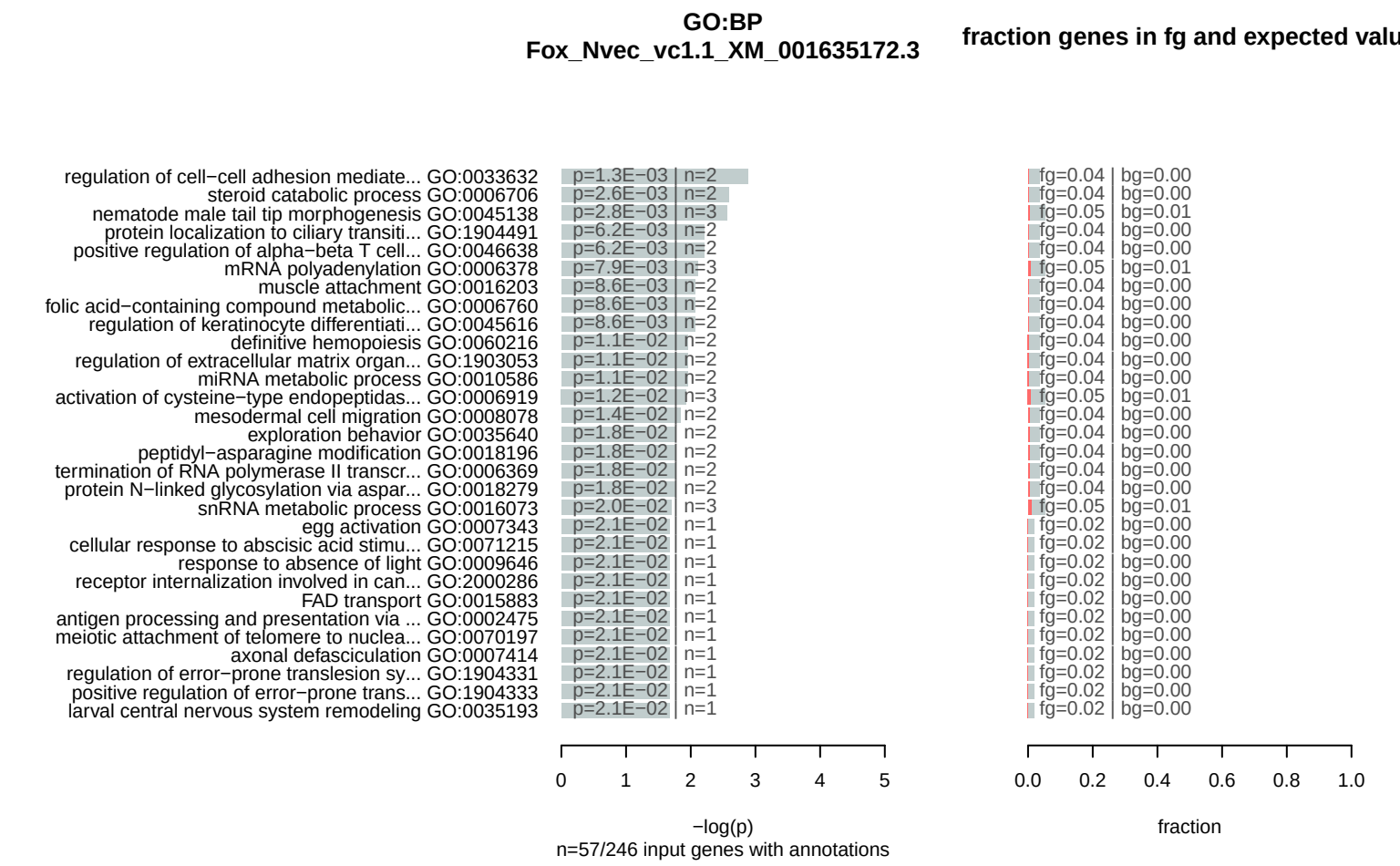
GO:BP
Fox_Nvec_vc1.1_XM_001635172.3
fraction genes in fg and expected valu
regulation of cell−cell adhesion mediate... GO:0033632 p=1.3E−03 n=2 fg=0.04 bg=0.00
steroid catabolic process GO:0006706 p=2.6E−03 n=2 fg=0.04 bg=0.00
nematode male tail tip morphogenesis GO:0045138 p=2.8E−03 n=3 fg=0.05 bg=0.01
protein localization to ciliary transiti... GO:1904491 p=6.2E−03 n=2 fg=0.04 bg=0.00
positive regulation of alpha−beta T cell... GO:0046638 p=6.2E−03 n=2 fg=0.04 bg=0.00
mRNA polyadenylation GO:0006378 p=7.9E−03 n=3 fg=0.05 bg=0.01
muscle attachment GO:0016203 p=8.6E−03 n=2 fg=0.04 bg=0.00
folic acid−containing compound metabolic... GO:0006760 p=8.6E−03 n=2 fg=0.04 bg=0.00
regulation of keratinocyte differentiati... GO:0045616 p=8.6E−03 n=2 fg=0.04 bg=0.00
definitive hemopoiesis GO:0060216 p=1.1E−02 n=2 fg=0.04 bg=0.00
regulation of extracellular matrix organ... GO:1903053 p=1.1E−02 n=2 fg=0.04 bg=0.00
miRNA metabolic process GO:0010586 p=1.1E−02 n=2 fg=0.04 bg=0.00
activation of cysteine−type endopeptidas... GO:0006919 p=1.2E−02 n=3 fg=0.05 bg=0.01
mesodermal cell migration GO:0008078 p=1.4E−02 n=2 fg=0.04 bg=0.00
exploration behavior GO:0035640 p=1.8E−02 n=2 fg=0.04 bg=0.00
peptidyl−asparagine modification GO:0018196 p=1.8E−02 n=2 fg=0.04 bg=0.00
termination of RNA polymerase II transcr... GO:0006369 p=1.8E−02 n=2 fg=0.04 bg=0.00
protein N−linked glycosylation via aspar... GO:0018279 p=1.8E−02 n=2 fg=0.04 bg=0.00
snRNA metabolic process GO:0016073 p=2.0E−02 n=3 fg=0.05 bg=0.01
egg activation GO:0007343 p=2.1E−02 n=1 fg=0.02 bg=0.00
cellular response to abscisic acid stimu... GO:0071215 p=2.1E−02 n=1 fg=0.02 bg=0.00
response to absence of light GO:0009646 p=2.1E−02 n=1 fg=0.02 bg=0.00
receptor internalization involved in can... GO:2000286 p=2.1E−02 n=1 fg=0.02 bg=0.00
FAD transport GO:0015883 p=2.1E−02 n=1 fg=0.02 bg=0.00
antigen processing and presentation via ... GO:0002475 p=2.1E−02 n=1 fg=0.02 bg=0.00
meiotic attachment of telomere to nuclea... GO:0070197 p=2.1E−02 n=1 fg=0.02 bg=0.00
axonal defasciculation GO:0007414 p=2.1E−02 n=1 fg=0.02 bg=0.00
regulation of error−prone translesion sy... GO:1904331 p=2.1E−02 n=1 fg=0.02 bg=0.00
positive regulation of error−prone trans... GO:1904333 p=2.1E−02 n=1 fg=0.02 bg=0.00
larval central nervous system remodeling GO:0035193 p=2.1E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=57/246 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_001635172.3
fraction genes in fg and expected valu
polynucleotide adenylyltransferase activ... GO:0004652 p=3.3E−04 n=3 fg=0.06 bg=0.00
protease binding GO:0002020 p=1.1E−02 n=3 fg=0.06 bg=0.01
collagen binding GO:0005518 p=1.2E−02 n=2 fg=0.04 bg=0.00
organophosphate ester transmembrane tran... GO:0015605 p=1.5E−02 n=2 fg=0.04 bg=0.00
vitamin transmembrane transporter activi... GO:0090482 p=1.5E−02 n=2 fg=0.04 bg=0.00
all−trans retinol 3,4−desaturase activit... GO:0061896 p=2.2E−02 n=1 fg=0.02 bg=0.00
all−trans retinal 3,4−desaturase activit... GO:0061897 p=2.2E−02 n=1 fg=0.02 bg=0.00
all−trans retinoic acid 3,4−desaturase a... GO:0061898 p=2.2E−02 n=1 fg=0.02 bg=0.00
11−cis−retinal 3,4−desaturase activity GO:0061899 p=2.2E−02 n=1 fg=0.02 bg=0.00
3−phosphoinositide−dependent protein kin... GO:0004676 p=2.2E−02 n=1 fg=0.02 bg=0.00
all−trans−retinol binding GO:1904768 p=2.2E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on the C... GO:0046997 p=2.2E−02 n=1 fg=0.02 bg=0.00
dimethylglycine dehydrogenase activity GO:0047865 p=2.2E−02 n=1 fg=0.02 bg=0.00
calcidiol 1−monooxygenase activity GO:0004498 p=2.2E−02 n=1 fg=0.02 bg=0.00
25−hydroxycholecalciferol−24−hydroxylase... GO:0008403 p=2.2E−02 n=1 fg=0.02 bg=0.00
retinol binding GO:0019841 p=2.2E−02 n=1 fg=0.02 bg=0.00
steroid hydroxylase activity GO:0008395 p=2.2E−02 n=1 fg=0.02 bg=0.00
neuregulin binding GO:0038132 p=2.2E−02 n=1 fg=0.02 bg=0.00
ubiquitin−like protein−specific endopept... GO:0070137 p=2.2E−02 n=1 fg=0.02 bg=0.00
SUMO−specific endopeptidase activity GO:0070139 p=2.2E−02 n=1 fg=0.02 bg=0.00
vitamin D 24−hydroxylase activity GO:0070576 p=2.2E−02 n=1 fg=0.02 bg=0.00
insulin−like growth factor I binding GO:0031994 p=2.2E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on paire... GO:0016709 p=2.2E−02 n=1 fg=0.02 bg=0.00
vitamin D 25−hydroxylase activity GO:0070643 p=2.2E−02 n=1 fg=0.02 bg=0.00
alpha−1,6−mannosylglycoprotein 2−beta−N−... GO:0008455 p=2.2E−02 n=1 fg=0.02 bg=0.00
hedgehog receptor activity GO:0008158 p=2.2E−02 n=1 fg=0.02 bg=0.00
1−alpha,25−dihydroxyvitamin D3 24−hydrox... GO:0030342 p=2.2E−02 n=1 fg=0.02 bg=0.00
vitamin D3 25−hydroxylase activity GO:0030343 p=2.2E−02 n=1 fg=0.02 bg=0.00
steryl−sulfatase activity GO:0004773 p=2.2E−02 n=1 fg=0.02 bg=0.00
cholesterol 26−hydroxylase activity GO:0031073 p=2.2E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=52/246 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001635172.3
fraction genes in fg and expected valu
muscle tendon junction GO:0005927 p=2.6E−03 n=2 fg=0.03 bg=0.00
nuclear envelope GO:0005635 p=1.5E−02 n=7 fg=0.12 bg=0.05
organelle envelope GO:0031967 p=1.6E−02 n=12 fg=0.21 bg=0.11
envelope GO:0031975 p=1.6E−02 n=12 fg=0.21 bg=0.11
polytene chromosome interband GO:0005705 p=1.8E−02 n=2 fg=0.03 bg=0.00
integrin alpha3−beta1 complex GO:0034667 p=2.1E−02 n=1 fg=0.02 bg=0.00
eukaryotic translation initiation factor... GO:0071540 p=2.1E−02 n=1 fg=0.02 bg=0.00
RNA−directed RNA polymerase complex GO:0031379 p=2.1E−02 n=1 fg=0.02 bg=0.00
integrin alpha6−beta4 complex GO:0034676 p=2.1E−02 n=1 fg=0.02 bg=0.00
integrin alpha7−beta1 complex GO:0034677 p=2.1E−02 n=1 fg=0.02 bg=0.00
core−binding factor complex GO:0016513 p=2.1E−02 n=1 fg=0.02 bg=0.00
AP−3 adaptor complex GO:0030123 p=2.1E−02 n=1 fg=0.02 bg=0.00
nuclear RNA−directed RNA polymerase comp... GO:0031380 p=2.1E−02 n=1 fg=0.02 bg=0.00
intracellular anatomical structure GO:0005622 p=3.3E−02 n=58 fg=1.00 bg=0.94
adherens junction GO:0005912 p=3.4E−02 n=4 fg=0.07 bg=0.02
nuclear protein−containing complex GO:0140513 p=3.5E−02 n=12 fg=0.21 bg=0.12
nuclear membrane GO:0031965 p=4.3E−02 n=4 fg=0.07 bg=0.02
box H/ACA RNP complex GO:0072588 p=4.3E−02 n=1 fg=0.02 bg=0.00
box H/ACA scaRNP complex GO:0072589 p=4.3E−02 n=1 fg=0.02 bg=0.00
box H/ACA telomerase RNP complex GO:0090661 p=4.3E−02 n=1 fg=0.02 bg=0.00
DRM complex GO:0070176 p=4.3E−02 n=1 fg=0.02 bg=0.00
TORC2 complex GO:0031932 p=4.3E−02 n=1 fg=0.02 bg=0.00
NELF complex GO:0032021 p=4.3E−02 n=1 fg=0.02 bg=0.00
box H/ACA snoRNP complex GO:0031429 p=4.3E−02 n=1 fg=0.02 bg=0.00
RSF complex GO:0031213 p=4.3E−02 n=1 fg=0.02 bg=0.00
U2AF complex GO:0089701 p=4.3E−02 n=1 fg=0.02 bg=0.00
transcription repressor complex GO:0017053 p=5.6E−02 n=2 fg=0.03 bg=0.01
ciliary basal body GO:0036064 p=6.0E−02 n=3 fg=0.05 bg=0.02
intracellular organelle GO:0043229 p=6.1E−02 n=53 fg=0.91 bg=0.83
TORC1 complex GO:0031931 p=6.3E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=58/246 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction