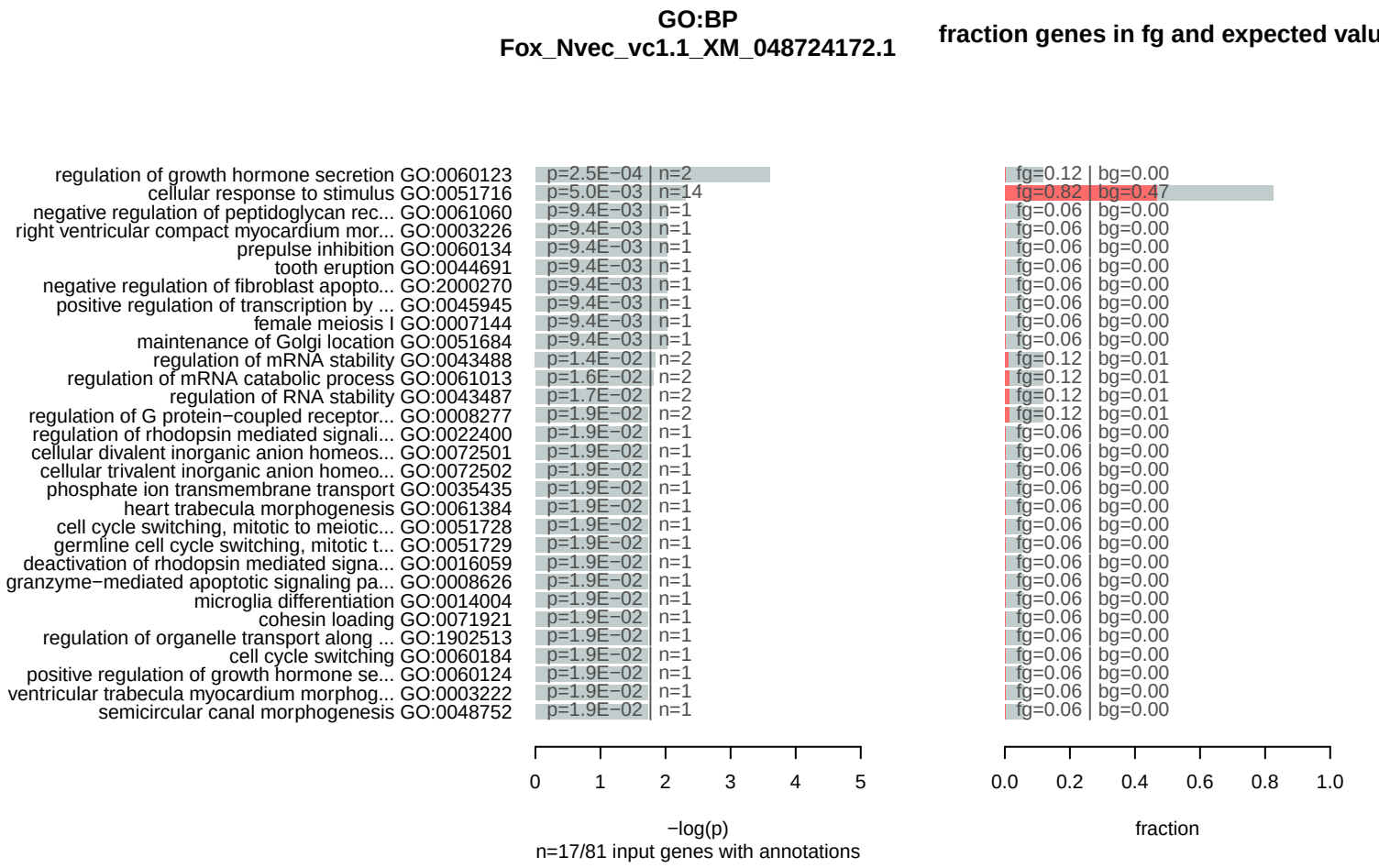
GO:BP
Fox_Nvec_vc1.1_XM_048724172.1
fraction genes in fg and expected valu
regulation of growth hormone secretion GO:0060123 p=2.5E−04 n=2 fg=0.12 bg=0.00
cellular response to stimulus GO:0051716 p=5.0E−03 n=14 fg=0.82 bg=0.47
negative regulation of peptidoglycan rec... GO:0061060 p=9.4E−03 n=1 fg=0.06 bg=0.00
right ventricular compact myocardium mor... GO:0003226 p=9.4E−03 n=1 fg=0.06 bg=0.00
prepulse inhibition GO:0060134 p=9.4E−03 n=1 fg=0.06 bg=0.00
tooth eruption GO:0044691 p=9.4E−03 n=1 fg=0.06 bg=0.00
negative regulation of fibroblast apopto... GO:2000270 p=9.4E−03 n=1 fg=0.06 bg=0.00
positive regulation of transcription by ... GO:0045945 p=9.4E−03 n=1 fg=0.06 bg=0.00
female meiosis I GO:0007144 p=9.4E−03 n=1 fg=0.06 bg=0.00
maintenance of Golgi location GO:0051684 p=9.4E−03 n=1 fg=0.06 bg=0.00
regulation of mRNA stability GO:0043488 p=1.4E−02 n=2 fg=0.12 bg=0.01
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regulation of RNA stability GO:0043487 p=1.7E−02 n=2 fg=0.12 bg=0.01
regulation of G protein−coupled receptor... GO:0008277 p=1.9E−02 n=2 fg=0.12 bg=0.01
regulation of rhodopsin mediated signali... GO:0022400 p=1.9E−02 n=1 fg=0.06 bg=0.00
cellular divalent inorganic anion homeos... GO:0072501 p=1.9E−02 n=1 fg=0.06 bg=0.00
cellular trivalent inorganic anion homeo... GO:0072502 p=1.9E−02 n=1 fg=0.06 bg=0.00
phosphate ion transmembrane transport GO:0035435 p=1.9E−02 n=1 fg=0.06 bg=0.00
heart trabecula morphogenesis GO:0061384 p=1.9E−02 n=1 fg=0.06 bg=0.00
cell cycle switching, mitotic to meiotic... GO:0051728 p=1.9E−02 n=1 fg=0.06 bg=0.00
germline cell cycle switching, mitotic t... GO:0051729 p=1.9E−02 n=1 fg=0.06 bg=0.00
deactivation of rhodopsin mediated signa... GO:0016059 p=1.9E−02 n=1 fg=0.06 bg=0.00
granzyme−mediated apoptotic signaling pa... GO:0008626 p=1.9E−02 n=1 fg=0.06 bg=0.00
microglia differentiation GO:0014004 p=1.9E−02 n=1 fg=0.06 bg=0.00
cohesin loading GO:0071921 p=1.9E−02 n=1 fg=0.06 bg=0.00
regulation of organelle transport along ... GO:1902513 p=1.9E−02 n=1 fg=0.06 bg=0.00
cell cycle switching GO:0060184 p=1.9E−02 n=1 fg=0.06 bg=0.00
positive regulation of growth hormone se... GO:0060124 p=1.9E−02 n=1 fg=0.06 bg=0.00
ventricular trabecula myocardium morphog... GO:0003222 p=1.9E−02 n=1 fg=0.06 bg=0.00
semicircular canal morphogenesis GO:0048752 p=1.9E−02 n=1 fg=0.06 bg=0.00
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−log(p)
n=17/81 input genes with annotations
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fraction
GO:MF
Fox_Nvec_vc1.1_XM_048724172.1
fraction genes in fg and expected valu
anion binding GO:0043168 p=4.6E−03 n=6 fg=0.43 bg=0.13
phosphatidylinositol binding GO:0035091 p=6.6E−03 n=3 fg=0.21 bg=0.03
efflux transmembrane transporter activit... GO:0015562 p=8.8E−03 n=1 fg=0.07 bg=0.00
phosphatidylcholine transporter activity GO:0008525 p=8.8E−03 n=1 fg=0.07 bg=0.00
selenium binding GO:0008430 p=8.8E−03 n=1 fg=0.07 bg=0.00
thioredoxin−disulfide reductase activity GO:0004791 p=8.8E−03 n=1 fg=0.07 bg=0.00
ribokinase activity GO:0004747 p=8.8E−03 n=1 fg=0.07 bg=0.00
acid−sensing ion channel activity GO:0044736 p=8.8E−03 n=1 fg=0.07 bg=0.00
nucleoside−triphosphatase activity GO:0017111 p=1.5E−02 n=4 fg=0.29 bg=0.07
hydrolase activity, acting on acid anhyd... GO:0016817 p=1.7E−02 n=4 fg=0.29 bg=0.07
hydrolase activity, acting on acid anhyd... GO:0016818 p=1.7E−02 n=4 fg=0.29 bg=0.07
pyrophosphatase activity GO:0016462 p=1.7E−02 n=4 fg=0.29 bg=0.07
armadillo repeat domain binding GO:0070016 p=1.8E−02 n=1 fg=0.07 bg=0.00
1−phosphatidylinositol binding GO:0005545 p=1.8E−02 n=1 fg=0.07 bg=0.00
exogenous protein binding GO:0140272 p=1.8E−02 n=1 fg=0.07 bg=0.00
inositol hexakisphosphate binding GO:0000822 p=1.8E−02 n=1 fg=0.07 bg=0.00
phosphate ion transmembrane transporter ... GO:0015114 p=1.8E−02 n=1 fg=0.07 bg=0.00
phosphatidylinositol transfer activity GO:0008526 p=1.8E−02 n=1 fg=0.07 bg=0.00
phosphatidic acid transfer activity GO:1990050 p=1.8E−02 n=1 fg=0.07 bg=0.00
GDP−dissociation inhibitor activity GO:0005092 p=1.8E−02 n=1 fg=0.07 bg=0.00
virus receptor activity GO:0001618 p=1.8E−02 n=1 fg=0.07 bg=0.00
ATP hydrolysis activity GO:0016887 p=2.5E−02 n=3 fg=0.21 bg=0.05
phospholipid transfer activity GO:0120014 p=2.6E−02 n=1 fg=0.07 bg=0.00
P−type calcium transporter activity GO:0005388 p=2.6E−02 n=1 fg=0.07 bg=0.00
microfilament motor activity GO:0000146 p=2.6E−02 n=1 fg=0.07 bg=0.00
ATP−dependent activity GO:0140657 p=3.3E−02 n=3 fg=0.21 bg=0.05
phosphatidic acid binding GO:0070300 p=3.5E−02 n=1 fg=0.07 bg=0.00
voltage−gated sodium channel activity GO:0005248 p=3.5E−02 n=1 fg=0.07 bg=0.00
small molecule binding GO:0036094 p=4.2E−02 n=4 fg=0.29 bg=0.10
lipid transfer activity GO:0120013 p=4.3E−02 n=1 fg=0.07 bg=0.00
0 1 2 3 4 5
−log(p)
n=14/81 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_048724172.1
fraction genes in fg and expected valu
cuticular plate GO:0032437 p=1.1E−02 n=1 fg=0.05 bg=0.00
apical cytoplasm GO:0090651 p=1.1E−02 n=1 fg=0.05 bg=0.00
phagolysosome membrane GO:0061474 p=1.1E−02 n=1 fg=0.05 bg=0.00
phagolysosome GO:0032010 p=1.1E−02 n=1 fg=0.05 bg=0.00
alveolar lamellar body GO:0097208 p=1.1E−02 n=1 fg=0.05 bg=0.00
Scc2−Scc4 cohesin loading complex GO:0090694 p=1.1E−02 n=1 fg=0.05 bg=0.00
SMC loading complex GO:0032116 p=1.1E−02 n=1 fg=0.05 bg=0.00
intrinsic component of plasma membrane GO:0031226 p=1.5E−02 n=5 fg=0.26 bg=0.08
filamentous actin GO:0031941 p=2.1E−02 n=1 fg=0.05 bg=0.00
smooth endoplasmic reticulum cisterna GO:0120082 p=3.1E−02 n=1 fg=0.05 bg=0.00
cytolytic granule GO:0044194 p=3.1E−02 n=1 fg=0.05 bg=0.00
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subrhabdomeral cisterna GO:0016029 p=3.1E−02 n=1 fg=0.05 bg=0.00
lamellar body GO:0042599 p=3.1E−02 n=1 fg=0.05 bg=0.00
microtubule organizing center GO:0005815 p=3.3E−02 n=4 fg=0.21 bg=0.07
extrinsic component of endosome membrane GO:0031313 p=4.1E−02 n=1 fg=0.05 bg=0.00
integral component of plasma membrane GO:0005887 p=4.9E−02 n=4 fg=0.21 bg=0.08
autolysosome GO:0044754 p=5.1E−02 n=1 fg=0.05 bg=0.00
unconventional myosin complex GO:0016461 p=5.1E−02 n=1 fg=0.05 bg=0.00
MLL1 complex GO:0071339 p=5.1E−02 n=1 fg=0.05 bg=0.00
myosin complex GO:0016459 p=5.1E−02 n=1 fg=0.05 bg=0.00
actin filament GO:0005884 p=5.1E−02 n=1 fg=0.05 bg=0.00
ficolin−1−rich granule membrane GO:0101003 p=6.1E−02 n=1 fg=0.05 bg=0.00
MLL1/2 complex GO:0044665 p=7.1E−02 n=1 fg=0.05 bg=0.00
secondary lysosome GO:0005767 p=7.1E−02 n=1 fg=0.05 bg=0.00
endosome GO:0005768 p=7.9E−02 n=4 fg=0.21 bg=0.09
azurophil granule membrane GO:0035577 p=8.1E−02 n=1 fg=0.05 bg=0.00
rhabdomere GO:0016028 p=8.1E−02 n=1 fg=0.05 bg=0.00
multivesicular body GO:0005771 p=9.1E−02 n=1 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=19/81 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction