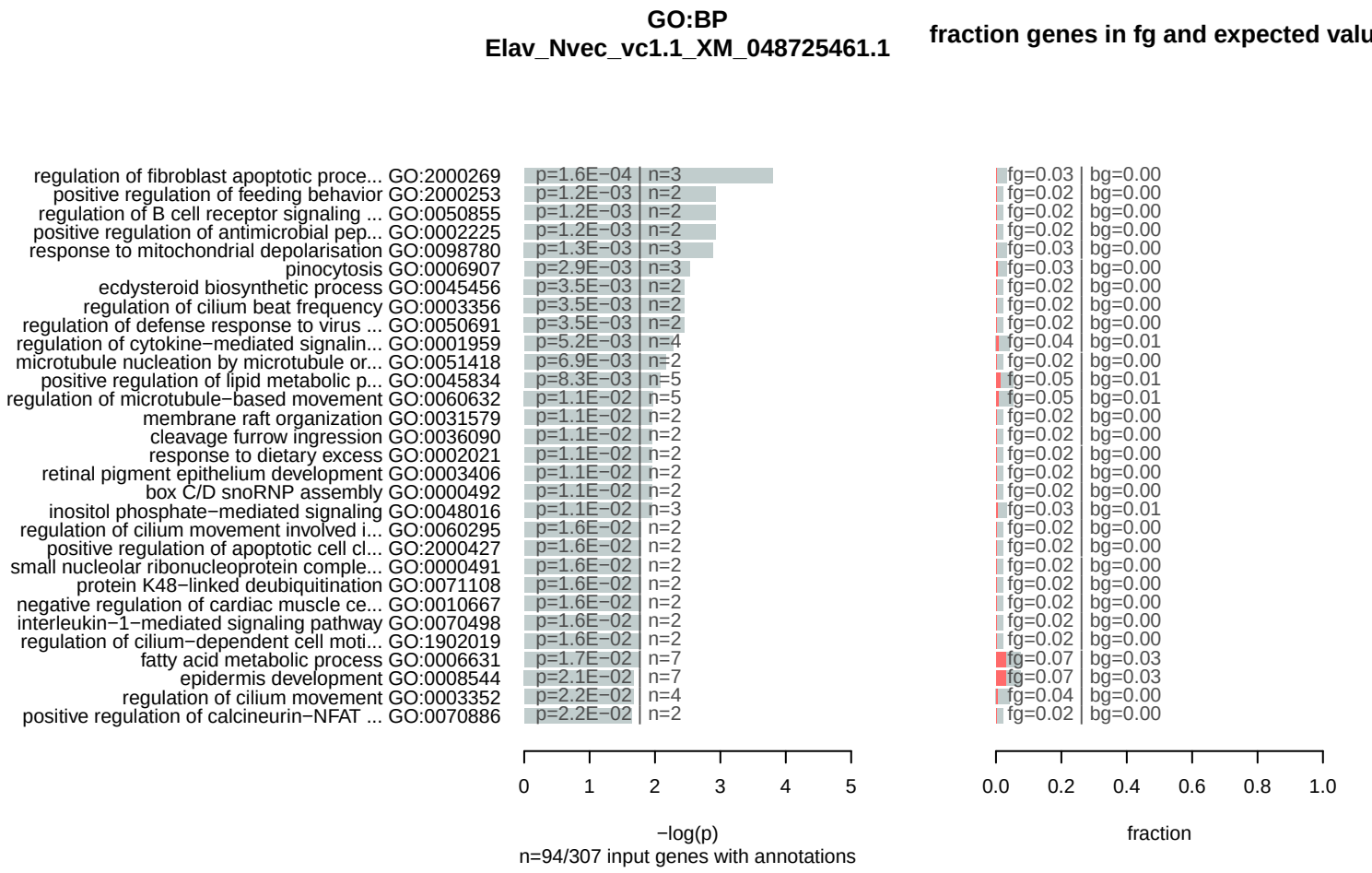
GO:BP
Elav_Nvec_vc1.1_XM_048725461.1
fraction genes in fg and expected valu
regulation of fibroblast apoptotic proce... GO:2000269 p=1.6E−04 n=3 fg=0.03 bg=0.00
positive regulation of feeding behavior GO:2000253 p=1.2E−03 n=2 fg=0.02 bg=0.00
regulation of B cell receptor signaling ... GO:0050855 p=1.2E−03 n=2 fg=0.02 bg=0.00
positive regulation of antimicrobial pep... GO:0002225 p=1.2E−03 n=2 fg=0.02 bg=0.00
response to mitochondrial depolarisation GO:0098780 p=1.3E−03 n=3 fg=0.03 bg=0.00
pinocytosis GO:0006907 p=2.9E−03 n=3 fg=0.03 bg=0.00
ecdysteroid biosynthetic process GO:0045456 p=3.5E−03 n=2 fg=0.02 bg=0.00
regulation of cilium beat frequency GO:0003356 p=3.5E−03 n=2 fg=0.02 bg=0.00
regulation of defense response to virus ... GO:0050691 p=3.5E−03 n=2 fg=0.02 bg=0.00
regulation of cytokine−mediated signalin... GO:0001959 p=5.2E−03 n=4 fg=0.04 bg=0.01
microtubule nucleation by microtubule or... GO:0051418 p=6.9E−03 n=2 fg=0.02 bg=0.00
positive regulation of lipid metabolic p... GO:0045834 p=8.3E−03 n=5 fg=0.05 bg=0.01
regulation of microtubule−based movement GO:0060632 p=1.1E−02 n=5 fg=0.05 bg=0.01
membrane raft organization GO:0031579 p=1.1E−02 n=2 fg=0.02 bg=0.00
cleavage furrow ingression GO:0036090 p=1.1E−02 n=2 fg=0.02 bg=0.00
response to dietary excess GO:0002021 p=1.1E−02 n=2 fg=0.02 bg=0.00
retinal pigment epithelium development GO:0003406 p=1.1E−02 n=2 fg=0.02 bg=0.00
box C/D snoRNP assembly GO:0000492 p=1.1E−02 n=2 fg=0.02 bg=0.00
inositol phosphate−mediated signaling GO:0048016 p=1.1E−02 n=3 fg=0.03 bg=0.01
regulation of cilium movement involved i... GO:0060295 p=1.6E−02 n=2 fg=0.02 bg=0.00
positive regulation of apoptotic cell cl... GO:2000427 p=1.6E−02 n=2 fg=0.02 bg=0.00
small nucleolar ribonucleoprotein comple... GO:0000491 p=1.6E−02 n=2 fg=0.02 bg=0.00
protein K48−linked deubiquitination GO:0071108 p=1.6E−02 n=2 fg=0.02 bg=0.00
negative regulation of cardiac muscle ce... GO:0010667 p=1.6E−02 n=2 fg=0.02 bg=0.00
interleukin−1−mediated signaling pathway GO:0070498 p=1.6E−02 n=2 fg=0.02 bg=0.00
regulation of cilium−dependent cell moti... GO:1902019 p=1.6E−02 n=2 fg=0.02 bg=0.00
fatty acid metabolic process GO:0006631 p=1.7E−02 n=7 fg=0.07 bg=0.03
epidermis development GO:0008544 p=2.1E−02 n=7 fg=0.07 bg=0.03
regulation of cilium movement GO:0003352 p=2.2E−02 n=4 fg=0.04 bg=0.00
positive regulation of calcineurin−NFAT ... GO:0070886 p=2.2E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=94/307 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_048725461.1
fraction genes in fg and expected valu
phospholipase A2 activity GO:0004623 p=7.7E−04 n=3 fg=0.04 bg=0.00
dopamine receptor binding GO:0050780 p=1.3E−03 n=3 fg=0.04 bg=0.00
DNA−binding transcription repressor acti... GO:0001227 p=2.1E−03 n=5 fg=0.06 bg=0.01
arrestin family protein binding GO:1990763 p=1.1E−02 n=2 fg=0.02 bg=0.00
Wnt−protein binding GO:0017147 p=1.7E−02 n=2 fg=0.02 bg=0.00
amino acid binding GO:0016597 p=1.7E−02 n=3 fg=0.04 bg=0.01
oxidoreductase activity, acting on perox... GO:0016684 p=2.3E−02 n=2 fg=0.02 bg=0.00
biotinidase activity GO:0047708 p=3.5E−02 n=1 fg=0.01 bg=0.00
GDP−mannose 4,6−dehydratase activity GO:0008446 p=3.5E−02 n=1 fg=0.01 bg=0.00
nucleoside:sodium symporter activity GO:0005415 p=3.5E−02 n=1 fg=0.01 bg=0.00
sphingolipid transfer activity GO:0120016 p=3.5E−02 n=1 fg=0.01 bg=0.00
ceramide transfer activity GO:0120017 p=3.5E−02 n=1 fg=0.01 bg=0.00
IkappaB kinase activity GO:0008384 p=3.5E−02 n=1 fg=0.01 bg=0.00
pyrimidine nucleobase transmembrane tran... GO:0005350 p=3.5E−02 n=1 fg=0.01 bg=0.00
lysophosphatidic acid binding GO:0035727 p=3.5E−02 n=1 fg=0.01 bg=0.00
ammonia ligase activity GO:0016211 p=3.5E−02 n=1 fg=0.01 bg=0.00
calcium:sodium antiporter activity invol... GO:0086038 p=3.5E−02 n=1 fg=0.01 bg=0.00
purine nucleoside transmembrane transpor... GO:0015211 p=3.5E−02 n=1 fg=0.01 bg=0.00
T cell receptor binding GO:0042608 p=3.5E−02 n=1 fg=0.01 bg=0.00
G−protein beta−subunit binding GO:0031681 p=3.5E−02 n=1 fg=0.01 bg=0.00
tRNA 2'−phosphotransferase activity GO:0000215 p=3.5E−02 n=1 fg=0.01 bg=0.00
mono−olein transacylation activity GO:0051264 p=3.5E−02 n=1 fg=0.01 bg=0.00
diolein transacylation activity GO:0051265 p=3.5E−02 n=1 fg=0.01 bg=0.00
leucine binding GO:0070728 p=3.5E−02 n=1 fg=0.01 bg=0.00
NADP+ binding GO:0070401 p=3.5E−02 n=1 fg=0.01 bg=0.00
cysteine−type exopeptidase activity GO:0070004 p=3.5E−02 n=1 fg=0.01 bg=0.00
cyclic GMP−AMP synthase activity GO:0140699 p=3.5E−02 n=1 fg=0.01 bg=0.00
purine−specific nucleoside:sodium sympor... GO:0015390 p=3.5E−02 n=1 fg=0.01 bg=0.00
nucleobase:cation symporter activity GO:0015391 p=3.5E−02 n=1 fg=0.01 bg=0.00
lipoprotein lipase activity GO:0004465 p=3.5E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=83/307 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048725461.1
fraction genes in fg and expected valu
nuclear matrix GO:0016363 p=1.9E−02 n=4 fg=0.04 bg=0.01
extrinsic component of membrane GO:0019898 p=2.2E−02 n=6 fg=0.06 bg=0.02
polar microtubule GO:0005827 p=3.6E−02 n=1 fg=0.01 bg=0.00
protein phosphatase 4 complex GO:0030289 p=3.6E−02 n=1 fg=0.01 bg=0.00
perichromatin fibrils GO:0005726 p=3.6E−02 n=1 fg=0.01 bg=0.00
ATF4−CREB1 transcription factor complex GO:1990589 p=3.6E−02 n=1 fg=0.01 bg=0.00
gamma−tubulin small complex GO:0008275 p=3.6E−02 n=1 fg=0.01 bg=0.00
core−binding factor complex GO:0016513 p=3.6E−02 n=1 fg=0.01 bg=0.00
equatorial microtubule organizing center GO:0000923 p=3.6E−02 n=1 fg=0.01 bg=0.00
macropinocytic cup GO:0070685 p=3.6E−02 n=1 fg=0.01 bg=0.00
tubular endosome GO:0097422 p=3.6E−02 n=1 fg=0.01 bg=0.00
postsynaptic endosome GO:0098845 p=3.6E−02 n=1 fg=0.01 bg=0.00
postsynaptic recycling endosome GO:0098837 p=3.6E−02 n=1 fg=0.01 bg=0.00
presynaptic active zone GO:0048786 p=4.7E−02 n=3 fg=0.03 bg=0.01
Cul4−RING E3 ubiquitin ligase complex GO:0080008 p=4.8E−02 n=2 fg=0.02 bg=0.00
integral component of mitochondrial memb... GO:0032592 p=6.7E−02 n=2 fg=0.02 bg=0.00
intrinsic component of mitochondrial mem... GO:0098573 p=6.7E−02 n=2 fg=0.02 bg=0.00
DNA replication preinitiation complex GO:0031261 p=7.1E−02 n=1 fg=0.01 bg=0.00
IkappaB kinase complex GO:0008385 p=7.1E−02 n=1 fg=0.01 bg=0.00
GATOR2 complex GO:0061700 p=7.1E−02 n=1 fg=0.01 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000220 p=7.1E−02 n=1 fg=0.01 bg=0.00
proton−transporting V−type ATPase, V0 do... GO:0033179 p=7.1E−02 n=1 fg=0.01 bg=0.00
mitochondrial pyruvate dehydrogenase (li... GO:0019910 p=7.1E−02 n=1 fg=0.01 bg=0.00
Cul7−RING ubiquitin ligase complex GO:0031467 p=7.1E−02 n=1 fg=0.01 bg=0.00
gamma−tubulin complex GO:0000930 p=7.1E−02 n=1 fg=0.01 bg=0.00
retromer, tubulation complex GO:0030905 p=7.1E−02 n=1 fg=0.01 bg=0.00
Seh1−associated complex GO:0035859 p=7.1E−02 n=1 fg=0.01 bg=0.00
GINS complex GO:0000811 p=7.1E−02 n=1 fg=0.01 bg=0.00
Swr1 complex GO:0000812 p=7.1E−02 n=1 fg=0.01 bg=0.00
pleated septate junction GO:0005919 p=7.1E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=97/307 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction