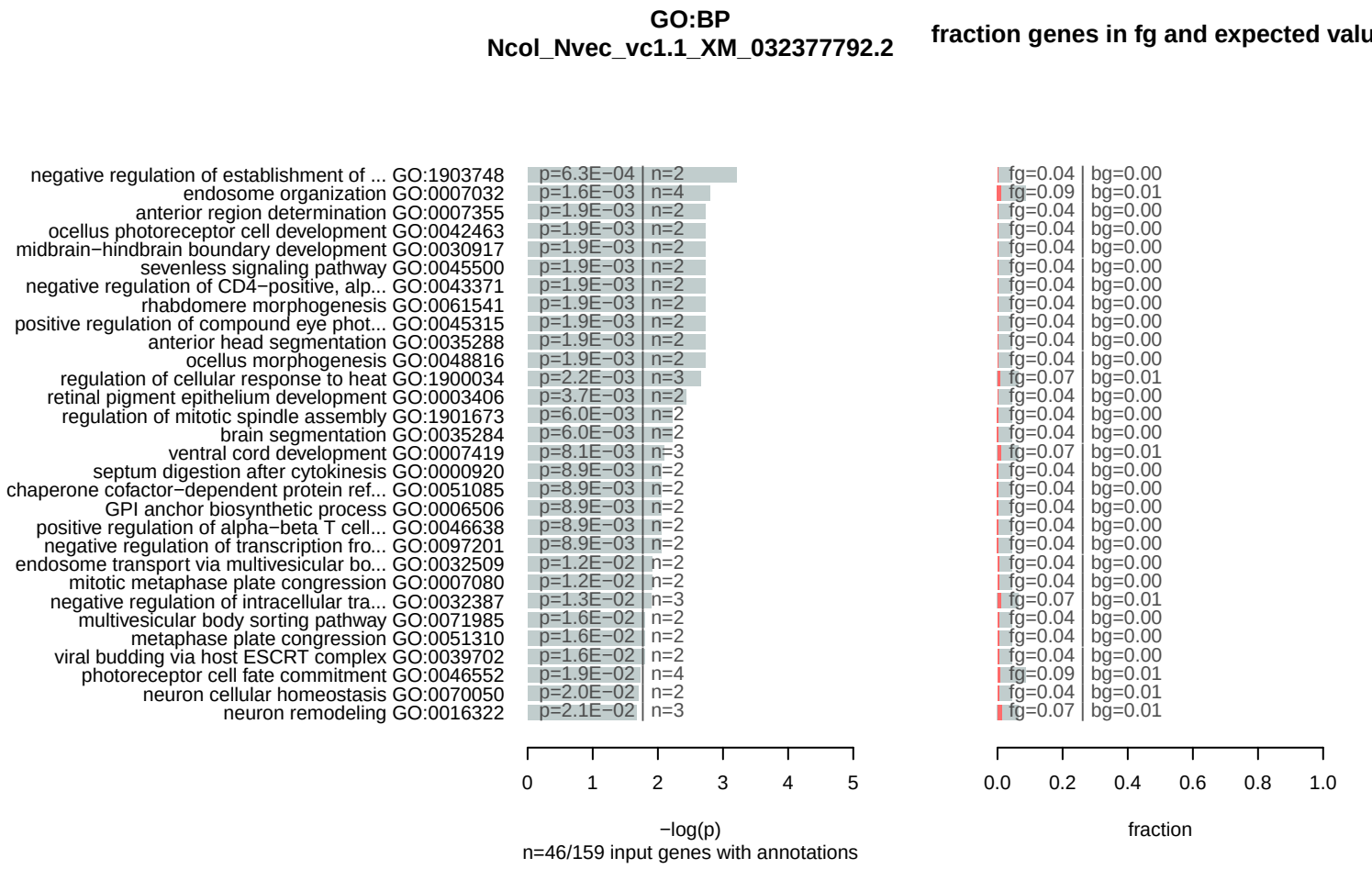
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Ncol_Nvec_vc1.1_XM_032377792.2
fraction genes in fg and expected valu
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endosome organization GO:0007032 p=1.6E−03 n=4 fg=0.09 bg=0.01
anterior region determination GO:0007355 p=1.9E−03 n=2 fg=0.04 bg=0.00
ocellus photoreceptor cell development GO:0042463 p=1.9E−03 n=2 fg=0.04 bg=0.00
midbrain−hindbrain boundary development GO:0030917 p=1.9E−03 n=2 fg=0.04 bg=0.00
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negative regulation of CD4−positive, alp... GO:0043371 p=1.9E−03 n=2 fg=0.04 bg=0.00
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anterior head segmentation GO:0035288 p=1.9E−03 n=2 fg=0.04 bg=0.00
ocellus morphogenesis GO:0048816 p=1.9E−03 n=2 fg=0.04 bg=0.00
regulation of cellular response to heat GO:1900034 p=2.2E−03 n=3 fg=0.07 bg=0.01
retinal pigment epithelium development GO:0003406 p=3.7E−03 n=2 fg=0.04 bg=0.00
regulation of mitotic spindle assembly GO:1901673 p=6.0E−03 n=2 fg=0.04 bg=0.00
brain segmentation GO:0035284 p=6.0E−03 n=2 fg=0.04 bg=0.00
ventral cord development GO:0007419 p=8.1E−03 n=3 fg=0.07 bg=0.01
septum digestion after cytokinesis GO:0000920 p=8.9E−03 n=2 fg=0.04 bg=0.00
chaperone cofactor−dependent protein ref... GO:0051085 p=8.9E−03 n=2 fg=0.04 bg=0.00
GPI anchor biosynthetic process GO:0006506 p=8.9E−03 n=2 fg=0.04 bg=0.00
positive regulation of alpha−beta T cell... GO:0046638 p=8.9E−03 n=2 fg=0.04 bg=0.00
negative regulation of transcription fro... GO:0097201 p=8.9E−03 n=2 fg=0.04 bg=0.00
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negative regulation of intracellular tra... GO:0032387 p=1.3E−02 n=3 fg=0.07 bg=0.01
multivesicular body sorting pathway GO:0071985 p=1.6E−02 n=2 fg=0.04 bg=0.00
metaphase plate congression GO:0051310 p=1.6E−02 n=2 fg=0.04 bg=0.00
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neuron cellular homeostasis GO:0070050 p=2.0E−02 n=2 fg=0.04 bg=0.01
neuron remodeling GO:0016322 p=2.1E−02 n=3 fg=0.07 bg=0.01
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n=46/159 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032377792.2
fraction genes in fg and expected valu
adenyl−nucleotide exchange factor activi... GO:0000774 p=2.2E−03 n=2 fg=0.05 bg=0.00
spermine:oxygen oxidoreductase (spermidi... GO:0052901 p=2.8E−02 n=1 fg=0.02 bg=0.00
N1−acetylspermidine:oxygen oxidoreductas... GO:0052904 p=2.8E−02 n=1 fg=0.02 bg=0.00
NEDD8 conjugating enzyme activity GO:0061654 p=2.8E−02 n=1 fg=0.02 bg=0.00
translation termination factor activity GO:0008079 p=2.8E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on the C... GO:0016647 p=2.8E−02 n=1 fg=0.02 bg=0.00
farnesyltranstransferase activity GO:0004311 p=2.8E−02 n=1 fg=0.02 bg=0.00
DNA topoisomerase binding GO:0044547 p=2.8E−02 n=1 fg=0.02 bg=0.00
translation release factor activity GO:0003747 p=2.8E−02 n=1 fg=0.02 bg=0.00
protein farnesyltransferase activity GO:0004660 p=2.8E−02 n=1 fg=0.02 bg=0.00
polyamine oxidase activity GO:0046592 p=2.8E−02 n=1 fg=0.02 bg=0.00
7SK snRNA binding GO:0097322 p=2.8E−02 n=1 fg=0.02 bg=0.00
SNAP receptor activity GO:0005484 p=3.5E−02 n=2 fg=0.05 bg=0.01
phosphatidylinositol binding GO:0035091 p=3.6E−02 n=4 fg=0.09 bg=0.03
receptor tyrosine kinase binding GO:0030971 p=4.1E−02 n=2 fg=0.05 bg=0.01
ubiquitin−like protein conjugating enzym... GO:0061650 p=4.1E−02 n=2 fg=0.05 bg=0.01
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protein−cysteine S−palmitoyltransferase ... GO:0019706 p=5.4E−02 n=1 fg=0.02 bg=0.00
protein−cysteine S−acyltransferase activ... GO:0019707 p=5.4E−02 n=1 fg=0.02 bg=0.00
histone methyltransferase activity (H3−K... GO:0042800 p=5.4E−02 n=1 fg=0.02 bg=0.00
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transmembrane receptor protein tyrosine ... GO:0005068 p=5.4E−02 n=1 fg=0.02 bg=0.00
cyclin−dependent protein serine/threonin... GO:0004861 p=5.4E−02 n=1 fg=0.02 bg=0.00
1−phosphatidylinositol binding GO:0005545 p=5.4E−02 n=1 fg=0.02 bg=0.00
1−alkylglycerophosphocholine O−acetyltra... GO:0047192 p=5.4E−02 n=1 fg=0.02 bg=0.00
protein prenyltransferase activity GO:0008318 p=5.4E−02 n=1 fg=0.02 bg=0.00
high voltage−gated calcium channel activ... GO:0008331 p=5.4E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=44/159 input genes with annotations
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fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032377792.2
fraction genes in fg and expected valu
ESCRT III complex GO:0000815 p=3.8E−03 n=2 fg=0.04 bg=0.00
core−binding factor complex GO:0016513 p=2.6E−02 n=1 fg=0.02 bg=0.00
endocytic vesicle lumen GO:0071682 p=2.6E−02 n=1 fg=0.02 bg=0.00
apical cytoplasm GO:0090651 p=2.6E−02 n=1 fg=0.02 bg=0.00
protein farnesyltransferase complex GO:0005965 p=2.6E−02 n=1 fg=0.02 bg=0.00
SNARE complex GO:0031201 p=4.9E−02 n=2 fg=0.04 bg=0.01
endoplasmic reticulum chaperone complex GO:0034663 p=5.1E−02 n=1 fg=0.02 bg=0.00
caspase complex GO:0008303 p=5.1E−02 n=1 fg=0.02 bg=0.00
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pleated septate junction GO:0005919 p=5.1E−02 n=1 fg=0.02 bg=0.00
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endoplasmic reticulum exit site GO:0070971 p=7.6E−02 n=1 fg=0.02 bg=0.00
proximal dendrite GO:1990635 p=7.6E−02 n=1 fg=0.02 bg=0.00
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integral component of endoplasmic reticu... GO:0030176 p=8.8E−02 n=3 fg=0.06 bg=0.02
intrinsic component of endoplasmic retic... GO:0031227 p=8.8E−02 n=3 fg=0.06 bg=0.02
cytoplasmic side of plasma membrane GO:0009898 p=9.3E−02 n=3 fg=0.06 bg=0.02
endoplasmic reticulum−Golgi intermediate... GO:0005793 p=9.3E−02 n=2 fg=0.04 bg=0.01
microbody lumen GO:0031907 p=1.0E−01 n=1 fg=0.02 bg=0.00
sperm head GO:0061827 p=1.0E−01 n=1 fg=0.02 bg=0.00
extrinsic component of endosome membrane GO:0031313 p=1.0E−01 n=1 fg=0.02 bg=0.00
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septate junction GO:0005918 p=1.0E−01 n=1 fg=0.02 bg=0.00
peroxisomal matrix GO:0005782 p=1.0E−01 n=1 fg=0.02 bg=0.00
nuclear envelope GO:0005635 p=1.1E−01 n=4 fg=0.09 bg=0.04
cytoplasmic side of membrane GO:0098562 p=1.2E−01 n=3 fg=0.06 bg=0.03
contractile ring GO:0070938 p=1.2E−01 n=1 fg=0.02 bg=0.00
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−log(p)
n=47/159 input genes with annotations
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fraction