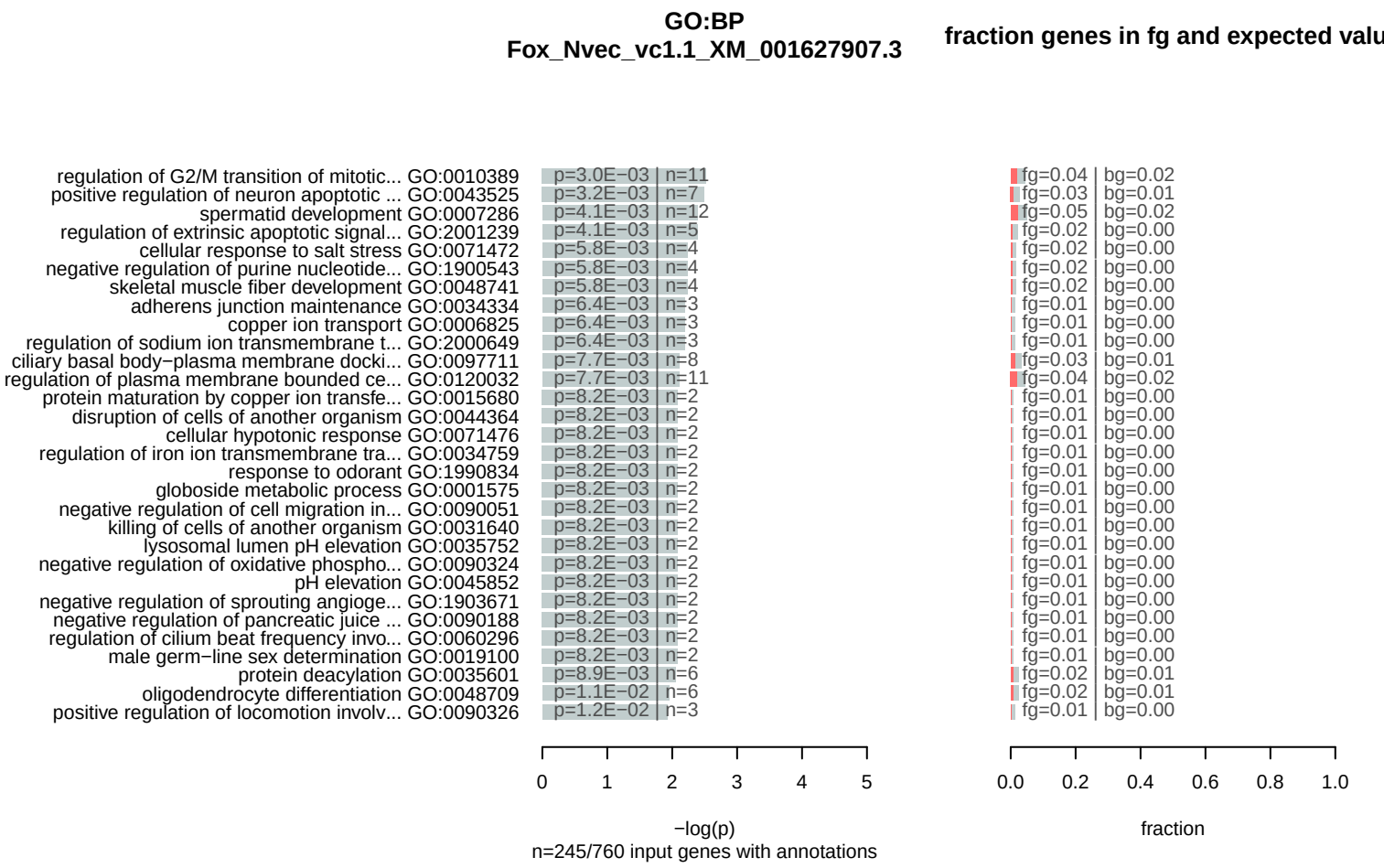
GO:BP
Fox_Nvec_vc1.1_XM_001627907.3
fraction genes in fg and expected valu
regulation of G2/M transition of mitotic... GO:0010389 p=3.0E−03 n=11 fg=0.04 bg=0.02
positive regulation of neuron apoptotic ... GO:0043525 p=3.2E−03 n=7 fg=0.03 bg=0.01
spermatid development GO:0007286 p=4.1E−03 n=12 fg=0.05 bg=0.02
regulation of extrinsic apoptotic signal... GO:2001239 p=4.1E−03 n=5 fg=0.02 bg=0.00
cellular response to salt stress GO:0071472 p=5.8E−03 n=4 fg=0.02 bg=0.00
negative regulation of purine nucleotide... GO:1900543 p=5.8E−03 n=4 fg=0.02 bg=0.00
skeletal muscle fiber development GO:0048741 p=5.8E−03 n=4 fg=0.02 bg=0.00
adherens junction maintenance GO:0034334 p=6.4E−03 n=3 fg=0.01 bg=0.00
copper ion transport GO:0006825 p=6.4E−03 n=3 fg=0.01 bg=0.00
regulation of sodium ion transmembrane t... GO:2000649 p=6.4E−03 n=3 fg=0.01 bg=0.00
ciliary basal body−plasma membrane docki... GO:0097711 p=7.7E−03 n=8 fg=0.03 bg=0.01
regulation of plasma membrane bounded ce... GO:0120032 p=7.7E−03 n=11 fg=0.04 bg=0.02
protein maturation by copper ion transfe... GO:0015680 p=8.2E−03 n=2 fg=0.01 bg=0.00
disruption of cells of another organism GO:0044364 p=8.2E−03 n=2 fg=0.01 bg=0.00
cellular hypotonic response GO:0071476 p=8.2E−03 n=2 fg=0.01 bg=0.00
regulation of iron ion transmembrane tra... GO:0034759 p=8.2E−03 n=2 fg=0.01 bg=0.00
response to odorant GO:1990834 p=8.2E−03 n=2 fg=0.01 bg=0.00
globoside metabolic process GO:0001575 p=8.2E−03 n=2 fg=0.01 bg=0.00
negative regulation of cell migration in... GO:0090051 p=8.2E−03 n=2 fg=0.01 bg=0.00
killing of cells of another organism GO:0031640 p=8.2E−03 n=2 fg=0.01 bg=0.00
lysosomal lumen pH elevation GO:0035752 p=8.2E−03 n=2 fg=0.01 bg=0.00
negative regulation of oxidative phospho... GO:0090324 p=8.2E−03 n=2 fg=0.01 bg=0.00
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negative regulation of sprouting angioge... GO:1903671 p=8.2E−03 n=2 fg=0.01 bg=0.00
negative regulation of pancreatic juice ... GO:0090188 p=8.2E−03 n=2 fg=0.01 bg=0.00
regulation of cilium beat frequency invo... GO:0060296 p=8.2E−03 n=2 fg=0.01 bg=0.00
male germ−line sex determination GO:0019100 p=8.2E−03 n=2 fg=0.01 bg=0.00
protein deacylation GO:0035601 p=8.9E−03 n=6 fg=0.02 bg=0.01
oligodendrocyte differentiation GO:0048709 p=1.1E−02 n=6 fg=0.02 bg=0.01
positive regulation of locomotion involv... GO:0090326 p=1.2E−02 n=3 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=245/760 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_001627907.3
fraction genes in fg and expected valu
translation factor activity, RNA binding GO:0008135 p=2.9E−03 n=8 fg=0.04 bg=0.01
ribosome binding GO:0043022 p=6.6E−03 n=5 fg=0.02 bg=0.01
calcium−activated potassium channel acti... GO:0015269 p=6.9E−03 n=3 fg=0.01 bg=0.00
BH3 domain binding GO:0051434 p=8.6E−03 n=2 fg=0.01 bg=0.00
flap−structured DNA binding GO:0070336 p=8.6E−03 n=2 fg=0.01 bg=0.00
superoxide dismutase copper chaperone ac... GO:0016532 p=8.6E−03 n=2 fg=0.01 bg=0.00
histone deacetylase activity GO:0004407 p=9.7E−03 n=4 fg=0.02 bg=0.00
carbohydrate derivative binding GO:0097367 p=1.8E−02 n=26 fg=0.12 bg=0.08
carbohydrate kinase activity GO:0019200 p=2.1E−02 n=3 fg=0.01 bg=0.00
G−quadruplex DNA binding GO:0051880 p=2.4E−02 n=2 fg=0.01 bg=0.00
microtubule motor activity GO:0003777 p=2.6E−02 n=4 fg=0.02 bg=0.01
DNA−directed 5'−3' RNA polymerase activi... GO:0003899 p=3.1E−02 n=3 fg=0.01 bg=0.00
hydrolase activity, acting on ester bond... GO:0016788 p=4.0E−02 n=22 fg=0.10 bg=0.07
purine nucleotide binding GO:0017076 p=4.3E−02 n=22 fg=0.10 bg=0.07
5'−3' RNA polymerase activity GO:0034062 p=4.4E−02 n=3 fg=0.01 bg=0.00
RNA polymerase activity GO:0097747 p=4.4E−02 n=3 fg=0.01 bg=0.00
ADP binding GO:0043531 p=4.4E−02 n=4 fg=0.02 bg=0.01
dynein light intermediate chain binding GO:0051959 p=4.5E−02 n=2 fg=0.01 bg=0.00
palmitoyl−(protein) hydrolase activity GO:0008474 p=4.5E−02 n=2 fg=0.01 bg=0.00
5'−3' exonuclease activity GO:0008409 p=4.5E−02 n=2 fg=0.01 bg=0.00
palmitoyl hydrolase activity GO:0098599 p=4.5E−02 n=2 fg=0.01 bg=0.00
nucleotide binding GO:0000166 p=4.9E−02 n=25 fg=0.11 bg=0.08
nucleoside phosphate binding GO:1901265 p=4.9E−02 n=25 fg=0.11 bg=0.08
transferase activity GO:0016740 p=5.1E−02 n=55 fg=0.25 bg=0.20
ribonucleotide binding GO:0032553 p=5.1E−02 n=21 fg=0.10 bg=0.07
purine ribonucleotide binding GO:0032555 p=5.1E−02 n=21 fg=0.10 bg=0.07
translation initiation factor activity GO:0003743 p=5.4E−02 n=4 fg=0.02 bg=0.01
purine ribonucleoside triphosphate bindi... GO:0035639 p=5.5E−02 n=19 fg=0.09 bg=0.06
heparin binding GO:0008201 p=5.8E−02 n=3 fg=0.01 bg=0.00
transferase activity, transferring phosp... GO:0016772 p=5.9E−02 n=26 fg=0.12 bg=0.09
0 1 2 3 4 5
−log(p)
n=220/760 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001627907.3
fraction genes in fg and expected valu
intermediate filament cytoskeleton GO:0045111 p=1.5E−02 n=4 fg=0.02 bg=0.00
lipid droplet GO:0005811 p=2.1E−02 n=6 fg=0.02 bg=0.01
centriole GO:0005814 p=2.2E−02 n=7 fg=0.03 bg=0.01
EARP complex GO:1990745 p=2.5E−02 n=2 fg=0.01 bg=0.00
eukaryotic translation initiation factor... GO:0005850 p=2.5E−02 n=2 fg=0.01 bg=0.00
GARP complex GO:0000938 p=2.5E−02 n=2 fg=0.01 bg=0.00
Bcl−2 family protein complex GO:0097136 p=2.5E−02 n=2 fg=0.01 bg=0.00
tertiary granule GO:0070820 p=2.5E−02 n=6 fg=0.02 bg=0.01
histone deacetylase complex GO:0000118 p=2.8E−02 n=4 fg=0.02 bg=0.00
fibrillar center GO:0001650 p=3.1E−02 n=7 fg=0.03 bg=0.01
tertiary granule membrane GO:0070821 p=3.3E−02 n=3 fg=0.01 bg=0.00
sperm flagellum GO:0036126 p=3.6E−02 n=7 fg=0.03 bg=0.01
RNA polymerase I complex GO:0005736 p=4.7E−02 n=2 fg=0.01 bg=0.00
9+2 motile cilium GO:0097729 p=4.8E−02 n=7 fg=0.03 bg=0.01
endocytic vesicle membrane GO:0030666 p=6.9E−02 n=5 fg=0.02 bg=0.01
endocytic vesicle GO:0030139 p=6.9E−02 n=9 fg=0.04 bg=0.02
sensory dendrite GO:0071683 p=7.3E−02 n=2 fg=0.01 bg=0.00
eukaryotic translation initiation factor... GO:0005851 p=7.3E−02 n=2 fg=0.01 bg=0.00
RNA polymerase II, core complex GO:0005665 p=7.3E−02 n=2 fg=0.01 bg=0.00
intermediate filament GO:0005882 p=7.3E−02 n=2 fg=0.01 bg=0.00
sperm fibrous sheath GO:0035686 p=7.3E−02 n=2 fg=0.01 bg=0.00
intrinsic component of the cytoplasmic s... GO:0031235 p=7.3E−02 n=2 fg=0.01 bg=0.00
neuron projection cytoplasm GO:0120111 p=7.8E−02 n=3 fg=0.01 bg=0.00
organelle envelope GO:0031967 p=8.2E−02 n=34 fg=0.13 bg=0.11
envelope GO:0031975 p=8.2E−02 n=34 fg=0.13 bg=0.11
A band GO:0031672 p=8.3E−02 n=4 fg=0.02 bg=0.01
phagocytic vesicle GO:0045335 p=9.2E−02 n=5 fg=0.02 bg=0.01
nuclear speck GO:0016607 p=9.3E−02 n=12 fg=0.05 bg=0.03
protein kinase CK2 complex GO:0005956 p=9.4E−02 n=1 fg=0.00 bg=0.00
ciliary cap GO:0061822 p=9.4E−02 n=1 fg=0.00 bg=0.00
0 1 2 3 4 5
−log(p)
n=255/760 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction