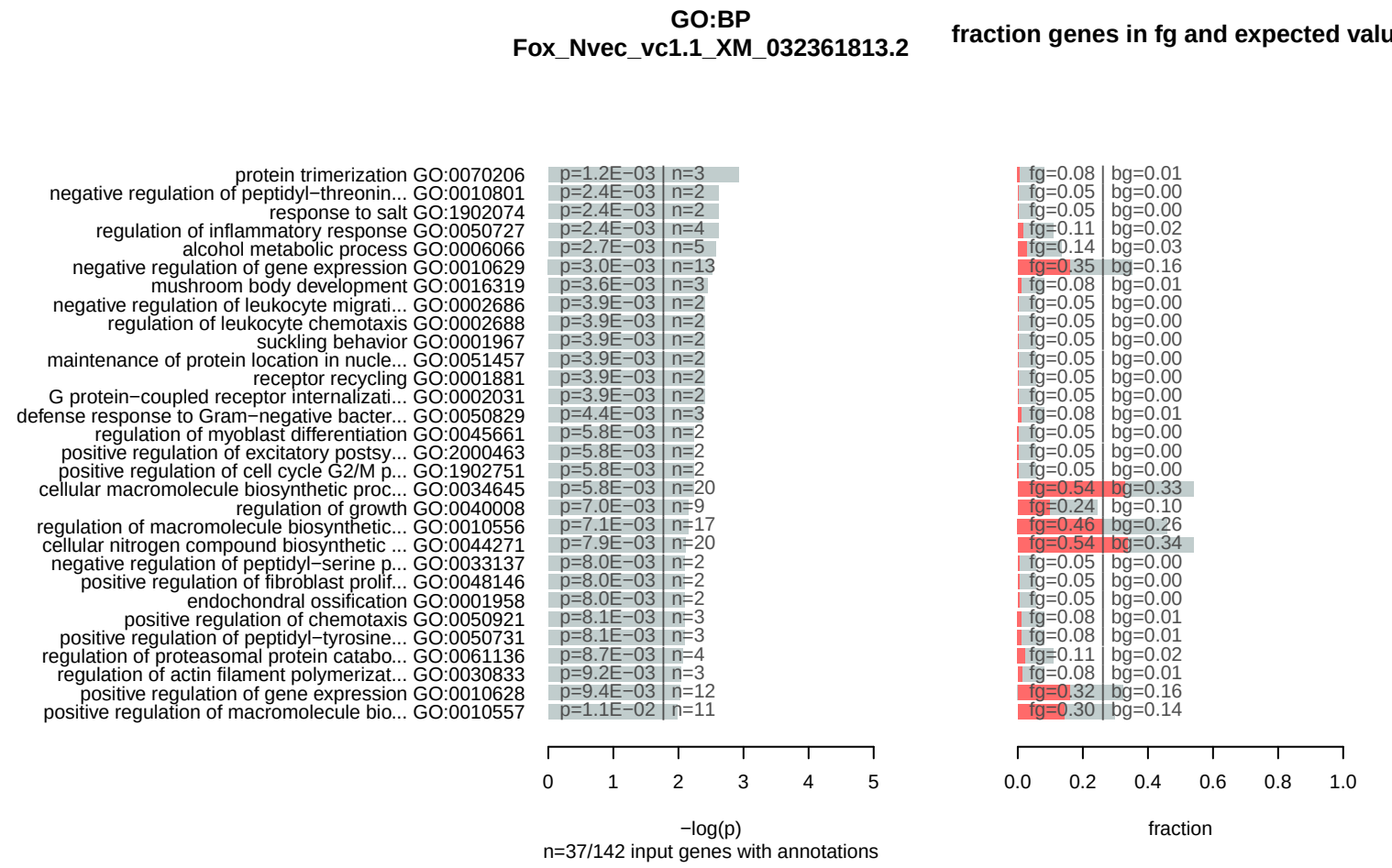
GO:BP
Fox_Nvec_vc1.1_XM_032361813.2
fraction genes in fg and expected valu
protein trimerization GO:0070206 p=1.2E−03 n=3 fg=0.08 bg=0.01
negative regulation of peptidyl−threonin... GO:0010801 p=2.4E−03 n=2 fg=0.05 bg=0.00
response to salt GO:1902074 p=2.4E−03 n=2 fg=0.05 bg=0.00
regulation of inflammatory response GO:0050727 p=2.4E−03 n=4 fg=0.11 bg=0.02
alcohol metabolic process GO:0006066 p=2.7E−03 n=5 fg=0.14 bg=0.03
negative regulation of gene expression GO:0010629 p=3.0E−03 n=13 fg=0.35 bg=0.16
mushroom body development GO:0016319 p=3.6E−03 n=3 fg=0.08 bg=0.01
negative regulation of leukocyte migrati... GO:0002686 p=3.9E−03 n=2 fg=0.05 bg=0.00
regulation of leukocyte chemotaxis GO:0002688 p=3.9E−03 n=2 fg=0.05 bg=0.00
suckling behavior GO:0001967 p=3.9E−03 n=2 fg=0.05 bg=0.00
maintenance of protein location in nucle... GO:0051457 p=3.9E−03 n=2 fg=0.05 bg=0.00
receptor recycling GO:0001881 p=3.9E−03 n=2 fg=0.05 bg=0.00
G protein−coupled receptor internalizati... GO:0002031 p=3.9E−03 n=2 fg=0.05 bg=0.00
defense response to Gram−negative bacter... GO:0050829 p=4.4E−03 n=3 fg=0.08 bg=0.01
regulation of myoblast differentiation GO:0045661 p=5.8E−03 n=2 fg=0.05 bg=0.00
positive regulation of excitatory postsy... GO:2000463 p=5.8E−03 n=2 fg=0.05 bg=0.00
positive regulation of cell cycle G2/M p... GO:1902751 p=5.8E−03 n=2 fg=0.05 bg=0.00
cellular macromolecule biosynthetic proc... GO:0034645 p=5.8E−03 n=20 fg=0.54 bg=0.33
regulation of growth GO:0040008 p=7.0E−03 n=9 fg=0.24 bg=0.10
regulation of macromolecule biosynthetic... GO:0010556 p=7.1E−03 n=17 fg=0.46 bg=0.26
cellular nitrogen compound biosynthetic ... GO:0044271 p=7.9E−03 n=20 fg=0.54 bg=0.34
negative regulation of peptidyl−serine p... GO:0033137 p=8.0E−03 n=2 fg=0.05 bg=0.00
positive regulation of fibroblast prolif... GO:0048146 p=8.0E−03 n=2 fg=0.05 bg=0.00
endochondral ossification GO:0001958 p=8.0E−03 n=2 fg=0.05 bg=0.00
positive regulation of chemotaxis GO:0050921 p=8.1E−03 n=3 fg=0.08 bg=0.01
positive regulation of peptidyl−tyrosine... GO:0050731 p=8.1E−03 n=3 fg=0.08 bg=0.01
regulation of proteasomal protein catabo... GO:0061136 p=8.7E−03 n=4 fg=0.11 bg=0.02
regulation of actin filament polymerizat... GO:0030833 p=9.2E−03 n=3 fg=0.08 bg=0.01
positive regulation of gene expression GO:0010628 p=9.4E−03 n=12 fg=0.32 bg=0.16
positive regulation of macromolecule bio... GO:0010557 p=1.1E−02 n=11 fg=0.30 bg=0.14
0 1 2 3 4 5
−log(p)
n=37/142 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032361813.2
fraction genes in fg and expected valu
lipid binding GO:0008289 p=2.0E−03 n=7 fg=0.19 bg=0.05
transcription factor binding GO:0008134 p=3.9E−03 n=8 fg=0.22 bg=0.07
phospholipid binding GO:0005543 p=1.5E−02 n=5 fg=0.14 bg=0.04
phosphatidylinositol binding GO:0035091 p=1.8E−02 n=4 fg=0.11 bg=0.03
ribonuclease III activity GO:0004525 p=2.3E−02 n=1 fg=0.03 bg=0.00
double−stranded RNA−specific ribonucleas... GO:0032296 p=2.3E−02 n=1 fg=0.03 bg=0.00
beta−adrenergic receptor kinase activity GO:0047696 p=2.3E−02 n=1 fg=0.03 bg=0.00
methylmalonyl−CoA mutase activity GO:0004494 p=2.3E−02 n=1 fg=0.03 bg=0.00
acetylcholine receptor regulator activit... GO:0030548 p=2.3E−02 n=1 fg=0.03 bg=0.00
acetylcholine receptor activator activit... GO:0030549 p=2.3E−02 n=1 fg=0.03 bg=0.00
endothelial differentiation G protein−co... GO:0031753 p=2.3E−02 n=1 fg=0.03 bg=0.00
Edg−2 lysophosphatidic acid receptor bin... GO:0031755 p=2.3E−02 n=1 fg=0.03 bg=0.00
rhodopsin kinase activity GO:0050254 p=2.3E−02 n=1 fg=0.03 bg=0.00
G protein−coupled receptor kinase activi... GO:0004703 p=2.3E−02 n=1 fg=0.03 bg=0.00
delta−type opioid receptor binding GO:0031850 p=2.3E−02 n=1 fg=0.03 bg=0.00
kappa−type opioid receptor binding GO:0031851 p=2.3E−02 n=1 fg=0.03 bg=0.00
cobalamin binding GO:0031419 p=2.3E−02 n=1 fg=0.03 bg=0.00
translation elongation factor binding GO:0061770 p=2.3E−02 n=1 fg=0.03 bg=0.00
RNA strand−exchange activity GO:0034057 p=2.3E−02 n=1 fg=0.03 bg=0.00
RNA strand annealing activity GO:0033592 p=2.3E−02 n=1 fg=0.03 bg=0.00
calcitonin family binding GO:0097644 p=2.3E−02 n=1 fg=0.03 bg=0.00
neurotransmitter receptor regulator acti... GO:0099602 p=2.3E−02 n=1 fg=0.03 bg=0.00
amylin binding GO:0097645 p=2.3E−02 n=1 fg=0.03 bg=0.00
lipopolysaccharide binding GO:0001530 p=2.3E−02 n=1 fg=0.03 bg=0.00
protein O−GlcNAc transferase activity GO:0097363 p=2.3E−02 n=1 fg=0.03 bg=0.00
heparan sulfate binding GO:1904399 p=2.3E−02 n=1 fg=0.03 bg=0.00
opioid receptor binding GO:0031628 p=2.3E−02 n=1 fg=0.03 bg=0.00
protein N−acetylglucosaminyltransferase ... GO:0016262 p=2.3E−02 n=1 fg=0.03 bg=0.00
glycoprotein endo−alpha−1,2−mannosidase ... GO:0004569 p=2.3E−02 n=1 fg=0.03 bg=0.00
platelet−derived growth factor receptor ... GO:0005161 p=2.3E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=36/142 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032361813.2
fraction genes in fg and expected valu
PML body GO:0016605 p=9.8E−03 n=2 fg=0.05 bg=0.00
euchromatin GO:0000791 p=1.3E−02 n=2 fg=0.05 bg=0.00
large ribosomal subunit GO:0015934 p=1.3E−02 n=2 fg=0.05 bg=0.00
late endosome GO:0005770 p=1.7E−02 n=4 fg=0.10 bg=0.02
early endosome GO:0005769 p=1.8E−02 n=5 fg=0.12 bg=0.04
ribonucleoprotein complex GO:1990904 p=2.1E−02 n=7 fg=0.17 bg=0.07
non−membrane−bounded organelle GO:0043228 p=2.2E−02 n=19 fg=0.46 bg=0.30
intracellular non−membrane−bounded organ... GO:0043232 p=2.2E−02 n=19 fg=0.46 bg=0.30
RNA polymerase III transcription regulat... GO:0090576 p=2.3E−02 n=1 fg=0.02 bg=0.00
ribonuclease III complex GO:1903095 p=2.3E−02 n=1 fg=0.02 bg=0.00
amyloid−beta complex GO:0106003 p=2.3E−02 n=1 fg=0.02 bg=0.00
microprocessor complex GO:0070877 p=2.3E−02 n=1 fg=0.02 bg=0.00
intermediate−density lipoprotein particl... GO:0034363 p=2.3E−02 n=1 fg=0.02 bg=0.00
high−density lipoprotein particle GO:0034364 p=2.3E−02 n=1 fg=0.02 bg=0.00
lipoprotein particle GO:1990777 p=2.3E−02 n=1 fg=0.02 bg=0.00
transcription factor TFIIIC complex GO:0000127 p=2.3E−02 n=1 fg=0.02 bg=0.00
plasma lipoprotein particle GO:0034358 p=2.3E−02 n=1 fg=0.02 bg=0.00
varicosity GO:0043196 p=2.3E−02 n=1 fg=0.02 bg=0.00
triglyceride−rich plasma lipoprotein par... GO:0034385 p=2.3E−02 n=1 fg=0.02 bg=0.00
zeta DNA polymerase complex GO:0016035 p=2.3E−02 n=1 fg=0.02 bg=0.00
polytene chromosome chromocenter GO:0005701 p=2.3E−02 n=1 fg=0.02 bg=0.00
endosome to plasma membrane transport ve... GO:0070381 p=2.3E−02 n=1 fg=0.02 bg=0.00
eukaryotic translation initiation factor... GO:0016281 p=2.3E−02 n=1 fg=0.02 bg=0.00
bleb GO:0032059 p=2.3E−02 n=1 fg=0.02 bg=0.00
transcription regulator complex GO:0005667 p=2.8E−02 n=5 fg=0.12 bg=0.04
neuromuscular junction GO:0031594 p=3.7E−02 n=3 fg=0.07 bg=0.02
striated muscle thin filament GO:0005865 p=4.5E−02 n=1 fg=0.02 bg=0.00
endosome lumen GO:0031904 p=4.5E−02 n=1 fg=0.02 bg=0.00
ciliary rootlet GO:0035253 p=4.5E−02 n=1 fg=0.02 bg=0.00
platelet alpha granule membrane GO:0031092 p=4.5E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=41/142 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction