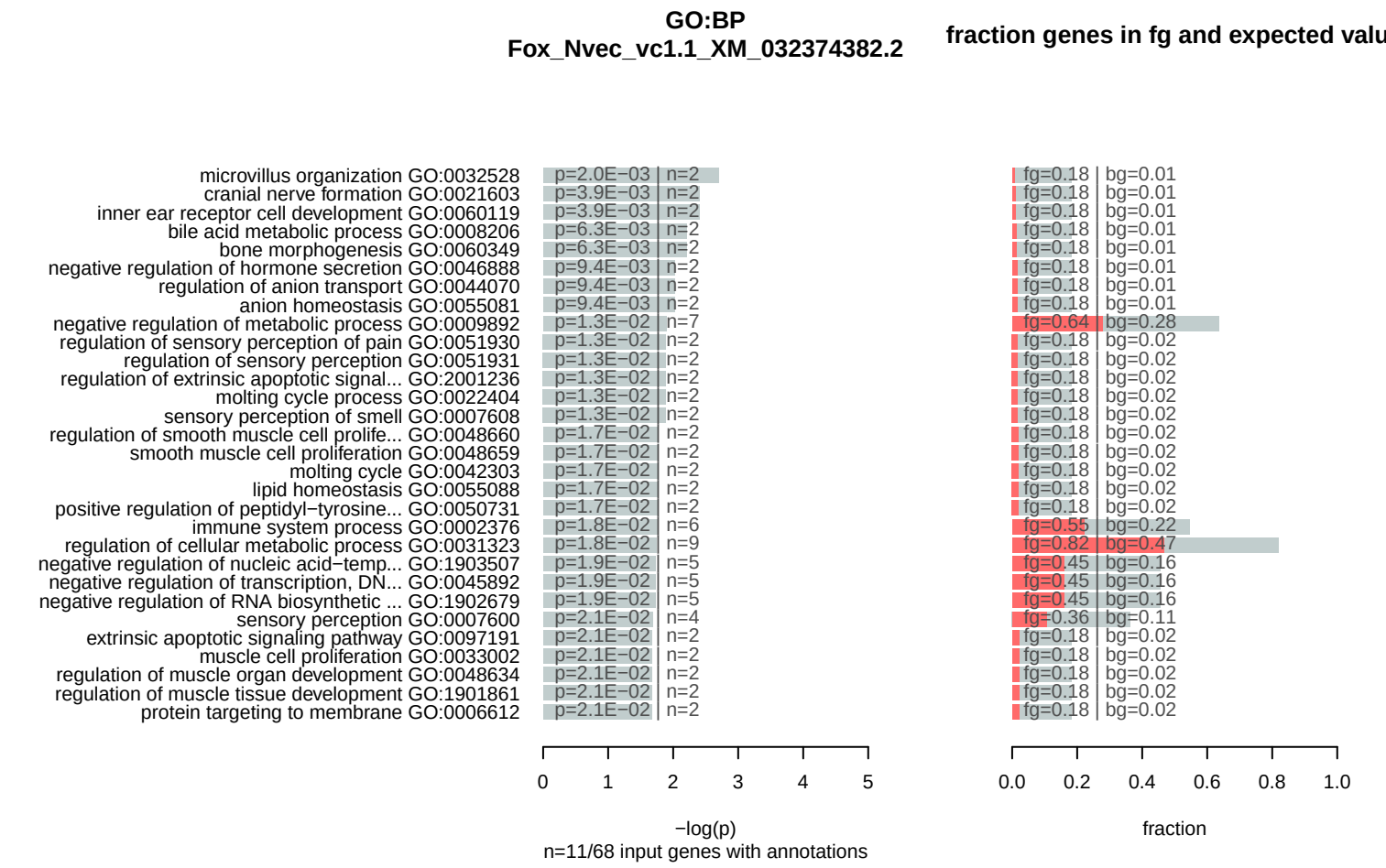
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fraction genes in fg and expected valu
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inner ear receptor cell development GO:0060119 p=3.9E−03 n=2 fg=0.18 bg=0.01
bile acid metabolic process GO:0008206 p=6.3E−03 n=2 fg=0.18 bg=0.01
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negative regulation of hormone secretion GO:0046888 p=9.4E−03 n=2 fg=0.18 bg=0.01
regulation of anion transport GO:0044070 p=9.4E−03 n=2 fg=0.18 bg=0.01
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regulation of extrinsic apoptotic signal... GO:2001236 p=1.3E−02 n=2 fg=0.18 bg=0.02
molting cycle process GO:0022404 p=1.3E−02 n=2 fg=0.18 bg=0.02
sensory perception of smell GO:0007608 p=1.3E−02 n=2 fg=0.18 bg=0.02
regulation of smooth muscle cell prolife... GO:0048660 p=1.7E−02 n=2 fg=0.18 bg=0.02
smooth muscle cell proliferation GO:0048659 p=1.7E−02 n=2 fg=0.18 bg=0.02
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lipid homeostasis GO:0055088 p=1.7E−02 n=2 fg=0.18 bg=0.02
positive regulation of peptidyl−tyrosine... GO:0050731 p=1.7E−02 n=2 fg=0.18 bg=0.02
immune system process GO:0002376 p=1.8E−02 n=6 fg=0.55 bg=0.22
regulation of cellular metabolic process GO:0031323 p=1.8E−02 n=9 fg=0.82 bg=0.47
negative regulation of nucleic acid−temp... GO:1903507 p=1.9E−02 n=5 fg=0.45 bg=0.16
negative regulation of transcription, DN... GO:0045892 p=1.9E−02 n=5 fg=0.45 bg=0.16
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sensory perception GO:0007600 p=2.1E−02 n=4 fg=0.36 bg=0.11
extrinsic apoptotic signaling pathway GO:0097191 p=2.1E−02 n=2 fg=0.18 bg=0.02
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regulation of muscle organ development GO:0048634 p=2.1E−02 n=2 fg=0.18 bg=0.02
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protein targeting to membrane GO:0006612 p=2.1E−02 n=2 fg=0.18 bg=0.02
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−log(p)
n=11/68 input genes with annotations
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fraction
GO:MF
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fraction genes in fg and expected valu
heat shock protein binding GO:0031072 p=5.2E−03 n=2 fg=0.22 bg=0.01
phosphoric diester hydrolase activity GO:0008081 p=2.2E−02 n=2 fg=0.22 bg=0.03
calmodulin−activated 3',5'−cyclic−GMP ph... GO:0048101 p=2.5E−02 n=1 fg=0.11 bg=0.00
1−phosphatidylinositol−3−kinase activity GO:0016303 p=2.5E−02 n=1 fg=0.11 bg=0.00
phosphatidylinositol 3−kinase activity GO:0035004 p=2.5E−02 n=1 fg=0.11 bg=0.00
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organophosphate ester transmembrane tran... GO:0015605 p=2.5E−02 n=1 fg=0.11 bg=0.00
phosphatidylinositol bisphosphate kinase... GO:0052813 p=2.5E−02 n=1 fg=0.11 bg=0.00
calmodulin−activated dual specificity 3'... GO:0004117 p=2.5E−02 n=1 fg=0.11 bg=0.00
phosphatidylinositol−4,5−bisphosphate 3−... GO:0046934 p=2.5E−02 n=1 fg=0.11 bg=0.00
phosphatidylglycerol binding GO:1901611 p=2.5E−02 n=1 fg=0.11 bg=0.00
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ATPase−coupled intramembrane lipid trans... GO:0140326 p=2.5E−02 n=1 fg=0.11 bg=0.00
flippase activity GO:0140327 p=2.5E−02 n=1 fg=0.11 bg=0.00
aminophospholipid flippase activity GO:0015247 p=2.5E−02 n=1 fg=0.11 bg=0.00
carbohydrate derivative binding GO:0097367 p=2.5E−02 n=3 fg=0.33 bg=0.08
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protein−containing complex binding GO:0044877 p=3.9E−02 n=3 fg=0.33 bg=0.09
molecular transducer activity GO:0060089 p=3.9E−02 n=3 fg=0.33 bg=0.09
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receptor−receptor interaction GO:0090722 p=4.9E−02 n=1 fg=0.11 bg=0.01
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molecular function activator activity GO:0140677 p=4.9E−02 n=1 fg=0.11 bg=0.01
heparin binding GO:0008201 p=4.9E−02 n=1 fg=0.11 bg=0.01
ribosome binding GO:0043022 p=4.9E−02 n=1 fg=0.11 bg=0.01
ATPase activator activity GO:0001671 p=4.9E−02 n=1 fg=0.11 bg=0.01
G protein−coupled adenosine receptor act... GO:0001609 p=4.9E−02 n=1 fg=0.11 bg=0.01
G−protein beta/gamma−subunit complex bin... GO:0031683 p=4.9E−02 n=1 fg=0.11 bg=0.01
sulfur compound binding GO:1901681 p=4.9E−02 n=1 fg=0.11 bg=0.01
fibroblast growth factor binding GO:0017134 p=4.9E−02 n=1 fg=0.11 bg=0.01
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−log(p)
n=9/68 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032374382.2
fraction genes in fg and expected valu
collagen and cuticulin−based cuticle ext... GO:0060102 p=2.7E−02 n=1 fg=0.09 bg=0.00
excitatory synapse GO:0060076 p=2.7E−02 n=1 fg=0.09 bg=0.00
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specific granule GO:0042581 p=5.4E−02 n=1 fg=0.09 bg=0.00
phagocytic vesicle membrane GO:0030670 p=5.4E−02 n=1 fg=0.09 bg=0.00
stereocilium GO:0032420 p=5.4E−02 n=1 fg=0.09 bg=0.00
stereocilium bundle GO:0032421 p=5.4E−02 n=1 fg=0.09 bg=0.00
cytosolic region GO:0099522 p=5.4E−02 n=1 fg=0.09 bg=0.00
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integral component of plasma membrane GO:0005887 p=6.2E−02 n=4 fg=0.36 bg=0.15
somatodendritic compartment GO:0036477 p=7.3E−02 n=4 fg=0.36 bg=0.15
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tertiary granule membrane GO:0070821 p=8.0E−02 n=1 fg=0.09 bg=0.01
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external encapsulating structure GO:0030312 p=8.0E−02 n=1 fg=0.09 bg=0.01
collagen−containing extracellular matrix GO:0062023 p=8.0E−02 n=1 fg=0.09 bg=0.01
rough endoplasmic reticulum GO:0005791 p=8.0E−02 n=1 fg=0.09 bg=0.01
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sensory dendrite GO:0071683 p=8.0E−02 n=1 fg=0.09 bg=0.01
intrinsic component of plasma membrane GO:0031226 p=8.0E−02 n=4 fg=0.36 bg=0.16
neuron spine GO:0044309 p=9.9E−02 n=2 fg=0.18 bg=0.05
asymmetric synapse GO:0032279 p=9.9E−02 n=2 fg=0.18 bg=0.05
dendritic spine GO:0043197 p=9.9E−02 n=2 fg=0.18 bg=0.05
acrosomal vesicle GO:0001669 p=1.0E−01 n=1 fg=0.09 bg=0.01
terminal bouton GO:0043195 p=1.0E−01 n=1 fg=0.09 bg=0.01
brush border membrane GO:0031526 p=1.0E−01 n=1 fg=0.09 bg=0.01
axolemma GO:0030673 p=1.0E−01 n=1 fg=0.09 bg=0.01
0 1 2 3 4 5
−log(p)
n=11/68 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction