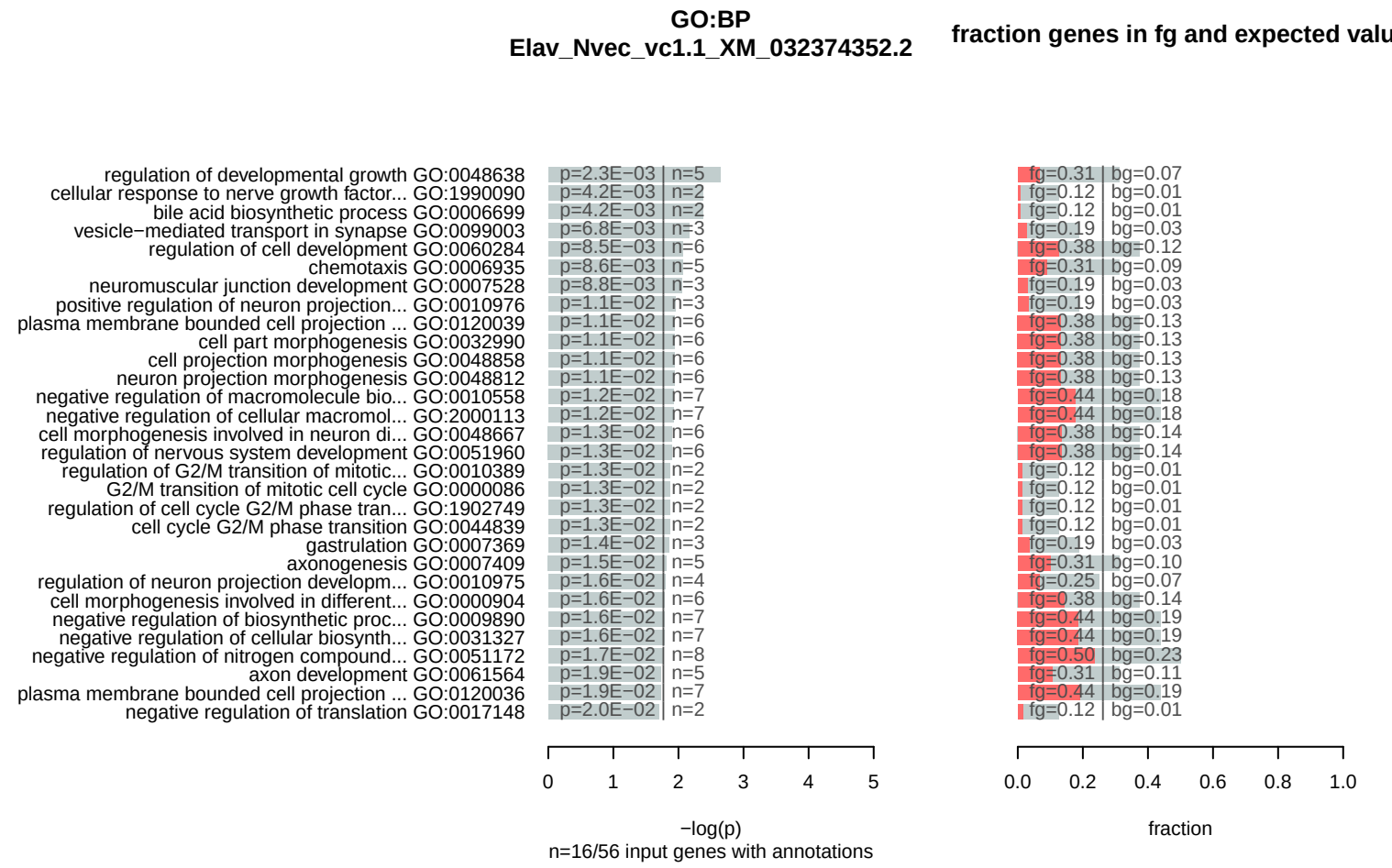
GO:BP
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cellular response to nerve growth factor... GO:1990090 p=4.2E−03 n=2 fg=0.12 bg=0.01
bile acid biosynthetic process GO:0006699 p=4.2E−03 n=2 fg=0.12 bg=0.01
vesicle−mediated transport in synapse GO:0099003 p=6.8E−03 n=3 fg=0.19 bg=0.03
regulation of cell development GO:0060284 p=8.5E−03 n=6 fg=0.38 bg=0.12
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plasma membrane bounded cell projection ... GO:0120039 p=1.1E−02 n=6 fg=0.38 bg=0.13
cell part morphogenesis GO:0032990 p=1.1E−02 n=6 fg=0.38 bg=0.13
cell projection morphogenesis GO:0048858 p=1.1E−02 n=6 fg=0.38 bg=0.13
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negative regulation of macromolecule bio... GO:0010558 p=1.2E−02 n=7 fg=0.44 bg=0.18
negative regulation of cellular macromol... GO:2000113 p=1.2E−02 n=7 fg=0.44 bg=0.18
cell morphogenesis involved in neuron di... GO:0048667 p=1.3E−02 n=6 fg=0.38 bg=0.14
regulation of nervous system development GO:0051960 p=1.3E−02 n=6 fg=0.38 bg=0.14
regulation of G2/M transition of mitotic... GO:0010389 p=1.3E−02 n=2 fg=0.12 bg=0.01
G2/M transition of mitotic cell cycle GO:0000086 p=1.3E−02 n=2 fg=0.12 bg=0.01
regulation of cell cycle G2/M phase tran... GO:1902749 p=1.3E−02 n=2 fg=0.12 bg=0.01
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gastrulation GO:0007369 p=1.4E−02 n=3 fg=0.19 bg=0.03
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cell morphogenesis involved in different... GO:0000904 p=1.6E−02 n=6 fg=0.38 bg=0.14
negative regulation of biosynthetic proc... GO:0009890 p=1.6E−02 n=7 fg=0.44 bg=0.19
negative regulation of cellular biosynth... GO:0031327 p=1.6E−02 n=7 fg=0.44 bg=0.19
negative regulation of nitrogen compound... GO:0051172 p=1.7E−02 n=8 fg=0.50 bg=0.23
axon development GO:0061564 p=1.9E−02 n=5 fg=0.31 bg=0.11
plasma membrane bounded cell projection ... GO:0120036 p=1.9E−02 n=7 fg=0.44 bg=0.19
negative regulation of translation GO:0017148 p=2.0E−02 n=2 fg=0.12 bg=0.01
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n=16/56 input genes with annotations
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fraction
GO:MF
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fraction genes in fg and expected valu
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mRNA 3'−UTR binding GO:0003730 p=7.9E−03 n=2 fg=0.14 bg=0.01
carbohydrate derivative binding GO:0097367 p=1.7E−02 n=4 fg=0.29 bg=0.08
adenyl ribonucleotide binding GO:0032559 p=3.0E−02 n=3 fg=0.21 bg=0.05
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poly−pyrimidine tract binding GO:0008187 p=3.8E−02 n=1 fg=0.07 bg=0.00
phosphatidylinositol 3−kinase activity GO:0035004 p=3.8E−02 n=1 fg=0.07 bg=0.00
P−type sodium transporter activity GO:0008554 p=3.8E−02 n=1 fg=0.07 bg=0.00
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cAMP−dependent protein kinase inhibitor ... GO:0004862 p=3.8E−02 n=1 fg=0.07 bg=0.00
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phosphatidylinositol bisphosphate kinase... GO:0052813 p=3.8E−02 n=1 fg=0.07 bg=0.00
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ABC−type bile acid transporter activity GO:0015432 p=3.8E−02 n=1 fg=0.07 bg=0.00
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cAMP−dependent protein kinase regulator ... GO:0008603 p=3.8E−02 n=1 fg=0.07 bg=0.00
translation factor activity, RNA binding GO:0008135 p=3.8E−02 n=1 fg=0.07 bg=0.00
mRNA 3'−UTR AU−rich region binding GO:0035925 p=3.8E−02 n=1 fg=0.07 bg=0.00
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ATPase−coupled monocarboxylic acid trans... GO:0033285 p=3.8E−02 n=1 fg=0.07 bg=0.00
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rRNA primary transcript binding GO:0042134 p=3.8E−02 n=1 fg=0.07 bg=0.00
beta−glucuronidase activity GO:0004566 p=3.8E−02 n=1 fg=0.07 bg=0.00
rRNA binding GO:0019843 p=3.8E−02 n=1 fg=0.07 bg=0.00
protein kinase A catalytic subunit bindi... GO:0034236 p=3.8E−02 n=1 fg=0.07 bg=0.00
1−phosphatidylinositol−3−kinase activity GO:0016303 p=3.8E−02 n=1 fg=0.07 bg=0.00
phosphatidylinositol kinase activity GO:0052742 p=3.8E−02 n=1 fg=0.07 bg=0.00
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−log(p)
n=14/56 input genes with annotations
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fraction
GO:CC
Elav_Nvec_vc1.1_XM_032374352.2
fraction genes in fg and expected valu
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presynaptic active zone GO:0048786 p=3.2E−02 n=2 fg=0.13 bg=0.02
messenger ribonucleoprotein complex GO:1990124 p=3.7E−02 n=1 fg=0.07 bg=0.00
excitatory synapse GO:0060076 p=3.7E−02 n=1 fg=0.07 bg=0.00
Cajal body GO:0015030 p=3.7E−02 n=1 fg=0.07 bg=0.00
polysomal ribosome GO:0042788 p=3.7E−02 n=1 fg=0.07 bg=0.00
gut granule GO:0044840 p=3.7E−02 n=1 fg=0.07 bg=0.00
gut granule membrane GO:0044841 p=3.7E−02 n=1 fg=0.07 bg=0.00
lysosomal lumen GO:0043202 p=3.7E−02 n=1 fg=0.07 bg=0.00
plasma membrane raft GO:0044853 p=4.9E−02 n=2 fg=0.13 bg=0.02
intracellular membrane−bounded organelle GO:0043231 p=6.4E−02 n=14 fg=0.93 bg=0.74
extracellular region GO:0005576 p=6.5E−02 n=3 fg=0.20 bg=0.06
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germinal vesicle GO:0042585 p=7.3E−02 n=1 fg=0.07 bg=0.00
nucleotide−activated protein kinase comp... GO:0031588 p=7.3E−02 n=1 fg=0.07 bg=0.00
intercellular canaliculus GO:0046581 p=7.3E−02 n=1 fg=0.07 bg=0.00
ribosome GO:0005840 p=7.3E−02 n=1 fg=0.07 bg=0.00
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cytoplasmic stress granule GO:0010494 p=7.3E−02 n=1 fg=0.07 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=7.3E−02 n=1 fg=0.07 bg=0.00
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nuclear body GO:0016604 p=1.0E−01 n=2 fg=0.13 bg=0.04
intracellular organelle GO:0043229 p=1.1E−01 n=14 fg=0.93 bg=0.77
perinuclear region of cytoplasm GO:0048471 p=1.1E−01 n=3 fg=0.20 bg=0.08
germ cell nucleus GO:0043073 p=1.1E−01 n=1 fg=0.07 bg=0.01
ficolin−1−rich granule lumen GO:1904813 p=1.1E−01 n=1 fg=0.07 bg=0.01
protein kinase complex GO:1902911 p=1.1E−01 n=1 fg=0.07 bg=0.01
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−log(p)
n=15/56 input genes with annotations
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fraction