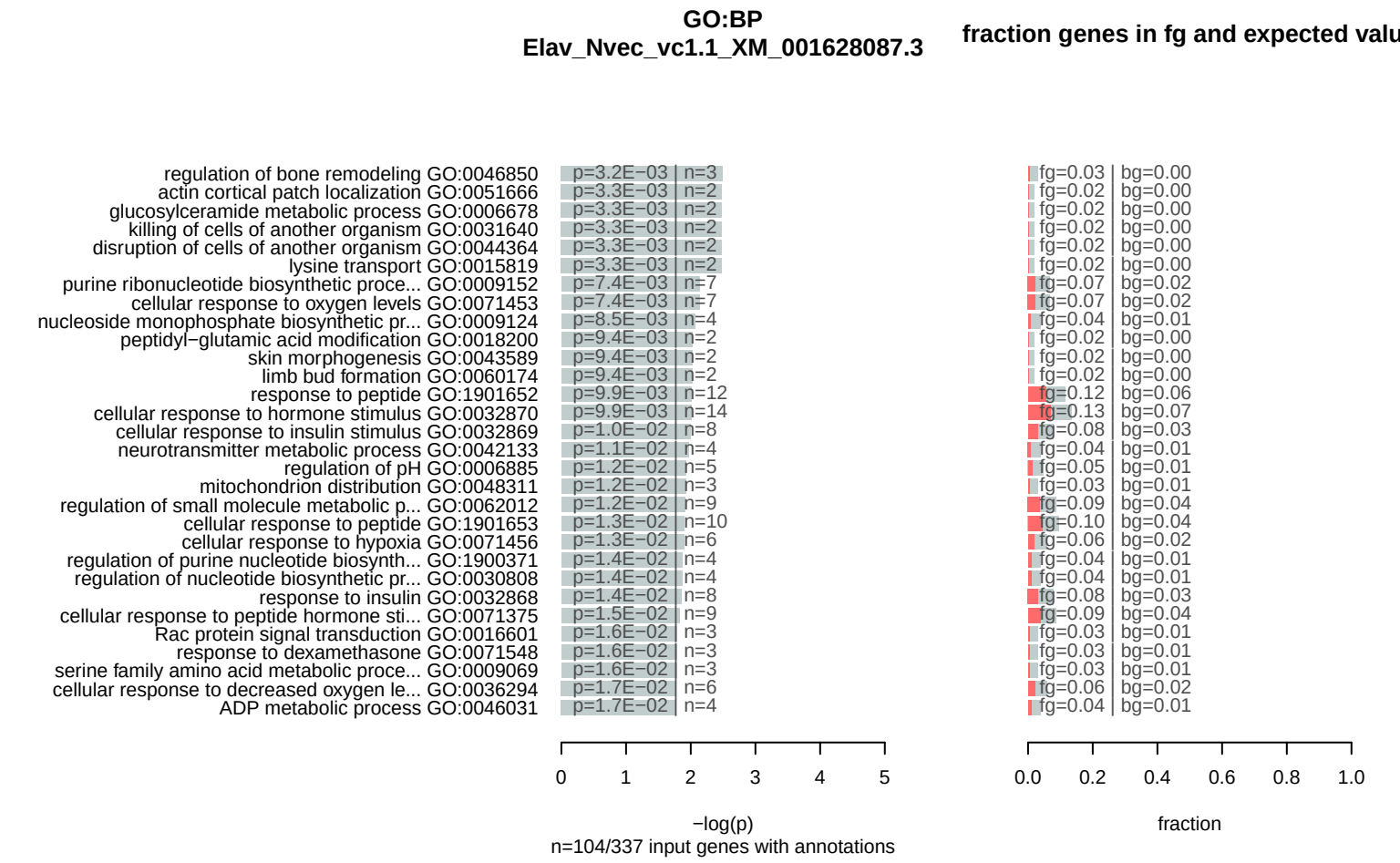
GO:BP
Elav_Nvec_vc1.1_XM_001628087.3
fraction genes in fg and expected valu
regulation of bone remodeling GO:0046850 p=3.2E−03 n=3 fg=0.03 bg=0.00
actin cortical patch localization GO:0051666 p=3.3E−03 n=2 fg=0.02 bg=0.00
glucosylceramide metabolic process GO:0006678 p=3.3E−03 n=2 fg=0.02 bg=0.00
killing of cells of another organism GO:0031640 p=3.3E−03 n=2 fg=0.02 bg=0.00
disruption of cells of another organism GO:0044364 p=3.3E−03 n=2 fg=0.02 bg=0.00
lysine transport GO:0015819 p=3.3E−03 n=2 fg=0.02 bg=0.00
purine ribonucleotide biosynthetic proce... GO:0009152 p=7.4E−03 n=7 fg=0.07 bg=0.02
cellular response to oxygen levels GO:0071453 p=7.4E−03 n=7 fg=0.07 bg=0.02
nucleoside monophosphate biosynthetic pr... GO:0009124 p=8.5E−03 n=4 fg=0.04 bg=0.01
peptidyl−glutamic acid modification GO:0018200 p=9.4E−03 n=2 fg=0.02 bg=0.00
skin morphogenesis GO:0043589 p=9.4E−03 n=2 fg=0.02 bg=0.00
limb bud formation GO:0060174 p=9.4E−03 n=2 fg=0.02 bg=0.00
response to peptide GO:1901652 p=9.9E−03 n=12 fg=0.12 bg=0.06
cellular response to hormone stimulus GO:0032870 p=9.9E−03 n=14 fg=0.13 bg=0.07
cellular response to insulin stimulus GO:0032869 p=1.0E−02 n=8 fg=0.08 bg=0.03
neurotransmitter metabolic process GO:0042133 p=1.1E−02 n=4 fg=0.04 bg=0.01
regulation of pH GO:0006885 p=1.2E−02 n=5 fg=0.05 bg=0.01
mitochondrion distribution GO:0048311 p=1.2E−02 n=3 fg=0.03 bg=0.01
regulation of small molecule metabolic p... GO:0062012 p=1.2E−02 n=9 fg=0.09 bg=0.04
cellular response to peptide GO:1901653 p=1.3E−02 n=10 fg=0.10 bg=0.04
cellular response to hypoxia GO:0071456 p=1.3E−02 n=6 fg=0.06 bg=0.02
regulation of purine nucleotide biosynth... GO:1900371 p=1.4E−02 n=4 fg=0.04 bg=0.01
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response to insulin GO:0032868 p=1.4E−02 n=8 fg=0.08 bg=0.03
cellular response to peptide hormone sti... GO:0071375 p=1.5E−02 n=9 fg=0.09 bg=0.04
Rac protein signal transduction GO:0016601 p=1.6E−02 n=3 fg=0.03 bg=0.01
response to dexamethasone GO:0071548 p=1.6E−02 n=3 fg=0.03 bg=0.01
serine family amino acid metabolic proce... GO:0009069 p=1.6E−02 n=3 fg=0.03 bg=0.01
cellular response to decreased oxygen le... GO:0036294 p=1.7E−02 n=6 fg=0.06 bg=0.02
ADP metabolic process GO:0046031 p=1.7E−02 n=4 fg=0.04 bg=0.01
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n=104/337 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_001628087.3
fraction genes in fg and expected valu
RNA binding GO:0003723 p=5.3E−03 n=16 fg=0.17 bg=0.09
tau protein binding GO:0048156 p=9.5E−03 n=2 fg=0.02 bg=0.00
deaminase activity GO:0019239 p=9.5E−03 n=2 fg=0.02 bg=0.00
O−acyltransferase activity GO:0008374 p=1.8E−02 n=2 fg=0.02 bg=0.00
hydrolase activity, acting on carbon−nit... GO:0016814 p=1.8E−02 n=2 fg=0.02 bg=0.00
mRNA binding GO:0003729 p=2.0E−02 n=7 fg=0.08 bg=0.03
proline−rich region binding GO:0070064 p=2.9E−02 n=2 fg=0.02 bg=0.00
phosphatidylinositol−3−phosphate binding GO:0032266 p=2.9E−02 n=2 fg=0.02 bg=0.00
DNA binding GO:0003677 p=3.1E−02 n=17 fg=0.18 bg=0.12
carboxy−lyase activity GO:0016831 p=4.3E−02 n=2 fg=0.02 bg=0.00
transcription regulatory region nucleic ... GO:0001067 p=5.1E−02 n=10 fg=0.11 bg=0.06
oxidoreductase activity, acting on CH−OH... GO:0016614 p=5.1E−02 n=3 fg=0.03 bg=0.01
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=5.8E−02 n=1 fg=0.01 bg=0.00
glyceraldehyde−3−phosphate dehydrogenase... GO:0004365 p=5.8E−02 n=1 fg=0.01 bg=0.00
glycerol−3−phosphate O−acyltransferase a... GO:0004366 p=5.8E−02 n=1 fg=0.01 bg=0.00
protein N−acetylglucosaminyltransferase ... GO:0016262 p=5.8E−02 n=1 fg=0.01 bg=0.00
testosterone 17−beta−dehydrogenase (NADP... GO:0047045 p=5.8E−02 n=1 fg=0.01 bg=0.00
tyrosyl−RNA phosphodiesterase activity GO:0036317 p=5.8E−02 n=1 fg=0.01 bg=0.00
poly(G) binding GO:0034046 p=5.8E−02 n=1 fg=0.01 bg=0.00
sialyltransferase activity GO:0008373 p=5.8E−02 n=1 fg=0.01 bg=0.00
regulatory region RNA binding GO:0001069 p=5.8E−02 n=1 fg=0.01 bg=0.00
steroid dehydrogenase activity GO:0016229 p=5.8E−02 n=1 fg=0.01 bg=0.00
RNA−3'−phosphate cyclase activity GO:0003963 p=5.8E−02 n=1 fg=0.01 bg=0.00
steroid dehydrogenase activity, acting o... GO:0033764 p=5.8E−02 n=1 fg=0.01 bg=0.00
ATP−dependent NAD(P)H−hydrate dehydratas... GO:0047453 p=5.8E−02 n=1 fg=0.01 bg=0.00
choline dehydrogenase activity GO:0008812 p=5.8E−02 n=1 fg=0.01 bg=0.00
amidophosphoribosyltransferase activity GO:0004044 p=5.8E−02 n=1 fg=0.01 bg=0.00
thiosulfate sulfurtransferase activity GO:0004792 p=5.8E−02 n=1 fg=0.01 bg=0.00
estradiol 17−beta−dehydrogenase activity GO:0004303 p=5.8E−02 n=1 fg=0.01 bg=0.00
acid−sensing ion channel activity GO:0044736 p=5.8E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=92/337 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001628087.3
fraction genes in fg and expected valu
dendritic spine membrane GO:0032591 p=9.6E−03 n=2 fg=0.02 bg=0.00
growth cone lamellipodium GO:1990761 p=9.6E−03 n=2 fg=0.02 bg=0.00
filopodium GO:0030175 p=1.1E−02 n=4 fg=0.04 bg=0.01
nucleolus GO:0005730 p=1.8E−02 n=14 fg=0.13 bg=0.07
fungal−type vacuole GO:0000324 p=1.8E−02 n=2 fg=0.02 bg=0.00
fungal−type vacuole membrane GO:0000329 p=1.8E−02 n=2 fg=0.02 bg=0.00
cell tip GO:0051286 p=1.8E−02 n=2 fg=0.02 bg=0.00
lipid droplet GO:0005811 p=2.1E−02 n=4 fg=0.04 bg=0.01
endoplasmic reticulum membrane GO:0005789 p=2.6E−02 n=14 fg=0.13 bg=0.08
intrinsic component of endoplasmic retic... GO:0031227 p=2.8E−02 n=6 fg=0.06 bg=0.02
integral component of endoplasmic reticu... GO:0030176 p=2.8E−02 n=6 fg=0.06 bg=0.02
intercellular bridge GO:0045171 p=2.9E−02 n=3 fg=0.03 bg=0.01
nuclear outer membrane−endoplasmic retic... GO:0042175 p=2.9E−02 n=14 fg=0.13 bg=0.08
storage vacuole GO:0000322 p=3.0E−02 n=2 fg=0.02 bg=0.00
sperm principal piece GO:0097228 p=3.0E−02 n=2 fg=0.02 bg=0.00
cell pole GO:0060187 p=3.0E−02 n=2 fg=0.02 bg=0.00
endoplasmic reticulum subcompartment GO:0098827 p=3.5E−02 n=14 fg=0.13 bg=0.08
A band GO:0031672 p=3.5E−02 n=3 fg=0.03 bg=0.01
cytoplasmic side of membrane GO:0098562 p=5.1E−02 n=6 fg=0.06 bg=0.03
lytic vacuole membrane GO:0098852 p=5.1E−02 n=6 fg=0.06 bg=0.03
cell division site GO:0032153 p=5.2E−02 n=3 fg=0.03 bg=0.01
Z disc GO:0030018 p=5.3E−02 n=4 fg=0.04 bg=0.01
extrinsic component of mitochondrial inn... GO:0031314 p=5.8E−02 n=1 fg=0.01 bg=0.00
transcription export complex GO:0000346 p=5.8E−02 n=1 fg=0.01 bg=0.00
THO complex GO:0000347 p=5.8E−02 n=1 fg=0.01 bg=0.00
H zone GO:0031673 p=5.8E−02 n=1 fg=0.01 bg=0.00
septin filament array GO:0032160 p=5.8E−02 n=1 fg=0.01 bg=0.00
RNA polymerase transcription factor SL1 ... GO:0005668 p=5.8E−02 n=1 fg=0.01 bg=0.00
RNA polymerase I transcription regulator... GO:0000120 p=5.8E−02 n=1 fg=0.01 bg=0.00
mitochondrial pyruvate dehydrogenase com... GO:0005967 p=5.8E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=105/337 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction