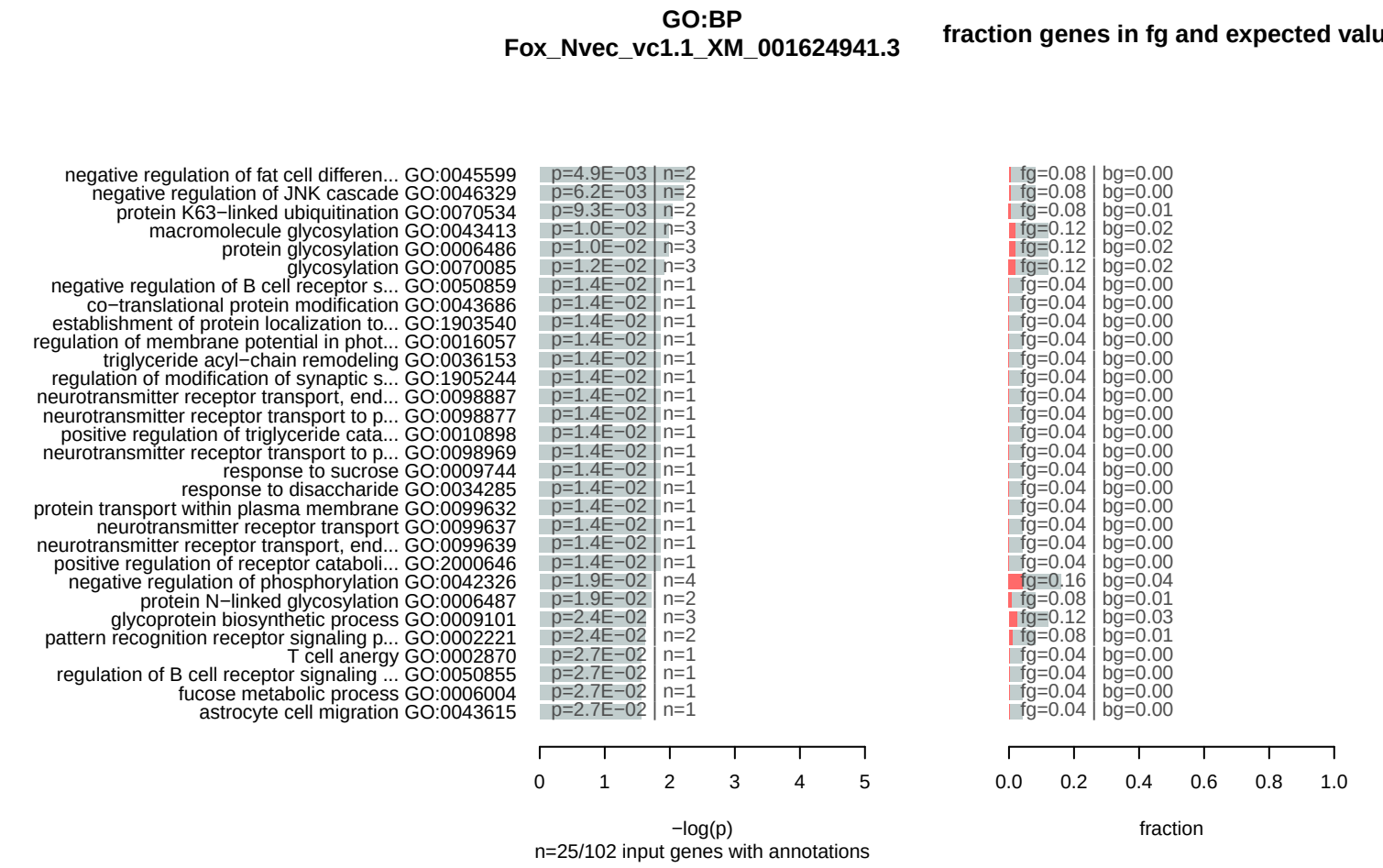
GO:BP
Fox_Nvec_vc1.1_XM_001624941.3
fraction genes in fg and expected valu
negative regulation of fat cell differen... GO:0045599 p=4.9E−03 n=2 fg=0.08 bg=0.00
negative regulation of JNK cascade GO:0046329 p=6.2E−03 n=2 fg=0.08 bg=0.00
protein K63−linked ubiquitination GO:0070534 p=9.3E−03 n=2 fg=0.08 bg=0.01
macromolecule glycosylation GO:0043413 p=1.0E−02 n=3 fg=0.12 bg=0.02
protein glycosylation GO:0006486 p=1.0E−02 n=3 fg=0.12 bg=0.02
glycosylation GO:0070085 p=1.2E−02 n=3 fg=0.12 bg=0.02
negative regulation of B cell receptor s... GO:0050859 p=1.4E−02 n=1 fg=0.04 bg=0.00
co−translational protein modification GO:0043686 p=1.4E−02 n=1 fg=0.04 bg=0.00
establishment of protein localization to... GO:1903540 p=1.4E−02 n=1 fg=0.04 bg=0.00
regulation of membrane potential in phot... GO:0016057 p=1.4E−02 n=1 fg=0.04 bg=0.00
triglyceride acyl−chain remodeling GO:0036153 p=1.4E−02 n=1 fg=0.04 bg=0.00
regulation of modification of synaptic s... GO:1905244 p=1.4E−02 n=1 fg=0.04 bg=0.00
neurotransmitter receptor transport, end... GO:0098887 p=1.4E−02 n=1 fg=0.04 bg=0.00
neurotransmitter receptor transport to p... GO:0098877 p=1.4E−02 n=1 fg=0.04 bg=0.00
positive regulation of triglyceride cata... GO:0010898 p=1.4E−02 n=1 fg=0.04 bg=0.00
neurotransmitter receptor transport to p... GO:0098969 p=1.4E−02 n=1 fg=0.04 bg=0.00
response to sucrose GO:0009744 p=1.4E−02 n=1 fg=0.04 bg=0.00
response to disaccharide GO:0034285 p=1.4E−02 n=1 fg=0.04 bg=0.00
protein transport within plasma membrane GO:0099632 p=1.4E−02 n=1 fg=0.04 bg=0.00
neurotransmitter receptor transport GO:0099637 p=1.4E−02 n=1 fg=0.04 bg=0.00
neurotransmitter receptor transport, end... GO:0099639 p=1.4E−02 n=1 fg=0.04 bg=0.00
positive regulation of receptor cataboli... GO:2000646 p=1.4E−02 n=1 fg=0.04 bg=0.00
negative regulation of phosphorylation GO:0042326 p=1.9E−02 n=4 fg=0.16 bg=0.04
protein N−linked glycosylation GO:0006487 p=1.9E−02 n=2 fg=0.08 bg=0.01
glycoprotein biosynthetic process GO:0009101 p=2.4E−02 n=3 fg=0.12 bg=0.03
pattern recognition receptor signaling p... GO:0002221 p=2.4E−02 n=2 fg=0.08 bg=0.01
T cell anergy GO:0002870 p=2.7E−02 n=1 fg=0.04 bg=0.00
regulation of B cell receptor signaling ... GO:0050855 p=2.7E−02 n=1 fg=0.04 bg=0.00
fucose metabolic process GO:0006004 p=2.7E−02 n=1 fg=0.04 bg=0.00
astrocyte cell migration GO:0043615 p=2.7E−02 n=1 fg=0.04 bg=0.00
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−log(p)
n=25/102 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_001624941.3
fraction genes in fg and expected valu
phospholipase A2 activity GO:0004623 p=1.1E−03 n=2 fg=0.09 bg=0.00
G protein−coupled receptor binding GO:0001664 p=1.0E−02 n=3 fg=0.14 bg=0.02
dolichyl−diphosphooligosaccharide−protei... GO:0004579 p=1.4E−02 n=1 fg=0.05 bg=0.00
mono−olein transacylation activity GO:0051264 p=1.4E−02 n=1 fg=0.05 bg=0.00
diolein transacylation activity GO:0051265 p=1.4E−02 n=1 fg=0.05 bg=0.00
1−alkyl−2−acetylglycerophosphocholine es... GO:0003847 p=1.4E−02 n=1 fg=0.05 bg=0.00
lysophosphatidic acid binding GO:0035727 p=1.4E−02 n=1 fg=0.05 bg=0.00
D5 dopamine receptor binding GO:0031752 p=1.4E−02 n=1 fg=0.05 bg=0.00
CXCR chemokine receptor binding GO:0045236 p=1.4E−02 n=1 fg=0.05 bg=0.00
lipoprotein lipase activity GO:0004465 p=1.4E−02 n=1 fg=0.05 bg=0.00
cAMP−dependent protein kinase inhibitor ... GO:0004862 p=2.8E−02 n=1 fg=0.05 bg=0.00
chemokine receptor binding GO:0042379 p=2.8E−02 n=1 fg=0.05 bg=0.00
platelet−activating factor acetyltransfe... GO:0047179 p=2.8E−02 n=1 fg=0.05 bg=0.00
long−chain fatty acyl−CoA binding GO:0036042 p=2.8E−02 n=1 fg=0.05 bg=0.00
high voltage−gated calcium channel activ... GO:0008331 p=2.8E−02 n=1 fg=0.05 bg=0.00
low voltage−gated calcium channel activi... GO:0008332 p=2.8E−02 n=1 fg=0.05 bg=0.00
cAMP−dependent protein kinase regulator ... GO:0008603 p=2.8E−02 n=1 fg=0.05 bg=0.00
metallochaperone activity GO:0016530 p=2.8E−02 n=1 fg=0.05 bg=0.00
copper chaperone activity GO:0016531 p=2.8E−02 n=1 fg=0.05 bg=0.00
superoxide dismutase copper chaperone ac... GO:0016532 p=2.8E−02 n=1 fg=0.05 bg=0.00
protein kinase A catalytic subunit bindi... GO:0034236 p=2.8E−02 n=1 fg=0.05 bg=0.00
asparaginase activity GO:0004067 p=2.8E−02 n=1 fg=0.05 bg=0.00
beta−2 adrenergic receptor binding GO:0031698 p=2.8E−02 n=1 fg=0.05 bg=0.00
oligosaccharyl transferase activity GO:0004576 p=2.8E−02 n=1 fg=0.05 bg=0.00
acyltransferase activity, transferring g... GO:0016747 p=3.3E−02 n=2 fg=0.09 bg=0.01
acyltransferase activity GO:0016746 p=3.9E−02 n=2 fg=0.09 bg=0.01
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=4.1E−02 n=1 fg=0.05 bg=0.00
acyl−CoA binding GO:0120227 p=4.1E−02 n=1 fg=0.05 bg=0.00
triglyceride lipase activity GO:0004806 p=4.1E−02 n=1 fg=0.05 bg=0.00
fatty−acyl−CoA binding GO:0000062 p=4.1E−02 n=1 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=22/102 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001624941.3
fraction genes in fg and expected valu
ciliary base GO:0097546 p=1.1E−02 n=2 fg=0.07 bg=0.01
postsynaptic endosome GO:0098845 p=1.5E−02 n=1 fg=0.04 bg=0.00
postsynaptic recycling endosome GO:0098837 p=1.5E−02 n=1 fg=0.04 bg=0.00
transcription repressor complex GO:0017053 p=1.5E−02 n=2 fg=0.07 bg=0.01
intracellular protein−containing complex GO:0140535 p=2.3E−02 n=6 fg=0.22 bg=0.09
transcription regulator complex GO:0005667 p=2.5E−02 n=4 fg=0.15 bg=0.04
presynaptic active zone GO:0048786 p=2.8E−02 n=2 fg=0.07 bg=0.01
oligosaccharyltransferase complex GO:0008250 p=3.0E−02 n=1 fg=0.04 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=4.4E−02 n=1 fg=0.04 bg=0.00
nucleotide−activated protein kinase comp... GO:0031588 p=4.4E−02 n=1 fg=0.04 bg=0.00
transferase complex GO:1990234 p=5.5E−02 n=5 fg=0.19 bg=0.08
germinal vesicle GO:0042585 p=5.8E−02 n=1 fg=0.04 bg=0.00
ubiquitin ligase complex GO:0000151 p=6.2E−02 n=3 fg=0.11 bg=0.03
catalytic complex GO:1902494 p=6.5E−02 n=7 fg=0.26 bg=0.14
endoplasmic reticulum lumen GO:0005788 p=7.2E−02 n=2 fg=0.07 bg=0.02
voltage−gated calcium channel complex GO:0005891 p=7.3E−02 n=1 fg=0.04 bg=0.00
female germ cell nucleus GO:0001674 p=7.3E−02 n=1 fg=0.04 bg=0.00
TRAPP complex GO:0030008 p=7.3E−02 n=1 fg=0.04 bg=0.00
presynaptic active zone membrane GO:0048787 p=7.3E−02 n=1 fg=0.04 bg=0.00
heterotrimeric G−protein complex GO:0005834 p=8.6E−02 n=1 fg=0.04 bg=0.00
GTPase complex GO:1905360 p=8.6E−02 n=1 fg=0.04 bg=0.00
secretory granule lumen GO:0034774 p=9.9E−02 n=2 fg=0.07 bg=0.02
Golgi cisterna membrane GO:0032580 p=1.0E−01 n=1 fg=0.04 bg=0.00
calcium channel complex GO:0034704 p=1.0E−01 n=1 fg=0.04 bg=0.00
Cul4−RING E3 ubiquitin ligase complex GO:0080008 p=1.0E−01 n=1 fg=0.04 bg=0.00
vesicle lumen GO:0031983 p=1.1E−01 n=2 fg=0.07 bg=0.02
cytoplasmic vesicle lumen GO:0060205 p=1.1E−01 n=2 fg=0.07 bg=0.02
germ cell nucleus GO:0043073 p=1.1E−01 n=1 fg=0.04 bg=0.00
T−tubule GO:0030315 p=1.4E−01 n=1 fg=0.04 bg=0.01
proteasome complex GO:0000502 p=1.5E−01 n=1 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=27/102 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction