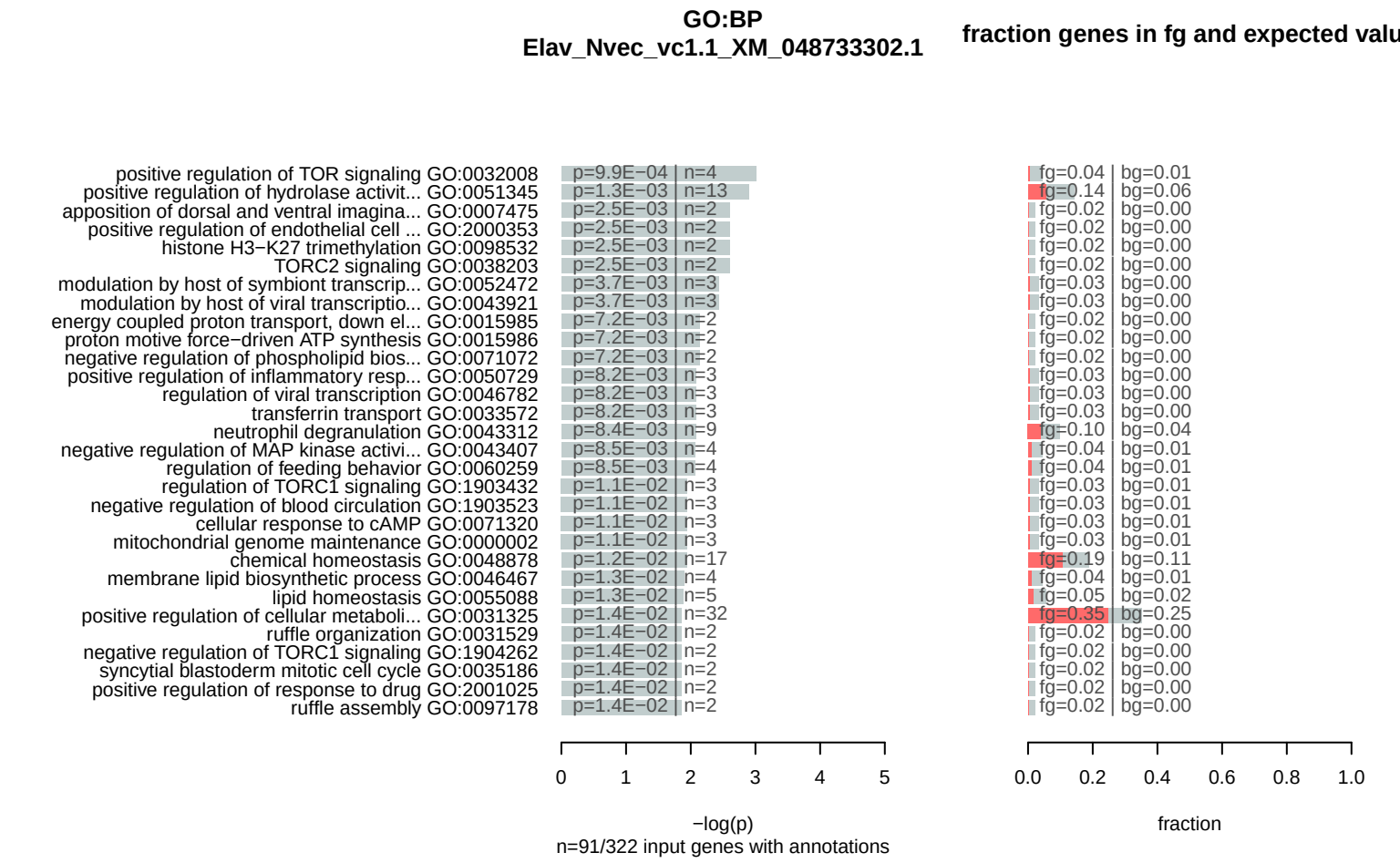
GO:BP
Elav_Nvec_vc1.1_XM_048733302.1
fraction genes in fg and expected valu
positive regulation of TOR signaling GO:0032008 p=9.9E−04 n=4 fg=0.04 bg=0.01
positive regulation of hydrolase activit... GO:0051345 p=1.3E−03 n=13 fg=0.14 bg=0.06
apposition of dorsal and ventral imagina... GO:0007475 p=2.5E−03 n=2 fg=0.02 bg=0.00
positive regulation of endothelial cell ... GO:2000353 p=2.5E−03 n=2 fg=0.02 bg=0.00
histone H3−K27 trimethylation GO:0098532 p=2.5E−03 n=2 fg=0.02 bg=0.00
TORC2 signaling GO:0038203 p=2.5E−03 n=2 fg=0.02 bg=0.00
modulation by host of symbiont transcrip... GO:0052472 p=3.7E−03 n=3 fg=0.03 bg=0.00
modulation by host of viral transcriptio... GO:0043921 p=3.7E−03 n=3 fg=0.03 bg=0.00
energy coupled proton transport, down el... GO:0015985 p=7.2E−03 n=2 fg=0.02 bg=0.00
proton motive force−driven ATP synthesis GO:0015986 p=7.2E−03 n=2 fg=0.02 bg=0.00
negative regulation of phospholipid bios... GO:0071072 p=7.2E−03 n=2 fg=0.02 bg=0.00
positive regulation of inflammatory resp... GO:0050729 p=8.2E−03 n=3 fg=0.03 bg=0.00
regulation of viral transcription GO:0046782 p=8.2E−03 n=3 fg=0.03 bg=0.00
transferrin transport GO:0033572 p=8.2E−03 n=3 fg=0.03 bg=0.00
neutrophil degranulation GO:0043312 p=8.4E−03 n=9 fg=0.10 bg=0.04
negative regulation of MAP kinase activi... GO:0043407 p=8.5E−03 n=4 fg=0.04 bg=0.01
regulation of feeding behavior GO:0060259 p=8.5E−03 n=4 fg=0.04 bg=0.01
regulation of TORC1 signaling GO:1903432 p=1.1E−02 n=3 fg=0.03 bg=0.01
negative regulation of blood circulation GO:1903523 p=1.1E−02 n=3 fg=0.03 bg=0.01
cellular response to cAMP GO:0071320 p=1.1E−02 n=3 fg=0.03 bg=0.01
mitochondrial genome maintenance GO:0000002 p=1.1E−02 n=3 fg=0.03 bg=0.01
chemical homeostasis GO:0048878 p=1.2E−02 n=17 fg=0.19 bg=0.11
membrane lipid biosynthetic process GO:0046467 p=1.3E−02 n=4 fg=0.04 bg=0.01
lipid homeostasis GO:0055088 p=1.3E−02 n=5 fg=0.05 bg=0.02
positive regulation of cellular metaboli... GO:0031325 p=1.4E−02 n=32 fg=0.35 bg=0.25
ruffle organization GO:0031529 p=1.4E−02 n=2 fg=0.02 bg=0.00
negative regulation of TORC1 signaling GO:1904262 p=1.4E−02 n=2 fg=0.02 bg=0.00
syncytial blastoderm mitotic cell cycle GO:0035186 p=1.4E−02 n=2 fg=0.02 bg=0.00
positive regulation of response to drug GO:2001025 p=1.4E−02 n=2 fg=0.02 bg=0.00
ruffle assembly GO:0097178 p=1.4E−02 n=2 fg=0.02 bg=0.00
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−log(p)
n=91/322 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_048733302.1
fraction genes in fg and expected valu
damaged DNA binding GO:0003684 p=5.1E−03 n=3 fg=0.04 bg=0.01
proton−transporting ATPase activity, rot... GO:0046961 p=2.1E−02 n=2 fg=0.03 bg=0.00
ATPase activity, coupled to transmembran... GO:0044769 p=2.1E−02 n=2 fg=0.03 bg=0.00
calcium−release channel activity GO:0015278 p=2.1E−02 n=2 fg=0.03 bg=0.00
pyrophosphate hydrolysis−driven proton t... GO:0009678 p=2.1E−02 n=2 fg=0.03 bg=0.00
collagen binding GO:0005518 p=3.0E−02 n=2 fg=0.03 bg=0.00
peptidase activator activity GO:0016504 p=3.0E−02 n=2 fg=0.03 bg=0.00
carboxy−lyase activity GO:0016831 p=3.0E−02 n=2 fg=0.03 bg=0.00
ligand−gated calcium channel activity GO:0099604 p=3.0E−02 n=2 fg=0.03 bg=0.00
proton transmembrane transporter activit... GO:0015078 p=4.5E−02 n=3 fg=0.04 bg=0.01
insulin−like growth factor I binding GO:0031994 p=4.8E−02 n=1 fg=0.01 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=4.8E−02 n=1 fg=0.01 bg=0.00
protein phosphatase 5 binding GO:1990634 p=4.8E−02 n=1 fg=0.01 bg=0.00
8−oxo−7,8−dihydroguanine DNA N−glycosyla... GO:0034039 p=4.8E−02 n=1 fg=0.01 bg=0.00
sphingolipid transporter activity GO:0046624 p=4.8E−02 n=1 fg=0.01 bg=0.00
oxalate transmembrane transporter activi... GO:0019531 p=4.8E−02 n=1 fg=0.01 bg=0.00
G−protein gamma−subunit binding GO:0031682 p=4.8E−02 n=1 fg=0.01 bg=0.00
fibronectin binding GO:0001968 p=4.8E−02 n=1 fg=0.01 bg=0.00
3−chloroallyl aldehyde dehydrogenase act... GO:0004028 p=4.8E−02 n=1 fg=0.01 bg=0.00
aldehyde dehydrogenase (NAD+) activity GO:0004029 p=4.8E−02 n=1 fg=0.01 bg=0.00
neurotrophin TRK receptor binding GO:0005167 p=4.8E−02 n=1 fg=0.01 bg=0.00
neurotrophin TRKA receptor binding GO:0005168 p=4.8E−02 n=1 fg=0.01 bg=0.00
intracellular phosphatidylinositol−3,5−b... GO:0097682 p=4.8E−02 n=1 fg=0.01 bg=0.00
neuregulin binding GO:0038132 p=4.8E−02 n=1 fg=0.01 bg=0.00
inositol bisphosphate phosphatase activi... GO:0016312 p=4.8E−02 n=1 fg=0.01 bg=0.00
transmembrane receptor protein phosphata... GO:0019198 p=4.8E−02 n=1 fg=0.01 bg=0.00
deubiquitinase activator activity GO:0035800 p=4.8E−02 n=1 fg=0.01 bg=0.00
aldehyde dehydrogenase [NAD(P)+] activit... GO:0004030 p=4.8E−02 n=1 fg=0.01 bg=0.00
ceramide binding GO:0097001 p=4.8E−02 n=1 fg=0.01 bg=0.00
leucine binding GO:0070728 p=4.8E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=77/322 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048733302.1
fraction genes in fg and expected valu
perinuclear region of cytoplasm GO:0048471 p=5.3E−04 n=16 fg=0.18 bg=0.07
endolysosome membrane GO:0036020 p=7.1E−03 n=2 fg=0.02 bg=0.00
secretory granule GO:0030141 p=7.1E−03 n=11 fg=0.12 bg=0.05
lipid droplet GO:0005811 p=1.3E−02 n=4 fg=0.04 bg=0.01
cytoplasmic vesicle membrane GO:0030659 p=1.8E−02 n=15 fg=0.17 bg=0.08
clathrin−coated vesicle GO:0030136 p=1.9E−02 n=5 fg=0.06 bg=0.02
vesicle membrane GO:0012506 p=2.0E−02 n=15 fg=0.17 bg=0.08
filopodium membrane GO:0031527 p=2.2E−02 n=2 fg=0.02 bg=0.00
synaptonemal structure GO:0099086 p=2.2E−02 n=2 fg=0.02 bg=0.00
synaptonemal complex GO:0000795 p=2.2E−02 n=2 fg=0.02 bg=0.00
transcription regulator complex GO:0005667 p=3.4E−02 n=8 fg=0.09 bg=0.04
secretory granule membrane GO:0030667 p=3.7E−02 n=5 fg=0.06 bg=0.02
intermediate filament cytoskeleton GO:0045111 p=4.4E−02 n=2 fg=0.02 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0016471 p=4.4E−02 n=2 fg=0.02 bg=0.00
collagen−containing extracellular matrix GO:0062023 p=4.4E−02 n=2 fg=0.02 bg=0.00
heterochromatin GO:0000792 p=4.9E−02 n=3 fg=0.03 bg=0.01
integrin alpha3−beta1 complex GO:0034667 p=5.0E−02 n=1 fg=0.01 bg=0.00
DNA ligase III−XRCC1 complex GO:0070421 p=5.0E−02 n=1 fg=0.01 bg=0.00
lamellipodium membrane GO:0031258 p=5.0E−02 n=1 fg=0.01 bg=0.00
TSC1−TSC2 complex GO:0033596 p=5.0E−02 n=1 fg=0.01 bg=0.00
integrin alpha6−beta4 complex GO:0034676 p=5.0E−02 n=1 fg=0.01 bg=0.00
integrin alpha7−beta1 complex GO:0034677 p=5.0E−02 n=1 fg=0.01 bg=0.00
integral component of lysosomal membrane GO:1905103 p=5.0E−02 n=1 fg=0.01 bg=0.00
GTPase activator complex GO:1902773 p=5.0E−02 n=1 fg=0.01 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=5.0E−02 n=1 fg=0.01 bg=0.00
apoptosome GO:0043293 p=5.0E−02 n=1 fg=0.01 bg=0.00
PR−DUB complex GO:0035517 p=5.0E−02 n=1 fg=0.01 bg=0.00
apical cytoplasm GO:0090651 p=5.0E−02 n=1 fg=0.01 bg=0.00
nuclear protein−containing complex GO:0140513 p=5.5E−02 n=15 fg=0.17 bg=0.11
proton−transporting two−sector ATPase co... GO:0016469 p=5.6E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=90/322 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction