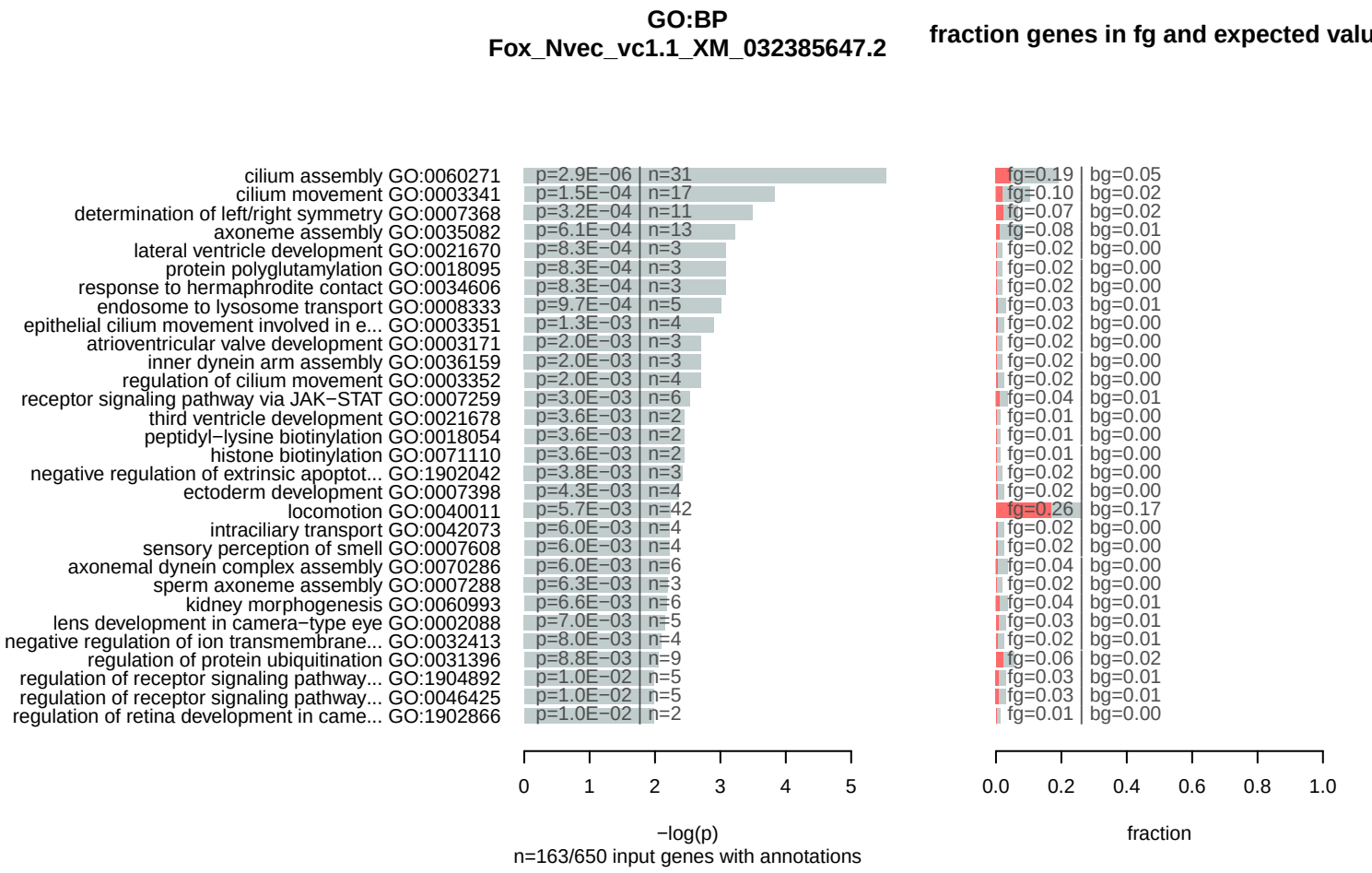
GO:BP
Fox_Nvec_vc1.1_XM_032385647.2
fraction genes in fg and expected valu
cilium assembly GO:0060271 p=2.9E−06 n=31 fg=0.19 bg=0.05
cilium movement GO:0003341 p=1.5E−04 n=17 fg=0.10 bg=0.02
determination of left/right symmetry GO:0007368 p=3.2E−04 n=11 fg=0.07 bg=0.02
axoneme assembly GO:0035082 p=6.1E−04 n=13 fg=0.08 bg=0.01
lateral ventricle development GO:0021670 p=8.3E−04 n=3 fg=0.02 bg=0.00
protein polyglutamylation GO:0018095 p=8.3E−04 n=3 fg=0.02 bg=0.00
response to hermaphrodite contact GO:0034606 p=8.3E−04 n=3 fg=0.02 bg=0.00
endosome to lysosome transport GO:0008333 p=9.7E−04 n=5 fg=0.03 bg=0.01
epithelial cilium movement involved in e... GO:0003351 p=1.3E−03 n=4 fg=0.02 bg=0.00
atrioventricular valve development GO:0003171 p=2.0E−03 n=3 fg=0.02 bg=0.00
inner dynein arm assembly GO:0036159 p=2.0E−03 n=3 fg=0.02 bg=0.00
regulation of cilium movement GO:0003352 p=2.0E−03 n=4 fg=0.02 bg=0.00
receptor signaling pathway via JAK−STAT GO:0007259 p=3.0E−03 n=6 fg=0.04 bg=0.01
third ventricle development GO:0021678 p=3.6E−03 n=2 fg=0.01 bg=0.00
peptidyl−lysine biotinylation GO:0018054 p=3.6E−03 n=2 fg=0.01 bg=0.00
histone biotinylation GO:0071110 p=3.6E−03 n=2 fg=0.01 bg=0.00
negative regulation of extrinsic apoptot... GO:1902042 p=3.8E−03 n=3 fg=0.02 bg=0.00
ectoderm development GO:0007398 p=4.3E−03 n=4 fg=0.02 bg=0.00
locomotion GO:0040011 p=5.7E−03 n=42 fg=0.26 bg=0.17
intraciliary transport GO:0042073 p=6.0E−03 n=4 fg=0.02 bg=0.00
sensory perception of smell GO:0007608 p=6.0E−03 n=4 fg=0.02 bg=0.00
axonemal dynein complex assembly GO:0070286 p=6.0E−03 n=6 fg=0.04 bg=0.00
sperm axoneme assembly GO:0007288 p=6.3E−03 n=3 fg=0.02 bg=0.00
kidney morphogenesis GO:0060993 p=6.6E−03 n=6 fg=0.04 bg=0.01
lens development in camera−type eye GO:0002088 p=7.0E−03 n=5 fg=0.03 bg=0.01
negative regulation of ion transmembrane... GO:0032413 p=8.0E−03 n=4 fg=0.02 bg=0.01
regulation of protein ubiquitination GO:0031396 p=8.8E−03 n=9 fg=0.06 bg=0.02
regulation of receptor signaling pathway... GO:1904892 p=1.0E−02 n=5 fg=0.03 bg=0.01
regulation of receptor signaling pathway... GO:0046425 p=1.0E−02 n=5 fg=0.03 bg=0.01
regulation of retina development in came... GO:1902866 p=1.0E−02 n=2 fg=0.01 bg=0.00
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−log(p)
n=163/650 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032385647.2
fraction genes in fg and expected valu
dynein light chain binding GO:0045503 p=5.0E−05 n=4 fg=0.03 bg=0.00
transmembrane transporter binding GO:0044325 p=2.7E−03 n=5 fg=0.04 bg=0.01
dynein heavy chain binding GO:0045504 p=3.3E−03 n=3 fg=0.02 bg=0.00
dynein intermediate chain binding GO:0045505 p=3.3E−03 n=3 fg=0.02 bg=0.00
tubulin−glycine ligase activity GO:0070738 p=3.3E−03 n=2 fg=0.01 bg=0.00
calcium−dependent protein kinase inhibit... GO:0008427 p=3.3E−03 n=2 fg=0.01 bg=0.00
uridine kinase activity GO:0004849 p=3.3E−03 n=2 fg=0.01 bg=0.00
protein serine/threonine kinase inhibito... GO:0030291 p=8.4E−03 n=3 fg=0.02 bg=0.00
fatty acid ligase activity GO:0015645 p=9.4E−03 n=2 fg=0.01 bg=0.00
minus−end−directed microtubule motor act... GO:0008569 p=9.4E−03 n=2 fg=0.01 bg=0.00
palmitoyl hydrolase activity GO:0098599 p=1.8E−02 n=2 fg=0.01 bg=0.00
dynein light intermediate chain binding GO:0051959 p=1.8E−02 n=2 fg=0.01 bg=0.00
palmitoyl−(protein) hydrolase activity GO:0008474 p=1.8E−02 n=2 fg=0.01 bg=0.00
cAMP binding GO:0030552 p=1.8E−02 n=2 fg=0.01 bg=0.00
calcium activated cation channel activit... GO:0005227 p=2.2E−02 n=3 fg=0.02 bg=0.00
cyclic nucleotide binding GO:0030551 p=2.9E−02 n=2 fg=0.01 bg=0.00
histone H3−methyl−lysine−4 demethylase a... GO:0032453 p=2.9E−02 n=2 fg=0.01 bg=0.00
protein kinase regulator activity GO:0019887 p=3.0E−02 n=9 fg=0.07 bg=0.02
protease binding GO:0002020 p=3.4E−02 n=4 fg=0.03 bg=0.01
nuclear localization sequence binding GO:0008139 p=4.2E−02 n=2 fg=0.01 bg=0.00
kinase regulator activity GO:0019207 p=4.3E−02 n=9 fg=0.07 bg=0.02
DNA−binding transcription factor activit... GO:0003700 p=5.1E−02 n=15 fg=0.11 bg=0.07
biotin−protein ligase activity GO:0018271 p=5.7E−02 n=1 fg=0.01 bg=0.00
neuregulin binding GO:0038132 p=5.7E−02 n=1 fg=0.01 bg=0.00
dihydrouridine synthase activity GO:0106413 p=5.7E−02 n=1 fg=0.01 bg=0.00
poly−ADP−D−ribose binding GO:0072572 p=5.7E−02 n=1 fg=0.01 bg=0.00
tRNA dihydrouridine synthase activity GO:0017150 p=5.7E−02 n=1 fg=0.01 bg=0.00
pantetheine hydrolase activity GO:0017159 p=5.7E−02 n=1 fg=0.01 bg=0.00
unmethylated CpG binding GO:0045322 p=5.7E−02 n=1 fg=0.01 bg=0.00
protein−glycine ligase activity, initiat... GO:0070736 p=5.7E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=136/650 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032385647.2
fraction genes in fg and expected valu
axoneme GO:0005930 p=1.6E−08 n=17 fg=0.10 bg=0.01
motile cilium GO:0031514 p=3.4E−04 n=11 fg=0.07 bg=0.02
centrosome GO:0005813 p=6.0E−04 n=19 fg=0.12 bg=0.05
ciliary basal body GO:0036064 p=7.1E−04 n=9 fg=0.05 bg=0.02
inner dynein arm GO:0036156 p=8.4E−04 n=3 fg=0.02 bg=0.00
radial spoke GO:0001534 p=3.7E−03 n=2 fg=0.01 bg=0.00
lateral plasma membrane GO:0016328 p=4.4E−03 n=4 fg=0.02 bg=0.00
cilium GO:0005929 p=7.9E−03 n=36 fg=0.22 bg=0.06
ciliary base GO:0097546 p=8.1E−03 n=4 fg=0.02 bg=0.01
cytoplasmic dynein complex GO:0005868 p=9.8E−03 n=3 fg=0.02 bg=0.00
non−motile cilium GO:0097730 p=1.2E−02 n=7 fg=0.04 bg=0.02
ciliary tip GO:0097542 p=2.5E−02 n=3 fg=0.02 bg=0.00
actin−based cell projection GO:0098858 p=3.2E−02 n=7 fg=0.04 bg=0.02
U2−type prespliceosome GO:0071004 p=3.2E−02 n=2 fg=0.01 bg=0.00
intraciliary transport particle GO:0030990 p=3.2E−02 n=2 fg=0.01 bg=0.00
ESCRT complex GO:0036452 p=4.0E−02 n=3 fg=0.02 bg=0.00
filopodium GO:0030175 p=4.1E−02 n=4 fg=0.02 bg=0.01
filopodium membrane GO:0031527 p=4.7E−02 n=2 fg=0.01 bg=0.00
perinuclear region of cytoplasm GO:0048471 p=5.9E−02 n=16 fg=0.10 bg=0.06
Kibra−Ex−Mer complex GO:0036375 p=6.1E−02 n=1 fg=0.01 bg=0.00
FHF complex GO:0070695 p=6.1E−02 n=1 fg=0.01 bg=0.00
integrin alpha3−beta1 complex GO:0034667 p=6.1E−02 n=1 fg=0.01 bg=0.00
postsynaptic endosome GO:0098845 p=6.1E−02 n=1 fg=0.01 bg=0.00
integrin alpha6−beta4 complex GO:0034676 p=6.1E−02 n=1 fg=0.01 bg=0.00
integrin alpha7−beta1 complex GO:0034677 p=6.1E−02 n=1 fg=0.01 bg=0.00
postsynaptic recycling endosome GO:0098837 p=6.1E−02 n=1 fg=0.01 bg=0.00
plus−end kinesin complex GO:0005873 p=6.1E−02 n=1 fg=0.01 bg=0.00
cyclin D2−CDK4 complex GO:0097129 p=6.1E−02 n=1 fg=0.01 bg=0.00
cyclin D2−CDK6 complex GO:0097132 p=6.1E−02 n=1 fg=0.01 bg=0.00
XPC complex GO:0071942 p=6.1E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=164/650 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction