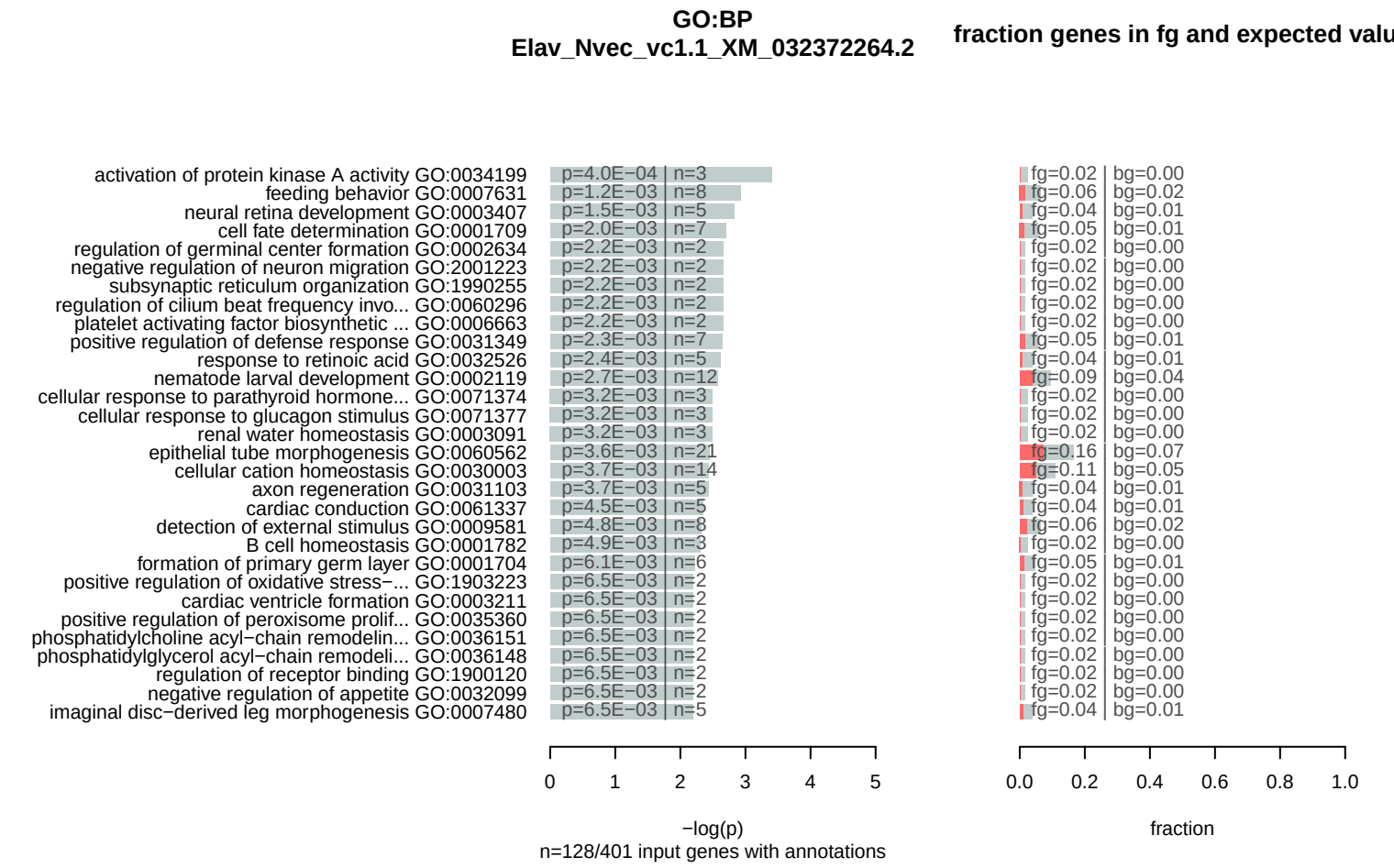
GO:BP
Elav_Nvec_vc1.1_XM_032372264.2
fraction genes in fg and expected valu
activation of protein kinase A activity GO:0034199 p=4.0E−04 n=3 fg=0.02 bg=0.00
feeding behavior GO:0007631 p=1.2E−03 n=8 fg=0.06 bg=0.02
neural retina development GO:0003407 p=1.5E−03 n=5 fg=0.04 bg=0.01
cell fate determination GO:0001709 p=2.0E−03 n=7 fg=0.05 bg=0.01
regulation of germinal center formation GO:0002634 p=2.2E−03 n=2 fg=0.02 bg=0.00
negative regulation of neuron migration GO:2001223 p=2.2E−03 n=2 fg=0.02 bg=0.00
subsynaptic reticulum organization GO:1990255 p=2.2E−03 n=2 fg=0.02 bg=0.00
regulation of cilium beat frequency invo... GO:0060296 p=2.2E−03 n=2 fg=0.02 bg=0.00
platelet activating factor biosynthetic ... GO:0006663 p=2.2E−03 n=2 fg=0.02 bg=0.00
positive regulation of defense response GO:0031349 p=2.3E−03 n=7 fg=0.05 bg=0.01
response to retinoic acid GO:0032526 p=2.4E−03 n=5 fg=0.04 bg=0.01
nematode larval development GO:0002119 p=2.7E−03 n=12 fg=0.09 bg=0.04
cellular response to parathyroid hormone... GO:0071374 p=3.2E−03 n=3 fg=0.02 bg=0.00
cellular response to glucagon stimulus GO:0071377 p=3.2E−03 n=3 fg=0.02 bg=0.00
renal water homeostasis GO:0003091 p=3.2E−03 n=3 fg=0.02 bg=0.00
epithelial tube morphogenesis GO:0060562 p=3.6E−03 n=21 fg=0.16 bg=0.07
cellular cation homeostasis GO:0030003 p=3.7E−03 n=14 fg=0.11 bg=0.05
axon regeneration GO:0031103 p=3.7E−03 n=5 fg=0.04 bg=0.01
cardiac conduction GO:0061337 p=4.5E−03 n=5 fg=0.04 bg=0.01
detection of external stimulus GO:0009581 p=4.8E−03 n=8 fg=0.06 bg=0.02
B cell homeostasis GO:0001782 p=4.9E−03 n=3 fg=0.02 bg=0.00
formation of primary germ layer GO:0001704 p=6.1E−03 n=6 fg=0.05 bg=0.01
positive regulation of oxidative stress−... GO:1903223 p=6.5E−03 n=2 fg=0.02 bg=0.00
cardiac ventricle formation GO:0003211 p=6.5E−03 n=2 fg=0.02 bg=0.00
positive regulation of peroxisome prolif... GO:0035360 p=6.5E−03 n=2 fg=0.02 bg=0.00
phosphatidylcholine acyl−chain remodelin... GO:0036151 p=6.5E−03 n=2 fg=0.02 bg=0.00
phosphatidylglycerol acyl−chain remodeli... GO:0036148 p=6.5E−03 n=2 fg=0.02 bg=0.00
regulation of receptor binding GO:1900120 p=6.5E−03 n=2 fg=0.02 bg=0.00
negative regulation of appetite GO:0032099 p=6.5E−03 n=2 fg=0.02 bg=0.00
imaginal disc−derived leg morphogenesis GO:0007480 p=6.5E−03 n=5 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=128/401 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032372264.2
fraction genes in fg and expected valu
protein kinase A regulatory subunit bind... GO:0034237 p=9.6E−04 n=3 fg=0.03 bg=0.00
protein domain specific binding GO:0019904 p=1.6E−03 n=19 fg=0.17 bg=0.08
1−alkylglycerophosphocholine O−acetyltra... GO:0047192 p=2.2E−03 n=2 fg=0.02 bg=0.00
ATPase−coupled cation transmembrane tran... GO:0019829 p=4.3E−03 n=4 fg=0.04 bg=0.01
ATPase−coupled ion transmembrane transpo... GO:0042625 p=5.5E−03 n=4 fg=0.04 bg=0.01
ubiquitin protein ligase binding GO:0031625 p=5.8E−03 n=10 fg=0.09 bg=0.04
1−acylglycerophosphocholine O−acyltransf... GO:0047184 p=6.4E−03 n=2 fg=0.02 bg=0.00
2−acylglycerol−3−phosphate O−acyltransfe... GO:0047144 p=6.4E−03 n=2 fg=0.02 bg=0.00
mRNA binding GO:0003729 p=7.8E−03 n=9 fg=0.08 bg=0.03
potassium channel activity GO:0005267 p=8.7E−03 n=4 fg=0.04 bg=0.01
carbohydrate derivative binding GO:0097367 p=1.2E−02 n=16 fg=0.14 bg=0.08
WW domain binding GO:0050699 p=1.2E−02 n=2 fg=0.02 bg=0.00
voltage−gated potassium channel activity GO:0005249 p=1.3E−02 n=3 fg=0.03 bg=0.00
ribonucleotide binding GO:0032553 p=1.4E−02 n=14 fg=0.12 bg=0.07
purine ribonucleotide binding GO:0032555 p=1.4E−02 n=14 fg=0.12 bg=0.07
purine nucleotide binding GO:0017076 p=1.9E−02 n=14 fg=0.12 bg=0.07
ephrin receptor binding GO:0046875 p=2.0E−02 n=2 fg=0.02 bg=0.00
P−type calcium transporter activity GO:0005388 p=2.0E−02 n=2 fg=0.02 bg=0.00
leak channel activity GO:0022840 p=2.0E−02 n=2 fg=0.02 bg=0.00
acetylcholine receptor binding GO:0033130 p=2.0E−02 n=2 fg=0.02 bg=0.00
potassium ion leak channel activity GO:0022841 p=2.0E−02 n=2 fg=0.02 bg=0.00
narrow pore channel activity GO:0022842 p=2.0E−02 n=2 fg=0.02 bg=0.00
phospholipid transporter activity GO:0005548 p=2.6E−02 n=3 fg=0.03 bg=0.01
E−box binding GO:0070888 p=2.6E−02 n=3 fg=0.03 bg=0.01
lipid transfer activity GO:0120013 p=2.9E−02 n=2 fg=0.02 bg=0.00
Wnt−protein binding GO:0017147 p=2.9E−02 n=2 fg=0.02 bg=0.00
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=2.9E−02 n=2 fg=0.02 bg=0.00
protein phosphatase 2B binding GO:0030346 p=2.9E−02 n=2 fg=0.02 bg=0.00
bicarbonate transmembrane transporter ac... GO:0015106 p=2.9E−02 n=2 fg=0.02 bg=0.00
tumor necrosis factor receptor binding GO:0005164 p=2.9E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=112/401 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032372264.2
fraction genes in fg and expected valu
plasma membrane GO:0005886 p=1.9E−03 n=44 fg=0.35 bg=0.23
growth cone filopodium GO:1990812 p=2.2E−03 n=2 fg=0.02 bg=0.00
dendritic spine GO:0043197 p=2.4E−03 n=8 fg=0.06 bg=0.02
cAMP−dependent protein kinase complex GO:0005952 p=6.3E−03 n=2 fg=0.02 bg=0.00
ciliary rootlet GO:0035253 p=6.3E−03 n=2 fg=0.02 bg=0.00
stress fiber GO:0001725 p=9.4E−03 n=3 fg=0.02 bg=0.00
nucleotide−activated protein kinase comp... GO:0031588 p=1.2E−02 n=2 fg=0.02 bg=0.00
growth cone lamellipodium GO:1990761 p=1.2E−02 n=2 fg=0.02 bg=0.00
neuromuscular junction GO:0031594 p=1.3E−02 n=6 fg=0.05 bg=0.02
lipid droplet GO:0005811 p=2.3E−02 n=4 fg=0.03 bg=0.01
intrinsic component of plasma membrane GO:0031226 p=2.4E−02 n=15 fg=0.12 bg=0.07
plasma membrane region GO:0098590 p=2.6E−02 n=17 fg=0.13 bg=0.08
integral component of plasma membrane GO:0005887 p=2.8E−02 n=14 fg=0.11 bg=0.06
secretory granule membrane GO:0030667 p=2.9E−02 n=6 fg=0.05 bg=0.02
intrinsic component of membrane GO:0031224 p=3.5E−02 n=27 fg=0.21 bg=0.15
lamellipodium GO:0030027 p=3.5E−02 n=6 fg=0.05 bg=0.02
germinal vesicle GO:0042585 p=3.9E−02 n=2 fg=0.02 bg=0.00
nuclear body GO:0016604 p=3.9E−02 n=13 fg=0.10 bg=0.06
host cell nucleus GO:0042025 p=4.7E−02 n=1 fg=0.01 bg=0.00
endosome to plasma membrane transport ve... GO:0070381 p=4.7E−02 n=1 fg=0.01 bg=0.00
lipoprotein particle GO:1990777 p=4.7E−02 n=1 fg=0.01 bg=0.00
host intracellular region GO:0043656 p=4.7E−02 n=1 fg=0.01 bg=0.00
host cell GO:0043657 p=4.7E−02 n=1 fg=0.01 bg=0.00
amyloid−beta complex GO:0106003 p=4.7E−02 n=1 fg=0.01 bg=0.00
septin collar GO:0032173 p=4.7E−02 n=1 fg=0.01 bg=0.00
host cell PML body GO:0075341 p=4.7E−02 n=1 fg=0.01 bg=0.00
host cellular component GO:0018995 p=4.7E−02 n=1 fg=0.01 bg=0.00
mitochondrial isocitrate dehydrogenase c... GO:0005962 p=4.7E−02 n=1 fg=0.01 bg=0.00
host cell part GO:0033643 p=4.7E−02 n=1 fg=0.01 bg=0.00
host intracellular part GO:0033646 p=4.7E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=126/401 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction