valu
pi−body GO:0071546 p=2.2E−02 n=1 fg=0.10 bg=0.00
chromatoid body GO:0033391 p=2.2E−02 n=1 fg=0.10 bg=0.00
cytosolic small ribosomal subunit GO:0022627 p=3.8E−02 n=1 fg=0.10 bg=0.00
small ribosomal subunit GO:0015935 p=5.4E−02 n=1 fg=0.10 bg=0.01
P granule GO:0043186 p=6.5E−02 n=1 fg=0.10 bg=0.01
germ plasm GO:0060293 p=7.0E−02 n=1 fg=0.10 bg=0.01
pole plasm GO:0045495 p=7.0E−02 n=1 fg=0.10 bg=0.01
cytosolic ribosome GO:0022626 p=7.5E−02 n=1 fg=0.10 bg=0.01
ribosomal subunit GO:0044391 p=9.5E−02 n=1 fg=0.10 bg=0.01
autophagosome GO:0005776 p=1.2E−01 n=1 fg=0.10 bg=0.01
ribosome GO:0005840 p=1.3E−01 n=1 fg=0.10 bg=0.01
ribonucleoprotein complex GO:1990904 p=1.5E−01 n=2 fg=0.20 bg=0.07
RNA polymerase II transcription regulato... GO:0090575 p=1.7E−01 n=1 fg=0.10 bg=0.02
secretory granule membrane GO:0030667 p=1.9E−01 n=1 fg=0.10 bg=0.02
cytoplasmic ribonucleoprotein granule GO:0036464 p=2.2E−01 n=1 fg=0.10 bg=0.02
ribonucleoprotein granule GO:0035770 p=2.3E−01 n=1 fg=0.10 bg=0.03
nuclear speck GO:0016607 p=2.9E−01 n=1 fg=0.10 bg=0.03
nuclear chromosome GO:0000228 p=3.2E−01 n=1 fg=0.10 bg=0.04
cytosol GO:0005829 p=3.4E−01 n=5 fg=0.50 bg=0.39
mitochondrial matrix GO:0005759 p=3.5E−01 n=1 fg=0.10 bg=0.04
transcription regulator complex GO:0005667 p=3.5E−01 n=1 fg=0.10 bg=0.04
chromatin GO:0000785 p=3.6E−01 n=1 fg=0.10 bg=0.04
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secretory granule GO:0030141 p=4.2E−01 n=1 fg=0.10 bg=0.05
nuclear body GO:0016604 p=4.8E−01 n=1 fg=0.10 bg=0.06
vacuole GO:0005773 p=5.2E−01 n=1 fg=0.10 bg=0.07
integral component of plasma membrane GO:0005887 p=5.4E−01 n=1 fg=0.10 bg=0.07
secretory vesicle GO:0099503 p=5.5E−01 n=1 fg=0.10 bg=0.08
supramolecular complex GO:0099080 p=5.5E−01 n=1 fg=0.10 bg=0.08
0 1 2 3 4 5
−log(p)
n=10/73 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction