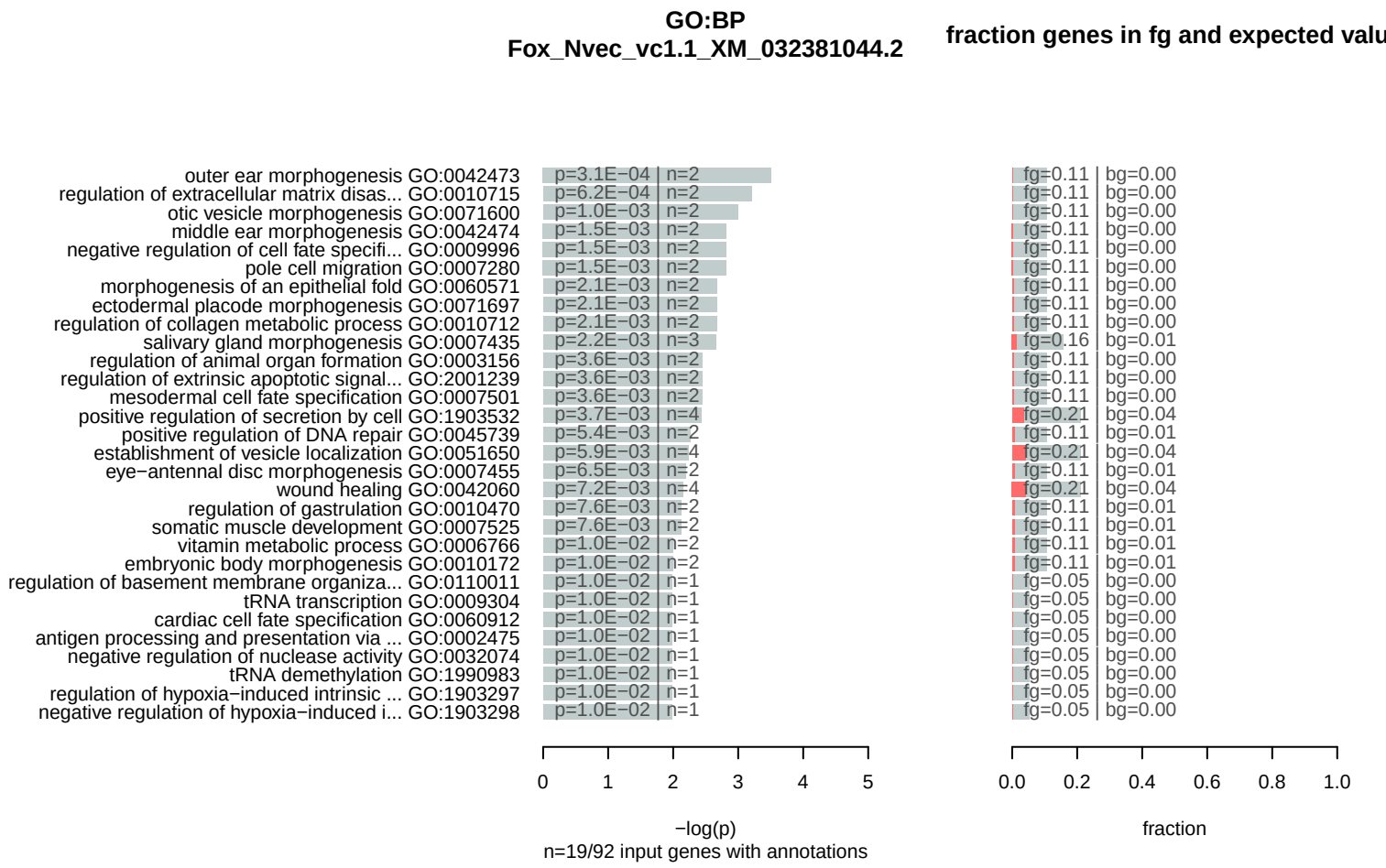
GO:BP
Fox_Nvec_vc1.1_XM_032381044.2
fraction genes in fg and expected valu
outer ear morphogenesis GO:0042473 p=3.1E−04 n=2 fg=0.11 bg=0.00
regulation of extracellular matrix disas... GO:0010715 p=6.2E−04 n=2 fg=0.11 bg=0.00
otic vesicle morphogenesis GO:0071600 p=1.0E−03 n=2 fg=0.11 bg=0.00
middle ear morphogenesis GO:0042474 p=1.5E−03 n=2 fg=0.11 bg=0.00
negative regulation of cell fate specifi... GO:0009996 p=1.5E−03 n=2 fg=0.11 bg=0.00
pole cell migration GO:0007280 p=1.5E−03 n=2 fg=0.11 bg=0.00
morphogenesis of an epithelial fold GO:0060571 p=2.1E−03 n=2 fg=0.11 bg=0.00
ectodermal placode morphogenesis GO:0071697 p=2.1E−03 n=2 fg=0.11 bg=0.00
regulation of collagen metabolic process GO:0010712 p=2.1E−03 n=2 fg=0.11 bg=0.00
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regulation of animal organ formation GO:0003156 p=3.6E−03 n=2 fg=0.11 bg=0.00
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mesodermal cell fate specification GO:0007501 p=3.6E−03 n=2 fg=0.11 bg=0.00
positive regulation of secretion by cell GO:1903532 p=3.7E−03 n=4 fg=0.21 bg=0.04
positive regulation of DNA repair GO:0045739 p=5.4E−03 n=2 fg=0.11 bg=0.01
establishment of vesicle localization GO:0051650 p=5.9E−03 n=4 fg=0.21 bg=0.04
eye−antennal disc morphogenesis GO:0007455 p=6.5E−03 n=2 fg=0.11 bg=0.01
wound healing GO:0042060 p=7.2E−03 n=4 fg=0.21 bg=0.04
regulation of gastrulation GO:0010470 p=7.6E−03 n=2 fg=0.11 bg=0.01
somatic muscle development GO:0007525 p=7.6E−03 n=2 fg=0.11 bg=0.01
vitamin metabolic process GO:0006766 p=1.0E−02 n=2 fg=0.11 bg=0.01
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regulation of basement membrane organiza... GO:0110011 p=1.0E−02 n=1 fg=0.05 bg=0.00
tRNA transcription GO:0009304 p=1.0E−02 n=1 fg=0.05 bg=0.00
cardiac cell fate specification GO:0060912 p=1.0E−02 n=1 fg=0.05 bg=0.00
antigen processing and presentation via ... GO:0002475 p=1.0E−02 n=1 fg=0.05 bg=0.00
negative regulation of nuclease activity GO:0032074 p=1.0E−02 n=1 fg=0.05 bg=0.00
tRNA demethylation GO:1990983 p=1.0E−02 n=1 fg=0.05 bg=0.00
regulation of hypoxia−induced intrinsic ... GO:1903297 p=1.0E−02 n=1 fg=0.05 bg=0.00
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n=19/92 input genes with annotations
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fraction
GO:MF
Fox_Nvec_vc1.1_XM_032381044.2
fraction genes in fg and expected valu
G−protein alpha−subunit binding GO:0001965 p=1.6E−03 n=2 fg=0.12 bg=0.00
endoribonuclease inhibitor activity GO:0060698 p=1.1E−02 n=1 fg=0.06 bg=0.00
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protein tyrosine phosphatase activity, m... GO:0030946 p=1.1E−02 n=1 fg=0.06 bg=0.00
methylcytosine dioxygenase activity GO:0070579 p=1.1E−02 n=1 fg=0.06 bg=0.00
proteinase activated receptor binding GO:0031871 p=1.1E−02 n=1 fg=0.06 bg=0.00
dystroglycan binding GO:0002162 p=1.1E−02 n=1 fg=0.06 bg=0.00
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L−malate dehydrogenase activity GO:0030060 p=1.1E−02 n=1 fg=0.06 bg=0.00
oxidative RNA demethylase activity GO:0035515 p=1.1E−02 n=1 fg=0.06 bg=0.00
propionyl−CoA carboxylase activity GO:0004658 p=1.1E−02 n=1 fg=0.06 bg=0.00
CoA carboxylase activity GO:0016421 p=1.1E−02 n=1 fg=0.06 bg=0.00
kinetochore binding GO:0043515 p=1.1E−02 n=1 fg=0.06 bg=0.00
heparan−alpha−glucosaminide N−acetyltran... GO:0015019 p=2.1E−02 n=1 fg=0.06 bg=0.00
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GDP−dissociation inhibitor activity GO:0005092 p=2.1E−02 n=1 fg=0.06 bg=0.00
ubiquitin−protein transferase activator ... GO:0097027 p=2.1E−02 n=1 fg=0.06 bg=0.00
malic enzyme activity GO:0004470 p=2.1E−02 n=1 fg=0.06 bg=0.00
ligase activity, forming carbon−carbon b... GO:0016885 p=2.1E−02 n=1 fg=0.06 bg=0.00
malate dehydrogenase activity GO:0016615 p=2.1E−02 n=1 fg=0.06 bg=0.00
fibroblast growth factor−activated recep... GO:0005007 p=3.2E−02 n=1 fg=0.06 bg=0.00
tumor necrosis factor receptor binding GO:0005164 p=3.2E−02 n=1 fg=0.06 bg=0.00
NAD binding GO:0051287 p=3.2E−02 n=1 fg=0.06 bg=0.00
ubiquitin−protein transferase regulator ... GO:0055106 p=3.2E−02 n=1 fg=0.06 bg=0.00
DNA−(apurinic or apyrimidinic site) endo... GO:0003906 p=3.2E−02 n=1 fg=0.06 bg=0.00
receptor−receptor interaction GO:0090722 p=3.2E−02 n=1 fg=0.06 bg=0.00
molecular function regulator activity GO:0098772 p=4.1E−02 n=5 fg=0.29 bg=0.12
GTP−dependent protein binding GO:0030742 p=4.2E−02 n=1 fg=0.06 bg=0.00
chemoattractant activity GO:0042056 p=4.2E−02 n=1 fg=0.06 bg=0.00
0 1 2 3 4 5
−log(p)
n=17/92 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032381044.2
fraction genes in fg and expected valu
trans−Golgi network GO:0005802 p=4.4E−03 n=4 fg=0.21 bg=0.04
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cortical microtubule plus−end GO:1903754 p=1.1E−02 n=1 fg=0.05 bg=0.00
cytoplasmic microtubule plus−end GO:1904511 p=1.1E−02 n=1 fg=0.05 bg=0.00
lumenal side of Golgi membrane GO:0098547 p=1.1E−02 n=1 fg=0.05 bg=0.00
centrosomal corona GO:0031592 p=1.1E−02 n=1 fg=0.05 bg=0.00
cortical microtubule GO:0055028 p=1.1E−02 n=1 fg=0.05 bg=0.00
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transcription factor TFIIIC complex GO:0000127 p=1.1E−02 n=1 fg=0.05 bg=0.00
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cytoplasmic vesicle GO:0031410 p=1.2E−02 n=8 fg=0.42 bg=0.18
vesicle GO:0031982 p=1.7E−02 n=8 fg=0.42 bg=0.19
extracellular space GO:0005615 p=1.8E−02 n=3 fg=0.16 bg=0.03
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extrinsic component of Golgi membrane GO:0090498 p=2.1E−02 n=1 fg=0.05 bg=0.00
nuclear chromosome GO:0000228 p=3.1E−02 n=3 fg=0.16 bg=0.04
microtubule plus−end GO:0035371 p=3.1E−02 n=1 fg=0.05 bg=0.00
NuRD complex GO:0016581 p=3.1E−02 n=1 fg=0.05 bg=0.00
intercalary heterochromatin GO:0005725 p=3.1E−02 n=1 fg=0.05 bg=0.00
endoplasmic reticulum exit site GO:0070971 p=3.1E−02 n=1 fg=0.05 bg=0.00
CHD−type complex GO:0090545 p=3.1E−02 n=1 fg=0.05 bg=0.00
PRC1 complex GO:0035102 p=3.1E−02 n=1 fg=0.05 bg=0.00
kinetochore microtubule GO:0005828 p=3.1E−02 n=1 fg=0.05 bg=0.00
extracellular region GO:0005576 p=3.8E−02 n=4 fg=0.21 bg=0.07
cell cortex GO:0005938 p=4.0E−02 n=3 fg=0.16 bg=0.04
myelin sheath GO:0043209 p=4.1E−02 n=2 fg=0.11 bg=0.02
basal cortex GO:0045180 p=4.1E−02 n=1 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=19/92 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction