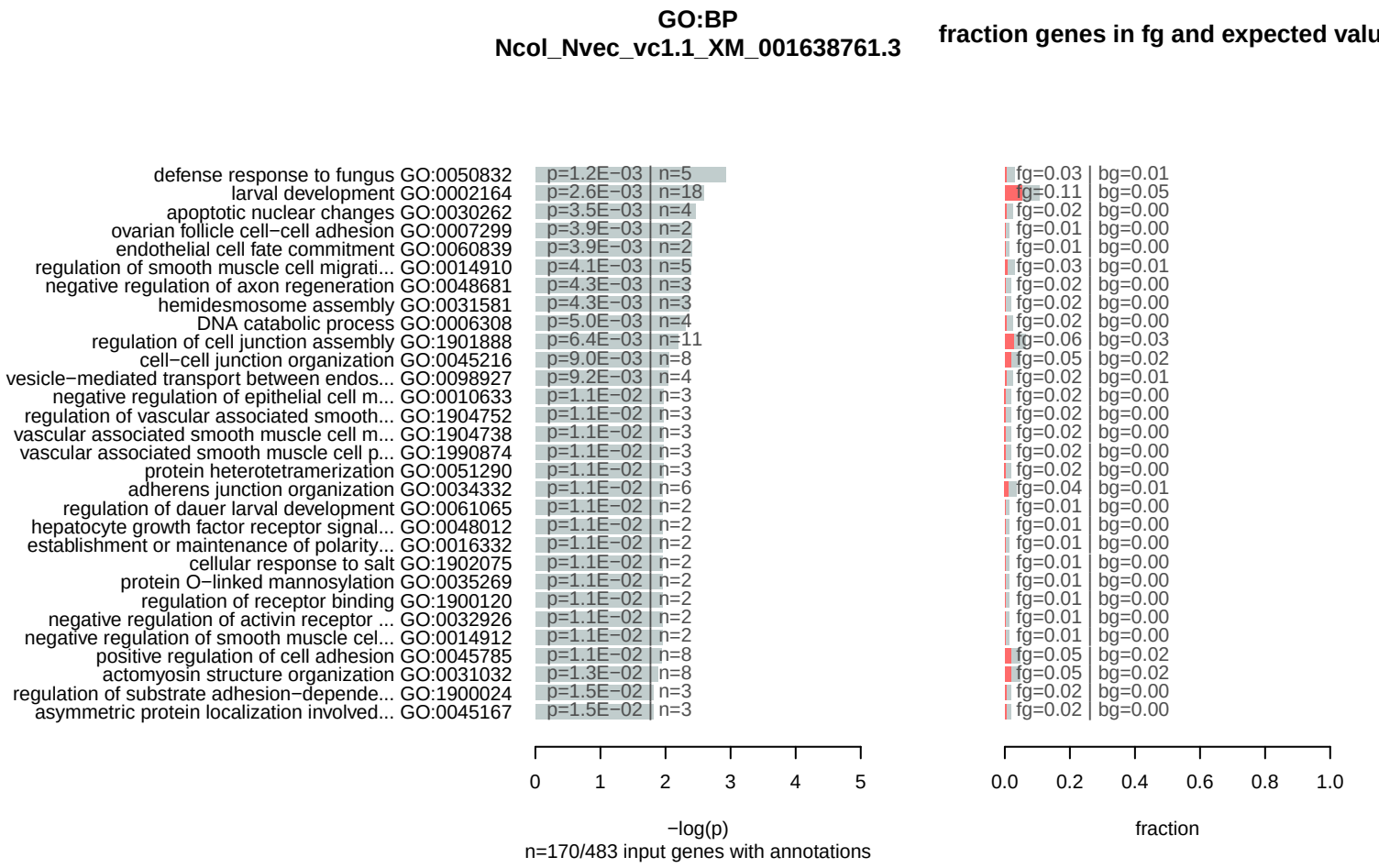
GO:BP
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larval development GO:0002164 p=2.6E−03 n=18 fg=0.11 bg=0.05
apoptotic nuclear changes GO:0030262 p=3.5E−03 n=4 fg=0.02 bg=0.00
ovarian follicle cell−cell adhesion GO:0007299 p=3.9E−03 n=2 fg=0.01 bg=0.00
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regulation of smooth muscle cell migrati... GO:0014910 p=4.1E−03 n=5 fg=0.03 bg=0.01
negative regulation of axon regeneration GO:0048681 p=4.3E−03 n=3 fg=0.02 bg=0.00
hemidesmosome assembly GO:0031581 p=4.3E−03 n=3 fg=0.02 bg=0.00
DNA catabolic process GO:0006308 p=5.0E−03 n=4 fg=0.02 bg=0.00
regulation of cell junction assembly GO:1901888 p=6.4E−03 n=11 fg=0.06 bg=0.03
cell−cell junction organization GO:0045216 p=9.0E−03 n=8 fg=0.05 bg=0.02
vesicle−mediated transport between endos... GO:0098927 p=9.2E−03 n=4 fg=0.02 bg=0.01
negative regulation of epithelial cell m... GO:0010633 p=1.1E−02 n=3 fg=0.02 bg=0.00
regulation of vascular associated smooth... GO:1904752 p=1.1E−02 n=3 fg=0.02 bg=0.00
vascular associated smooth muscle cell m... GO:1904738 p=1.1E−02 n=3 fg=0.02 bg=0.00
vascular associated smooth muscle cell p... GO:1990874 p=1.1E−02 n=3 fg=0.02 bg=0.00
protein heterotetramerization GO:0051290 p=1.1E−02 n=3 fg=0.02 bg=0.00
adherens junction organization GO:0034332 p=1.1E−02 n=6 fg=0.04 bg=0.01
regulation of dauer larval development GO:0061065 p=1.1E−02 n=2 fg=0.01 bg=0.00
hepatocyte growth factor receptor signal... GO:0048012 p=1.1E−02 n=2 fg=0.01 bg=0.00
establishment or maintenance of polarity... GO:0016332 p=1.1E−02 n=2 fg=0.01 bg=0.00
cellular response to salt GO:1902075 p=1.1E−02 n=2 fg=0.01 bg=0.00
protein O−linked mannosylation GO:0035269 p=1.1E−02 n=2 fg=0.01 bg=0.00
regulation of receptor binding GO:1900120 p=1.1E−02 n=2 fg=0.01 bg=0.00
negative regulation of activin receptor ... GO:0032926 p=1.1E−02 n=2 fg=0.01 bg=0.00
negative regulation of smooth muscle cel... GO:0014912 p=1.1E−02 n=2 fg=0.01 bg=0.00
positive regulation of cell adhesion GO:0045785 p=1.1E−02 n=8 fg=0.05 bg=0.02
actomyosin structure organization GO:0031032 p=1.3E−02 n=8 fg=0.05 bg=0.02
regulation of substrate adhesion−depende... GO:1900024 p=1.5E−02 n=3 fg=0.02 bg=0.00
asymmetric protein localization involved... GO:0045167 p=1.5E−02 n=3 fg=0.02 bg=0.00
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−log(p)
n=170/483 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001638761.3
fraction genes in fg and expected valu
histone deacetylase binding GO:0042826 p=4.4E−03 n=6 fg=0.04 bg=0.01
enzyme binding GO:0019899 p=6.1E−03 n=49 fg=0.33 bg=0.22
snRNA binding GO:0017069 p=1.1E−02 n=3 fg=0.02 bg=0.00
pre−mRNA intronic binding GO:0097157 p=1.1E−02 n=2 fg=0.01 bg=0.00
U2 snRNA binding GO:0030620 p=1.1E−02 n=2 fg=0.01 bg=0.00
xylosyltransferase activity GO:0042285 p=2.1E−02 n=2 fg=0.01 bg=0.00
FAD binding GO:0071949 p=2.1E−02 n=2 fg=0.01 bg=0.00
UDP−xylosyltransferase activity GO:0035252 p=2.1E−02 n=2 fg=0.01 bg=0.00
ubiquitin binding GO:0043130 p=2.2E−02 n=4 fg=0.03 bg=0.01
protein dimerization activity GO:0046983 p=2.3E−02 n=28 fg=0.19 bg=0.13
oxidoreductase activity, acting on paire... GO:0016705 p=2.7E−02 n=4 fg=0.03 bg=0.01
growth factor binding GO:0019838 p=2.7E−02 n=4 fg=0.03 bg=0.01
dynein light chain binding GO:0045503 p=3.4E−02 n=2 fg=0.01 bg=0.00
satellite DNA binding GO:0003696 p=3.4E−02 n=2 fg=0.01 bg=0.00
calcium−activated potassium channel acti... GO:0015269 p=3.4E−02 n=2 fg=0.01 bg=0.00
misfolded protein binding GO:0051787 p=3.4E−02 n=2 fg=0.01 bg=0.00
protein kinase C binding GO:0005080 p=3.5E−02 n=3 fg=0.02 bg=0.01
pentosyltransferase activity GO:0016763 p=3.5E−02 n=3 fg=0.02 bg=0.01
protein homodimerization activity GO:0042803 p=4.3E−02 n=21 fg=0.14 bg=0.10
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coreceptor activity GO:0015026 p=4.9E−02 n=2 fg=0.01 bg=0.00
dynein intermediate chain binding GO:0045505 p=4.9E−02 n=2 fg=0.01 bg=0.00
MAP kinase kinase activity GO:0004708 p=4.9E−02 n=2 fg=0.01 bg=0.00
gamma−tubulin binding GO:0043015 p=4.9E−02 n=2 fg=0.01 bg=0.00
ubiquitin−like protein binding GO:0032182 p=5.1E−02 n=4 fg=0.03 bg=0.01
E−box binding GO:0070888 p=5.2E−02 n=3 fg=0.02 bg=0.01
ribosome binding GO:0043022 p=5.2E−02 n=3 fg=0.02 bg=0.01
catalytic activity, acting on DNA GO:0140097 p=5.8E−02 n=8 fg=0.05 bg=0.03
adenosylselenohomocysteinase activity GO:0098604 p=6.2E−02 n=1 fg=0.01 bg=0.00
nerve growth factor binding GO:0048406 p=6.2E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=148/483 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001638761.3
fraction genes in fg and expected valu
U12−type spliceosomal complex GO:0005689 p=1.2E−02 n=3 fg=0.02 bg=0.00
intraciliary transport particle A GO:0030991 p=1.2E−02 n=2 fg=0.01 bg=0.00
myelin sheath GO:0043209 p=2.1E−02 n=7 fg=0.04 bg=0.02
zonula adherens GO:0005915 p=3.6E−02 n=2 fg=0.01 bg=0.00
intraciliary transport particle GO:0030990 p=3.6E−02 n=2 fg=0.01 bg=0.00
early endosome GO:0005769 p=4.1E−02 n=10 fg=0.06 bg=0.03
extracellular exosome GO:0070062 p=5.6E−02 n=4 fg=0.02 bg=0.01
actin filament GO:0005884 p=5.7E−02 n=3 fg=0.02 bg=0.01
extracellular vesicle GO:1903561 p=6.4E−02 n=4 fg=0.02 bg=0.01
heterochromatin GO:0000792 p=6.4E−02 n=4 fg=0.02 bg=0.01
apical junction complex GO:0043296 p=6.4E−02 n=4 fg=0.02 bg=0.01
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protein kinase CK2 complex GO:0005956 p=6.4E−02 n=1 fg=0.01 bg=0.00
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anterior cell cortex GO:0061802 p=6.4E−02 n=1 fg=0.01 bg=0.00
omegasome membrane GO:1903349 p=6.4E−02 n=1 fg=0.01 bg=0.00
nuclear RNA export factor complex GO:0042272 p=6.4E−02 n=1 fg=0.01 bg=0.00
pinosome GO:0044352 p=6.4E−02 n=1 fg=0.01 bg=0.00
macropinosome GO:0044354 p=6.4E−02 n=1 fg=0.01 bg=0.00
BAT3 complex GO:0071818 p=6.4E−02 n=1 fg=0.01 bg=0.00
endodeoxyribonuclease complex GO:1905347 p=6.4E−02 n=1 fg=0.01 bg=0.00
internode region of axon GO:0033269 p=6.4E−02 n=1 fg=0.01 bg=0.00
eukaryotic 43S preinitiation complex GO:0016282 p=6.4E−02 n=1 fg=0.01 bg=0.00
bub1−bub3 complex GO:1990298 p=6.4E−02 n=1 fg=0.01 bg=0.00
methionyl glutamyl tRNA synthetase compl... GO:0017102 p=6.4E−02 n=1 fg=0.01 bg=0.00
omegasome GO:1990462 p=6.4E−02 n=1 fg=0.01 bg=0.00
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066 p=6.4E−02 n=1 fg=0.01 bg=0.00
U7 snRNP GO:0005683 p=6.4E−02 n=1 fg=0.01 bg=0.00
intrinsic component of omegasome membran... GO:0097630 p=6.4E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=174/483 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction