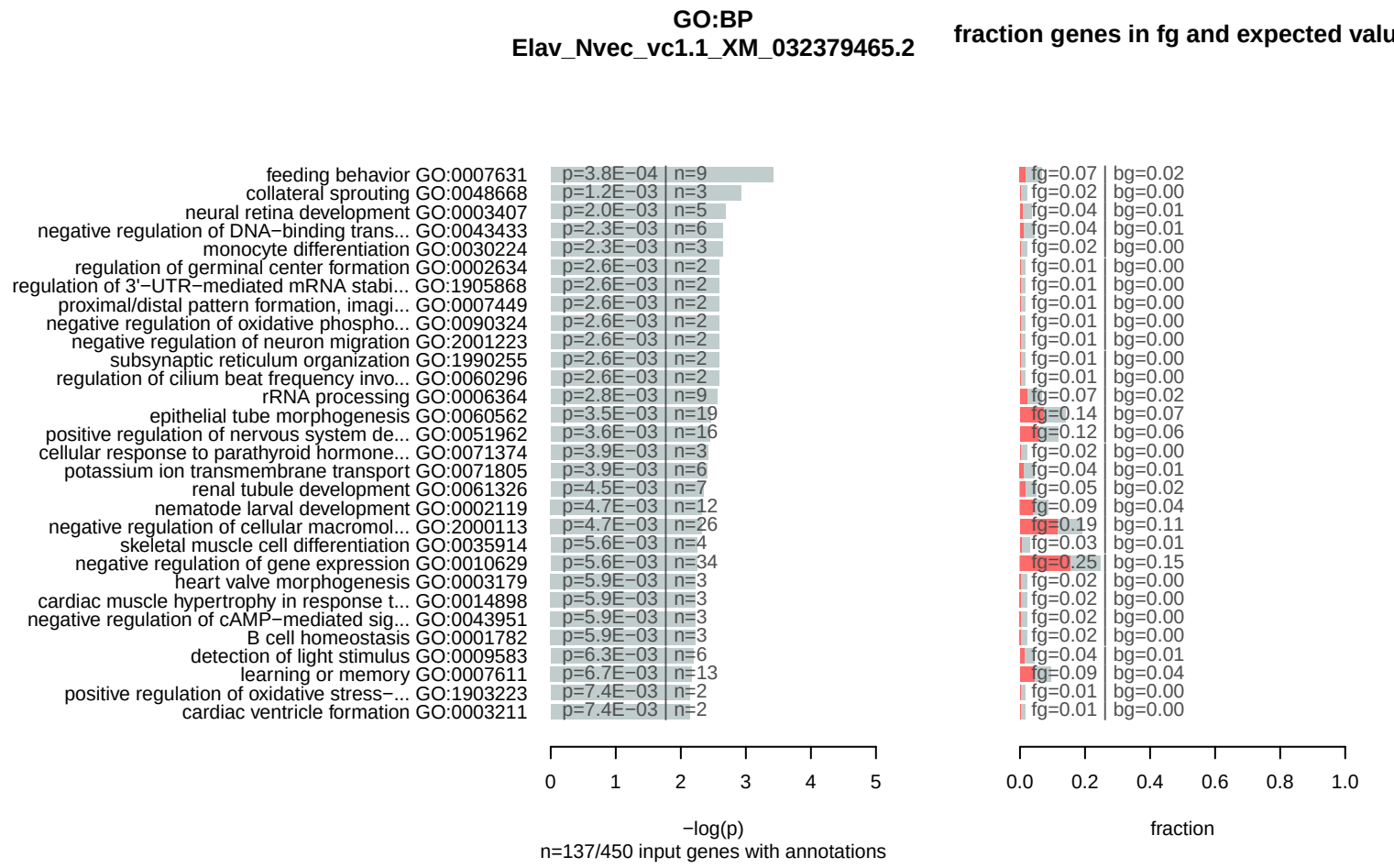
GO:BP
Elav_Nvec_vc1.1_XM_032379465.2
fraction genes in fg and expected valu
feeding behavior GO:0007631 p=3.8E−04 n=9 fg=0.07 bg=0.02
collateral sprouting GO:0048668 p=1.2E−03 n=3 fg=0.02 bg=0.00
neural retina development GO:0003407 p=2.0E−03 n=5 fg=0.04 bg=0.01
negative regulation of DNA−binding trans... GO:0043433 p=2.3E−03 n=6 fg=0.04 bg=0.01
monocyte differentiation GO:0030224 p=2.3E−03 n=3 fg=0.02 bg=0.00
regulation of germinal center formation GO:0002634 p=2.6E−03 n=2 fg=0.01 bg=0.00
regulation of 3'−UTR−mediated mRNA stabi... GO:1905868 p=2.6E−03 n=2 fg=0.01 bg=0.00
proximal/distal pattern formation, imagi... GO:0007449 p=2.6E−03 n=2 fg=0.01 bg=0.00
negative regulation of oxidative phospho... GO:0090324 p=2.6E−03 n=2 fg=0.01 bg=0.00
negative regulation of neuron migration GO:2001223 p=2.6E−03 n=2 fg=0.01 bg=0.00
subsynaptic reticulum organization GO:1990255 p=2.6E−03 n=2 fg=0.01 bg=0.00
regulation of cilium beat frequency invo... GO:0060296 p=2.6E−03 n=2 fg=0.01 bg=0.00
rRNA processing GO:0006364 p=2.8E−03 n=9 fg=0.07 bg=0.02
epithelial tube morphogenesis GO:0060562 p=3.5E−03 n=19 fg=0.14 bg=0.07
positive regulation of nervous system de... GO:0051962 p=3.6E−03 n=16 fg=0.12 bg=0.06
cellular response to parathyroid hormone... GO:0071374 p=3.9E−03 n=3 fg=0.02 bg=0.00
potassium ion transmembrane transport GO:0071805 p=3.9E−03 n=6 fg=0.04 bg=0.01
renal tubule development GO:0061326 p=4.5E−03 n=7 fg=0.05 bg=0.02
nematode larval development GO:0002119 p=4.7E−03 n=12 fg=0.09 bg=0.04
negative regulation of cellular macromol... GO:2000113 p=4.7E−03 n=26 fg=0.19 bg=0.11
skeletal muscle cell differentiation GO:0035914 p=5.6E−03 n=4 fg=0.03 bg=0.01
negative regulation of gene expression GO:0010629 p=5.6E−03 n=34 fg=0.25 bg=0.15
heart valve morphogenesis GO:0003179 p=5.9E−03 n=3 fg=0.02 bg=0.00
cardiac muscle hypertrophy in response t... GO:0014898 p=5.9E−03 n=3 fg=0.02 bg=0.00
negative regulation of cAMP−mediated sig... GO:0043951 p=5.9E−03 n=3 fg=0.02 bg=0.00
B cell homeostasis GO:0001782 p=5.9E−03 n=3 fg=0.02 bg=0.00
detection of light stimulus GO:0009583 p=6.3E−03 n=6 fg=0.04 bg=0.01
learning or memory GO:0007611 p=6.7E−03 n=13 fg=0.09 bg=0.04
positive regulation of oxidative stress−... GO:1903223 p=7.4E−03 n=2 fg=0.01 bg=0.00
cardiac ventricle formation GO:0003211 p=7.4E−03 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=137/450 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032379465.2
fraction genes in fg and expected valu
DNA−binding transcription factor activit... GO:0000981 p=6.1E−04 n=17 fg=0.14 bg=0.06
voltage−gated potassium channel activity GO:0005249 p=1.7E−03 n=4 fg=0.03 bg=0.00
ATPase−coupled cation transmembrane tran... GO:0019829 p=6.0E−03 n=4 fg=0.03 bg=0.01
ATPase−coupled ion transmembrane transpo... GO:0042625 p=7.7E−03 n=4 fg=0.03 bg=0.01
mRNA 3'−UTR binding GO:0003730 p=7.7E−03 n=4 fg=0.03 bg=0.01
miRNA binding GO:0035198 p=7.7E−03 n=2 fg=0.02 bg=0.00
mRNA regulatory element binding translat... GO:0000900 p=7.7E−03 n=2 fg=0.02 bg=0.00
snoRNA binding GO:0030515 p=9.1E−03 n=3 fg=0.02 bg=0.00
RNA polymerase II transcription regulato... GO:0000977 p=1.2E−02 n=11 fg=0.09 bg=0.04
DNA−binding transcription activator acti... GO:0001228 p=1.3E−02 n=9 fg=0.07 bg=0.03
DNA−binding transcription activator acti... GO:0001216 p=1.3E−02 n=9 fg=0.07 bg=0.03
cis−regulatory region sequence−specific ... GO:0000987 p=1.4E−02 n=9 fg=0.07 bg=0.03
RNA polymerase II cis−regulatory region ... GO:0000978 p=1.4E−02 n=9 fg=0.07 bg=0.03
cAMP binding GO:0030552 p=1.5E−02 n=2 fg=0.02 bg=0.00
bHLH transcription factor binding GO:0043425 p=1.5E−02 n=2 fg=0.02 bg=0.00
acetylcholine receptor binding GO:0033130 p=2.4E−02 n=2 fg=0.02 bg=0.00
leak channel activity GO:0022840 p=2.4E−02 n=2 fg=0.02 bg=0.00
potassium ion leak channel activity GO:0022841 p=2.4E−02 n=2 fg=0.02 bg=0.00
narrow pore channel activity GO:0022842 p=2.4E−02 n=2 fg=0.02 bg=0.00
cyclic nucleotide binding GO:0030551 p=2.4E−02 n=2 fg=0.02 bg=0.00
ephrin receptor binding GO:0046875 p=2.4E−02 n=2 fg=0.02 bg=0.00
P−type calcium transporter activity GO:0005388 p=2.4E−02 n=2 fg=0.02 bg=0.00
chemoattractant activity GO:0042056 p=2.4E−02 n=2 fg=0.02 bg=0.00
microtubule motor activity GO:0003777 p=2.7E−02 n=3 fg=0.02 bg=0.01
transcription cis−regulatory region bind... GO:0000976 p=2.8E−02 n=11 fg=0.09 bg=0.05
RNA methyltransferase activity GO:0008173 p=2.8E−02 n=4 fg=0.03 bg=0.01
catalytic activity, acting on RNA GO:0140098 p=3.2E−02 n=10 fg=0.08 bg=0.04
phospholipid transporter activity GO:0005548 p=3.3E−02 n=3 fg=0.02 bg=0.01
E−box binding GO:0070888 p=3.3E−02 n=3 fg=0.02 bg=0.01
O−methyltransferase activity GO:0008171 p=3.5E−02 n=2 fg=0.02 bg=0.00
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−log(p)
n=123/450 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032379465.2
fraction genes in fg and expected valu
voltage−gated potassium channel complex GO:0008076 p=1.0E−03 n=4 fg=0.03 bg=0.00
hippocampal mossy fiber GO:0097457 p=2.5E−03 n=2 fg=0.01 bg=0.00
growth cone filopodium GO:1990812 p=2.5E−03 n=2 fg=0.01 bg=0.00
actomyosin GO:0042641 p=8.8E−03 n=4 fg=0.03 bg=0.01
transcription repressor complex GO:0017053 p=1.1E−02 n=4 fg=0.03 bg=0.01
90S preribosome GO:0030686 p=1.2E−02 n=3 fg=0.02 bg=0.00
stress fiber GO:0001725 p=1.2E−02 n=3 fg=0.02 bg=0.00
contractile actin filament bundle GO:0097517 p=1.2E−02 n=3 fg=0.02 bg=0.00
neuron spine GO:0044309 p=1.4E−02 n=7 fg=0.05 bg=0.02
dendritic spine GO:0043197 p=1.4E−02 n=7 fg=0.05 bg=0.02
RNA polymerase II transcription represso... GO:0090571 p=1.4E−02 n=2 fg=0.01 bg=0.00
growth cone lamellipodium GO:1990761 p=1.4E−02 n=2 fg=0.01 bg=0.00
actin filament bundle GO:0032432 p=1.5E−02 n=3 fg=0.02 bg=0.00
nuclear body GO:0016604 p=1.6E−02 n=15 fg=0.11 bg=0.06
rough endoplasmic reticulum GO:0005791 p=2.2E−02 n=4 fg=0.03 bg=0.01
synapse GO:0045202 p=2.6E−02 n=18 fg=0.13 bg=0.08
cell junction GO:0030054 p=3.1E−02 n=23 fg=0.17 bg=0.11
sno(s)RNA−containing ribonucleoprotein c... GO:0005732 p=3.3E−02 n=2 fg=0.01 bg=0.00
dendrite GO:0030425 p=3.4E−02 n=14 fg=0.10 bg=0.06
dendritic tree GO:0097447 p=3.5E−02 n=14 fg=0.10 bg=0.06
somatodendritic compartment GO:0036477 p=3.8E−02 n=18 fg=0.13 bg=0.09
cell periphery GO:0071944 p=4.8E−02 n=46 fg=0.34 bg=0.25
host cell nucleus GO:0042025 p=5.0E−02 n=1 fg=0.01 bg=0.00
endosome to plasma membrane transport ve... GO:0070381 p=5.0E−02 n=1 fg=0.01 bg=0.00
lipoprotein particle GO:1990777 p=5.0E−02 n=1 fg=0.01 bg=0.00
host intracellular region GO:0043656 p=5.0E−02 n=1 fg=0.01 bg=0.00
host cell GO:0043657 p=5.0E−02 n=1 fg=0.01 bg=0.00
amyloid−beta complex GO:0106003 p=5.0E−02 n=1 fg=0.01 bg=0.00
AP−3 adaptor complex GO:0030123 p=5.0E−02 n=1 fg=0.01 bg=0.00
septin collar GO:0032173 p=5.0E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=136/450 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction