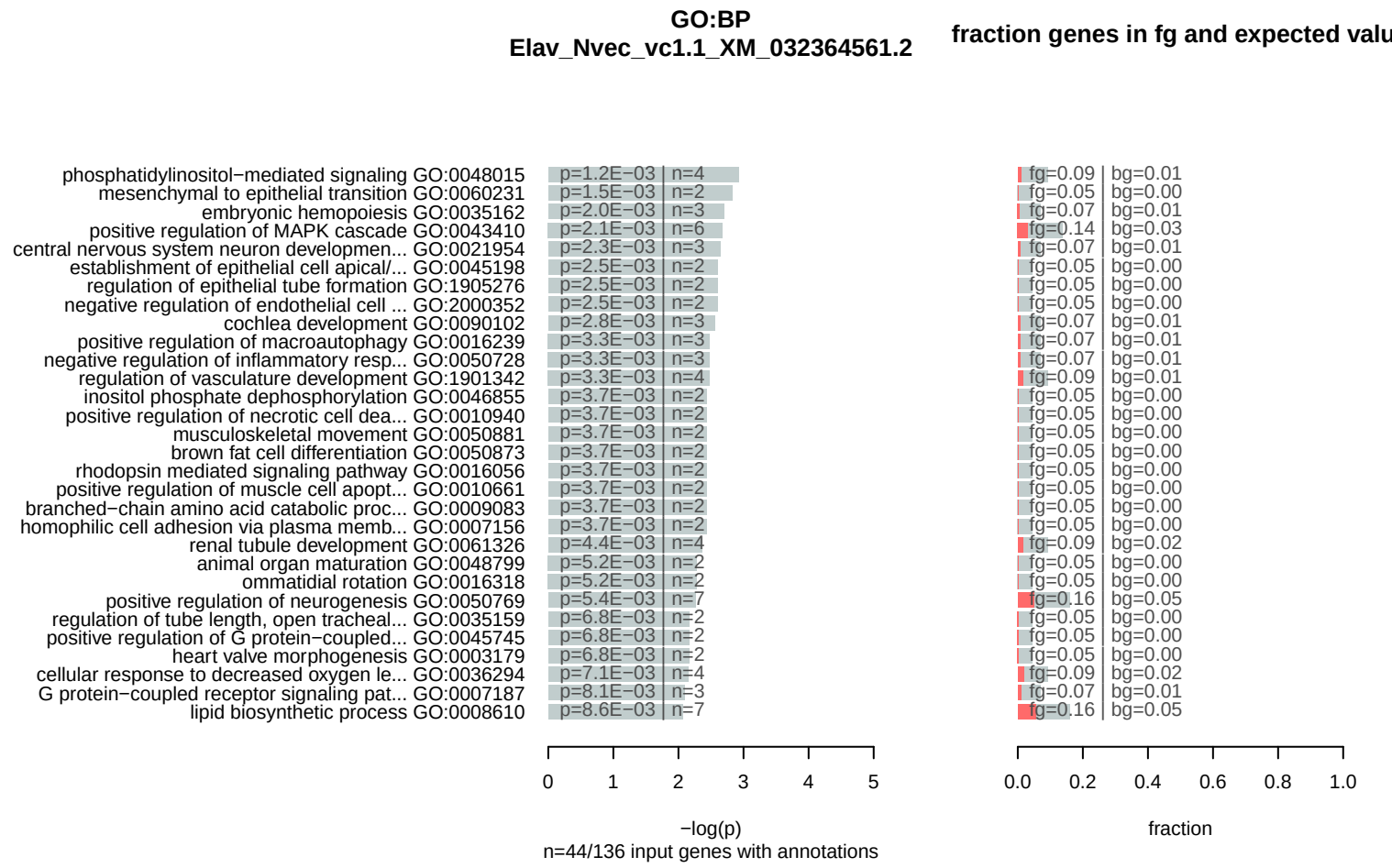
GO:BP
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fraction genes in fg and expected valu
phosphatidylinositol−mediated signaling GO:0048015 p=1.2E−03 n=4 fg=0.09 bg=0.01
mesenchymal to epithelial transition GO:0060231 p=1.5E−03 n=2 fg=0.05 bg=0.00
embryonic hemopoiesis GO:0035162 p=2.0E−03 n=3 fg=0.07 bg=0.01
positive regulation of MAPK cascade GO:0043410 p=2.1E−03 n=6 fg=0.14 bg=0.03
central nervous system neuron developmen... GO:0021954 p=2.3E−03 n=3 fg=0.07 bg=0.01
establishment of epithelial cell apical/... GO:0045198 p=2.5E−03 n=2 fg=0.05 bg=0.00
regulation of epithelial tube formation GO:1905276 p=2.5E−03 n=2 fg=0.05 bg=0.00
negative regulation of endothelial cell ... GO:2000352 p=2.5E−03 n=2 fg=0.05 bg=0.00
cochlea development GO:0090102 p=2.8E−03 n=3 fg=0.07 bg=0.01
positive regulation of macroautophagy GO:0016239 p=3.3E−03 n=3 fg=0.07 bg=0.01
negative regulation of inflammatory resp... GO:0050728 p=3.3E−03 n=3 fg=0.07 bg=0.01
regulation of vasculature development GO:1901342 p=3.3E−03 n=4 fg=0.09 bg=0.01
inositol phosphate dephosphorylation GO:0046855 p=3.7E−03 n=2 fg=0.05 bg=0.00
positive regulation of necrotic cell dea... GO:0010940 p=3.7E−03 n=2 fg=0.05 bg=0.00
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brown fat cell differentiation GO:0050873 p=3.7E−03 n=2 fg=0.05 bg=0.00
rhodopsin mediated signaling pathway GO:0016056 p=3.7E−03 n=2 fg=0.05 bg=0.00
positive regulation of muscle cell apopt... GO:0010661 p=3.7E−03 n=2 fg=0.05 bg=0.00
branched−chain amino acid catabolic proc... GO:0009083 p=3.7E−03 n=2 fg=0.05 bg=0.00
homophilic cell adhesion via plasma memb... GO:0007156 p=3.7E−03 n=2 fg=0.05 bg=0.00
renal tubule development GO:0061326 p=4.4E−03 n=4 fg=0.09 bg=0.02
animal organ maturation GO:0048799 p=5.2E−03 n=2 fg=0.05 bg=0.00
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positive regulation of neurogenesis GO:0050769 p=5.4E−03 n=7 fg=0.16 bg=0.05
regulation of tube length, open tracheal... GO:0035159 p=6.8E−03 n=2 fg=0.05 bg=0.00
positive regulation of G protein−coupled... GO:0045745 p=6.8E−03 n=2 fg=0.05 bg=0.00
heart valve morphogenesis GO:0003179 p=6.8E−03 n=2 fg=0.05 bg=0.00
cellular response to decreased oxygen le... GO:0036294 p=7.1E−03 n=4 fg=0.09 bg=0.02
G protein−coupled receptor signaling pat... GO:0007187 p=8.1E−03 n=3 fg=0.07 bg=0.01
lipid biosynthetic process GO:0008610 p=8.6E−03 n=7 fg=0.16 bg=0.05
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fraction
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Elav_Nvec_vc1.1_XM_032364561.2
fraction genes in fg and expected valu
phosphatidylinositol−3,5−bisphosphate 3−... GO:0052629 p=7.4E−04 n=2 fg=0.05 bg=0.00
ammonium ion binding GO:0070405 p=9.8E−04 n=3 fg=0.08 bg=0.01
protein homodimerization activity GO:0042803 p=2.4E−03 n=10 fg=0.26 bg=0.10
phosphatidylinositol−3−phosphatase activ... GO:0004438 p=2.4E−03 n=2 fg=0.05 bg=0.00
inositol phosphate phosphatase activity GO:0052745 p=5.0E−03 n=2 fg=0.05 bg=0.00
phosphatidylcholine binding GO:0031210 p=5.0E−03 n=2 fg=0.05 bg=0.00
metal ion transmembrane transporter acti... GO:0046873 p=9.9E−03 n=5 fg=0.13 bg=0.04
estradiol 17−beta−dehydrogenase activity GO:0004303 p=1.6E−02 n=1 fg=0.03 bg=0.00
[3−methyl−2−oxobutanoate dehydrogenase (... GO:0047323 p=1.6E−02 n=1 fg=0.03 bg=0.00
interleukin−2 receptor binding GO:0005134 p=1.6E−02 n=1 fg=0.03 bg=0.00
C−acyltransferase activity GO:0016408 p=1.6E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol−3,5−bisphosphate 5−... GO:0043813 p=1.6E−02 n=1 fg=0.03 bg=0.00
long−chain fatty acid transporter activi... GO:0005324 p=1.6E−02 n=1 fg=0.03 bg=0.00
aminomethyltransferase activity GO:0004047 p=1.6E−02 n=1 fg=0.03 bg=0.00
dopamine binding GO:0035240 p=1.6E−02 n=1 fg=0.03 bg=0.00
semaphorin receptor binding GO:0030215 p=1.6E−02 n=1 fg=0.03 bg=0.00
light−activated ion channel activity GO:0010461 p=1.6E−02 n=1 fg=0.03 bg=0.00
acetyl−CoA C−acetyltransferase activity GO:0003985 p=1.6E−02 n=1 fg=0.03 bg=0.00
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EH domain binding GO:1990175 p=1.6E−02 n=1 fg=0.03 bg=0.00
ribokinase activity GO:0004747 p=1.6E−02 n=1 fg=0.03 bg=0.00
testosterone 17−beta−dehydrogenase (NADP... GO:0047045 p=1.6E−02 n=1 fg=0.03 bg=0.00
bradykinin receptor binding GO:0031711 p=1.6E−02 n=1 fg=0.03 bg=0.00
B2 bradykinin receptor binding GO:0031713 p=1.6E−02 n=1 fg=0.03 bg=0.00
C−acetyltransferase activity GO:0016453 p=1.6E−02 n=1 fg=0.03 bg=0.00
phosphatidylcholine transporter activity GO:0008525 p=1.6E−02 n=1 fg=0.03 bg=0.00
beta1−adrenergic receptor activity GO:0004940 p=1.6E−02 n=1 fg=0.03 bg=0.00
beta2−adrenergic receptor activity GO:0004941 p=1.6E−02 n=1 fg=0.03 bg=0.00
beta−adrenergic receptor activity GO:0004939 p=1.6E−02 n=1 fg=0.03 bg=0.00
tRNA 2'−phosphotransferase activity GO:0000215 p=1.6E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=38/136 input genes with annotations
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fraction
GO:CC
Elav_Nvec_vc1.1_XM_032364561.2
fraction genes in fg and expected valu
rhabdomere GO:0016028 p=9.4E−03 n=2 fg=0.05 bg=0.00
Cul4−RING E3 ubiquitin ligase complex GO:0080008 p=9.4E−03 n=2 fg=0.05 bg=0.00
rhabdomere membrane GO:0033583 p=1.5E−02 n=1 fg=0.02 bg=0.00
cytoplasmic periphery of the nuclear por... GO:1990723 p=1.5E−02 n=1 fg=0.02 bg=0.00
rhabdomere microvillus GO:0035996 p=1.5E−02 n=1 fg=0.02 bg=0.00
rhabdomere microvillus membrane GO:0035997 p=1.5E−02 n=1 fg=0.02 bg=0.00
nuclear pore cytoplasmic filaments GO:0044614 p=1.5E−02 n=1 fg=0.02 bg=0.00
clathrin−coated vesicle membrane GO:0030665 p=2.6E−02 n=2 fg=0.05 bg=0.01
mitochondrial alpha−ketoglutarate dehydr... GO:0005947 p=3.0E−02 n=1 fg=0.02 bg=0.00
glycine cleavage complex GO:0005960 p=3.0E−02 n=1 fg=0.02 bg=0.00
Seh1−associated complex GO:0035859 p=3.0E−02 n=1 fg=0.02 bg=0.00
dihydrolipoyl dehydrogenase complex GO:0045240 p=3.0E−02 n=1 fg=0.02 bg=0.00
Wnt signalosome GO:1990909 p=3.0E−02 n=1 fg=0.02 bg=0.00
growth cone filopodium GO:1990812 p=3.0E−02 n=1 fg=0.02 bg=0.00
GATOR2 complex GO:0061700 p=3.0E−02 n=1 fg=0.02 bg=0.00
nuclear envelope GO:0005635 p=3.6E−02 n=5 fg=0.12 bg=0.05
actin−based cell projection GO:0098858 p=4.1E−02 n=3 fg=0.07 bg=0.02
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filopodium GO:0030175 p=4.3E−02 n=2 fg=0.05 bg=0.01
intercalary heterochromatin GO:0005725 p=4.5E−02 n=1 fg=0.02 bg=0.00
glycogen granule GO:0042587 p=4.5E−02 n=1 fg=0.02 bg=0.00
PRC1 complex GO:0035102 p=4.5E−02 n=1 fg=0.02 bg=0.00
subrhabdomeral cisterna GO:0016029 p=4.5E−02 n=1 fg=0.02 bg=0.00
mitochondrial tricarboxylic acid cycle e... GO:0030062 p=4.5E−02 n=1 fg=0.02 bg=0.00
endoplasmic reticulum cisternal network GO:0071781 p=4.5E−02 n=1 fg=0.02 bg=0.00
smooth endoplasmic reticulum cisterna GO:0120082 p=4.5E−02 n=1 fg=0.02 bg=0.00
tricarboxylic acid cycle enzyme complex GO:0045239 p=4.5E−02 n=1 fg=0.02 bg=0.00
RSC−type complex GO:0016586 p=4.5E−02 n=1 fg=0.02 bg=0.00
neuron projection GO:0043005 p=4.6E−02 n=9 fg=0.22 bg=0.12
motile cilium GO:0031514 p=4.9E−02 n=3 fg=0.07 bg=0.02
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−log(p)
n=41/136 input genes with annotations
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fraction