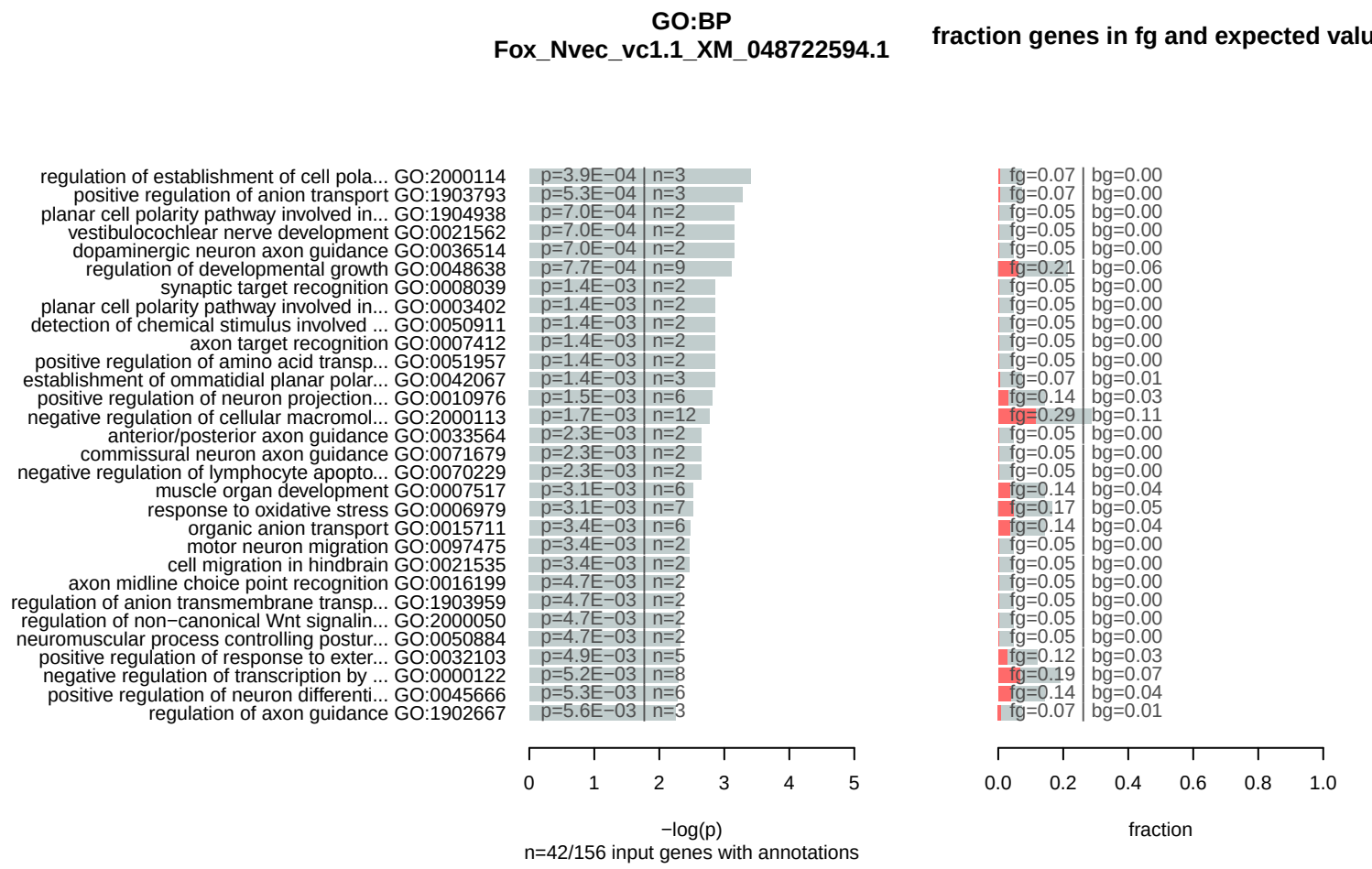
GO:BP
Fox_Nvec_vc1.1_XM_048722594.1
fraction genes in fg and expected valu
regulation of establishment of cell pola... GO:2000114 p=3.9E−04 n=3 fg=0.07 bg=0.00
positive regulation of anion transport GO:1903793 p=5.3E−04 n=3 fg=0.07 bg=0.00
planar cell polarity pathway involved in... GO:1904938 p=7.0E−04 n=2 fg=0.05 bg=0.00
vestibulocochlear nerve development GO:0021562 p=7.0E−04 n=2 fg=0.05 bg=0.00
dopaminergic neuron axon guidance GO:0036514 p=7.0E−04 n=2 fg=0.05 bg=0.00
regulation of developmental growth GO:0048638 p=7.7E−04 n=9 fg=0.21 bg=0.06
synaptic target recognition GO:0008039 p=1.4E−03 n=2 fg=0.05 bg=0.00
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detection of chemical stimulus involved ... GO:0050911 p=1.4E−03 n=2 fg=0.05 bg=0.00
axon target recognition GO:0007412 p=1.4E−03 n=2 fg=0.05 bg=0.00
positive regulation of amino acid transp... GO:0051957 p=1.4E−03 n=2 fg=0.05 bg=0.00
establishment of ommatidial planar polar... GO:0042067 p=1.4E−03 n=3 fg=0.07 bg=0.01
positive regulation of neuron projection... GO:0010976 p=1.5E−03 n=6 fg=0.14 bg=0.03
negative regulation of cellular macromol... GO:2000113 p=1.7E−03 n=12 fg=0.29 bg=0.11
anterior/posterior axon guidance GO:0033564 p=2.3E−03 n=2 fg=0.05 bg=0.00
commissural neuron axon guidance GO:0071679 p=2.3E−03 n=2 fg=0.05 bg=0.00
negative regulation of lymphocyte apopto... GO:0070229 p=2.3E−03 n=2 fg=0.05 bg=0.00
muscle organ development GO:0007517 p=3.1E−03 n=6 fg=0.14 bg=0.04
response to oxidative stress GO:0006979 p=3.1E−03 n=7 fg=0.17 bg=0.05
organic anion transport GO:0015711 p=3.4E−03 n=6 fg=0.14 bg=0.04
motor neuron migration GO:0097475 p=3.4E−03 n=2 fg=0.05 bg=0.00
cell migration in hindbrain GO:0021535 p=3.4E−03 n=2 fg=0.05 bg=0.00
axon midline choice point recognition GO:0016199 p=4.7E−03 n=2 fg=0.05 bg=0.00
regulation of anion transmembrane transp... GO:1903959 p=4.7E−03 n=2 fg=0.05 bg=0.00
regulation of non−canonical Wnt signalin... GO:2000050 p=4.7E−03 n=2 fg=0.05 bg=0.00
neuromuscular process controlling postur... GO:0050884 p=4.7E−03 n=2 fg=0.05 bg=0.00
positive regulation of response to exter... GO:0032103 p=4.9E−03 n=5 fg=0.12 bg=0.03
negative regulation of transcription by ... GO:0000122 p=5.2E−03 n=8 fg=0.19 bg=0.07
positive regulation of neuron differenti... GO:0045666 p=5.3E−03 n=6 fg=0.14 bg=0.04
regulation of axon guidance GO:1902667 p=5.6E−03 n=3 fg=0.07 bg=0.01
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n=42/156 input genes with annotations
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fraction
GO:MF
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fraction genes in fg and expected valu
frizzled binding GO:0005109 p=4.6E−04 n=3 fg=0.08 bg=0.00
promoter−specific chromatin binding GO:1990841 p=6.2E−04 n=3 fg=0.08 bg=0.00
RNA polymerase II cis−regulatory region ... GO:0000978 p=6.9E−03 n=5 fg=0.13 bg=0.03
transcription regulatory region nucleic ... GO:0001067 p=8.0E−03 n=9 fg=0.23 bg=0.05
DNA−binding transcription repressor acti... GO:0001227 p=9.2E−03 n=3 fg=0.08 bg=0.01
endopeptidase regulator activity GO:0061135 p=1.1E−02 n=2 fg=0.05 bg=0.00
double−stranded DNA binding GO:0003690 p=1.4E−02 n=9 fg=0.23 bg=0.06
amide transmembrane transporter activity GO:0042887 p=1.6E−02 n=2 fg=0.05 bg=0.01
transcription cis−regulatory region bind... GO:0000976 p=1.6E−02 n=8 fg=0.21 bg=0.05
phosphatidylglycerol binding GO:1901611 p=1.6E−02 n=1 fg=0.03 bg=0.00
cardiolipin binding GO:1901612 p=1.6E−02 n=1 fg=0.03 bg=0.00
amino acid:proton symporter activity GO:0005280 p=1.6E−02 n=1 fg=0.03 bg=0.00
Rho−dependent protein serine/threonine k... GO:0072518 p=1.6E−02 n=1 fg=0.03 bg=0.00
L−proline transmembrane transporter acti... GO:0015193 p=1.6E−02 n=1 fg=0.03 bg=0.00
peroxynitrite reductase activity GO:0072541 p=1.6E−02 n=1 fg=0.03 bg=0.00
L−tryptophan transmembrane transporter a... GO:0015196 p=1.6E−02 n=1 fg=0.03 bg=0.00
methotrexate transmembrane transporter a... GO:0015350 p=1.6E−02 n=1 fg=0.03 bg=0.00
lipoprotein lipase activity GO:0004465 p=1.6E−02 n=1 fg=0.03 bg=0.00
peroxiredoxin activity GO:0051920 p=1.6E−02 n=1 fg=0.03 bg=0.00
phosphatidylserine decarboxylase activit... GO:0004609 p=1.6E−02 n=1 fg=0.03 bg=0.00
glycine transmembrane transporter activi... GO:0015187 p=1.6E−02 n=1 fg=0.03 bg=0.00
lysophosphatidic acid binding GO:0035727 p=1.6E−02 n=1 fg=0.03 bg=0.00
thioredoxin peroxidase activity GO:0008379 p=1.6E−02 n=1 fg=0.03 bg=0.00
mono−olein transacylation activity GO:0051264 p=1.6E−02 n=1 fg=0.03 bg=0.00
diolein transacylation activity GO:0051265 p=1.6E−02 n=1 fg=0.03 bg=0.00
nickel cation binding GO:0016151 p=1.6E−02 n=1 fg=0.03 bg=0.00
ATPase−coupled intramembrane lipid trans... GO:0140326 p=1.6E−02 n=1 fg=0.03 bg=0.00
flippase activity GO:0140327 p=1.6E−02 n=1 fg=0.03 bg=0.00
aminophospholipid flippase activity GO:0015247 p=1.6E−02 n=1 fg=0.03 bg=0.00
peptidase regulator activity GO:0061134 p=2.1E−02 n=2 fg=0.05 bg=0.01
0 1 2 3 4 5
−log(p)
n=39/156 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_048722594.1
fraction genes in fg and expected valu
cytoplasmic ribonucleoprotein granule GO:0036464 p=2.6E−03 n=5 fg=0.11 bg=0.02
fusome GO:0045169 p=9.1E−03 n=2 fg=0.04 bg=0.00
specific granule GO:0042581 p=1.3E−02 n=3 fg=0.07 bg=0.01
actin filament bundle GO:0032432 p=1.4E−02 n=2 fg=0.04 bg=0.00
lateral plasma membrane GO:0016328 p=1.6E−02 n=2 fg=0.04 bg=0.00
spectrosome GO:0045170 p=1.7E−02 n=1 fg=0.02 bg=0.00
spectrin GO:0008091 p=1.7E−02 n=1 fg=0.02 bg=0.00
apicomedial cortex GO:0106037 p=1.7E−02 n=1 fg=0.02 bg=0.00
plastid GO:0009536 p=1.7E−02 n=1 fg=0.02 bg=0.00
extrinsic component of presynaptic activ... GO:0098891 p=1.7E−02 n=1 fg=0.02 bg=0.00
symplast GO:0055044 p=1.7E−02 n=1 fg=0.02 bg=0.00
plasmodesma GO:0009506 p=1.7E−02 n=1 fg=0.02 bg=0.00
chloroplast GO:0009507 p=1.7E−02 n=1 fg=0.02 bg=0.00
extrinsic component of synaptic membrane GO:0099243 p=1.7E−02 n=1 fg=0.02 bg=0.00
actin rod GO:0031002 p=1.7E−02 n=1 fg=0.02 bg=0.00
extrinsic component of presynaptic membr... GO:0098888 p=1.7E−02 n=1 fg=0.02 bg=0.00
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cofilin−actin rod GO:0090732 p=1.7E−02 n=1 fg=0.02 bg=0.00
chromatin GO:0000785 p=1.8E−02 n=6 fg=0.13 bg=0.05
contractile fiber GO:0043292 p=2.6E−02 n=4 fg=0.09 bg=0.03
vacuolar membrane GO:0005774 p=3.0E−02 n=4 fg=0.09 bg=0.03
Sin3 complex GO:0016580 p=3.3E−02 n=1 fg=0.02 bg=0.00
PTW/PP1 phosphatase complex GO:0072357 p=3.3E−02 n=1 fg=0.02 bg=0.00
nucleus GO:0005634 p=3.3E−02 n=29 fg=0.64 bg=0.50
brush border membrane GO:0031526 p=3.5E−02 n=2 fg=0.04 bg=0.01
specific granule membrane GO:0035579 p=4.3E−02 n=2 fg=0.04 bg=0.01
cortical actin cytoskeleton GO:0030864 p=4.3E−02 n=2 fg=0.04 bg=0.01
actin cytoskeleton GO:0015629 p=4.4E−02 n=4 fg=0.09 bg=0.03
cytolytic granule GO:0044194 p=4.9E−02 n=1 fg=0.02 bg=0.00
zymogen granule membrane GO:0042589 p=4.9E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=45/156 input genes with annotations
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fraction