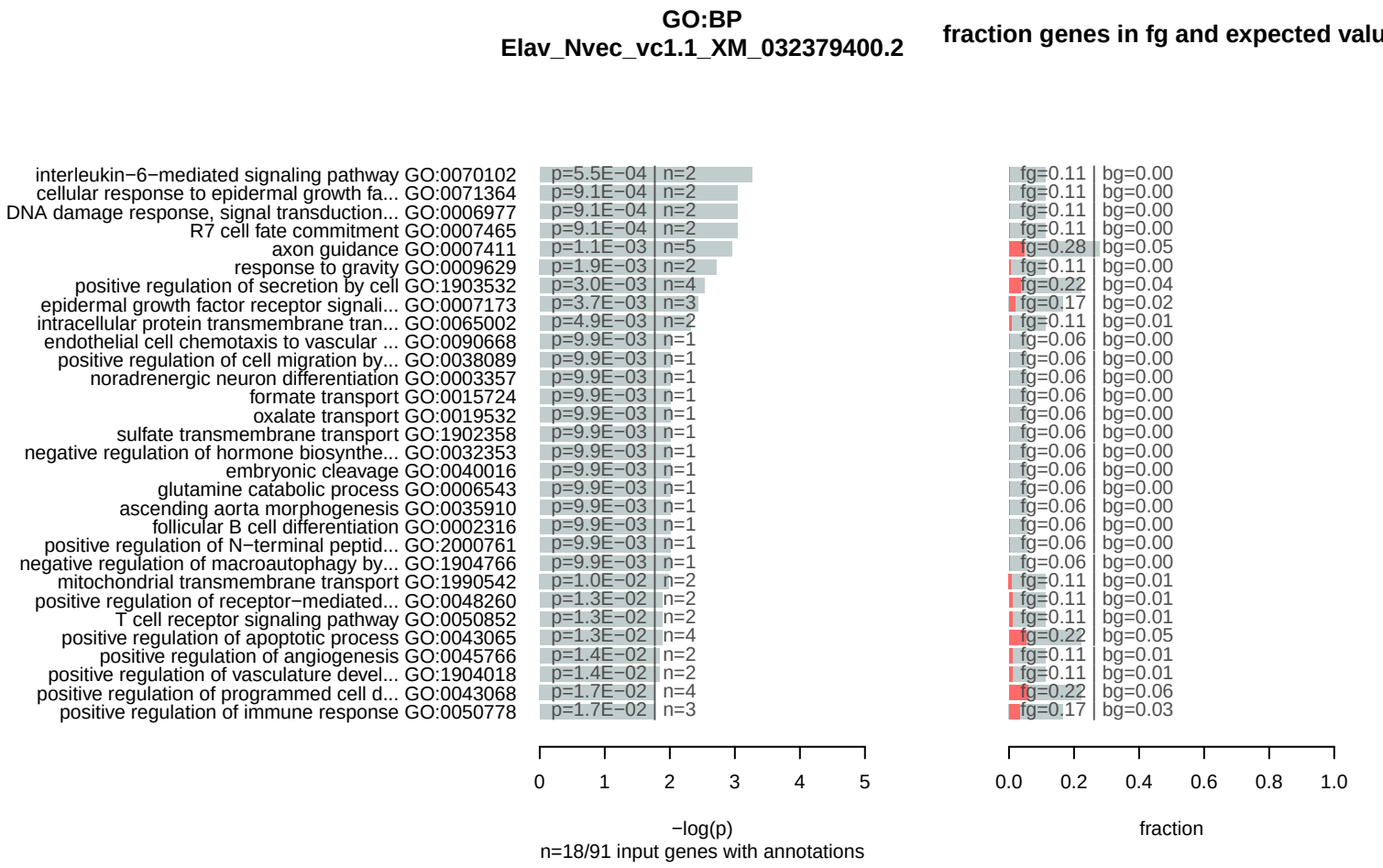
GO:BP
Elav_Nvec_vc1.1_XM_032379400.2
fraction genes in fg and expected valu
interleukin−6−mediated signaling pathway GO:0070102 p=5.5E−04 n=2 fg=0.11 bg=0.00
cellular response to epidermal growth fa... GO:0071364 p=9.1E−04 n=2 fg=0.11 bg=0.00
DNA damage response, signal transduction... GO:0006977 p=9.1E−04 n=2 fg=0.11 bg=0.00
R7 cell fate commitment GO:0007465 p=9.1E−04 n=2 fg=0.11 bg=0.00
axon guidance GO:0007411 p=1.1E−03 n=5 fg=0.28 bg=0.05
response to gravity GO:0009629 p=1.9E−03 n=2 fg=0.11 bg=0.00
positive regulation of secretion by cell GO:1903532 p=3.0E−03 n=4 fg=0.22 bg=0.04
epidermal growth factor receptor signali... GO:0007173 p=3.7E−03 n=3 fg=0.17 bg=0.02
intracellular protein transmembrane tran... GO:0065002 p=4.9E−03 n=2 fg=0.11 bg=0.01
endothelial cell chemotaxis to vascular ... GO:0090668 p=9.9E−03 n=1 fg=0.06 bg=0.00
positive regulation of cell migration by... GO:0038089 p=9.9E−03 n=1 fg=0.06 bg=0.00
noradrenergic neuron differentiation GO:0003357 p=9.9E−03 n=1 fg=0.06 bg=0.00
formate transport GO:0015724 p=9.9E−03 n=1 fg=0.06 bg=0.00
oxalate transport GO:0019532 p=9.9E−03 n=1 fg=0.06 bg=0.00
sulfate transmembrane transport GO:1902358 p=9.9E−03 n=1 fg=0.06 bg=0.00
negative regulation of hormone biosynthe... GO:0032353 p=9.9E−03 n=1 fg=0.06 bg=0.00
embryonic cleavage GO:0040016 p=9.9E−03 n=1 fg=0.06 bg=0.00
glutamine catabolic process GO:0006543 p=9.9E−03 n=1 fg=0.06 bg=0.00
ascending aorta morphogenesis GO:0035910 p=9.9E−03 n=1 fg=0.06 bg=0.00
follicular B cell differentiation GO:0002316 p=9.9E−03 n=1 fg=0.06 bg=0.00
positive regulation of N−terminal peptid... GO:2000761 p=9.9E−03 n=1 fg=0.06 bg=0.00
negative regulation of macroautophagy by... GO:1904766 p=9.9E−03 n=1 fg=0.06 bg=0.00
mitochondrial transmembrane transport GO:1990542 p=1.0E−02 n=2 fg=0.11 bg=0.01
positive regulation of receptor−mediated... GO:0048260 p=1.3E−02 n=2 fg=0.11 bg=0.01
T cell receptor signaling pathway GO:0050852 p=1.3E−02 n=2 fg=0.11 bg=0.01
positive regulation of apoptotic process GO:0043065 p=1.3E−02 n=4 fg=0.22 bg=0.05
positive regulation of angiogenesis GO:0045766 p=1.4E−02 n=2 fg=0.11 bg=0.01
positive regulation of vasculature devel... GO:1904018 p=1.4E−02 n=2 fg=0.11 bg=0.01
positive regulation of programmed cell d... GO:0043068 p=1.7E−02 n=4 fg=0.22 bg=0.06
positive regulation of immune response GO:0050778 p=1.7E−02 n=3 fg=0.17 bg=0.03
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n=18/91 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032379400.2
fraction genes in fg and expected valu
receptor tyrosine kinase binding GO:0030971 p=1.7E−04 n=3 fg=0.19 bg=0.01
DNA−binding transcription activator acti... GO:0001228 p=2.5E−03 n=4 fg=0.25 bg=0.04
phosphotyrosine residue binding GO:0001784 p=2.6E−03 n=2 fg=0.12 bg=0.01
oxalate transmembrane transporter activi... GO:0019531 p=1.0E−02 n=1 fg=0.06 bg=0.00
amidophosphoribosyltransferase activity GO:0004044 p=1.0E−02 n=1 fg=0.06 bg=0.00
formate transmembrane transporter activi... GO:0015499 p=1.0E−02 n=1 fg=0.06 bg=0.00
K48−linked polyubiquitin modification−de... GO:0036435 p=1.0E−02 n=1 fg=0.06 bg=0.00
phosphatidylinositol phospholipase C act... GO:0004435 p=1.0E−02 n=1 fg=0.06 bg=0.00
sulfate transmembrane transporter activi... GO:0015116 p=1.0E−02 n=1 fg=0.06 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=1.0E−02 n=1 fg=0.06 bg=0.00
neurotrophin TRK receptor binding GO:0005167 p=1.0E−02 n=1 fg=0.06 bg=0.00
neurotrophin TRKA receptor binding GO:0005168 p=1.0E−02 n=1 fg=0.06 bg=0.00
cis−regulatory region sequence−specific ... GO:0000987 p=1.8E−02 n=3 fg=0.19 bg=0.04
RNA polymerase II cis−regulatory region ... GO:0000978 p=1.8E−02 n=3 fg=0.19 bg=0.04
transmembrane receptor protein tyrosine ... GO:0005068 p=2.0E−02 n=1 fg=0.06 bg=0.00
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phosphatidylinositol 3−kinase regulatory... GO:0036312 p=2.0E−02 n=1 fg=0.06 bg=0.00
sequence−specific DNA binding GO:0043565 p=2.2E−02 n=4 fg=0.25 bg=0.07
bicarbonate transmembrane transporter ac... GO:0015106 p=3.0E−02 n=1 fg=0.06 bg=0.00
pyrimidine nucleotide transmembrane tran... GO:0015218 p=3.0E−02 n=1 fg=0.06 bg=0.00
tau protein binding GO:0048156 p=3.0E−02 n=1 fg=0.06 bg=0.00
calcium−activated potassium channel acti... GO:0015269 p=3.0E−02 n=1 fg=0.06 bg=0.00
solute:anion antiporter activity GO:0140323 p=4.0E−02 n=1 fg=0.06 bg=0.00
anion:anion antiporter activity GO:0015301 p=4.0E−02 n=1 fg=0.06 bg=0.00
dicarboxylic acid transmembrane transpor... GO:0005310 p=4.0E−02 n=1 fg=0.06 bg=0.00
inorganic anion exchanger activity GO:0005452 p=4.0E−02 n=1 fg=0.06 bg=0.00
phospholipase C activity GO:0004629 p=4.0E−02 n=1 fg=0.06 bg=0.00
phosphatidylinositol−3,4−bisphosphate bi... GO:0043325 p=4.0E−02 n=1 fg=0.06 bg=0.00
RNA polymerase II transcription regulato... GO:0000977 p=4.1E−02 n=3 fg=0.19 bg=0.05
phosphatidylinositol 3−kinase activity GO:0035004 p=4.9E−02 n=1 fg=0.06 bg=0.00
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−log(p)
n=16/91 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032379400.2
fraction genes in fg and expected valu
growth cone filopodium GO:1990812 p=2.2E−02 n=1 fg=0.05 bg=0.00
COP9 signalosome GO:0008180 p=2.2E−02 n=1 fg=0.05 bg=0.00
membrane GO:0016020 p=2.8E−02 n=14 fg=0.70 bg=0.46
endolysosome membrane GO:0036020 p=3.3E−02 n=1 fg=0.05 bg=0.00
growth cone lamellipodium GO:1990761 p=3.3E−02 n=1 fg=0.05 bg=0.00
endolysosome GO:0036019 p=3.3E−02 n=1 fg=0.05 bg=0.00
anchored component of membrane GO:0031225 p=5.4E−02 n=1 fg=0.05 bg=0.00
lamellipodium GO:0030027 p=5.6E−02 n=2 fg=0.10 bg=0.02
growth cone GO:0030426 p=7.4E−02 n=2 fg=0.10 bg=0.02
site of polarized growth GO:0030427 p=8.0E−02 n=2 fg=0.10 bg=0.02
voltage−gated potassium channel complex GO:0008076 p=9.5E−02 n=1 fg=0.05 bg=0.01
mediator complex GO:0016592 p=9.5E−02 n=1 fg=0.05 bg=0.01
potassium channel complex GO:0034705 p=9.5E−02 n=1 fg=0.05 bg=0.01
membrane raft GO:0045121 p=1.1E−01 n=2 fg=0.10 bg=0.03
membrane microdomain GO:0098857 p=1.1E−01 n=2 fg=0.10 bg=0.03
intrinsic component of membrane GO:0031224 p=1.2E−01 n=6 fg=0.30 bg=0.17
lateral plasma membrane GO:0016328 p=1.2E−01 n=1 fg=0.05 bg=0.01
focal adhesion GO:0005925 p=1.5E−01 n=1 fg=0.05 bg=0.01
cell leading edge GO:0031252 p=1.6E−01 n=2 fg=0.10 bg=0.04
cis−Golgi network GO:0005801 p=1.6E−01 n=1 fg=0.05 bg=0.01
filopodium GO:0030175 p=1.6E−01 n=1 fg=0.05 bg=0.01
main axon GO:0044304 p=1.6E−01 n=1 fg=0.05 bg=0.01
cell−substrate junction GO:0030055 p=1.8E−01 n=1 fg=0.05 bg=0.01
ruffle GO:0001726 p=1.8E−01 n=1 fg=0.05 bg=0.01
nucleus GO:0005634 p=1.8E−01 n=12 fg=0.60 bg=0.48
axon GO:0030424 p=2.0E−01 n=3 fg=0.15 bg=0.08
cation channel complex GO:0034703 p=2.1E−01 n=1 fg=0.05 bg=0.01
integral component of membrane GO:0016021 p=2.2E−01 n=5 fg=0.25 bg=0.16
ion channel complex GO:0034702 p=2.3E−01 n=1 fg=0.05 bg=0.01
cell−cell junction GO:0005911 p=2.3E−01 n=2 fg=0.10 bg=0.05
0 1 2 3 4 5
−log(p)
n=20/91 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction