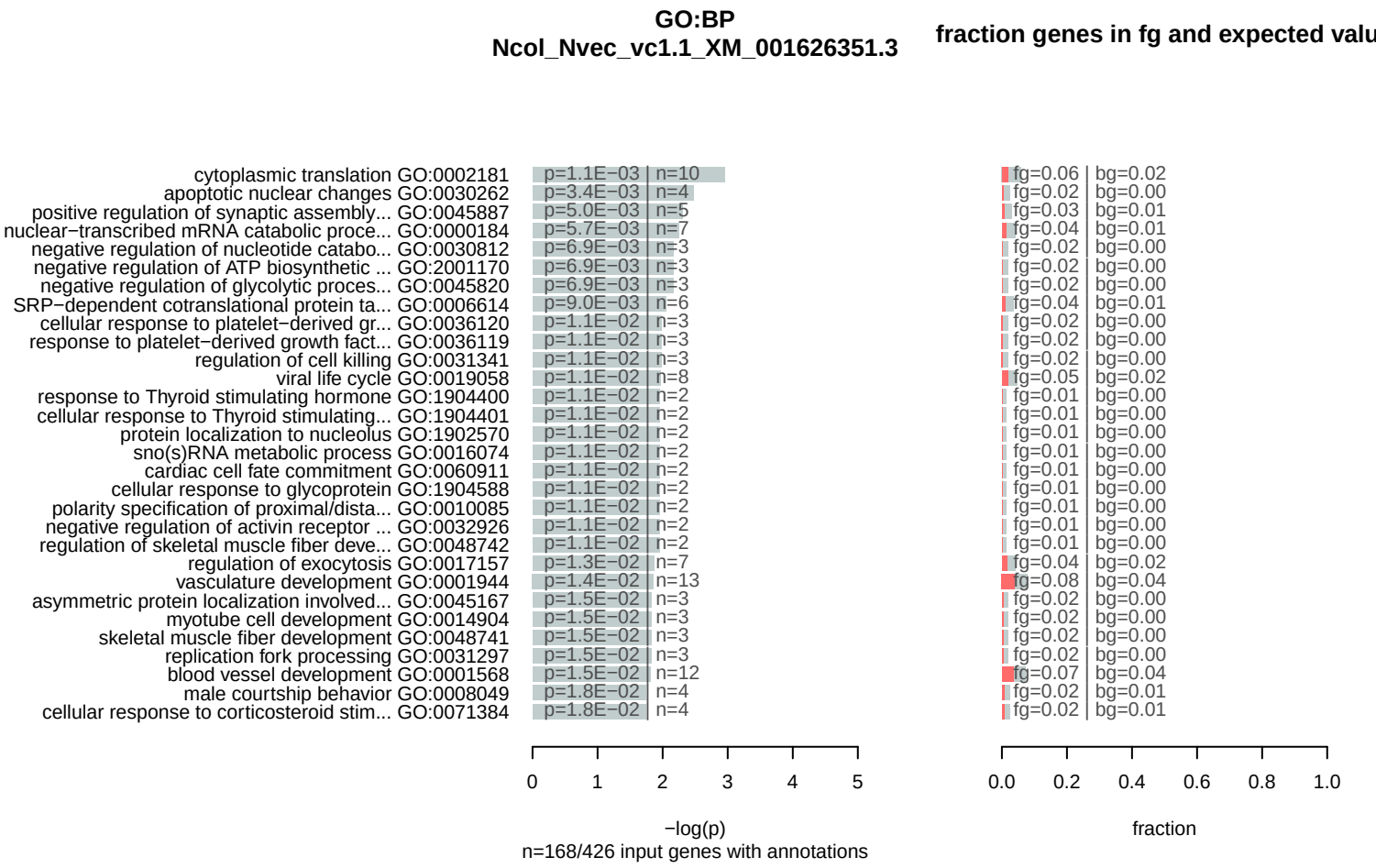
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apoptotic nuclear changes GO:0030262 p=3.4E−03 n=4 fg=0.02 bg=0.00
positive regulation of synaptic assembly... GO:0045887 p=5.0E−03 n=5 fg=0.03 bg=0.01
nuclear−transcribed mRNA catabolic proce... GO:0000184 p=5.7E−03 n=7 fg=0.04 bg=0.01
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negative regulation of glycolytic proces... GO:0045820 p=6.9E−03 n=3 fg=0.02 bg=0.00
SRP−dependent cotranslational protein ta... GO:0006614 p=9.0E−03 n=6 fg=0.04 bg=0.01
cellular response to platelet−derived gr... GO:0036120 p=1.1E−02 n=3 fg=0.02 bg=0.00
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regulation of cell killing GO:0031341 p=1.1E−02 n=3 fg=0.02 bg=0.00
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response to Thyroid stimulating hormone GO:1904400 p=1.1E−02 n=2 fg=0.01 bg=0.00
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protein localization to nucleolus GO:1902570 p=1.1E−02 n=2 fg=0.01 bg=0.00
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cardiac cell fate commitment GO:0060911 p=1.1E−02 n=2 fg=0.01 bg=0.00
cellular response to glycoprotein GO:1904588 p=1.1E−02 n=2 fg=0.01 bg=0.00
polarity specification of proximal/dista... GO:0010085 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
regulation of skeletal muscle fiber deve... GO:0048742 p=1.1E−02 n=2 fg=0.01 bg=0.00
regulation of exocytosis GO:0017157 p=1.3E−02 n=7 fg=0.04 bg=0.02
vasculature development GO:0001944 p=1.4E−02 n=13 fg=0.08 bg=0.04
asymmetric protein localization involved... GO:0045167 p=1.5E−02 n=3 fg=0.02 bg=0.00
myotube cell development GO:0014904 p=1.5E−02 n=3 fg=0.02 bg=0.00
skeletal muscle fiber development GO:0048741 p=1.5E−02 n=3 fg=0.02 bg=0.00
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blood vessel development GO:0001568 p=1.5E−02 n=12 fg=0.07 bg=0.04
male courtship behavior GO:0008049 p=1.8E−02 n=4 fg=0.02 bg=0.01
cellular response to corticosteroid stim... GO:0071384 p=1.8E−02 n=4 fg=0.02 bg=0.01
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001626351.3
fraction genes in fg and expected valu
structural constituent of ribosome GO:0003735 p=2.3E−03 n=10 fg=0.07 bg=0.02
RNA binding GO:0003723 p=3.6E−03 n=26 fg=0.18 bg=0.10
four−way junction DNA binding GO:0000400 p=3.9E−03 n=2 fg=0.01 bg=0.00
protein serine/threonine phosphatase act... GO:0004722 p=5.1E−03 n=5 fg=0.03 bg=0.01
ribosome binding GO:0043022 p=8.9E−03 n=4 fg=0.03 bg=0.01
molecular carrier activity GO:0140104 p=1.1E−02 n=3 fg=0.02 bg=0.00
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ATP−dependent activity, acting on RNA GO:0008186 p=2.7E−02 n=4 fg=0.03 bg=0.01
endodeoxyribonuclease activity GO:0004520 p=2.7E−02 n=3 fg=0.02 bg=0.00
protein lysine deacetylase activity GO:0033558 p=2.7E−02 n=3 fg=0.02 bg=0.00
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metal ion binding GO:0046872 p=3.3E−02 n=22 fg=0.15 bg=0.10
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
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deacetylase activity GO:0019213 p=3.5E−02 n=3 fg=0.02 bg=0.01
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nucleoside−triphosphatase activity GO:0017111 p=5.0E−02 n=16 fg=0.11 bg=0.07
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helicase activity GO:0004386 p=5.7E−02 n=5 fg=0.03 bg=0.01
amide binding GO:0033218 p=5.8E−02 n=8 fg=0.05 bg=0.03
catalytic activity, acting on DNA GO:0140097 p=5.8E−02 n=8 fg=0.05 bg=0.03
nerve growth factor binding GO:0048406 p=6.2E−02 n=1 fg=0.01 bg=0.00
acyl binding GO:0000035 p=6.2E−02 n=1 fg=0.01 bg=0.00
acyl carrier activity GO:0000036 p=6.2E−02 n=1 fg=0.01 bg=0.00
oxidoreductase activity, acting on paire... GO:0016717 p=6.2E−02 n=1 fg=0.01 bg=0.00
guanylate cyclase activator activity GO:0030250 p=6.2E−02 n=1 fg=0.01 bg=0.00
3'−tyrosyl−DNA phosphodiesterase activit... GO:0017005 p=6.2E−02 n=1 fg=0.01 bg=0.00
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fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001626351.3
fraction genes in fg and expected valu
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translation initiation ternary complex GO:0044207 p=6.0E−02 n=1 fg=0.01 bg=0.00
eukaryotic 48S preinitiation complex GO:0033290 p=6.0E−02 n=1 fg=0.01 bg=0.00
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glial limiting end−foot GO:0097451 p=6.0E−02 n=1 fg=0.01 bg=0.00
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bub1−bub3 complex GO:1990298 p=6.0E−02 n=1 fg=0.01 bg=0.00
methionyl glutamyl tRNA synthetase compl... GO:0017102 p=6.0E−02 n=1 fg=0.01 bg=0.00
histone pre−mRNA 3'end processing comple... GO:0071204 p=6.0E−02 n=1 fg=0.01 bg=0.00
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066 p=6.0E−02 n=1 fg=0.01 bg=0.00
septin collar GO:0032173 p=6.0E−02 n=1 fg=0.01 bg=0.00
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n=163/426 input genes with annotations
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fraction