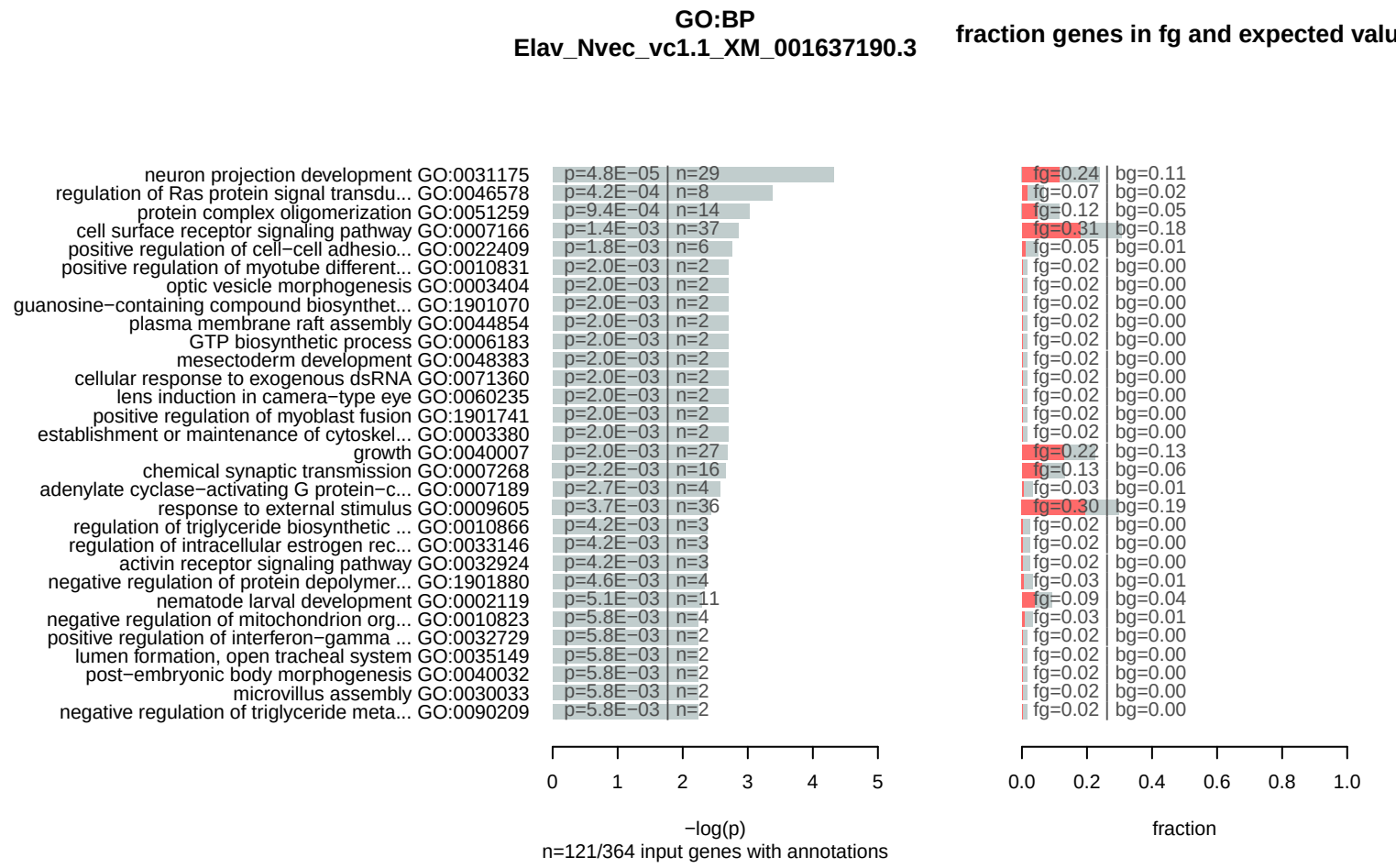
GO:BP
Elav_Nvec_vc1.1_XM_001637190.3
fraction genes in fg and expected valu
neuron projection development GO:0031175 p=4.8E−05 n=29 fg=0.24 bg=0.11
regulation of Ras protein signal transdu... GO:0046578 p=4.2E−04 n=8 fg=0.07 bg=0.02
protein complex oligomerization GO:0051259 p=9.4E−04 n=14 fg=0.12 bg=0.05
cell surface receptor signaling pathway GO:0007166 p=1.4E−03 n=37 fg=0.31 bg=0.18
positive regulation of cell−cell adhesio... GO:0022409 p=1.8E−03 n=6 fg=0.05 bg=0.01
positive regulation of myotube different... GO:0010831 p=2.0E−03 n=2 fg=0.02 bg=0.00
optic vesicle morphogenesis GO:0003404 p=2.0E−03 n=2 fg=0.02 bg=0.00
guanosine−containing compound biosynthet... GO:1901070 p=2.0E−03 n=2 fg=0.02 bg=0.00
plasma membrane raft assembly GO:0044854 p=2.0E−03 n=2 fg=0.02 bg=0.00
GTP biosynthetic process GO:0006183 p=2.0E−03 n=2 fg=0.02 bg=0.00
mesectoderm development GO:0048383 p=2.0E−03 n=2 fg=0.02 bg=0.00
cellular response to exogenous dsRNA GO:0071360 p=2.0E−03 n=2 fg=0.02 bg=0.00
lens induction in camera−type eye GO:0060235 p=2.0E−03 n=2 fg=0.02 bg=0.00
positive regulation of myoblast fusion GO:1901741 p=2.0E−03 n=2 fg=0.02 bg=0.00
establishment or maintenance of cytoskel... GO:0003380 p=2.0E−03 n=2 fg=0.02 bg=0.00
growth GO:0040007 p=2.0E−03 n=27 fg=0.22 bg=0.13
chemical synaptic transmission GO:0007268 p=2.2E−03 n=16 fg=0.13 bg=0.06
adenylate cyclase−activating G protein−c... GO:0007189 p=2.7E−03 n=4 fg=0.03 bg=0.01
response to external stimulus GO:0009605 p=3.7E−03 n=36 fg=0.30 bg=0.19
regulation of triglyceride biosynthetic ... GO:0010866 p=4.2E−03 n=3 fg=0.02 bg=0.00
regulation of intracellular estrogen rec... GO:0033146 p=4.2E−03 n=3 fg=0.02 bg=0.00
activin receptor signaling pathway GO:0032924 p=4.2E−03 n=3 fg=0.02 bg=0.00
negative regulation of protein depolymer... GO:1901880 p=4.6E−03 n=4 fg=0.03 bg=0.01
nematode larval development GO:0002119 p=5.1E−03 n=11 fg=0.09 bg=0.04
negative regulation of mitochondrion org... GO:0010823 p=5.8E−03 n=4 fg=0.03 bg=0.01
positive regulation of interferon−gamma ... GO:0032729 p=5.8E−03 n=2 fg=0.02 bg=0.00
lumen formation, open tracheal system GO:0035149 p=5.8E−03 n=2 fg=0.02 bg=0.00
post−embryonic body morphogenesis GO:0040032 p=5.8E−03 n=2 fg=0.02 bg=0.00
microvillus assembly GO:0030033 p=5.8E−03 n=2 fg=0.02 bg=0.00
negative regulation of triglyceride meta... GO:0090209 p=5.8E−03 n=2 fg=0.02 bg=0.00
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n=121/364 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_001637190.3
fraction genes in fg and expected valu
phosphatidylcholine binding GO:0031210 p=2.9E−03 n=3 fg=0.03 bg=0.00
ligase activity, forming phosphoric este... GO:0016886 p=6.1E−03 n=2 fg=0.02 bg=0.00
enzyme inhibitor activity GO:0004857 p=1.1E−02 n=7 fg=0.06 bg=0.02
cytoskeletal protein binding GO:0008092 p=1.1E−02 n=16 fg=0.15 bg=0.08
phosphoric diester hydrolase activity GO:0008081 p=1.2E−02 n=4 fg=0.04 bg=0.01
phosphatidylethanolamine binding GO:0008429 p=1.2E−02 n=2 fg=0.02 bg=0.00
disordered domain specific binding GO:0097718 p=1.5E−02 n=3 fg=0.03 bg=0.01
microtubule binding GO:0008017 p=1.7E−02 n=7 fg=0.06 bg=0.02
glucosyltransferase activity GO:0046527 p=1.9E−02 n=2 fg=0.02 bg=0.00
AP−2 adaptor complex binding GO:0035612 p=1.9E−02 n=2 fg=0.02 bg=0.00
ammonium ion binding GO:0070405 p=1.9E−02 n=3 fg=0.03 bg=0.01
BH domain binding GO:0051400 p=2.8E−02 n=2 fg=0.02 bg=0.00
actin binding GO:0003779 p=3.3E−02 n=6 fg=0.06 bg=0.02
UDP−glycosyltransferase activity GO:0008194 p=3.3E−02 n=4 fg=0.04 bg=0.01
signaling receptor binding GO:0005102 p=3.7E−02 n=17 fg=0.16 bg=0.10
UDP−galactose:beta−N−acetylglucosamine b... GO:0008499 p=3.8E−02 n=2 fg=0.02 bg=0.00
UDP−galactosyltransferase activity GO:0035250 p=3.8E−02 n=2 fg=0.02 bg=0.00
phosphatase inhibitor activity GO:0019212 p=3.8E−02 n=2 fg=0.02 bg=0.00
spectrin binding GO:0030507 p=3.8E−02 n=2 fg=0.02 bg=0.00
hexosyltransferase activity GO:0016758 p=4.1E−02 n=5 fg=0.05 bg=0.02
neuregulin binding GO:0038132 p=4.6E−02 n=1 fg=0.01 bg=0.00
phosphatidylinositol phosphate kinase ac... GO:0016307 p=4.6E−02 n=1 fg=0.01 bg=0.00
1−phosphatidylinositol−4−phosphate 5−kin... GO:0016308 p=4.6E−02 n=1 fg=0.01 bg=0.00
1−phosphatidylinositol−5−phosphate 4−kin... GO:0016309 p=4.6E−02 n=1 fg=0.01 bg=0.00
oxidative DNA demethylase activity GO:0035516 p=4.6E−02 n=1 fg=0.01 bg=0.00
sodium:dicarboxylate symporter activity GO:0017153 p=4.6E−02 n=1 fg=0.01 bg=0.00
MHC protein complex binding GO:0023023 p=4.6E−02 n=1 fg=0.01 bg=0.00
MHC class Ib protein complex binding GO:0023025 p=4.6E−02 n=1 fg=0.01 bg=0.00
MHC class Ib protein binding GO:0023029 p=4.6E−02 n=1 fg=0.01 bg=0.00
glutaminase activity GO:0004359 p=4.6E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=109/364 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001637190.3
fraction genes in fg and expected valu
lamellipodium GO:0030027 p=3.5E−04 n=9 fg=0.08 bg=0.02
synaptic membrane GO:0097060 p=7.0E−04 n=9 fg=0.08 bg=0.02
photoreceptor outer segment membrane GO:0042622 p=1.9E−03 n=2 fg=0.02 bg=0.00
uropod GO:0001931 p=1.9E−03 n=2 fg=0.02 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=1.9E−03 n=2 fg=0.02 bg=0.00
cell projection membrane GO:0031253 p=1.9E−03 n=12 fg=0.10 bg=0.03
transcription elongation factor complex GO:0008023 p=3.2E−03 n=4 fg=0.03 bg=0.01
plasma membrane protein complex GO:0098797 p=5.3E−03 n=9 fg=0.08 bg=0.03
clathrin−coated pit GO:0005905 p=5.5E−03 n=3 fg=0.03 bg=0.00
presynapse GO:0098793 p=5.6E−03 n=12 fg=0.10 bg=0.05
growth cone GO:0030426 p=5.7E−03 n=7 fg=0.06 bg=0.02
cytoplasmic side of plasma membrane GO:0009898 p=7.8E−03 n=7 fg=0.06 bg=0.02
plasma membrane raft GO:0044853 p=8.4E−03 n=5 fg=0.04 bg=0.01
somatodendritic compartment GO:0036477 p=9.2E−03 n=18 fg=0.15 bg=0.09
extrinsic component of plasma membrane GO:0019897 p=9.7E−03 n=5 fg=0.04 bg=0.01
filamentous actin GO:0031941 p=1.1E−02 n=2 fg=0.02 bg=0.00
growth cone lamellipodium GO:1990761 p=1.1E−02 n=2 fg=0.02 bg=0.00
vacuolar lumen GO:0005775 p=1.1E−02 n=5 fg=0.04 bg=0.01
extrinsic component of cytoplasmic side ... GO:0031234 p=1.1E−02 n=4 fg=0.03 bg=0.01
secretory vesicle GO:0099503 p=1.4E−02 n=15 fg=0.13 bg=0.07
caveola GO:0005901 p=1.6E−02 n=4 fg=0.03 bg=0.01
brush border GO:0005903 p=1.6E−02 n=5 fg=0.04 bg=0.01
basolateral plasma membrane GO:0016323 p=1.6E−02 n=7 fg=0.06 bg=0.02
basal plasma membrane GO:0009925 p=1.6E−02 n=7 fg=0.06 bg=0.02
side of membrane GO:0098552 p=1.7E−02 n=12 fg=0.10 bg=0.03
sensory dendrite GO:0071683 p=1.7E−02 n=2 fg=0.02 bg=0.00
cytoplasmic vesicle GO:0031410 p=1.8E−02 n=27 fg=0.23 bg=0.15
intracellular vesicle GO:0097708 p=1.8E−02 n=27 fg=0.23 bg=0.15
anchoring junction GO:0070161 p=2.0E−02 n=10 fg=0.09 bg=0.04
cell−cell junction GO:0005911 p=2.0E−02 n=10 fg=0.09 bg=0.04
0 1 2 3 4 5
−log(p)
n=117/364 input genes with annotations
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fraction