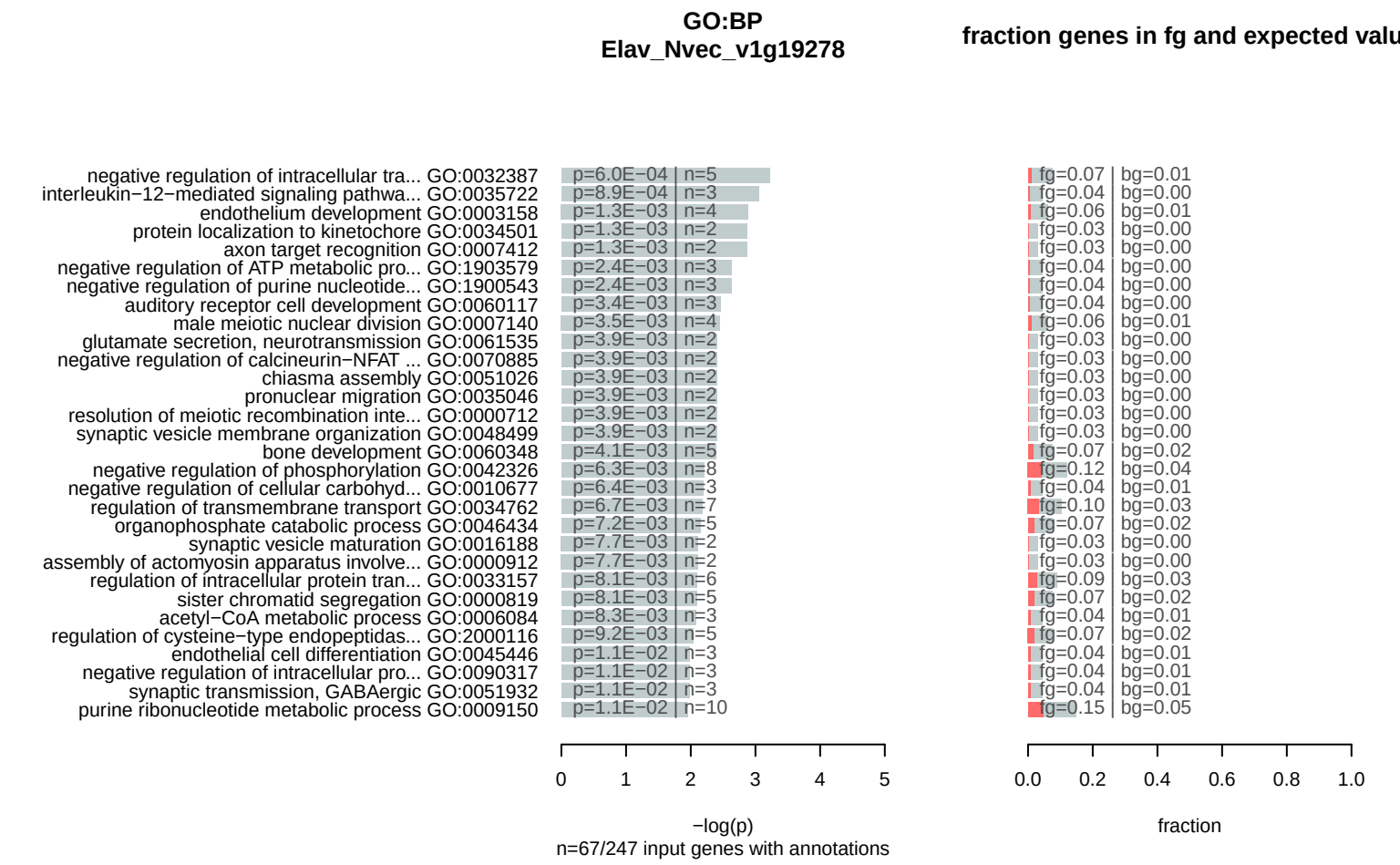
GO:BP
Elav_Nvec_v1g19278
fraction genes in fg and expected valu
negative regulation of intracellular tra... GO:0032387 p=6.0E−04 n=5 fg=0.07 bg=0.01
interleukin−12−mediated signaling pathwa... GO:0035722 p=8.9E−04 n=3 fg=0.04 bg=0.00
endothelium development GO:0003158 p=1.3E−03 n=4 fg=0.06 bg=0.01
protein localization to kinetochore GO:0034501 p=1.3E−03 n=2 fg=0.03 bg=0.00
axon target recognition GO:0007412 p=1.3E−03 n=2 fg=0.03 bg=0.00
negative regulation of ATP metabolic pro... GO:1903579 p=2.4E−03 n=3 fg=0.04 bg=0.00
negative regulation of purine nucleotide... GO:1900543 p=2.4E−03 n=3 fg=0.04 bg=0.00
auditory receptor cell development GO:0060117 p=3.4E−03 n=3 fg=0.04 bg=0.00
male meiotic nuclear division GO:0007140 p=3.5E−03 n=4 fg=0.06 bg=0.01
glutamate secretion, neurotransmission GO:0061535 p=3.9E−03 n=2 fg=0.03 bg=0.00
negative regulation of calcineurin−NFAT ... GO:0070885 p=3.9E−03 n=2 fg=0.03 bg=0.00
chiasma assembly GO:0051026 p=3.9E−03 n=2 fg=0.03 bg=0.00
pronuclear migration GO:0035046 p=3.9E−03 n=2 fg=0.03 bg=0.00
resolution of meiotic recombination inte... GO:0000712 p=3.9E−03 n=2 fg=0.03 bg=0.00
synaptic vesicle membrane organization GO:0048499 p=3.9E−03 n=2 fg=0.03 bg=0.00
bone development GO:0060348 p=4.1E−03 n=5 fg=0.07 bg=0.02
negative regulation of phosphorylation GO:0042326 p=6.3E−03 n=8 fg=0.12 bg=0.04
negative regulation of cellular carbohyd... GO:0010677 p=6.4E−03 n=3 fg=0.04 bg=0.01
regulation of transmembrane transport GO:0034762 p=6.7E−03 n=7 fg=0.10 bg=0.03
organophosphate catabolic process GO:0046434 p=7.2E−03 n=5 fg=0.07 bg=0.02
synaptic vesicle maturation GO:0016188 p=7.7E−03 n=2 fg=0.03 bg=0.00
assembly of actomyosin apparatus involve... GO:0000912 p=7.7E−03 n=2 fg=0.03 bg=0.00
regulation of intracellular protein tran... GO:0033157 p=8.1E−03 n=6 fg=0.09 bg=0.03
sister chromatid segregation GO:0000819 p=8.1E−03 n=5 fg=0.07 bg=0.02
acetyl−CoA metabolic process GO:0006084 p=8.3E−03 n=3 fg=0.04 bg=0.01
regulation of cysteine−type endopeptidas... GO:2000116 p=9.2E−03 n=5 fg=0.07 bg=0.02
endothelial cell differentiation GO:0045446 p=1.1E−02 n=3 fg=0.04 bg=0.01
negative regulation of intracellular pro... GO:0090317 p=1.1E−02 n=3 fg=0.04 bg=0.01
synaptic transmission, GABAergic GO:0051932 p=1.1E−02 n=3 fg=0.04 bg=0.01
purine ribonucleotide metabolic process GO:0009150 p=1.1E−02 n=10 fg=0.15 bg=0.05
0 1 2 3 4 5
−log(p)
n=67/247 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_v1g19278
fraction genes in fg and expected valu
phospholipase binding GO:0043274 p=4.1E−04 n=3 fg=0.05 bg=0.00
platelet−activating factor acetyltransfe... GO:0047179 p=1.3E−03 n=2 fg=0.04 bg=0.00
peroxidase activity GO:0004601 p=3.7E−03 n=2 fg=0.04 bg=0.00
ATP hydrolysis activity GO:0016887 p=4.2E−03 n=8 fg=0.14 bg=0.05
phospholipase A2 activity GO:0004623 p=7.2E−03 n=2 fg=0.04 bg=0.00
syntaxin−1 binding GO:0017075 p=7.2E−03 n=2 fg=0.04 bg=0.00
dynactin binding GO:0034452 p=1.2E−02 n=2 fg=0.04 bg=0.00
MAP kinase kinase kinase activity GO:0004709 p=1.7E−02 n=2 fg=0.04 bg=0.00
cholesterol binding GO:0015485 p=1.7E−02 n=2 fg=0.04 bg=0.00
sterol binding GO:0032934 p=2.4E−02 n=2 fg=0.04 bg=0.00
mRNA binding GO:0003729 p=2.8E−02 n=5 fg=0.09 bg=0.03
P−type transmembrane transporter activit... GO:0140358 p=3.1E−02 n=2 fg=0.04 bg=0.01
steroid binding GO:0005496 p=3.1E−02 n=2 fg=0.04 bg=0.01
P−type ion transporter activity GO:0015662 p=3.1E−02 n=2 fg=0.04 bg=0.01
P−Man:Man3GlcNAc2−PP−Dol alpha−1,2−man... GO:0004377 p=3.6E−02 n=1 fg=0.02 bg=0.00
alpha−N−acetylglucosaminidase activity GO:0004561 p=3.6E−02 n=1 fg=0.02 bg=0.00
C−acetyltransferase activity GO:0016453 p=3.6E−02 n=1 fg=0.02 bg=0.00
microtubule−severing ATPase activity GO:0008568 p=3.6E−02 n=1 fg=0.02 bg=0.00
acetyl−CoA C−acetyltransferase activity GO:0003985 p=3.6E−02 n=1 fg=0.02 bg=0.00
mevalonate kinase activity GO:0004496 p=3.6E−02 n=1 fg=0.02 bg=0.00
acetyl−CoA C−acyltransferase activity GO:0003988 p=3.6E−02 n=1 fg=0.02 bg=0.00
dynein light chain binding GO:0045503 p=3.6E−02 n=1 fg=0.02 bg=0.00
double−stranded methylated DNA binding GO:0010385 p=3.6E−02 n=1 fg=0.02 bg=0.00
dynein intermediate chain binding GO:0045505 p=3.6E−02 n=1 fg=0.02 bg=0.00
juvenile hormone response element bindin... GO:0070594 p=3.6E−02 n=1 fg=0.02 bg=0.00
cGMP−stimulated cyclic−nucleotide phosph... GO:0004118 p=3.6E−02 n=1 fg=0.02 bg=0.00
lysine N−acetyltransferase activity, act... GO:0004468 p=3.6E−02 n=1 fg=0.02 bg=0.00
taste receptor binding GO:0031883 p=3.6E−02 n=1 fg=0.02 bg=0.00
alpha−1,2−mannosyltransferase activity GO:0000026 p=3.6E−02 n=1 fg=0.02 bg=0.00
inositol bisphosphate phosphatase activi... GO:0016312 p=3.6E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=57/247 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_v1g19278
fraction genes in fg and expected valu
ficolin−1−rich granule membrane GO:0101003 p=1.0E−03 n=3 fg=0.04 bg=0.00
cluster of actin−based cell projections GO:0098862 p=3.7E−03 n=5 fg=0.07 bg=0.02
chromosome, centromeric region GO:0000775 p=3.7E−03 n=5 fg=0.07 bg=0.02
ruffle membrane GO:0032587 p=5.5E−03 n=3 fg=0.04 bg=0.01
cytoplasmic dynein complex GO:0005868 p=8.4E−03 n=2 fg=0.03 bg=0.00
perinuclear region of cytoplasm GO:0048471 p=1.1E−02 n=11 fg=0.16 bg=0.07
brush border GO:0005903 p=1.2E−02 n=4 fg=0.06 bg=0.01
distal axon GO:0150034 p=1.3E−02 n=8 fg=0.11 bg=0.05
pericentric heterochromatin GO:0005721 p=1.4E−02 n=2 fg=0.03 bg=0.00
axon GO:0030424 p=1.7E−02 n=11 fg=0.16 bg=0.08
growth cone GO:0030426 p=1.9E−02 n=5 fg=0.07 bg=0.02
supramolecular fiber GO:0099512 p=1.9E−02 n=8 fg=0.11 bg=0.05
supramolecular polymer GO:0099081 p=1.9E−02 n=8 fg=0.11 bg=0.05
cell junction GO:0030054 p=2.0E−02 n=16 fg=0.23 bg=0.13
site of polarized growth GO:0030427 p=2.3E−02 n=5 fg=0.07 bg=0.02
condensed chromosome GO:0000793 p=2.9E−02 n=4 fg=0.06 bg=0.02
presynaptic active zone GO:0048786 p=3.0E−02 n=3 fg=0.04 bg=0.01
stereocilium GO:0032420 p=3.5E−02 n=2 fg=0.03 bg=0.00
stereocilium bundle GO:0032421 p=3.5E−02 n=2 fg=0.03 bg=0.00
cytoplasmic microtubule GO:0005881 p=3.5E−02 n=2 fg=0.03 bg=0.00
synapse GO:0045202 p=3.8E−02 n=12 fg=0.17 bg=0.10
contractile fiber GO:0043292 p=3.8E−02 n=5 fg=0.07 bg=0.03
transverse filament GO:0000802 p=3.9E−02 n=1 fg=0.01 bg=0.00
chromaffin granule GO:0042583 p=3.9E−02 n=1 fg=0.01 bg=0.00
chromaffin granule membrane GO:0042584 p=3.9E−02 n=1 fg=0.01 bg=0.00
extrinsic component of presynaptic activ... GO:0098891 p=3.9E−02 n=1 fg=0.01 bg=0.00
FANCM−MHF complex GO:0071821 p=3.9E−02 n=1 fg=0.01 bg=0.00
extrinsic component of synaptic membrane GO:0099243 p=3.9E−02 n=1 fg=0.01 bg=0.00
astral microtubule GO:0000235 p=3.9E−02 n=1 fg=0.01 bg=0.00
hippocampal mossy fiber GO:0097457 p=3.9E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=70/247 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction