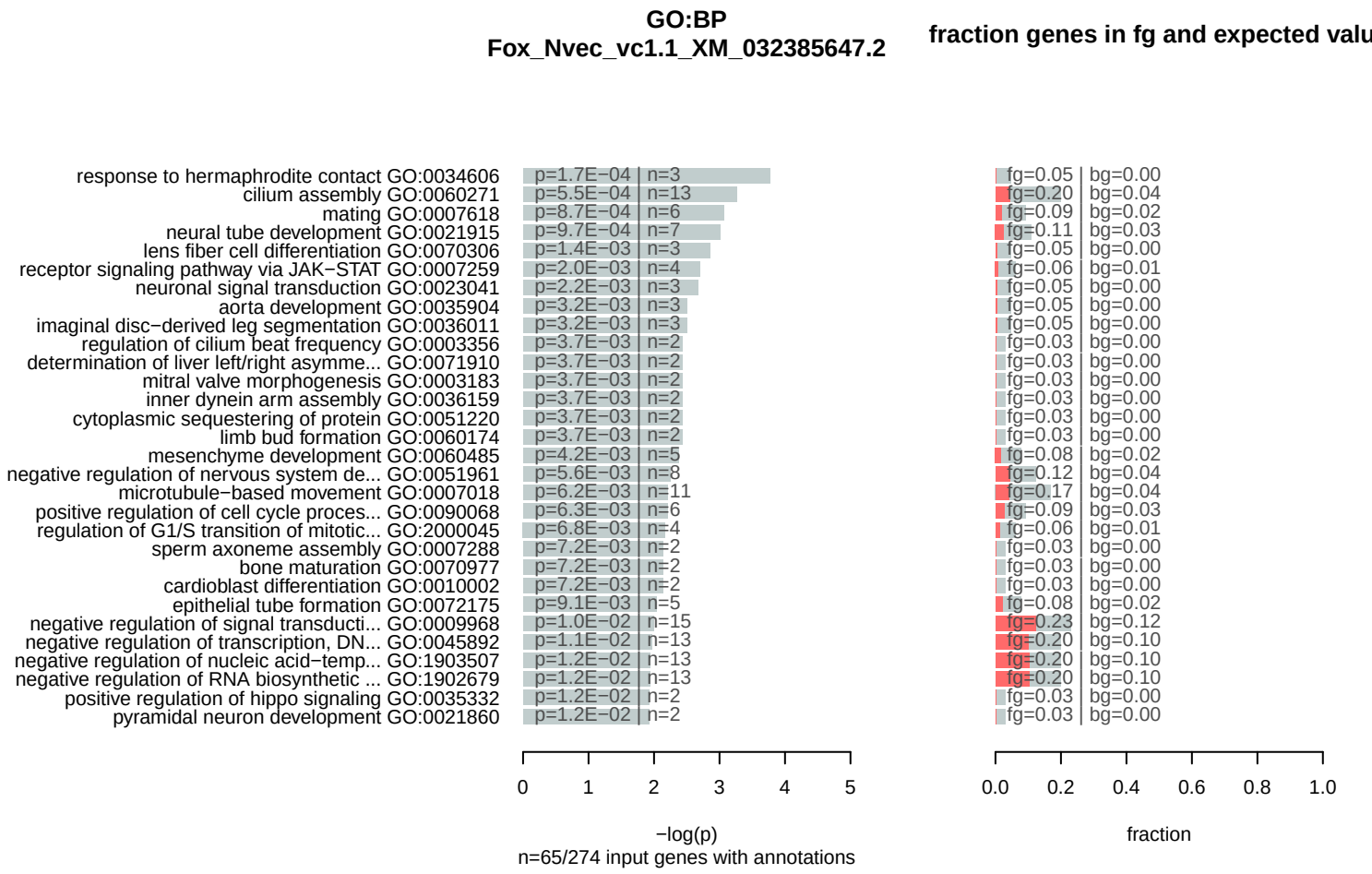
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fraction genes in fg and expected valu
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cilium assembly GO:0060271 p=5.5E−04 n=13 fg=0.20 bg=0.04
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neural tube development GO:0021915 p=9.7E−04 n=7 fg=0.11 bg=0.03
lens fiber cell differentiation GO:0070306 p=1.4E−03 n=3 fg=0.05 bg=0.00
receptor signaling pathway via JAK−STAT GO:0007259 p=2.0E−03 n=4 fg=0.06 bg=0.01
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aorta development GO:0035904 p=3.2E−03 n=3 fg=0.05 bg=0.00
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regulation of cilium beat frequency GO:0003356 p=3.7E−03 n=2 fg=0.03 bg=0.00
determination of liver left/right asymme... GO:0071910 p=3.7E−03 n=2 fg=0.03 bg=0.00
mitral valve morphogenesis GO:0003183 p=3.7E−03 n=2 fg=0.03 bg=0.00
inner dynein arm assembly GO:0036159 p=3.7E−03 n=2 fg=0.03 bg=0.00
cytoplasmic sequestering of protein GO:0051220 p=3.7E−03 n=2 fg=0.03 bg=0.00
limb bud formation GO:0060174 p=3.7E−03 n=2 fg=0.03 bg=0.00
mesenchyme development GO:0060485 p=4.2E−03 n=5 fg=0.08 bg=0.02
negative regulation of nervous system de... GO:0051961 p=5.6E−03 n=8 fg=0.12 bg=0.04
microtubule−based movement GO:0007018 p=6.2E−03 n=11 fg=0.17 bg=0.04
positive regulation of cell cycle proces... GO:0090068 p=6.3E−03 n=6 fg=0.09 bg=0.03
regulation of G1/S transition of mitotic... GO:2000045 p=6.8E−03 n=4 fg=0.06 bg=0.01
sperm axoneme assembly GO:0007288 p=7.2E−03 n=2 fg=0.03 bg=0.00
bone maturation GO:0070977 p=7.2E−03 n=2 fg=0.03 bg=0.00
cardioblast differentiation GO:0010002 p=7.2E−03 n=2 fg=0.03 bg=0.00
epithelial tube formation GO:0072175 p=9.1E−03 n=5 fg=0.08 bg=0.02
negative regulation of signal transducti... GO:0009968 p=1.0E−02 n=15 fg=0.23 bg=0.12
negative regulation of transcription, DN... GO:0045892 p=1.1E−02 n=13 fg=0.20 bg=0.10
negative regulation of nucleic acid−temp... GO:1903507 p=1.2E−02 n=13 fg=0.20 bg=0.10
negative regulation of RNA biosynthetic ... GO:1902679 p=1.2E−02 n=13 fg=0.20 bg=0.10
positive regulation of hippo signaling GO:0035332 p=1.2E−02 n=2 fg=0.03 bg=0.00
pyramidal neuron development GO:0021860 p=1.2E−02 n=2 fg=0.03 bg=0.00
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−log(p)
n=65/274 input genes with annotations
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fraction
GO:MF
Fox_Nvec_vc1.1_XM_032385647.2
fraction genes in fg and expected valu
cAMP binding GO:0030552 p=6.5E−03 n=2 fg=0.04 bg=0.00
transmembrane transporter binding GO:0044325 p=1.3E−02 n=3 fg=0.06 bg=0.01
outward rectifier potassium channel acti... GO:0015271 p=2.1E−02 n=2 fg=0.04 bg=0.00
protein serine/threonine kinase inhibito... GO:0030291 p=2.1E−02 n=2 fg=0.04 bg=0.00
DNA−binding transcription factor activit... GO:0003700 p=2.8E−02 n=9 fg=0.17 bg=0.08
actinin binding GO:0042805 p=2.8E−02 n=2 fg=0.04 bg=0.01
alpha−actinin binding GO:0051393 p=2.8E−02 n=2 fg=0.04 bg=0.01
DNA−binding transcription repressor acti... GO:0001227 p=3.2E−02 n=3 fg=0.06 bg=0.01
DNA−binding transcription repressor acti... GO:0001217 p=3.2E−02 n=3 fg=0.06 bg=0.01
protein−membrane adaptor activity GO:0043495 p=3.4E−02 n=1 fg=0.02 bg=0.00
N−acetylglucosaminyldiphosphodolichol N−... GO:0004577 p=3.4E−02 n=1 fg=0.02 bg=0.00
HLH domain binding GO:0043398 p=3.4E−02 n=1 fg=0.02 bg=0.00
growth hormone−releasing hormone recepto... GO:0016520 p=3.4E−02 n=1 fg=0.02 bg=0.00
ATPase−coupled inorganic anion transmemb... GO:0043225 p=3.4E−02 n=1 fg=0.02 bg=0.00
3−galactosyl−N−acetylglucosaminide 4−alp... GO:0017060 p=3.4E−02 n=1 fg=0.02 bg=0.00
muscle alpha−actinin binding GO:0051371 p=3.4E−02 n=1 fg=0.02 bg=0.00
calmodulin−activated 3',5'−cyclic−GMP ph... GO:0048101 p=3.4E−02 n=1 fg=0.02 bg=0.00
calmodulin−activated dual specificity 3'... GO:0004117 p=3.4E−02 n=1 fg=0.02 bg=0.00
interferon binding GO:0019961 p=3.4E−02 n=1 fg=0.02 bg=0.00
interferon−gamma binding GO:0019964 p=3.4E−02 n=1 fg=0.02 bg=0.00
phosphatidyl−N−methylethanolamine N−meth... GO:0000773 p=3.4E−02 n=1 fg=0.02 bg=0.00
pantetheine hydrolase activity GO:0017159 p=3.4E−02 n=1 fg=0.02 bg=0.00
phosphatidyl−N−dimethylethanolamine N−me... GO:0080101 p=3.4E−02 n=1 fg=0.02 bg=0.00
intracellular ligand−gated ion channel a... GO:0005217 p=4.3E−02 n=2 fg=0.04 bg=0.01
voltage−gated potassium channel activity GO:0005249 p=4.3E−02 n=2 fg=0.04 bg=0.01
DNA−binding transcription factor activit... GO:0000981 p=6.5E−02 n=7 fg=0.13 bg=0.07
protein kinase regulator activity GO:0019887 p=6.6E−02 n=3 fg=0.06 bg=0.02
nucleoside kinase activity GO:0019206 p=6.7E−02 n=1 fg=0.02 bg=0.00
dynein heavy chain binding GO:0045504 p=6.7E−02 n=1 fg=0.02 bg=0.00
calcium−dependent protein kinase inhibit... GO:0008427 p=6.7E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=54/274 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
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ciliary base GO:0097546 p=4.4E−04 n=4 fg=0.06 bg=0.01
motile cilium GO:0031514 p=1.5E−03 n=6 fg=0.09 bg=0.02
axoneme GO:0005930 p=3.4E−03 n=4 fg=0.06 bg=0.01
centrosome GO:0005813 p=5.1E−03 n=9 fg=0.14 bg=0.05
lateral plasma membrane GO:0016328 p=6.2E−03 n=3 fg=0.05 bg=0.01
filopodium GO:0030175 p=1.8E−02 n=3 fg=0.05 bg=0.01
dynein complex GO:0030286 p=2.4E−02 n=2 fg=0.03 bg=0.00
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transcription factor TFIIIC complex GO:0000127 p=3.6E−02 n=1 fg=0.02 bg=0.00
CORVET complex GO:0033263 p=3.6E−02 n=1 fg=0.02 bg=0.00
DNA replication factor C complex GO:0005663 p=3.6E−02 n=1 fg=0.02 bg=0.00
Ctf18 RFC−like complex GO:0031390 p=3.6E−02 n=1 fg=0.02 bg=0.00
Elg1 RFC−like complex GO:0031391 p=3.6E−02 n=1 fg=0.02 bg=0.00
RNA polymerase III transcription regulat... GO:0090576 p=3.6E−02 n=1 fg=0.02 bg=0.00
plus−end kinesin complex GO:0005873 p=3.6E−02 n=1 fg=0.02 bg=0.00
Kibra−Ex−Mer complex GO:0036375 p=3.6E−02 n=1 fg=0.02 bg=0.00
ESCRT−0 complex GO:0033565 p=3.6E−02 n=1 fg=0.02 bg=0.00
postsynaptic endosome GO:0098845 p=3.6E−02 n=1 fg=0.02 bg=0.00
CA3 pyramidal cell dendrite GO:0097442 p=3.6E−02 n=1 fg=0.02 bg=0.00
postsynaptic recycling endosome GO:0098837 p=3.6E−02 n=1 fg=0.02 bg=0.00
polycystin complex GO:0002133 p=3.6E−02 n=1 fg=0.02 bg=0.00
9+2 motile cilium GO:0097729 p=3.9E−02 n=3 fg=0.05 bg=0.01
actin−based cell projection GO:0098858 p=4.3E−02 n=4 fg=0.06 bg=0.02
ruffle membrane GO:0032587 p=4.9E−02 n=2 fg=0.03 bg=0.01
spindle pole GO:0000922 p=5.4E−02 n=3 fg=0.05 bg=0.01
transcription regulator complex GO:0005667 p=5.8E−02 n=6 fg=0.09 bg=0.04
inner dynein arm GO:0036156 p=7.2E−02 n=1 fg=0.02 bg=0.00
Nebenkern GO:0016006 p=7.2E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=66/274 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction