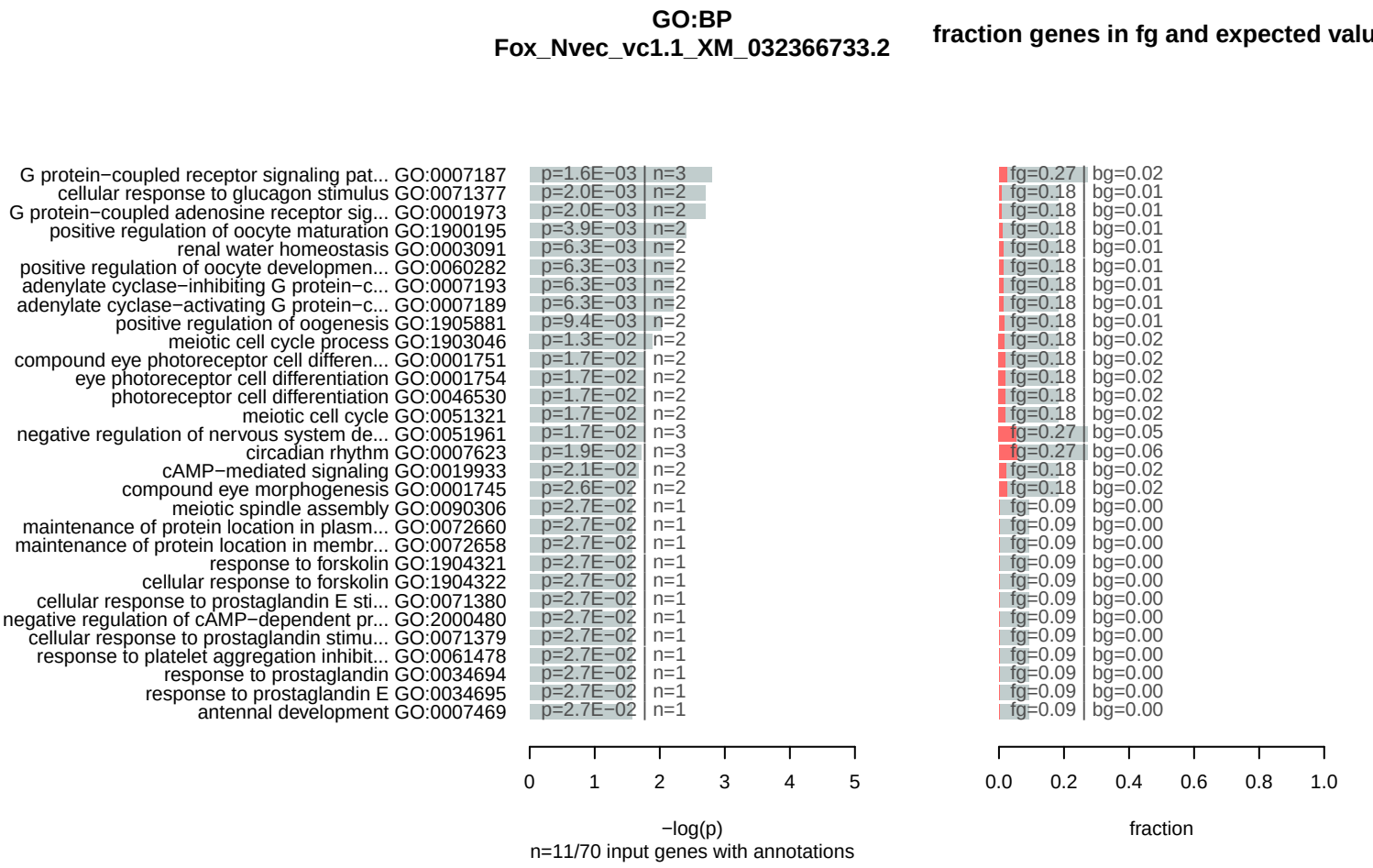
GO:BP
Fox_Nvec_vc1.1_XM_032366733.2
fraction genes in fg and expected valu
G protein−coupled receptor signaling pat... GO:0007187 p=1.6E−03 n=3 fg=0.27 bg=0.02
cellular response to glucagon stimulus GO:0071377 p=2.0E−03 n=2 fg=0.18 bg=0.01
G protein−coupled adenosine receptor sig... GO:0001973 p=2.0E−03 n=2 fg=0.18 bg=0.01
positive regulation of oocyte maturation GO:1900195 p=3.9E−03 n=2 fg=0.18 bg=0.01
renal water homeostasis GO:0003091 p=6.3E−03 n=2 fg=0.18 bg=0.01
positive regulation of oocyte developmen... GO:0060282 p=6.3E−03 n=2 fg=0.18 bg=0.01
adenylate cyclase−inhibiting G protein−c... GO:0007193 p=6.3E−03 n=2 fg=0.18 bg=0.01
adenylate cyclase−activating G protein−c... GO:0007189 p=6.3E−03 n=2 fg=0.18 bg=0.01
positive regulation of oogenesis GO:1905881 p=9.4E−03 n=2 fg=0.18 bg=0.01
meiotic cell cycle process GO:1903046 p=1.3E−02 n=2 fg=0.18 bg=0.02
compound eye photoreceptor cell differen... GO:0001751 p=1.7E−02 n=2 fg=0.18 bg=0.02
eye photoreceptor cell differentiation GO:0001754 p=1.7E−02 n=2 fg=0.18 bg=0.02
photoreceptor cell differentiation GO:0046530 p=1.7E−02 n=2 fg=0.18 bg=0.02
meiotic cell cycle GO:0051321 p=1.7E−02 n=2 fg=0.18 bg=0.02
negative regulation of nervous system de... GO:0051961 p=1.7E−02 n=3 fg=0.27 bg=0.05
circadian rhythm GO:0007623 p=1.9E−02 n=3 fg=0.27 bg=0.06
cAMP−mediated signaling GO:0019933 p=2.1E−02 n=2 fg=0.18 bg=0.02
compound eye morphogenesis GO:0001745 p=2.6E−02 n=2 fg=0.18 bg=0.02
meiotic spindle assembly GO:0090306 p=2.7E−02 n=1 fg=0.09 bg=0.00
maintenance of protein location in plasm... GO:0072660 p=2.7E−02 n=1 fg=0.09 bg=0.00
maintenance of protein location in membr... GO:0072658 p=2.7E−02 n=1 fg=0.09 bg=0.00
response to forskolin GO:1904321 p=2.7E−02 n=1 fg=0.09 bg=0.00
cellular response to forskolin GO:1904322 p=2.7E−02 n=1 fg=0.09 bg=0.00
cellular response to prostaglandin E sti... GO:0071380 p=2.7E−02 n=1 fg=0.09 bg=0.00
negative regulation of cAMP−dependent pr... GO:2000480 p=2.7E−02 n=1 fg=0.09 bg=0.00
cellular response to prostaglandin stimu... GO:0071379 p=2.7E−02 n=1 fg=0.09 bg=0.00
response to platelet aggregation inhibit... GO:0061478 p=2.7E−02 n=1 fg=0.09 bg=0.00
response to prostaglandin GO:0034694 p=2.7E−02 n=1 fg=0.09 bg=0.00
response to prostaglandin E GO:0034695 p=2.7E−02 n=1 fg=0.09 bg=0.00
antennal development GO:0007469 p=2.7E−02 n=1 fg=0.09 bg=0.00
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−log(p)
n=11/70 input genes with annotations
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fraction
GO:MF
Fox_Nvec_vc1.1_XM_032366733.2
fraction genes in fg and expected valu
G protein−coupled receptor activity GO:0004930 p=2.0E−02 n=3 fg=0.25 bg=0.05
phospholipase activity GO:0004620 p=3.2E−02 n=2 fg=0.17 bg=0.02
cAMP−dependent protein kinase regulator ... GO:0008603 p=3.3E−02 n=1 fg=0.08 bg=0.00
protein serine/threonine kinase inhibito... GO:0030291 p=3.3E−02 n=1 fg=0.08 bg=0.00
protein kinase A catalytic subunit bindi... GO:0034236 p=3.3E−02 n=1 fg=0.08 bg=0.00
calcium− and calmodulin−responsive adeny... GO:0008294 p=3.3E−02 n=1 fg=0.08 bg=0.00
phospholipase A2 activity GO:0004623 p=3.3E−02 n=1 fg=0.08 bg=0.00
cAMP−dependent protein kinase inhibitor ... GO:0004862 p=3.3E−02 n=1 fg=0.08 bg=0.00
ecdysis−triggering hormone receptor acti... GO:0042654 p=3.3E−02 n=1 fg=0.08 bg=0.00
beta−2 adrenergic receptor binding GO:0031698 p=3.3E−02 n=1 fg=0.08 bg=0.00
platelet−activating factor acetyltransfe... GO:0047179 p=3.3E−02 n=1 fg=0.08 bg=0.00
G protein−coupled receptor binding GO:0001664 p=3.9E−02 n=2 fg=0.17 bg=0.03
lipase activity GO:0016298 p=5.5E−02 n=2 fg=0.17 bg=0.03
signaling receptor binding GO:0005102 p=5.5E−02 n=4 fg=0.33 bg=0.13
G protein−coupled adenosine receptor act... GO:0001609 p=6.5E−02 n=1 fg=0.08 bg=0.01
G−protein beta/gamma−subunit complex bin... GO:0031683 p=6.5E−02 n=1 fg=0.08 bg=0.01
adenylate cyclase activity GO:0004016 p=6.5E−02 n=1 fg=0.08 bg=0.01
transcription corepressor binding GO:0001222 p=6.5E−02 n=1 fg=0.08 bg=0.01
transmembrane signaling receptor activit... GO:0004888 p=6.7E−02 n=3 fg=0.25 bg=0.08
molecular transducer activity GO:0060089 p=8.5E−02 n=3 fg=0.25 bg=0.09
signaling receptor activity GO:0038023 p=8.5E−02 n=3 fg=0.25 bg=0.09
adenylate cyclase binding GO:0008179 p=9.6E−02 n=1 fg=0.08 bg=0.01
cAMP binding GO:0030552 p=9.6E−02 n=1 fg=0.08 bg=0.01
microtubule motor activity GO:0003777 p=9.6E−02 n=1 fg=0.08 bg=0.01
heterotrimeric G−protein binding GO:0032795 p=9.6E−02 n=1 fg=0.08 bg=0.01
protein kinase A binding GO:0051018 p=9.6E−02 n=1 fg=0.08 bg=0.01
protein kinase inhibitor activity GO:0004860 p=9.6E−02 n=1 fg=0.08 bg=0.01
kinase inhibitor activity GO:0019210 p=9.6E−02 n=1 fg=0.08 bg=0.01
transcription coregulator binding GO:0001221 p=9.6E−02 n=1 fg=0.08 bg=0.01
ATP hydrolysis activity GO:0016887 p=1.1E−01 n=2 fg=0.17 bg=0.05
0 1 2 3 4 5
−log(p)
n=12/70 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032366733.2
fraction genes in fg and expected valu
cilium GO:0005929 p=3.2E−02 n=3 fg=0.23 bg=0.06
Barr body GO:0001740 p=3.2E−02 n=1 fg=0.08 bg=0.00
microvillus membrane GO:0031528 p=3.2E−02 n=1 fg=0.08 bg=0.00
X chromosome GO:0000805 p=3.2E−02 n=1 fg=0.08 bg=0.00
plus−end kinesin complex GO:0005873 p=3.2E−02 n=1 fg=0.08 bg=0.00
cell periphery GO:0071944 p=4.1E−02 n=9 fg=0.69 bg=0.42
cell projection membrane GO:0031253 p=4.5E−02 n=3 fg=0.23 bg=0.06
centrosome GO:0005813 p=6.2E−02 n=2 fg=0.15 bg=0.03
germinal vesicle GO:0042585 p=6.4E−02 n=1 fg=0.08 bg=0.00
nucleotide−activated protein kinase comp... GO:0031588 p=6.4E−02 n=1 fg=0.08 bg=0.00
female germ cell nucleus GO:0001674 p=6.4E−02 n=1 fg=0.08 bg=0.00
sex chromosome GO:0000803 p=6.4E−02 n=1 fg=0.08 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=6.4E−02 n=1 fg=0.08 bg=0.00
endosome GO:0005768 p=8.8E−02 n=3 fg=0.23 bg=0.08
germ cell nucleus GO:0043073 p=9.4E−02 n=1 fg=0.08 bg=0.01
ficolin−1−rich granule lumen GO:1904813 p=9.4E−02 n=1 fg=0.08 bg=0.01
ciliary membrane GO:0060170 p=9.4E−02 n=1 fg=0.08 bg=0.01
protein kinase complex GO:1902911 p=9.4E−02 n=1 fg=0.08 bg=0.01
kinesin complex GO:0005871 p=9.4E−02 n=1 fg=0.08 bg=0.01
microvillus GO:0005902 p=9.4E−02 n=1 fg=0.08 bg=0.01
cell cortex GO:0005938 p=1.0E−01 n=2 fg=0.15 bg=0.04
plasma membrane region GO:0098590 p=1.1E−01 n=4 fg=0.31 bg=0.15
cytoplasmic region GO:0099568 p=1.1E−01 n=2 fg=0.15 bg=0.04
microtubule organizing center GO:0005815 p=1.1E−01 n=2 fg=0.15 bg=0.04
fibrillar center GO:0001650 p=1.2E−01 n=1 fg=0.08 bg=0.01
axolemma GO:0030673 p=1.2E−01 n=1 fg=0.08 bg=0.01
spindle pole GO:0000922 p=1.2E−01 n=1 fg=0.08 bg=0.01
early endosome membrane GO:0031901 p=1.2E−01 n=1 fg=0.08 bg=0.01
ciliary base GO:0097546 p=1.2E−01 n=1 fg=0.08 bg=0.01
ficolin−1−rich granule GO:0101002 p=1.2E−01 n=1 fg=0.08 bg=0.01
0 1 2 3 4 5
−log(p)
n=13/70 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction