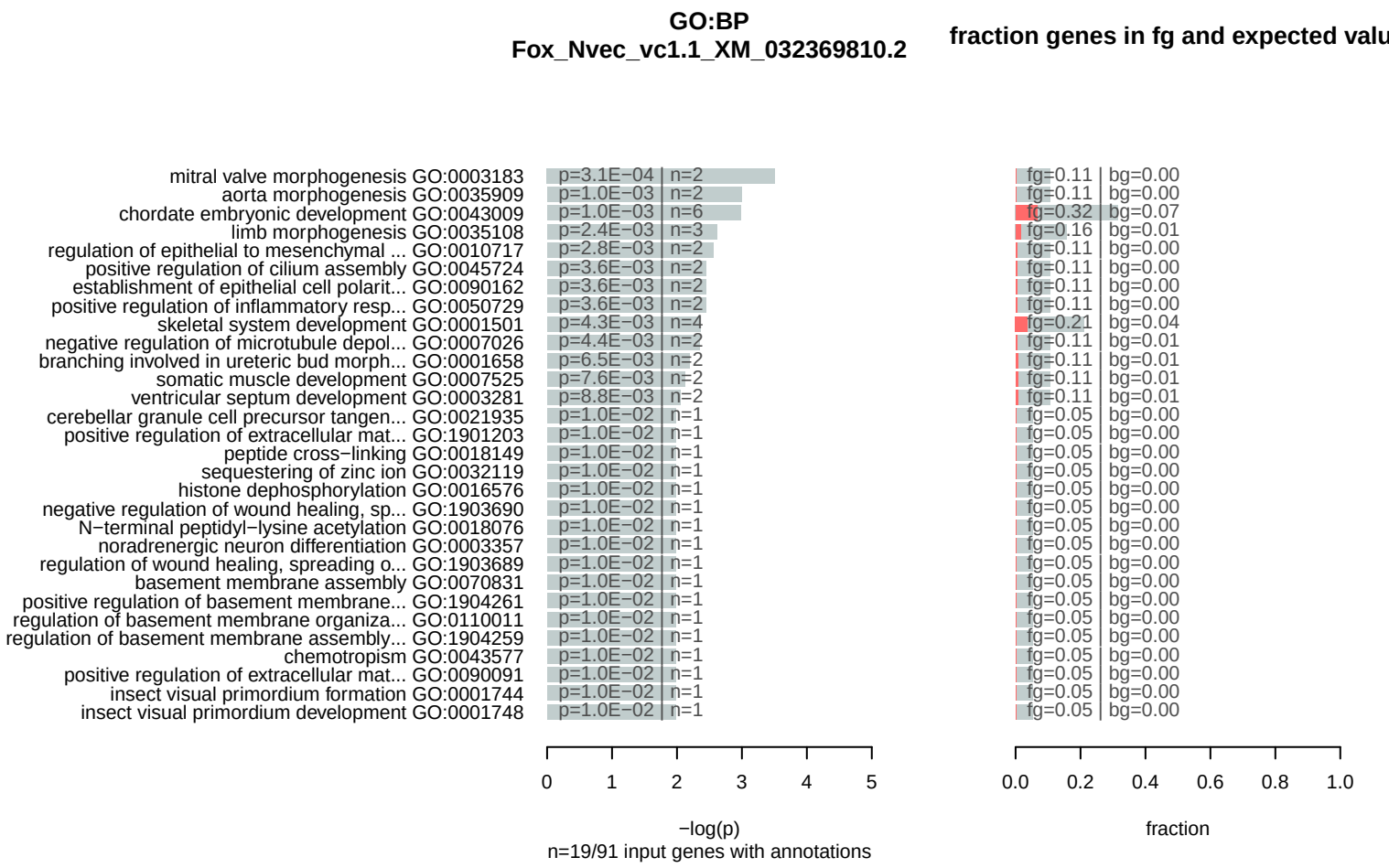
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fraction genes in fg and expected valu
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aorta morphogenesis GO:0035909 p=1.0E−03 n=2 fg=0.11 bg=0.00
chordate embryonic development GO:0043009 p=1.0E−03 n=6 fg=0.32 bg=0.07
limb morphogenesis GO:0035108 p=2.4E−03 n=3 fg=0.16 bg=0.01
regulation of epithelial to mesenchymal ... GO:0010717 p=2.8E−03 n=2 fg=0.11 bg=0.00
positive regulation of cilium assembly GO:0045724 p=3.6E−03 n=2 fg=0.11 bg=0.00
establishment of epithelial cell polarit... GO:0090162 p=3.6E−03 n=2 fg=0.11 bg=0.00
positive regulation of inflammatory resp... GO:0050729 p=3.6E−03 n=2 fg=0.11 bg=0.00
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branching involved in ureteric bud morph... GO:0001658 p=6.5E−03 n=2 fg=0.11 bg=0.01
somatic muscle development GO:0007525 p=7.6E−03 n=2 fg=0.11 bg=0.01
ventricular septum development GO:0003281 p=8.8E−03 n=2 fg=0.11 bg=0.01
cerebellar granule cell precursor tangen... GO:0021935 p=1.0E−02 n=1 fg=0.05 bg=0.00
positive regulation of extracellular mat... GO:1901203 p=1.0E−02 n=1 fg=0.05 bg=0.00
peptide cross−linking GO:0018149 p=1.0E−02 n=1 fg=0.05 bg=0.00
sequestering of zinc ion GO:0032119 p=1.0E−02 n=1 fg=0.05 bg=0.00
histone dephosphorylation GO:0016576 p=1.0E−02 n=1 fg=0.05 bg=0.00
negative regulation of wound healing, sp... GO:1903690 p=1.0E−02 n=1 fg=0.05 bg=0.00
N−terminal peptidyl−lysine acetylation GO:0018076 p=1.0E−02 n=1 fg=0.05 bg=0.00
noradrenergic neuron differentiation GO:0003357 p=1.0E−02 n=1 fg=0.05 bg=0.00
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basement membrane assembly GO:0070831 p=1.0E−02 n=1 fg=0.05 bg=0.00
positive regulation of basement membrane... GO:1904261 p=1.0E−02 n=1 fg=0.05 bg=0.00
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chemotropism GO:0043577 p=1.0E−02 n=1 fg=0.05 bg=0.00
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insect visual primordium formation GO:0001744 p=1.0E−02 n=1 fg=0.05 bg=0.00
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−log(p)
n=19/91 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032369810.2
fraction genes in fg and expected valu
microtubule plus−end binding GO:0051010 p=5.6E−04 n=2 fg=0.12 bg=0.00
RNA binding GO:0003723 p=9.9E−03 n=5 fg=0.31 bg=0.09
growth hormone−releasing hormone recepto... GO:0016520 p=1.0E−02 n=1 fg=0.06 bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946 p=1.0E−02 n=1 fg=0.06 bg=0.00
dystroglycan binding GO:0002162 p=1.0E−02 n=1 fg=0.06 bg=0.00
cysteine−tRNA ligase activity GO:0004817 p=1.0E−02 n=1 fg=0.06 bg=0.00
regulatory region RNA binding GO:0001069 p=1.0E−02 n=1 fg=0.06 bg=0.00
kinetochore binding GO:0043515 p=1.0E−02 n=1 fg=0.06 bg=0.00
interleukin−5 receptor binding GO:0005137 p=1.0E−02 n=1 fg=0.06 bg=0.00
cGMP−stimulated cyclic−nucleotide phosph... GO:0004118 p=1.0E−02 n=1 fg=0.06 bg=0.00
phosphoric ester hydrolase activity GO:0042578 p=1.8E−02 n=3 fg=0.19 bg=0.04
GAF domain binding GO:0036004 p=2.0E−02 n=1 fg=0.06 bg=0.00
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zinc ion transmembrane transporter activ... GO:0005385 p=3.0E−02 n=1 fg=0.06 bg=0.00
3',5'−cyclic−AMP phosphodiesterase activ... GO:0004115 p=3.0E−02 n=1 fg=0.06 bg=0.00
neurexin family protein binding GO:0042043 p=3.0E−02 n=1 fg=0.06 bg=0.00
cell adhesion molecule binding GO:0050839 p=3.3E−02 n=2 fg=0.12 bg=0.02
syndecan binding GO:0045545 p=4.0E−02 n=1 fg=0.06 bg=0.00
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cyclic nucleotide binding GO:0030551 p=4.9E−02 n=1 fg=0.06 bg=0.00
ephrin receptor binding GO:0046875 p=4.9E−02 n=1 fg=0.06 bg=0.00
proteoglycan binding GO:0043394 p=4.9E−02 n=1 fg=0.06 bg=0.00
phosphatase activity GO:0016791 p=5.7E−02 n=2 fg=0.12 bg=0.02
3',5'−cyclic−GMP phosphodiesterase activ... GO:0047555 p=5.9E−02 n=1 fg=0.06 bg=0.00
signaling receptor activator activity GO:0030546 p=5.9E−02 n=1 fg=0.06 bg=0.00
0 1 2 3 4 5
−log(p)
n=16/91 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032369810.2
fraction genes in fg and expected valu
ciliary basal body GO:0036064 p=2.5E−03 n=3 fg=0.16 bg=0.01
cytoplasmic microtubule plus−end GO:1904511 p=1.1E−02 n=1 fg=0.05 bg=0.00
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interleukin−5 receptor complex GO:0005895 p=1.1E−02 n=1 fg=0.05 bg=0.00
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spindle microtubule GO:0005876 p=1.0E−01 n=1 fg=0.05 bg=0.01
membrane raft GO:0045121 p=1.0E−01 n=2 fg=0.11 bg=0.03
membrane microdomain GO:0098857 p=1.0E−01 n=2 fg=0.11 bg=0.03
somatodendritic compartment GO:0036477 p=1.1E−01 n=4 fg=0.21 bg=0.10
A band GO:0031672 p=1.3E−01 n=1 fg=0.05 bg=0.01
azurophil granule lumen GO:0035578 p=1.4E−01 n=1 fg=0.05 bg=0.01
0 1 2 3 4 5
−log(p)
n=19/91 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction