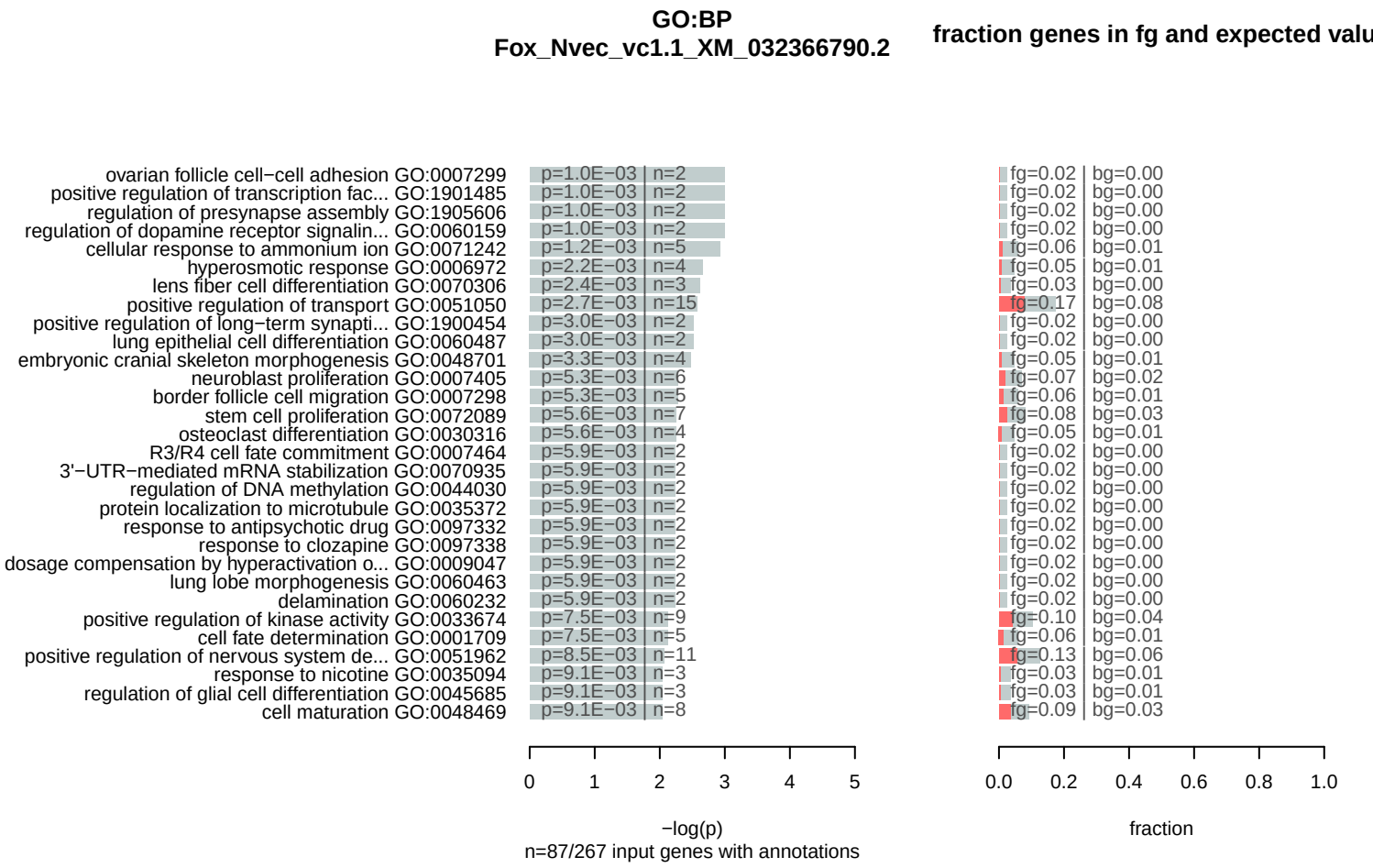
GO:BP
Fox_Nvec_vc1.1_XM_032366790.2
fraction genes in fg and expected valu
ovarian follicle cell−cell adhesion GO:0007299 p=1.0E−03 n=2 fg=0.02 bg=0.00
positive regulation of transcription fac... GO:1901485 p=1.0E−03 n=2 fg=0.02 bg=0.00
regulation of presynapse assembly GO:1905606 p=1.0E−03 n=2 fg=0.02 bg=0.00
regulation of dopamine receptor signalin... GO:0060159 p=1.0E−03 n=2 fg=0.02 bg=0.00
cellular response to ammonium ion GO:0071242 p=1.2E−03 n=5 fg=0.06 bg=0.01
hyperosmotic response GO:0006972 p=2.2E−03 n=4 fg=0.05 bg=0.01
lens fiber cell differentiation GO:0070306 p=2.4E−03 n=3 fg=0.03 bg=0.00
positive regulation of transport GO:0051050 p=2.7E−03 n=15 fg=0.17 bg=0.08
positive regulation of long−term synapti... GO:1900454 p=3.0E−03 n=2 fg=0.02 bg=0.00
lung epithelial cell differentiation GO:0060487 p=3.0E−03 n=2 fg=0.02 bg=0.00
embryonic cranial skeleton morphogenesis GO:0048701 p=3.3E−03 n=4 fg=0.05 bg=0.01
neuroblast proliferation GO:0007405 p=5.3E−03 n=6 fg=0.07 bg=0.02
border follicle cell migration GO:0007298 p=5.3E−03 n=5 fg=0.06 bg=0.01
stem cell proliferation GO:0072089 p=5.6E−03 n=7 fg=0.08 bg=0.03
osteoclast differentiation GO:0030316 p=5.6E−03 n=4 fg=0.05 bg=0.01
R3/R4 cell fate commitment GO:0007464 p=5.9E−03 n=2 fg=0.02 bg=0.00
3'−UTR−mediated mRNA stabilization GO:0070935 p=5.9E−03 n=2 fg=0.02 bg=0.00
regulation of DNA methylation GO:0044030 p=5.9E−03 n=2 fg=0.02 bg=0.00
protein localization to microtubule GO:0035372 p=5.9E−03 n=2 fg=0.02 bg=0.00
response to antipsychotic drug GO:0097332 p=5.9E−03 n=2 fg=0.02 bg=0.00
response to clozapine GO:0097338 p=5.9E−03 n=2 fg=0.02 bg=0.00
dosage compensation by hyperactivation o... GO:0009047 p=5.9E−03 n=2 fg=0.02 bg=0.00
lung lobe morphogenesis GO:0060463 p=5.9E−03 n=2 fg=0.02 bg=0.00
delamination GO:0060232 p=5.9E−03 n=2 fg=0.02 bg=0.00
positive regulation of kinase activity GO:0033674 p=7.5E−03 n=9 fg=0.10 bg=0.04
cell fate determination GO:0001709 p=7.5E−03 n=5 fg=0.06 bg=0.01
positive regulation of nervous system de... GO:0051962 p=8.5E−03 n=11 fg=0.13 bg=0.06
response to nicotine GO:0035094 p=9.1E−03 n=3 fg=0.03 bg=0.01
regulation of glial cell differentiation GO:0045685 p=9.1E−03 n=3 fg=0.03 bg=0.01
cell maturation GO:0048469 p=9.1E−03 n=8 fg=0.09 bg=0.03
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−log(p)
n=87/267 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032366790.2
fraction genes in fg and expected valu
protein kinase activity GO:0004672 p=3.6E−03 n=10 fg=0.14 bg=0.05
protein binding GO:0005515 p=5.1E−03 n=53 fg=0.74 bg=0.59
MAP kinase kinase activity GO:0004708 p=1.3E−02 n=2 fg=0.03 bg=0.00
kinesin binding GO:0019894 p=1.3E−02 n=3 fg=0.04 bg=0.01
adrenergic receptor binding GO:0031690 p=1.7E−02 n=2 fg=0.03 bg=0.00
dopamine receptor binding GO:0050780 p=1.7E−02 n=2 fg=0.03 bg=0.00
scaffold protein binding GO:0097110 p=2.1E−02 n=3 fg=0.04 bg=0.01
DNA−binding transcription activator acti... GO:0001228 p=2.3E−02 n=6 fg=0.08 bg=0.03
DNA−binding transcription activator acti... GO:0001216 p=2.3E−02 n=6 fg=0.08 bg=0.03
protein serine/threonine kinase activity GO:0004674 p=2.7E−02 n=7 fg=0.10 bg=0.04
transcription coregulator binding GO:0001221 p=2.9E−02 n=2 fg=0.03 bg=0.00
beta−adrenergic receptor kinase activity GO:0047696 p=3.0E−02 n=1 fg=0.01 bg=0.00
nitrite reductase (NO−forming) activity GO:0050421 p=3.0E−02 n=1 fg=0.01 bg=0.00
protein−arginine omega−N symmetric methy... GO:0035243 p=3.0E−02 n=1 fg=0.01 bg=0.00
delta−type opioid receptor binding GO:0031850 p=3.0E−02 n=1 fg=0.01 bg=0.00
kappa−type opioid receptor binding GO:0031851 p=3.0E−02 n=1 fg=0.01 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=3.0E−02 n=1 fg=0.01 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=3.0E−02 n=1 fg=0.01 bg=0.00
fructose binding GO:0070061 p=3.0E−02 n=1 fg=0.01 bg=0.00
pre−miRNA binding GO:0070883 p=3.0E−02 n=1 fg=0.01 bg=0.00
rhodopsin kinase activity GO:0050254 p=3.0E−02 n=1 fg=0.01 bg=0.00
[myelin basic protein]−arginine N−methyl... GO:0016277 p=3.0E−02 n=1 fg=0.01 bg=0.00
fatty acid alpha−hydroxylase activity GO:0080132 p=3.0E−02 n=1 fg=0.01 bg=0.00
6−phosphofructokinase activity GO:0003872 p=3.0E−02 n=1 fg=0.01 bg=0.00
histone deacetylase regulator activity GO:0035033 p=3.0E−02 n=1 fg=0.01 bg=0.00
endothelial differentiation G protein−co... GO:0031753 p=3.0E−02 n=1 fg=0.01 bg=0.00
Edg−2 lysophosphatidic acid receptor bin... GO:0031755 p=3.0E−02 n=1 fg=0.01 bg=0.00
nitrite reductase activity GO:0098809 p=3.0E−02 n=1 fg=0.01 bg=0.00
CD4 receptor binding GO:0042609 p=3.0E−02 n=1 fg=0.01 bg=0.00
DNA clamp loader activity GO:0003689 p=3.0E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=72/267 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032366790.2
fraction genes in fg and expected valu
stress fiber GO:0001725 p=3.6E−03 n=3 fg=0.03 bg=0.00
dendritic shaft GO:0043198 p=5.3E−03 n=4 fg=0.04 bg=0.01
dendritic spine GO:0043197 p=6.9E−03 n=6 fg=0.07 bg=0.02
intracellular non−membrane−bounded organ... GO:0043232 p=7.5E−03 n=43 fg=0.48 bg=0.33
presynaptic periactive zone GO:0036062 p=1.0E−02 n=2 fg=0.02 bg=0.00
cytoplasmic region GO:0099568 p=1.4E−02 n=10 fg=0.11 bg=0.05
vacuolar proton−transporting V−type ATPa... GO:0016471 p=2.1E−02 n=2 fg=0.02 bg=0.00
sperm flagellum GO:0036126 p=2.5E−02 n=4 fg=0.04 bg=0.01
nuclear lumen GO:0031981 p=2.6E−02 n=40 fg=0.44 bg=0.34
proton−transporting V−type ATPase comple... GO:0033176 p=2.7E−02 n=2 fg=0.02 bg=0.00
9+2 motile cilium GO:0097729 p=3.0E−02 n=4 fg=0.04 bg=0.01
cytoplasmic side of dendritic spine plas... GO:1990780 p=3.3E−02 n=1 fg=0.01 bg=0.00
UBC13−UEV1A complex GO:0035370 p=3.3E−02 n=1 fg=0.01 bg=0.00
RCAF complex GO:0035059 p=3.3E−02 n=1 fg=0.01 bg=0.00
septin collar GO:0032173 p=3.3E−02 n=1 fg=0.01 bg=0.00
ATF4−CREB1 transcription factor complex GO:1990589 p=3.3E−02 n=1 fg=0.01 bg=0.00
growth cone leading edge GO:0061850 p=3.3E−02 n=1 fg=0.01 bg=0.00
RNA nuclear export complex GO:0042565 p=3.3E−02 n=1 fg=0.01 bg=0.00
Ski complex GO:0055087 p=3.3E−02 n=1 fg=0.01 bg=0.00
6−phosphofructokinase complex GO:0005945 p=3.3E−02 n=1 fg=0.01 bg=0.00
anterior cell cortex GO:0061802 p=3.3E−02 n=1 fg=0.01 bg=0.00
nuclear RNA export factor complex GO:0042272 p=3.3E−02 n=1 fg=0.01 bg=0.00
MSL complex GO:0072487 p=3.3E−02 n=1 fg=0.01 bg=0.00
Schmidt−Lanterman incisure GO:0043220 p=3.3E−02 n=1 fg=0.01 bg=0.00
internode region of axon GO:0033269 p=3.3E−02 n=1 fg=0.01 bg=0.00
dosage compensation complex GO:0046536 p=3.3E−02 n=1 fg=0.01 bg=0.00
compact myelin GO:0043218 p=3.3E−02 n=1 fg=0.01 bg=0.00
dendritic spine head GO:0044327 p=3.3E−02 n=1 fg=0.01 bg=0.00
X chromosome located dosage compensation... GO:0016456 p=3.3E−02 n=1 fg=0.01 bg=0.00
chromocenter GO:0010369 p=3.4E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=90/267 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction