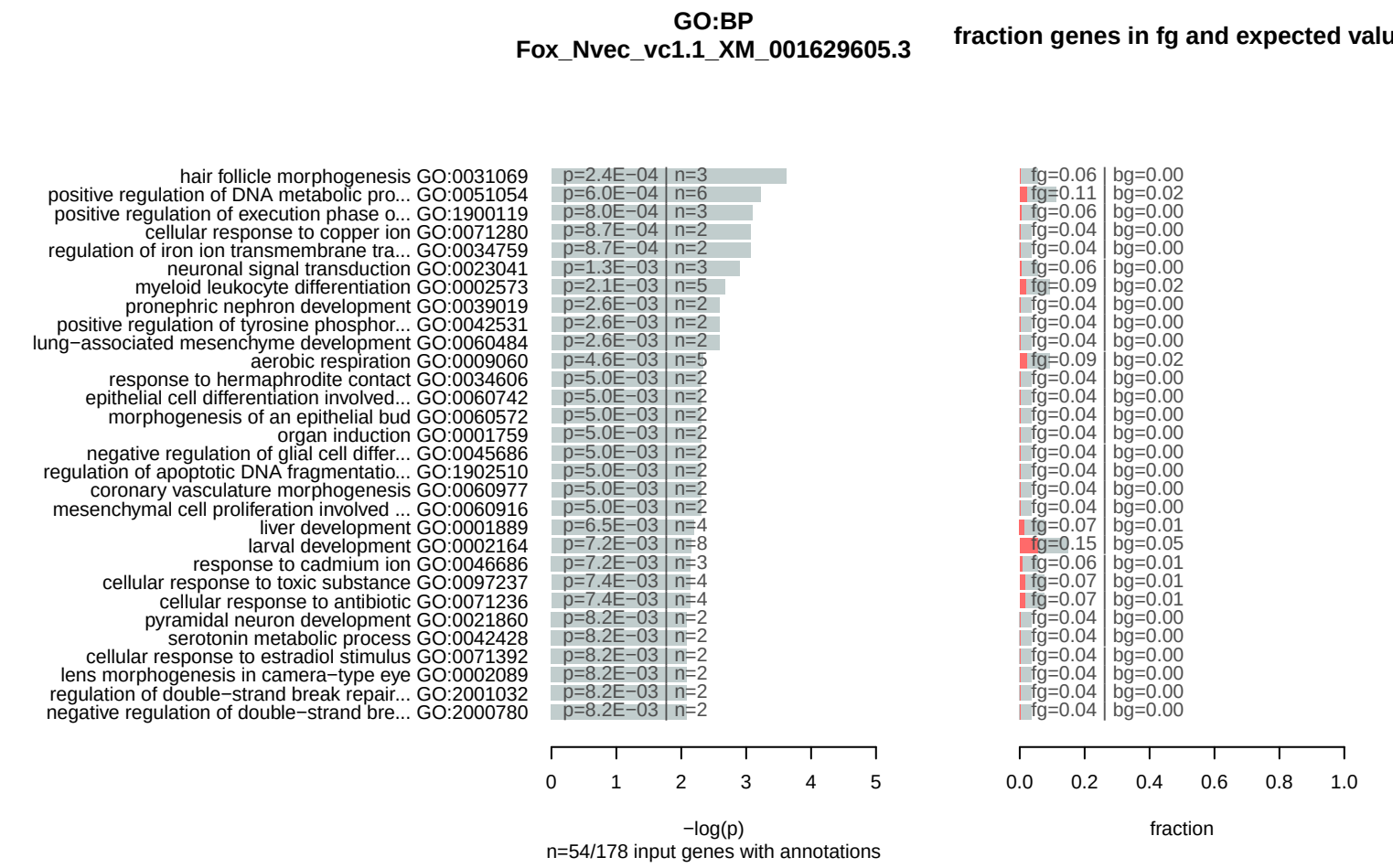
GO:BP
Fox_Nvec_vc1.1_XM_001629605.3
fraction genes in fg and expected valu
hair follicle morphogenesis GO:0031069 p=2.4E−04 n=3 fg=0.06 bg=0.00
positive regulation of DNA metabolic pro... GO:0051054 p=6.0E−04 n=6 fg=0.11 bg=0.02
positive regulation of execution phase o... GO:1900119 p=8.0E−04 n=3 fg=0.06 bg=0.00
cellular response to copper ion GO:0071280 p=8.7E−04 n=2 fg=0.04 bg=0.00
regulation of iron ion transmembrane tra... GO:0034759 p=8.7E−04 n=2 fg=0.04 bg=0.00
neuronal signal transduction GO:0023041 p=1.3E−03 n=3 fg=0.06 bg=0.00
myeloid leukocyte differentiation GO:0002573 p=2.1E−03 n=5 fg=0.09 bg=0.02
pronephric nephron development GO:0039019 p=2.6E−03 n=2 fg=0.04 bg=0.00
positive regulation of tyrosine phosphor... GO:0042531 p=2.6E−03 n=2 fg=0.04 bg=0.00
lung−associated mesenchyme development GO:0060484 p=2.6E−03 n=2 fg=0.04 bg=0.00
aerobic respiration GO:0009060 p=4.6E−03 n=5 fg=0.09 bg=0.02
response to hermaphrodite contact GO:0034606 p=5.0E−03 n=2 fg=0.04 bg=0.00
epithelial cell differentiation involved... GO:0060742 p=5.0E−03 n=2 fg=0.04 bg=0.00
morphogenesis of an epithelial bud GO:0060572 p=5.0E−03 n=2 fg=0.04 bg=0.00
organ induction GO:0001759 p=5.0E−03 n=2 fg=0.04 bg=0.00
negative regulation of glial cell differ... GO:0045686 p=5.0E−03 n=2 fg=0.04 bg=0.00
regulation of apoptotic DNA fragmentatio... GO:1902510 p=5.0E−03 n=2 fg=0.04 bg=0.00
coronary vasculature morphogenesis GO:0060977 p=5.0E−03 n=2 fg=0.04 bg=0.00
mesenchymal cell proliferation involved ... GO:0060916 p=5.0E−03 n=2 fg=0.04 bg=0.00
liver development GO:0001889 p=6.5E−03 n=4 fg=0.07 bg=0.01
larval development GO:0002164 p=7.2E−03 n=8 fg=0.15 bg=0.05
response to cadmium ion GO:0046686 p=7.2E−03 n=3 fg=0.06 bg=0.01
cellular response to toxic substance GO:0097237 p=7.4E−03 n=4 fg=0.07 bg=0.01
cellular response to antibiotic GO:0071236 p=7.4E−03 n=4 fg=0.07 bg=0.01
pyramidal neuron development GO:0021860 p=8.2E−03 n=2 fg=0.04 bg=0.00
serotonin metabolic process GO:0042428 p=8.2E−03 n=2 fg=0.04 bg=0.00
cellular response to estradiol stimulus GO:0071392 p=8.2E−03 n=2 fg=0.04 bg=0.00
lens morphogenesis in camera−type eye GO:0002089 p=8.2E−03 n=2 fg=0.04 bg=0.00
regulation of double−strand break repair... GO:2001032 p=8.2E−03 n=2 fg=0.04 bg=0.00
negative regulation of double−strand bre... GO:2000780 p=8.2E−03 n=2 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=54/178 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_001629605.3
fraction genes in fg and expected valu
oxidized purine DNA binding GO:0032357 p=4.9E−03 n=2 fg=0.04 bg=0.00
ATP hydrolysis activity GO:0016887 p=2.1E−02 n=6 fg=0.13 bg=0.05
electron transfer activity GO:0009055 p=2.2E−02 n=3 fg=0.06 bg=0.01
disordered domain specific binding GO:0097718 p=2.7E−02 n=2 fg=0.04 bg=0.01
cuprous ion binding GO:1903136 p=2.9E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on diphe... GO:0016679 p=2.9E−02 n=1 fg=0.02 bg=0.00
ATP−dependent DNA/DNA annealing activity GO:0036310 p=2.9E−02 n=1 fg=0.02 bg=0.00
histone methyltransferase binding GO:1990226 p=2.9E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on NAD(P... GO:0050664 p=2.9E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on the C... GO:0016649 p=2.9E−02 n=1 fg=0.02 bg=0.00
protein phosphatase 5 binding GO:1990634 p=2.9E−02 n=1 fg=0.02 bg=0.00
NAD(P)H oxidase H2O2−forming activity GO:0016174 p=2.9E−02 n=1 fg=0.02 bg=0.00
mannosyl−oligosaccharide mannosidase act... GO:0015924 p=2.9E−02 n=1 fg=0.02 bg=0.00
calmodulin−activated 3',5'−cyclic−GMP ph... GO:0048101 p=2.9E−02 n=1 fg=0.02 bg=0.00
mevalonate kinase activity GO:0004496 p=2.9E−02 n=1 fg=0.02 bg=0.00
mannosyl−oligosaccharide 1,2−alpha−manno... GO:0004571 p=2.9E−02 n=1 fg=0.02 bg=0.00
electron−transferring−flavoprotein dehyd... GO:0004174 p=2.9E−02 n=1 fg=0.02 bg=0.00
supercoiled DNA binding GO:0097100 p=2.9E−02 n=1 fg=0.02 bg=0.00
calmodulin−activated dual specificity 3'... GO:0004117 p=2.9E−02 n=1 fg=0.02 bg=0.00
alpha−catenin binding GO:0045294 p=2.9E−02 n=1 fg=0.02 bg=0.00
ubiquinol−cytochrome−c reductase activit... GO:0008121 p=2.9E−02 n=1 fg=0.02 bg=0.00
DNA/DNA annealing activity GO:1990814 p=2.9E−02 n=1 fg=0.02 bg=0.00
acid−sensing ion channel activity GO:0044736 p=2.9E−02 n=1 fg=0.02 bg=0.00
P−type divalent copper transporter activ... GO:0043682 p=2.9E−02 n=1 fg=0.02 bg=0.00
small ribosomal subunit rRNA binding GO:0070181 p=2.9E−02 n=1 fg=0.02 bg=0.00
malate dehydrogenase (decarboxylating) (... GO:0004471 p=2.9E−02 n=1 fg=0.02 bg=0.00
malate dehydrogenase (decarboxylating) (... GO:0004473 p=2.9E−02 n=1 fg=0.02 bg=0.00
SMC family protein binding GO:0043221 p=2.9E−02 n=1 fg=0.02 bg=0.00
translation elongation factor binding GO:0061770 p=2.9E−02 n=1 fg=0.02 bg=0.00
oxidized pyrimidine DNA binding GO:0032358 p=2.9E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=47/178 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001629605.3
fraction genes in fg and expected valu
bicellular tight junction GO:0005923 p=3.7E−03 n=3 fg=0.05 bg=0.01
rough endoplasmic reticulum membrane GO:0030867 p=5.2E−03 n=2 fg=0.04 bg=0.00
extrinsic component of cytoplasmic side ... GO:0031234 p=9.3E−03 n=3 fg=0.05 bg=0.01
nuclear matrix GO:0016363 p=1.3E−02 n=3 fg=0.05 bg=0.01
euchromatin GO:0000791 p=2.3E−02 n=2 fg=0.04 bg=0.00
phagocytic vesicle membrane GO:0030670 p=2.9E−02 n=2 fg=0.04 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=3.0E−02 n=1 fg=0.02 bg=0.00
BLOC−3 complex GO:0031085 p=3.0E−02 n=1 fg=0.02 bg=0.00
fascia adherens GO:0005916 p=3.0E−02 n=1 fg=0.02 bg=0.00
catenin−TCF7L2 complex GO:0071664 p=3.0E−02 n=1 fg=0.02 bg=0.00
Scrib−APC−beta−catenin complex GO:0034750 p=3.0E−02 n=1 fg=0.02 bg=0.00
beta−catenin−TCF7L2 complex GO:0070369 p=3.0E−02 n=1 fg=0.02 bg=0.00
platelet dense granule GO:0042827 p=3.0E−02 n=1 fg=0.02 bg=0.00
piP−body GO:0071547 p=3.0E−02 n=1 fg=0.02 bg=0.00
Pwp2p−containing subcomplex of 90S preri... GO:0034388 p=3.0E−02 n=1 fg=0.02 bg=0.00
beta−catenin destruction complex GO:0030877 p=3.0E−02 n=1 fg=0.02 bg=0.00
NF−kappaB complex GO:0071159 p=3.0E−02 n=1 fg=0.02 bg=0.00
protein kinase CK2 complex GO:0005956 p=3.0E−02 n=1 fg=0.02 bg=0.00
catenin complex GO:0016342 p=3.0E−02 n=1 fg=0.02 bg=0.00
ciliary base GO:0097546 p=4.2E−02 n=2 fg=0.04 bg=0.01
nuclear periphery GO:0034399 p=4.2E−02 n=3 fg=0.05 bg=0.01
perinuclear region of cytoplasm GO:0048471 p=4.3E−02 n=8 fg=0.15 bg=0.07
late endosome GO:0005770 p=4.5E−02 n=4 fg=0.07 bg=0.02
P granule GO:0043186 p=4.9E−02 n=2 fg=0.04 bg=0.01
polysome GO:0005844 p=4.9E−02 n=2 fg=0.04 bg=0.01
integral component of plasma membrane GO:0005887 p=5.0E−02 n=8 fg=0.15 bg=0.08
germ plasm GO:0060293 p=5.7E−02 n=2 fg=0.04 bg=0.01
pole plasm GO:0045495 p=5.7E−02 n=2 fg=0.04 bg=0.01
intercalated disc GO:0014704 p=5.7E−02 n=2 fg=0.04 bg=0.01
inner dynein arm GO:0036156 p=6.0E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=55/178 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction