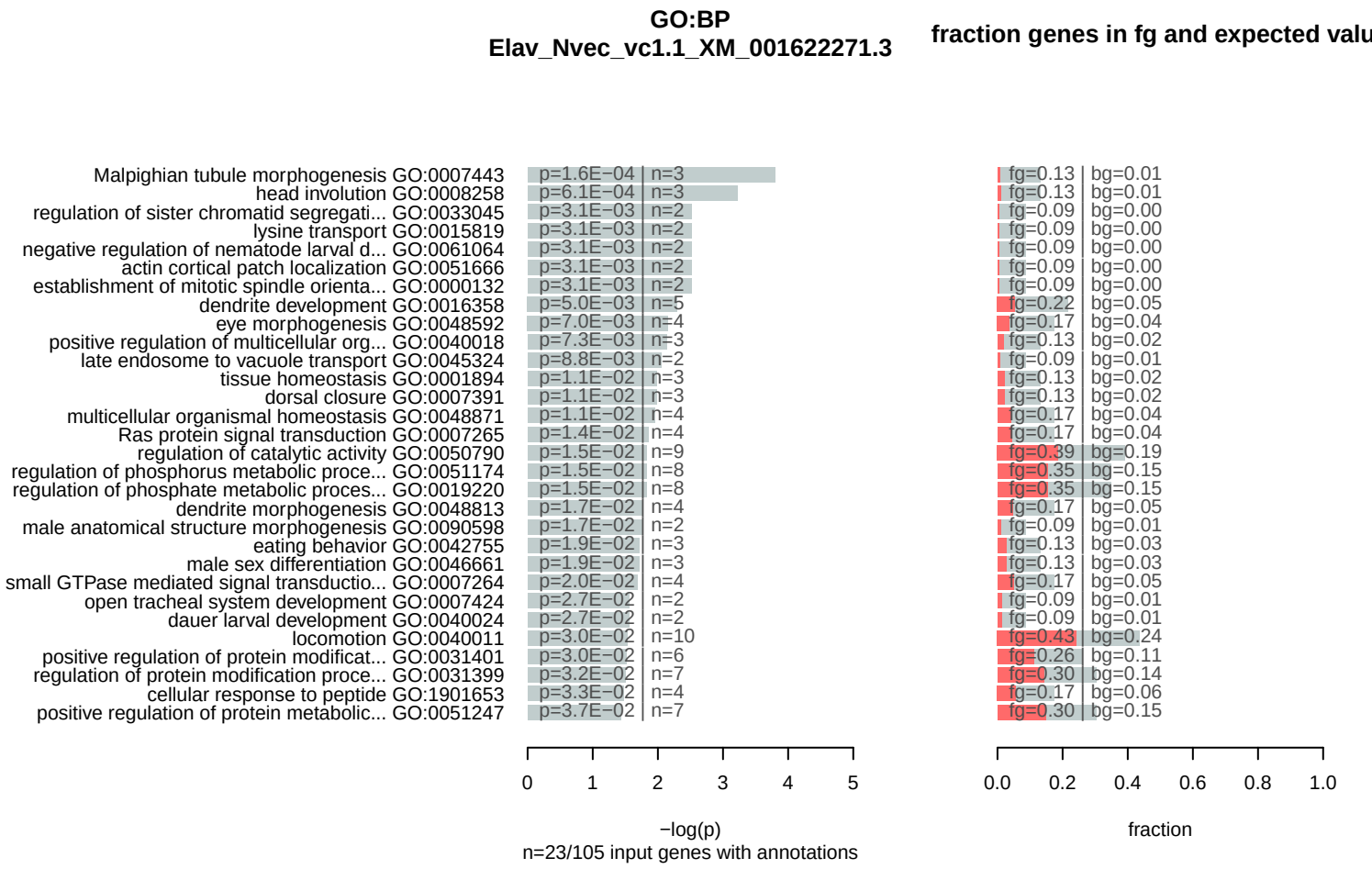
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negative regulation of nematode larval d... GO:0061064 p=3.1E−03 n=2 fg=0.09 bg=0.00
actin cortical patch localization GO:0051666 p=3.1E−03 n=2 fg=0.09 bg=0.00
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male anatomical structure morphogenesis GO:0090598 p=1.7E−02 n=2 fg=0.09 bg=0.01
eating behavior GO:0042755 p=1.9E−02 n=3 fg=0.13 bg=0.03
male sex differentiation GO:0046661 p=1.9E−02 n=3 fg=0.13 bg=0.03
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dauer larval development GO:0040024 p=2.7E−02 n=2 fg=0.09 bg=0.01
locomotion GO:0040011 p=3.0E−02 n=10 fg=0.43 bg=0.24
positive regulation of protein modificat... GO:0031401 p=3.0E−02 n=6 fg=0.26 bg=0.11
regulation of protein modification proce... GO:0031399 p=3.2E−02 n=7 fg=0.30 bg=0.14
cellular response to peptide GO:1901653 p=3.3E−02 n=4 fg=0.17 bg=0.06
positive regulation of protein metabolic... GO:0051247 p=3.7E−02 n=7 fg=0.30 bg=0.15
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n=23/105 input genes with annotations
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fraction
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Elav_Nvec_vc1.1_XM_001622271.3
fraction genes in fg and expected valu
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transmembrane receptor protein kinase ac... GO:0019199 p=2.4E−02 n=2 fg=0.11 bg=0.01
hydrolase activity, acting on acid anhyd... GO:0016817 p=2.9E−02 n=4 fg=0.21 bg=0.07
hydrolase activity, acting on acid anhyd... GO:0016818 p=2.9E−02 n=4 fg=0.21 bg=0.07
nucleoside−triphosphatase activity GO:0017111 p=2.9E−02 n=4 fg=0.21 bg=0.07
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inhibin binding GO:0034711 p=5.2E−02 n=1 fg=0.05 bg=0.00
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transforming growth factor beta−activate... GO:0005024 p=5.2E−02 n=1 fg=0.05 bg=0.00
protein serine/threonine kinase inhibito... GO:0030291 p=5.2E−02 n=1 fg=0.05 bg=0.00
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BMP receptor activity GO:0098821 p=5.2E−02 n=1 fg=0.05 bg=0.00
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ATP−dependent activity, acting on DNA GO:0008094 p=5.2E−02 n=1 fg=0.05 bg=0.00
activin−activated receptor activity GO:0017002 p=5.2E−02 n=1 fg=0.05 bg=0.00
activin binding GO:0048185 p=5.2E−02 n=1 fg=0.05 bg=0.00
BMP binding GO:0036122 p=5.2E−02 n=1 fg=0.05 bg=0.00
DNA helicase activity GO:0003678 p=5.2E−02 n=1 fg=0.05 bg=0.00
epidermal growth factor receptor binding GO:0005154 p=5.2E−02 n=1 fg=0.05 bg=0.00
beta−2 adrenergic receptor binding GO:0031698 p=5.2E−02 n=1 fg=0.05 bg=0.00
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n=19/105 input genes with annotations
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fraction
GO:CC
Elav_Nvec_vc1.1_XM_001622271.3
fraction genes in fg and expected valu
cell tip GO:0051286 p=3.1E−03 n=2 fg=0.09 bg=0.00
protein kinase complex GO:1902911 p=9.1E−03 n=2 fg=0.09 bg=0.01
fungal−type vacuole membrane GO:0000329 p=9.1E−03 n=2 fg=0.09 bg=0.01
fibrillar center GO:0001650 p=1.8E−02 n=2 fg=0.09 bg=0.01
Golgi cisterna GO:0031985 p=2.8E−02 n=2 fg=0.09 bg=0.01
cell division site GO:0032153 p=2.8E−02 n=2 fg=0.09 bg=0.01
cytoskeleton GO:0005856 p=4.3E−02 n=6 fg=0.26 bg=0.12
focal adhesion GO:0005925 p=5.5E−02 n=2 fg=0.09 bg=0.02
Golgi stack GO:0005795 p=5.5E−02 n=2 fg=0.09 bg=0.02
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serine/threonine protein kinase complex GO:1902554 p=5.7E−02 n=1 fg=0.04 bg=0.00
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adherens junction GO:0005912 p=1.1E−01 n=2 fg=0.09 bg=0.02
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P−body GO:0000932 p=1.1E−01 n=1 fg=0.04 bg=0.00
myosin V complex GO:0031475 p=1.1E−01 n=1 fg=0.04 bg=0.00
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−log(p)
n=23/105 input genes with annotations
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fraction