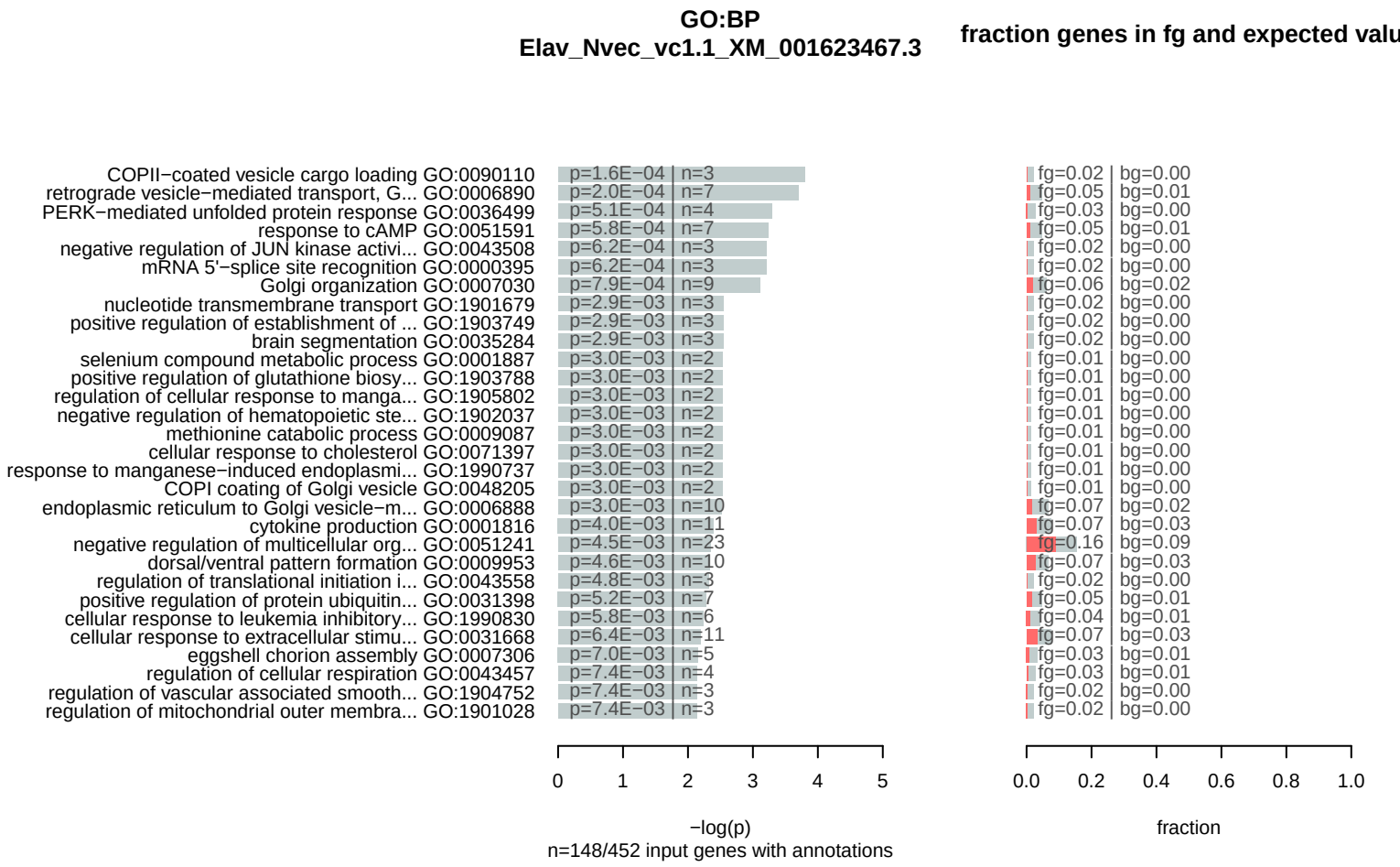
GO:BP
Elav_Nvec_vc1.1_XM_001623467.3
fraction genes in fg and expected valu
COPII−coated vesicle cargo loading GO:0090110 p=1.6E−04 n=3 fg=0.02 bg=0.00
retrograde vesicle−mediated transport, G... GO:0006890 p=2.0E−04 n=7 fg=0.05 bg=0.01
PERK−mediated unfolded protein response GO:0036499 p=5.1E−04 n=4 fg=0.03 bg=0.00
response to cAMP GO:0051591 p=5.8E−04 n=7 fg=0.05 bg=0.01
negative regulation of JUN kinase activi... GO:0043508 p=6.2E−04 n=3 fg=0.02 bg=0.00
mRNA 5'−splice site recognition GO:0000395 p=6.2E−04 n=3 fg=0.02 bg=0.00
Golgi organization GO:0007030 p=7.9E−04 n=9 fg=0.06 bg=0.02
nucleotide transmembrane transport GO:1901679 p=2.9E−03 n=3 fg=0.02 bg=0.00
positive regulation of establishment of ... GO:1903749 p=2.9E−03 n=3 fg=0.02 bg=0.00
brain segmentation GO:0035284 p=2.9E−03 n=3 fg=0.02 bg=0.00
selenium compound metabolic process GO:0001887 p=3.0E−03 n=2 fg=0.01 bg=0.00
positive regulation of glutathione biosy... GO:1903788 p=3.0E−03 n=2 fg=0.01 bg=0.00
regulation of cellular response to manga... GO:1905802 p=3.0E−03 n=2 fg=0.01 bg=0.00
negative regulation of hematopoietic ste... GO:1902037 p=3.0E−03 n=2 fg=0.01 bg=0.00
methionine catabolic process GO:0009087 p=3.0E−03 n=2 fg=0.01 bg=0.00
cellular response to cholesterol GO:0071397 p=3.0E−03 n=2 fg=0.01 bg=0.00
response to manganese−induced endoplasmi... GO:1990737 p=3.0E−03 n=2 fg=0.01 bg=0.00
COPI coating of Golgi vesicle GO:0048205 p=3.0E−03 n=2 fg=0.01 bg=0.00
endoplasmic reticulum to Golgi vesicle−m... GO:0006888 p=3.0E−03 n=10 fg=0.07 bg=0.02
cytokine production GO:0001816 p=4.0E−03 n=11 fg=0.07 bg=0.03
negative regulation of multicellular org... GO:0051241 p=4.5E−03 n=23 fg=0.16 bg=0.09
dorsal/ventral pattern formation GO:0009953 p=4.6E−03 n=10 fg=0.07 bg=0.03
regulation of translational initiation i... GO:0043558 p=4.8E−03 n=3 fg=0.02 bg=0.00
positive regulation of protein ubiquitin... GO:0031398 p=5.2E−03 n=7 fg=0.05 bg=0.01
cellular response to leukemia inhibitory... GO:1990830 p=5.8E−03 n=6 fg=0.04 bg=0.01
cellular response to extracellular stimu... GO:0031668 p=6.4E−03 n=11 fg=0.07 bg=0.03
eggshell chorion assembly GO:0007306 p=7.0E−03 n=5 fg=0.03 bg=0.01
regulation of cellular respiration GO:0043457 p=7.4E−03 n=4 fg=0.03 bg=0.01
regulation of vascular associated smooth... GO:1904752 p=7.4E−03 n=3 fg=0.02 bg=0.00
regulation of mitochondrial outer membra... GO:1901028 p=7.4E−03 n=3 fg=0.02 bg=0.00
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−log(p)
n=148/452 input genes with annotations
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fraction
GO:MF
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fraction genes in fg and expected valu
GTPase activity GO:0003924 p=1.6E−03 n=9 fg=0.06 bg=0.02
purine ribonucleoside triphosphate bindi... GO:0035639 p=2.9E−03 n=17 fg=0.12 bg=0.06
methionine adenosyltransferase activity GO:0004478 p=3.5E−03 n=2 fg=0.01 bg=0.00
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nucleotide transmembrane transporter act... GO:0015215 p=3.5E−03 n=3 fg=0.02 bg=0.00
purine ribonucleotide binding GO:0032555 p=9.4E−03 n=17 fg=0.12 bg=0.07
oxidoreductase activity, acting on singl... GO:0016702 p=1.0E−02 n=2 fg=0.01 bg=0.00
caspase binding GO:0089720 p=1.0E−02 n=2 fg=0.01 bg=0.00
magnesium ion binding GO:0000287 p=1.1E−02 n=8 fg=0.06 bg=0.02
ribonucleoprotein complex binding GO:0043021 p=1.2E−02 n=7 fg=0.05 bg=0.02
GTP binding GO:0005525 p=1.3E−02 n=7 fg=0.05 bg=0.02
translation regulator activity GO:0045182 p=1.5E−02 n=6 fg=0.04 bg=0.01
purine ribonucleoside binding GO:0032550 p=1.7E−02 n=7 fg=0.05 bg=0.02
ribonucleoside binding GO:0032549 p=1.7E−02 n=7 fg=0.05 bg=0.02
transition metal ion binding GO:0046914 p=1.9E−02 n=15 fg=0.11 bg=0.06
oxidoreductase activity, acting on singl... GO:0016701 p=1.9E−02 n=2 fg=0.01 bg=0.00
nuclear vitamin D receptor binding GO:0042809 p=1.9E−02 n=2 fg=0.01 bg=0.00
RNA stem−loop binding GO:0035613 p=1.9E−02 n=2 fg=0.01 bg=0.00
U1 snRNP binding GO:1990446 p=1.9E−02 n=2 fg=0.01 bg=0.00
purine nucleoside binding GO:0001883 p=2.1E−02 n=7 fg=0.05 bg=0.02
guanyl ribonucleotide binding GO:0032561 p=2.3E−02 n=7 fg=0.05 bg=0.02
nucleoside binding GO:0001882 p=2.3E−02 n=7 fg=0.05 bg=0.02
guanyl nucleotide binding GO:0019001 p=2.3E−02 n=7 fg=0.05 bg=0.02
translation regulator activity, nucleic ... GO:0090079 p=2.9E−02 n=5 fg=0.04 bg=0.01
zinc ion binding GO:0008270 p=2.9E−02 n=11 fg=0.08 bg=0.04
eukaryotic initiation factor eIF2 bindin... GO:0071074 p=3.1E−02 n=2 fg=0.01 bg=0.00
protein kinase A regulatory subunit bind... GO:0034237 p=3.1E−02 n=2 fg=0.01 bg=0.00
metal ion binding GO:0046872 p=3.3E−02 n=21 fg=0.15 bg=0.10
transporter activity GO:0005215 p=3.9E−02 n=23 fg=0.16 bg=0.10
anion transmembrane transporter activity GO:0008509 p=4.4E−02 n=8 fg=0.06 bg=0.03
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−log(p)
n=140/452 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001623467.3
fraction genes in fg and expected valu
endoplasmic reticulum−Golgi intermediate... GO:0033116 p=1.0E−04 n=5 fg=0.03 bg=0.00
COPI−coated vesicle GO:0030137 p=9.5E−04 n=4 fg=0.03 bg=0.00
Golgi cis cisterna GO:0000137 p=1.6E−03 n=3 fg=0.02 bg=0.00
post−mRNA release spliceosomal complex GO:0071014 p=3.1E−03 n=2 fg=0.01 bg=0.00
COPII vesicle coat GO:0030127 p=3.1E−03 n=2 fg=0.01 bg=0.00
Golgi−associated vesicle membrane GO:0030660 p=3.1E−03 n=5 fg=0.03 bg=0.01
endoplasmic reticulum membrane GO:0005789 p=5.6E−03 n=20 fg=0.13 bg=0.07
Golgi membrane GO:0000139 p=8.2E−03 n=15 fg=0.10 bg=0.05
methionine adenosyltransferase complex GO:0048269 p=9.0E−03 n=2 fg=0.01 bg=0.00
polysome GO:0005844 p=9.2E−03 n=5 fg=0.03 bg=0.01
subsynaptic reticulum GO:0071212 p=1.7E−02 n=2 fg=0.01 bg=0.00
basal dendrite GO:0097441 p=1.7E−02 n=2 fg=0.01 bg=0.00
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transport vesicle GO:0030133 p=2.6E−02 n=12 fg=0.08 bg=0.03
commitment complex GO:0000243 p=2.8E−02 n=2 fg=0.01 bg=0.00
polytene chromosome chromocenter GO:0005701 p=2.8E−02 n=2 fg=0.01 bg=0.00
protein phosphatase type 1 complex GO:0000164 p=2.8E−02 n=2 fg=0.01 bg=0.00
U1 snRNP GO:0005685 p=2.8E−02 n=2 fg=0.01 bg=0.00
ribosome GO:0005840 p=3.9E−02 n=8 fg=0.05 bg=0.03
catalytic step 2 spliceosome GO:0071013 p=4.2E−02 n=4 fg=0.03 bg=0.01
perikaryon GO:0043204 p=4.2E−02 n=4 fg=0.03 bg=0.01
Golgi medial cisterna GO:0005797 p=4.8E−02 n=3 fg=0.02 bg=0.01
transcription regulator complex GO:0005667 p=5.0E−02 n=10 fg=0.07 bg=0.04
prespliceosome GO:0071010 p=5.4E−02 n=2 fg=0.01 bg=0.00
alpha−heterochromatin GO:0005723 p=5.6E−02 n=1 fg=0.01 bg=0.00
AMPA glutamate receptor complex GO:0032281 p=5.6E−02 n=1 fg=0.01 bg=0.00
protein kinase CK2 complex GO:0005956 p=5.6E−02 n=1 fg=0.01 bg=0.00
translation release factor complex GO:0018444 p=5.6E−02 n=1 fg=0.01 bg=0.00
anchored component of synaptic vesicle m... GO:0098993 p=5.6E−02 n=1 fg=0.01 bg=0.00
translation initiation ternary complex GO:0044207 p=5.6E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=151/452 input genes with annotations
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fraction