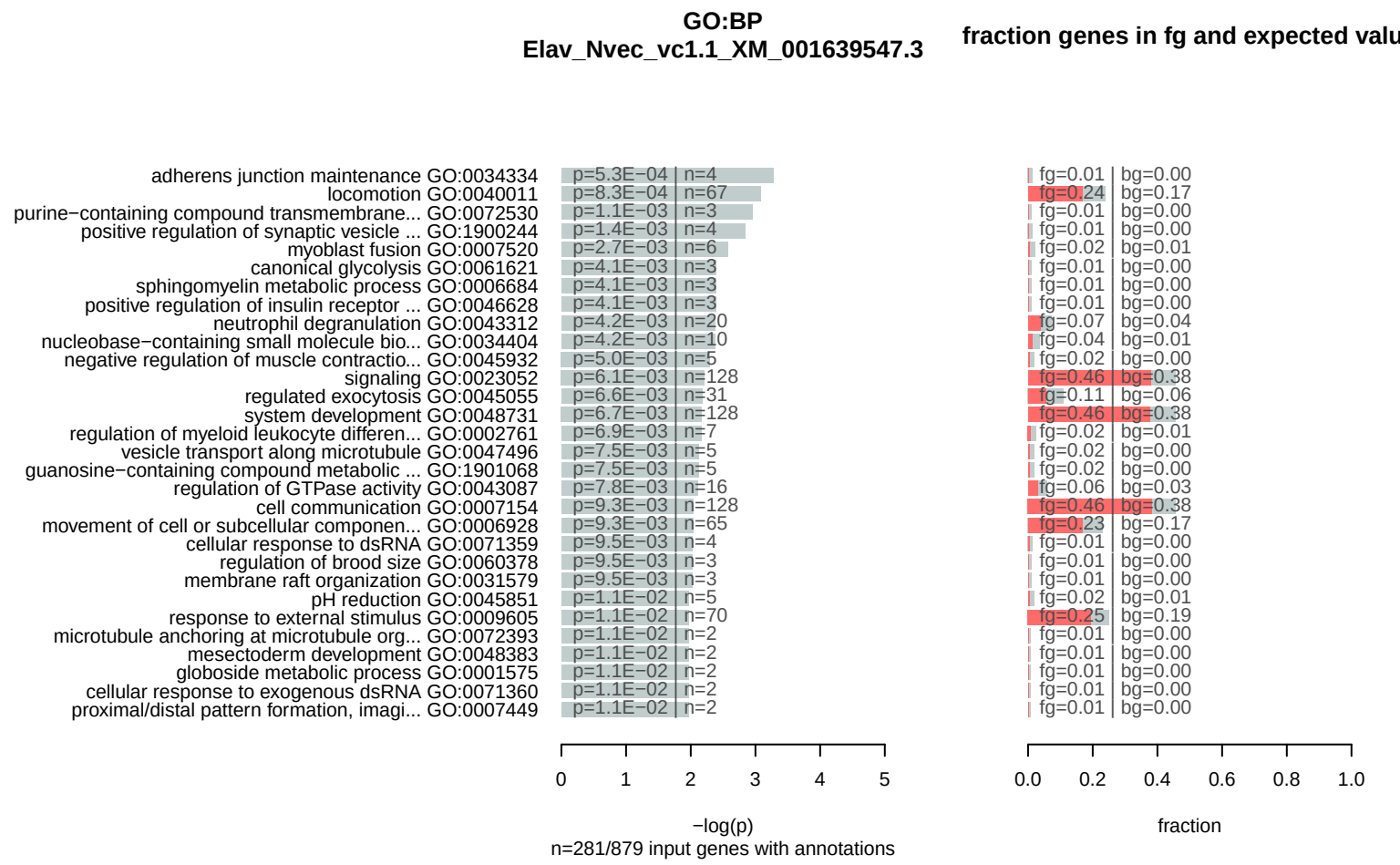
GO:BP
Elav_Nvec_vc1.1_XM_001639547.3
fraction genes in fg and expected valu
adherens junction maintenance GO:0034334 p=5.3E−04 n=4 fg=0.01 bg=0.00
locomotion GO:0040011 p=8.3E−04 n=67 fg=0.24 bg=0.17
purine−containing compound transmembrane... GO:0072530 p=1.1E−03 n=3 fg=0.01 bg=0.00
positive regulation of synaptic vesicle ... GO:1900244 p=1.4E−03 n=4 fg=0.01 bg=0.00
myoblast fusion GO:0007520 p=2.7E−03 n=6 fg=0.02 bg=0.01
canonical glycolysis GO:0061621 p=4.1E−03 n=3 fg=0.01 bg=0.00
sphingomyelin metabolic process GO:0006684 p=4.1E−03 n=3 fg=0.01 bg=0.00
positive regulation of insulin receptor ... GO:0046628 p=4.1E−03 n=3 fg=0.01 bg=0.00
neutrophil degranulation GO:0043312 p=4.2E−03 n=20 fg=0.07 bg=0.04
nucleobase−containing small molecule bio... GO:0034404 p=4.2E−03 n=10 fg=0.04 bg=0.01
negative regulation of muscle contractio... GO:0045932 p=5.0E−03 n=5 fg=0.02 bg=0.00
signaling GO:0023052 p=6.1E−03 n=128 fg=0.46 bg=0.38
regulated exocytosis GO:0045055 p=6.6E−03 n=31 fg=0.11 bg=0.06
system development GO:0048731 p=6.7E−03 n=128 fg=0.46 bg=0.38
regulation of myeloid leukocyte differen... GO:0002761 p=6.9E−03 n=7 fg=0.02 bg=0.01
vesicle transport along microtubule GO:0047496 p=7.5E−03 n=5 fg=0.02 bg=0.00
guanosine−containing compound metabolic ... GO:1901068 p=7.5E−03 n=5 fg=0.02 bg=0.00
regulation of GTPase activity GO:0043087 p=7.8E−03 n=16 fg=0.06 bg=0.03
cell communication GO:0007154 p=9.3E−03 n=128 fg=0.46 bg=0.38
movement of cell or subcellular componen... GO:0006928 p=9.3E−03 n=65 fg=0.23 bg=0.17
cellular response to dsRNA GO:0071359 p=9.5E−03 n=4 fg=0.01 bg=0.00
regulation of brood size GO:0060378 p=9.5E−03 n=3 fg=0.01 bg=0.00
membrane raft organization GO:0031579 p=9.5E−03 n=3 fg=0.01 bg=0.00
pH reduction GO:0045851 p=1.1E−02 n=5 fg=0.02 bg=0.01
response to external stimulus GO:0009605 p=1.1E−02 n=70 fg=0.25 bg=0.19
microtubule anchoring at microtubule org... GO:0072393 p=1.1E−02 n=2 fg=0.01 bg=0.00
mesectoderm development GO:0048383 p=1.1E−02 n=2 fg=0.01 bg=0.00
globoside metabolic process GO:0001575 p=1.1E−02 n=2 fg=0.01 bg=0.00
cellular response to exogenous dsRNA GO:0071360 p=1.1E−02 n=2 fg=0.01 bg=0.00
proximal/distal pattern formation, imagi... GO:0007449 p=1.1E−02 n=2 fg=0.01 bg=0.00
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−log(p)
n=281/879 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_001639547.3
fraction genes in fg and expected valu
nucleobase transmembrane transporter act... GO:0015205 p=1.2E−02 n=2 fg=0.01 bg=0.00
N4−(beta−N−acetylglucosaminyl)−L−asparag... GO:0003948 p=1.2E−02 n=2 fg=0.01 bg=0.00
gamma−butyrobetaine dioxygenase activity GO:0008336 p=1.2E−02 n=2 fg=0.01 bg=0.00
purine nucleobase transmembrane transpor... GO:0005345 p=1.2E−02 n=2 fg=0.01 bg=0.00
purine ribonucleotide transmembrane tran... GO:0005346 p=1.2E−02 n=2 fg=0.01 bg=0.00
purine nucleotide transmembrane transpor... GO:0015216 p=1.2E−02 n=2 fg=0.01 bg=0.00
GTPase regulator activity GO:0030695 p=1.4E−02 n=18 fg=0.07 bg=0.04
proton transmembrane transporter activit... GO:0015078 p=2.1E−02 n=6 fg=0.02 bg=0.01
guanyl−nucleotide exchange factor activi... GO:0005085 p=2.5E−02 n=9 fg=0.03 bg=0.02
phosphatidylcholine binding GO:0031210 p=3.2E−02 n=3 fg=0.01 bg=0.00
cyclin binding GO:0030332 p=3.2E−02 n=3 fg=0.01 bg=0.00
spectrin binding GO:0030507 p=3.2E−02 n=3 fg=0.01 bg=0.00
transferase activity, transferring nitro... GO:0016769 p=3.2E−02 n=3 fg=0.01 bg=0.00
oxidoreductase activity, acting on singl... GO:0016702 p=3.3E−02 n=2 fg=0.01 bg=0.00
insulin−like growth factor receptor bind... GO:0005159 p=3.3E−02 n=2 fg=0.01 bg=0.00
caspase binding GO:0089720 p=3.3E−02 n=2 fg=0.01 bg=0.00
LIM domain binding GO:0030274 p=3.3E−02 n=2 fg=0.01 bg=0.00
dioxygenase activity GO:0051213 p=3.9E−02 n=5 fg=0.02 bg=0.01
active ion transmembrane transporter act... GO:0022853 p=4.0E−02 n=10 fg=0.04 bg=0.02
microtubule motor activity GO:0003777 p=4.5E−02 n=4 fg=0.02 bg=0.01
carbohydrate derivative transmembrane tr... GO:1901505 p=4.8E−02 n=3 fg=0.01 bg=0.00
nucleoside−triphosphatase regulator acti... GO:0060589 p=4.9E−02 n=18 fg=0.07 bg=0.05
GTPase activator activity GO:0005096 p=5.7E−02 n=10 fg=0.04 bg=0.02
phosphoric diester hydrolase activity GO:0008081 p=5.9E−02 n=5 fg=0.02 bg=0.01
oxidoreductase activity, acting on singl... GO:0016701 p=6.2E−02 n=2 fg=0.01 bg=0.00
single−stranded telomeric DNA binding GO:0043047 p=6.2E−02 n=2 fg=0.01 bg=0.00
phosphatidylethanolamine binding GO:0008429 p=6.2E−02 n=2 fg=0.01 bg=0.00
GTPase binding GO:0051020 p=6.3E−02 n=20 fg=0.08 bg=0.05
small GTPase binding GO:0031267 p=6.4E−02 n=17 fg=0.07 bg=0.04
organophosphate ester transmembrane tran... GO:0015605 p=6.6E−02 n=3 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=259/879 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001639547.3
fraction genes in fg and expected valu
secretory granule GO:0030141 p=4.0E−04 n=28 fg=0.10 bg=0.05
caveola GO:0005901 p=1.5E−03 n=8 fg=0.03 bg=0.01
adherens junction GO:0005912 p=5.2E−03 n=13 fg=0.05 bg=0.02
cytoplasmic side of plasma membrane GO:0009898 p=7.7E−03 n=12 fg=0.04 bg=0.02
sperm fibrous sheath GO:0035686 p=9.4E−03 n=3 fg=0.01 bg=0.00
pericentriolar material GO:0000242 p=9.4E−03 n=3 fg=0.01 bg=0.00
photoreceptor outer segment membrane GO:0042622 p=1.1E−02 n=2 fg=0.01 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=1.1E−02 n=2 fg=0.01 bg=0.00
plasma membrane protein complex GO:0098797 p=1.1E−02 n=15 fg=0.05 bg=0.03
secretory granule lumen GO:0034774 p=1.4E−02 n=12 fg=0.04 bg=0.02
vacuolar membrane GO:0005774 p=1.4E−02 n=14 fg=0.05 bg=0.03
lytic vacuole GO:0000323 p=1.5E−02 n=21 fg=0.07 bg=0.05
cell−substrate junction GO:0030055 p=1.7E−02 n=7 fg=0.03 bg=0.01
heterotrimeric G−protein complex GO:0005834 p=1.7E−02 n=3 fg=0.01 bg=0.00
axon cytoplasm GO:1904115 p=1.7E−02 n=3 fg=0.01 bg=0.00
GTPase complex GO:1905360 p=1.7E−02 n=3 fg=0.01 bg=0.00
plasma membrane proton−transporting V−ty... GO:0033181 p=1.7E−02 n=3 fg=0.01 bg=0.00
lytic vacuole membrane GO:0098852 p=1.8E−02 n=11 fg=0.04 bg=0.02
cytoplasmic vesicle lumen GO:0060205 p=1.8E−02 n=12 fg=0.04 bg=0.02
vesicle lumen GO:0031983 p=1.8E−02 n=12 fg=0.04 bg=0.02
lysosome GO:0005764 p=1.8E−02 n=20 fg=0.07 bg=0.04
lysosomal membrane GO:0005765 p=2.2E−02 n=10 fg=0.04 bg=0.02
nuclear membrane GO:0031965 p=2.3E−02 n=12 fg=0.04 bg=0.02
extrinsic component of membrane GO:0019898 p=2.3E−02 n=12 fg=0.04 bg=0.02
Cul2−RING ubiquitin ligase complex GO:0031462 p=2.8E−02 n=3 fg=0.01 bg=0.00
bounding membrane of organelle GO:0098588 p=2.8E−02 n=48 fg=0.17 bg=0.13
mediator complex GO:0016592 p=2.9E−02 n=4 fg=0.01 bg=0.00
collagen−containing extracellular matrix GO:0062023 p=2.9E−02 n=4 fg=0.01 bg=0.00
EARP complex GO:1990745 p=3.0E−02 n=2 fg=0.01 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000221 p=3.0E−02 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=280/879 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction