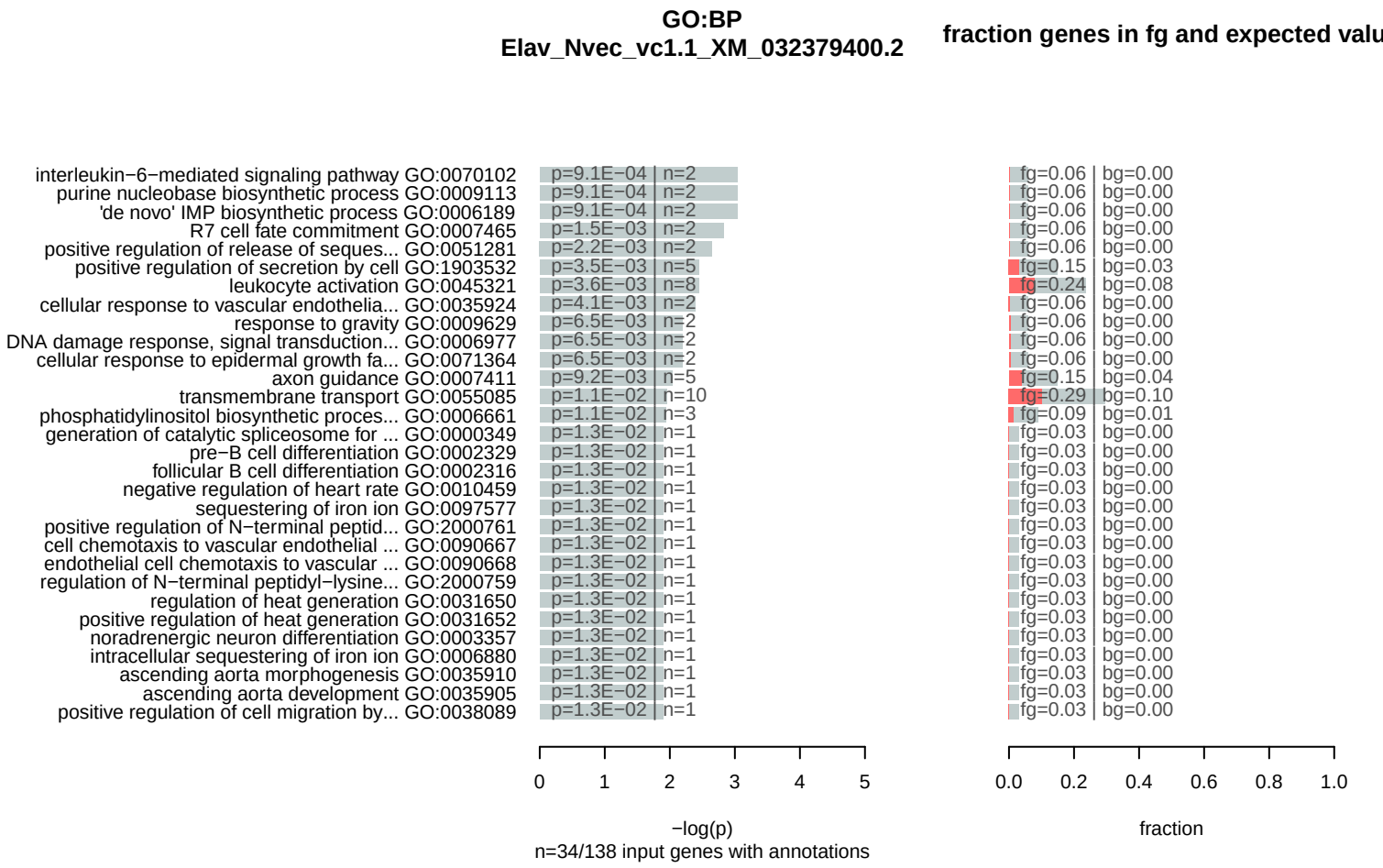
GO:BP
Elav_Nvec_vc1.1_XM_032379400.2
fraction genes in fg and expected valu
interleukin−6−mediated signaling pathway GO:0070102 p=9.1E−04 n=2 fg=0.06 bg=0.00
purine nucleobase biosynthetic process GO:0009113 p=9.1E−04 n=2 fg=0.06 bg=0.00
'de novo' IMP biosynthetic process GO:0006189 p=9.1E−04 n=2 fg=0.06 bg=0.00
R7 cell fate commitment GO:0007465 p=1.5E−03 n=2 fg=0.06 bg=0.00
positive regulation of release of seques... GO:0051281 p=2.2E−03 n=2 fg=0.06 bg=0.00
positive regulation of secretion by cell GO:1903532 p=3.5E−03 n=5 fg=0.15 bg=0.03
leukocyte activation GO:0045321 p=3.6E−03 n=8 fg=0.24 bg=0.08
cellular response to vascular endothelia... GO:0035924 p=4.1E−03 n=2 fg=0.06 bg=0.00
response to gravity GO:0009629 p=6.5E−03 n=2 fg=0.06 bg=0.00
DNA damage response, signal transduction... GO:0006977 p=6.5E−03 n=2 fg=0.06 bg=0.00
cellular response to epidermal growth fa... GO:0071364 p=6.5E−03 n=2 fg=0.06 bg=0.00
axon guidance GO:0007411 p=9.2E−03 n=5 fg=0.15 bg=0.04
transmembrane transport GO:0055085 p=1.1E−02 n=10 fg=0.29 bg=0.10
phosphatidylinositol biosynthetic proces... GO:0006661 p=1.1E−02 n=3 fg=0.09 bg=0.01
generation of catalytic spliceosome for ... GO:0000349 p=1.3E−02 n=1 fg=0.03 bg=0.00
pre−B cell differentiation GO:0002329 p=1.3E−02 n=1 fg=0.03 bg=0.00
follicular B cell differentiation GO:0002316 p=1.3E−02 n=1 fg=0.03 bg=0.00
negative regulation of heart rate GO:0010459 p=1.3E−02 n=1 fg=0.03 bg=0.00
sequestering of iron ion GO:0097577 p=1.3E−02 n=1 fg=0.03 bg=0.00
positive regulation of N−terminal peptid... GO:2000761 p=1.3E−02 n=1 fg=0.03 bg=0.00
cell chemotaxis to vascular endothelial ... GO:0090667 p=1.3E−02 n=1 fg=0.03 bg=0.00
endothelial cell chemotaxis to vascular ... GO:0090668 p=1.3E−02 n=1 fg=0.03 bg=0.00
regulation of N−terminal peptidyl−lysine... GO:2000759 p=1.3E−02 n=1 fg=0.03 bg=0.00
regulation of heat generation GO:0031650 p=1.3E−02 n=1 fg=0.03 bg=0.00
positive regulation of heat generation GO:0031652 p=1.3E−02 n=1 fg=0.03 bg=0.00
noradrenergic neuron differentiation GO:0003357 p=1.3E−02 n=1 fg=0.03 bg=0.00
intracellular sequestering of iron ion GO:0006880 p=1.3E−02 n=1 fg=0.03 bg=0.00
ascending aorta morphogenesis GO:0035910 p=1.3E−02 n=1 fg=0.03 bg=0.00
ascending aorta development GO:0035905 p=1.3E−02 n=1 fg=0.03 bg=0.00
positive regulation of cell migration by... GO:0038089 p=1.3E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=34/138 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=3.9E−04 n=3 fg=0.11 bg=0.01
phosphotyrosine residue binding GO:0001784 p=3.6E−03 n=2 fg=0.07 bg=0.00
ATPase activator activity GO:0001671 p=4.6E−03 n=2 fg=0.07 bg=0.00
polyubiquitin modification−dependent pro... GO:0031593 p=8.3E−03 n=2 fg=0.07 bg=0.01
monocarboxylic acid transmembrane transp... GO:0008028 p=8.3E−03 n=2 fg=0.07 bg=0.01
DNA−binding transcription activator acti... GO:0001228 p=1.0E−02 n=4 fg=0.14 bg=0.03
DNA−binding transcription activator acti... GO:0001216 p=1.0E−02 n=4 fg=0.14 bg=0.03
phosphoribosylaminoimidazole carboxylase... GO:0004638 p=1.2E−02 n=1 fg=0.04 bg=0.00
phosphoribosylaminoimidazolesuccinocarbo... GO:0004639 p=1.2E−02 n=1 fg=0.04 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=1.2E−02 n=1 fg=0.04 bg=0.00
long−chain fatty acid−CoA ligase activit... GO:0004467 p=1.2E−02 n=1 fg=0.04 bg=0.00
amidophosphoribosyltransferase activity GO:0004044 p=1.2E−02 n=1 fg=0.04 bg=0.00
glycogenin glucosyltransferase activity GO:0008466 p=1.2E−02 n=1 fg=0.04 bg=0.00
voltage−gated proton channel activity GO:0030171 p=1.2E−02 n=1 fg=0.04 bg=0.00
very long−chain fatty acid−CoA ligase ac... GO:0031957 p=1.2E−02 n=1 fg=0.04 bg=0.00
phosphatidylinositol phospholipase C act... GO:0004435 p=1.2E−02 n=1 fg=0.04 bg=0.00
neurotrophin TRK receptor binding GO:0005167 p=1.2E−02 n=1 fg=0.04 bg=0.00
neurotrophin TRKA receptor binding GO:0005168 p=1.2E−02 n=1 fg=0.04 bg=0.00
ATPase regulator activity GO:0060590 p=1.3E−02 n=2 fg=0.07 bg=0.01
ion channel activity GO:0005216 p=1.6E−02 n=4 fg=0.14 bg=0.04
channel activity GO:0015267 p=1.7E−02 n=4 fg=0.14 bg=0.04
passive transmembrane transporter activi... GO:0022803 p=1.7E−02 n=4 fg=0.14 bg=0.04
ubiquitin binding GO:0043130 p=1.8E−02 n=2 fg=0.07 bg=0.01
volume−sensitive anion channel activity GO:0005225 p=2.4E−02 n=1 fg=0.04 bg=0.00
phosphatidylinositol 3−kinase regulatory... GO:0036312 p=2.4E−02 n=1 fg=0.04 bg=0.00
transmembrane receptor protein tyrosine ... GO:0005068 p=2.4E−02 n=1 fg=0.04 bg=0.00
K48−linked polyubiquitin modification−de... GO:0036435 p=2.4E−02 n=1 fg=0.04 bg=0.00
neurotrophin receptor binding GO:0005165 p=2.4E−02 n=1 fg=0.04 bg=0.00
anion channel activity GO:0005253 p=2.5E−02 n=2 fg=0.07 bg=0.01
voltage−gated cation channel activity GO:0022843 p=2.7E−02 n=2 fg=0.07 bg=0.01
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−log(p)
n=28/138 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
ciliary plasm GO:0097014 p=9.8E−03 n=3 fg=0.09 bg=0.01
intrinsic component of membrane GO:0031224 p=1.1E−02 n=11 fg=0.31 bg=0.15
U2−type catalytic step 1 spliceosome GO:0071006 p=1.3E−02 n=1 fg=0.03 bg=0.00
catalytic step 1 spliceosome GO:0071012 p=1.3E−02 n=1 fg=0.03 bg=0.00
COP9 signalosome GO:0008180 p=2.6E−02 n=1 fg=0.03 bg=0.00
axonemal central apparatus GO:1990716 p=2.6E−02 n=1 fg=0.03 bg=0.00
dendritic spine neck GO:0044326 p=2.6E−02 n=1 fg=0.03 bg=0.00
growth cone filopodium GO:1990812 p=2.6E−02 n=1 fg=0.03 bg=0.00
F−actin capping protein complex GO:0008290 p=2.6E−02 n=1 fg=0.03 bg=0.00
transmembrane transporter complex GO:1902495 p=2.6E−02 n=3 fg=0.09 bg=0.02
transporter complex GO:1990351 p=3.2E−02 n=3 fg=0.09 bg=0.02
endolysosome membrane GO:0036020 p=3.8E−02 n=1 fg=0.03 bg=0.00
endolysosome GO:0036019 p=3.8E−02 n=1 fg=0.03 bg=0.00
extrinsic component of endoplasmic retic... GO:0042406 p=3.8E−02 n=1 fg=0.03 bg=0.00
ciliary rootlet GO:0035253 p=3.8E−02 n=1 fg=0.03 bg=0.00
membrane GO:0016020 p=4.1E−02 n=20 fg=0.57 bg=0.41
growth cone lamellipodium GO:1990761 p=5.1E−02 n=1 fg=0.03 bg=0.00
inner dynein arm GO:0036156 p=5.1E−02 n=1 fg=0.03 bg=0.00
integral component of membrane GO:0016021 p=5.5E−02 n=9 fg=0.26 bg=0.14
ion channel complex GO:0034702 p=5.7E−02 n=2 fg=0.06 bg=0.01
Prp19 complex GO:0000974 p=6.3E−02 n=1 fg=0.03 bg=0.00
vacuolar lumen GO:0005775 p=6.4E−02 n=2 fg=0.06 bg=0.01
membrane raft GO:0045121 p=6.7E−02 n=3 fg=0.09 bg=0.03
membrane microdomain GO:0098857 p=6.7E−02 n=3 fg=0.09 bg=0.03
axoneme GO:0005930 p=7.1E−02 n=2 fg=0.06 bg=0.01
sarcoplasmic reticulum membrane GO:0033017 p=7.5E−02 n=1 fg=0.03 bg=0.00
axon GO:0030424 p=7.8E−02 n=5 fg=0.14 bg=0.07
axonemal dynein complex GO:0005858 p=8.7E−02 n=1 fg=0.03 bg=0.00
U2−type catalytic step 2 spliceosome GO:0071007 p=9.9E−02 n=1 fg=0.03 bg=0.00
cytoplasmic side of endoplasmic reticulu... GO:0098554 p=9.9E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=35/138 input genes with annotations
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fraction