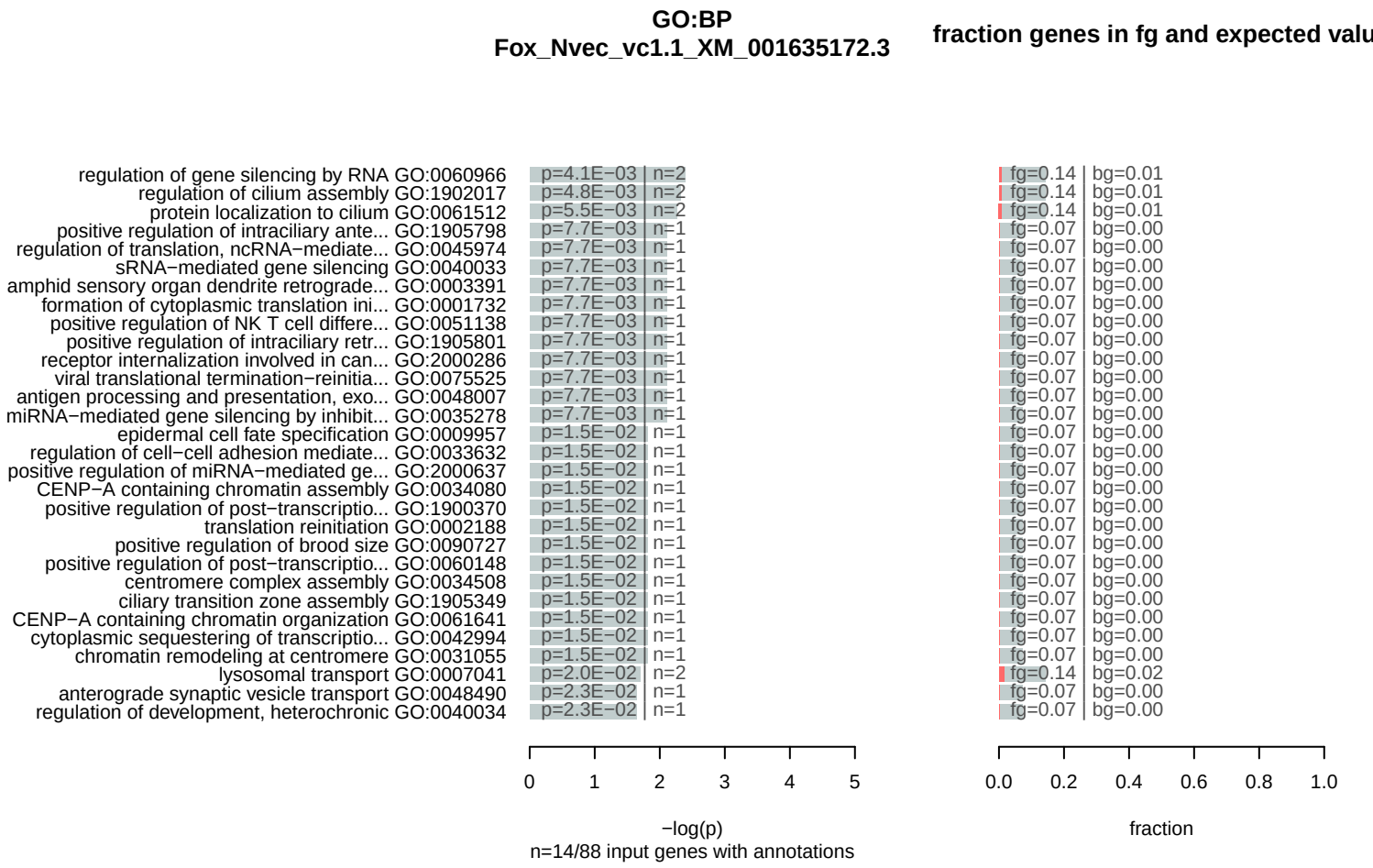
GO:BP
Fox_Nvec_vc1.1_XM_001635172.3
fraction genes in fg and expected valu
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regulation of cilium assembly GO:1902017 p=4.8E−03 n=2 fg=0.14 bg=0.01
protein localization to cilium GO:0061512 p=5.5E−03 n=2 fg=0.14 bg=0.01
positive regulation of intraciliary ante... GO:1905798 p=7.7E−03 n=1 fg=0.07 bg=0.00
regulation of translation, ncRNA−mediate... GO:0045974 p=7.7E−03 n=1 fg=0.07 bg=0.00
sRNA−mediated gene silencing GO:0040033 p=7.7E−03 n=1 fg=0.07 bg=0.00
amphid sensory organ dendrite retrograde... GO:0003391 p=7.7E−03 n=1 fg=0.07 bg=0.00
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positive regulation of NK T cell differe... GO:0051138 p=7.7E−03 n=1 fg=0.07 bg=0.00
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receptor internalization involved in can... GO:2000286 p=7.7E−03 n=1 fg=0.07 bg=0.00
viral translational termination−reinitia... GO:0075525 p=7.7E−03 n=1 fg=0.07 bg=0.00
antigen processing and presentation, exo... GO:0048007 p=7.7E−03 n=1 fg=0.07 bg=0.00
miRNA−mediated gene silencing by inhibit... GO:0035278 p=7.7E−03 n=1 fg=0.07 bg=0.00
epidermal cell fate specification GO:0009957 p=1.5E−02 n=1 fg=0.07 bg=0.00
regulation of cell−cell adhesion mediate... GO:0033632 p=1.5E−02 n=1 fg=0.07 bg=0.00
positive regulation of miRNA−mediated ge... GO:2000637 p=1.5E−02 n=1 fg=0.07 bg=0.00
CENP−A containing chromatin assembly GO:0034080 p=1.5E−02 n=1 fg=0.07 bg=0.00
positive regulation of post−transcriptio... GO:1900370 p=1.5E−02 n=1 fg=0.07 bg=0.00
translation reinitiation GO:0002188 p=1.5E−02 n=1 fg=0.07 bg=0.00
positive regulation of brood size GO:0090727 p=1.5E−02 n=1 fg=0.07 bg=0.00
positive regulation of post−transcriptio... GO:0060148 p=1.5E−02 n=1 fg=0.07 bg=0.00
centromere complex assembly GO:0034508 p=1.5E−02 n=1 fg=0.07 bg=0.00
ciliary transition zone assembly GO:1905349 p=1.5E−02 n=1 fg=0.07 bg=0.00
CENP−A containing chromatin organization GO:0061641 p=1.5E−02 n=1 fg=0.07 bg=0.00
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chromatin remodeling at centromere GO:0031055 p=1.5E−02 n=1 fg=0.07 bg=0.00
lysosomal transport GO:0007041 p=2.0E−02 n=2 fg=0.14 bg=0.02
anterograde synaptic vesicle transport GO:0048490 p=2.3E−02 n=1 fg=0.07 bg=0.00
regulation of development, heterochronic GO:0040034 p=2.3E−02 n=1 fg=0.07 bg=0.00
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fraction
GO:MF
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fraction genes in fg and expected valu
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translation regulator activity GO:0045182 p=1.1E−02 n=2 fg=0.17 bg=0.01
miRNA binding GO:0035198 p=2.2E−02 n=1 fg=0.08 bg=0.00
translation repressor activity GO:0030371 p=3.0E−02 n=1 fg=0.08 bg=0.00
regulatory RNA binding GO:0061980 p=3.0E−02 n=1 fg=0.08 bg=0.00
GTP−dependent protein binding GO:0030742 p=3.0E−02 n=1 fg=0.08 bg=0.00
RNA polymerase II complex binding GO:0000993 p=3.7E−02 n=1 fg=0.08 bg=0.00
RNA polymerase core enzyme binding GO:0043175 p=5.9E−02 n=1 fg=0.08 bg=0.01
basal transcription machinery binding GO:0001098 p=6.6E−02 n=1 fg=0.08 bg=0.01
basal RNA polymerase II transcription ma... GO:0001099 p=6.6E−02 n=1 fg=0.08 bg=0.01
glutamate receptor binding GO:0035254 p=8.0E−02 n=1 fg=0.08 bg=0.01
translation factor activity, RNA binding GO:0008135 p=8.0E−02 n=1 fg=0.08 bg=0.01
RNA polymerase binding GO:0070063 p=8.7E−02 n=1 fg=0.08 bg=0.01
receptor tyrosine kinase binding GO:0030971 p=8.7E−02 n=1 fg=0.08 bg=0.01
protein tyrosine kinase binding GO:1990782 p=1.0E−01 n=1 fg=0.08 bg=0.01
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translation regulator activity, nucleic ... GO:0090079 p=1.3E−01 n=1 fg=0.08 bg=0.01
ubiquitin−protein transferase activity GO:0004842 p=1.5E−01 n=2 fg=0.17 bg=0.06
ubiquitin−like protein transferase activ... GO:0019787 p=1.6E−01 n=2 fg=0.17 bg=0.06
histone binding GO:0042393 p=1.9E−01 n=1 fg=0.08 bg=0.02
PDZ domain binding GO:0030165 p=1.9E−01 n=1 fg=0.08 bg=0.02
protein phosphatase binding GO:0019903 p=2.0E−01 n=1 fg=0.08 bg=0.02
transcription corepressor activity GO:0003714 p=2.1E−01 n=1 fg=0.08 bg=0.02
phosphatase binding GO:0019902 p=2.8E−01 n=1 fg=0.08 bg=0.03
microtubule binding GO:0008017 p=2.8E−01 n=1 fg=0.08 bg=0.03
RNA binding GO:0003723 p=2.9E−01 n=2 fg=0.17 bg=0.09
molecular adaptor activity GO:0060090 p=3.1E−01 n=1 fg=0.08 bg=0.03
mRNA binding GO:0003729 p=3.1E−01 n=1 fg=0.08 bg=0.03
protein−macromolecule adaptor activity GO:0030674 p=3.1E−01 n=1 fg=0.08 bg=0.03
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−log(p)
n=12/88 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001635172.3
fraction genes in fg and expected valu
eukaryotic translation initiation factor... GO:0071540 p=8.3E−03 n=1 fg=0.07 bg=0.00
eukaryotic translation initiation factor... GO:0071541 p=8.3E−03 n=1 fg=0.07 bg=0.00
AP−3 adaptor complex GO:0030123 p=8.3E−03 n=1 fg=0.07 bg=0.00
trans−Golgi network GO:0005802 p=1.6E−02 n=3 fg=0.20 bg=0.04
multi−eIF complex GO:0043614 p=1.7E−02 n=1 fg=0.07 bg=0.00
RSF complex GO:0031213 p=1.7E−02 n=1 fg=0.07 bg=0.00
ciliary basal body GO:0036064 p=2.0E−02 n=2 fg=0.13 bg=0.01
spot adherens junction GO:0005914 p=2.5E−02 n=1 fg=0.07 bg=0.00
intraciliary transport particle GO:0030990 p=2.5E−02 n=1 fg=0.07 bg=0.00
intraciliary transport particle A GO:0030991 p=2.5E−02 n=1 fg=0.07 bg=0.00
ISWI−type complex GO:0031010 p=2.5E−02 n=1 fg=0.07 bg=0.00
muscle tendon junction GO:0005927 p=2.5E−02 n=1 fg=0.07 bg=0.00
zonula adherens GO:0005915 p=3.3E−02 n=1 fg=0.07 bg=0.00
Cul2−RING ubiquitin ligase complex GO:0031462 p=3.3E−02 n=1 fg=0.07 bg=0.00
centrosome GO:0005813 p=3.7E−02 n=3 fg=0.20 bg=0.05
messenger ribonucleoprotein complex GO:1990124 p=4.1E−02 n=1 fg=0.07 bg=0.00
sensory dendrite GO:0071683 p=4.1E−02 n=1 fg=0.07 bg=0.00
adherens junction GO:0005912 p=4.2E−02 n=2 fg=0.13 bg=0.02
non−membrane−bounded organelle GO:0043228 p=5.4E−02 n=8 fg=0.53 bg=0.30
intracellular non−membrane−bounded organ... GO:0043232 p=5.4E−02 n=8 fg=0.53 bg=0.30
microtubule cytoskeleton GO:0015630 p=5.4E−02 n=4 fg=0.27 bg=0.10
COPI−coated vesicle GO:0030137 p=5.7E−02 n=1 fg=0.07 bg=0.00
ciliary tip GO:0097542 p=5.7E−02 n=1 fg=0.07 bg=0.00
coated vesicle GO:0030135 p=6.2E−02 n=2 fg=0.13 bg=0.03
polytene chromosome interband GO:0005705 p=6.5E−02 n=1 fg=0.07 bg=0.00
microtubule organizing center GO:0005815 p=7.2E−02 n=3 fg=0.20 bg=0.07
photoreceptor connecting cilium GO:0032391 p=8.8E−02 n=1 fg=0.07 bg=0.01
nucleolus GO:0005730 p=9.2E−02 n=3 fg=0.20 bg=0.07
SWI/SNF superfamily−type complex GO:0070603 p=9.5E−02 n=1 fg=0.07 bg=0.01
Golgi apparatus subcompartment GO:0098791 p=1.2E−01 n=3 fg=0.20 bg=0.08
0 1 2 3 4 5
−log(p)
n=15/88 input genes with annotations
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fraction