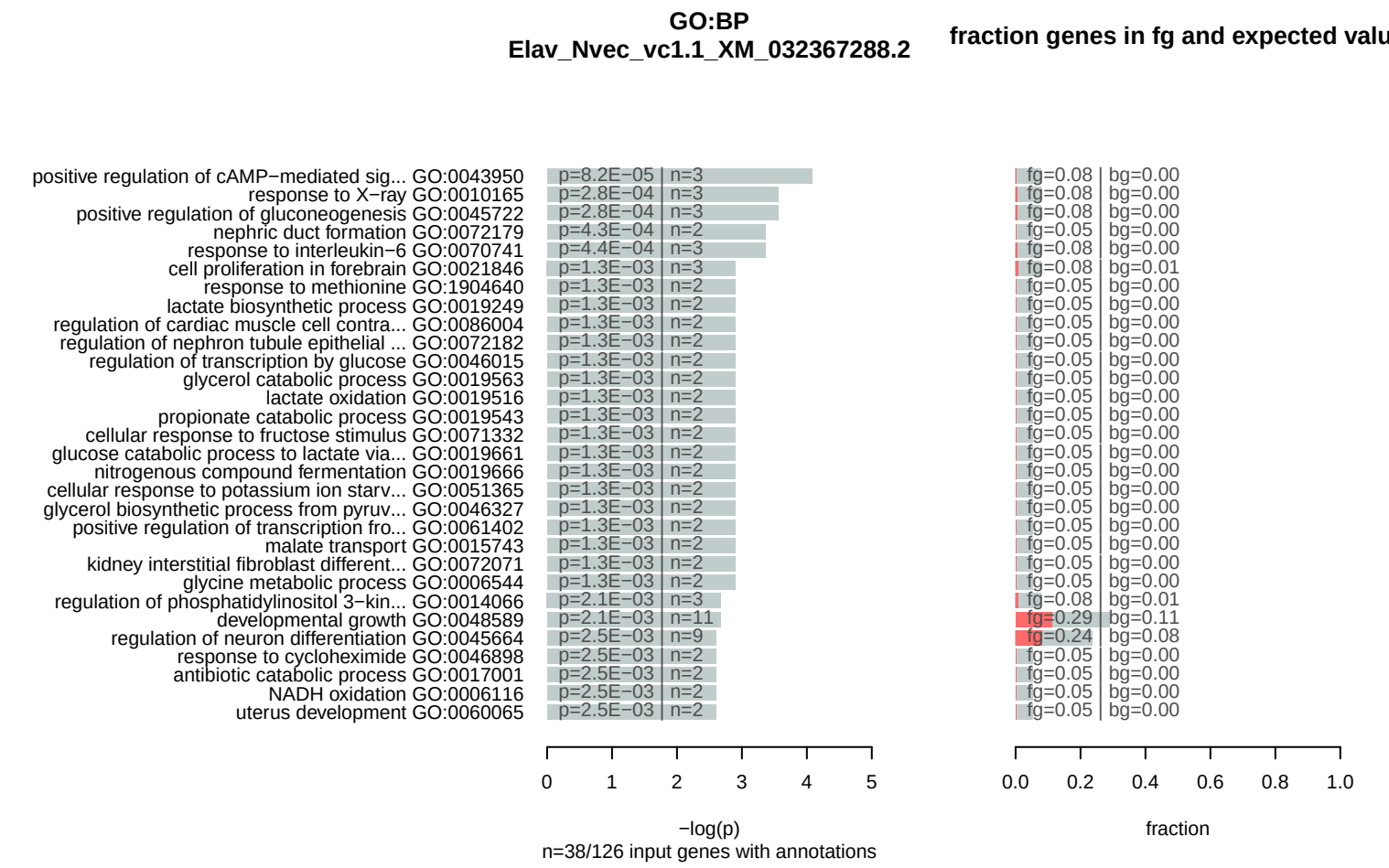
GO:BP
Elav_Nvec_vc1.1_XM_032367288.2
fraction genes in fg and expected valu
positive regulation of cAMP−mediated sig... GO:0043950 p=8.2E−05 n=3 fg=0.08 bg=0.00
response to X−ray GO:0010165 p=2.8E−04 n=3 fg=0.08 bg=0.00
positive regulation of gluconeogenesis GO:0045722 p=2.8E−04 n=3 fg=0.08 bg=0.00
nephric duct formation GO:0072179 p=4.3E−04 n=2 fg=0.05 bg=0.00
response to interleukin−6 GO:0070741 p=4.4E−04 n=3 fg=0.08 bg=0.00
cell proliferation in forebrain GO:0021846 p=1.3E−03 n=3 fg=0.08 bg=0.01
response to methionine GO:1904640 p=1.3E−03 n=2 fg=0.05 bg=0.00
lactate biosynthetic process GO:0019249 p=1.3E−03 n=2 fg=0.05 bg=0.00
regulation of cardiac muscle cell contra... GO:0086004 p=1.3E−03 n=2 fg=0.05 bg=0.00
regulation of nephron tubule epithelial ... GO:0072182 p=1.3E−03 n=2 fg=0.05 bg=0.00
regulation of transcription by glucose GO:0046015 p=1.3E−03 n=2 fg=0.05 bg=0.00
glycerol catabolic process GO:0019563 p=1.3E−03 n=2 fg=0.05 bg=0.00
lactate oxidation GO:0019516 p=1.3E−03 n=2 fg=0.05 bg=0.00
propionate catabolic process GO:0019543 p=1.3E−03 n=2 fg=0.05 bg=0.00
cellular response to fructose stimulus GO:0071332 p=1.3E−03 n=2 fg=0.05 bg=0.00
glucose catabolic process to lactate via... GO:0019661 p=1.3E−03 n=2 fg=0.05 bg=0.00
nitrogenous compound fermentation GO:0019666 p=1.3E−03 n=2 fg=0.05 bg=0.00
cellular response to potassium ion starv... GO:0051365 p=1.3E−03 n=2 fg=0.05 bg=0.00
glycerol biosynthetic process from pyruv... GO:0046327 p=1.3E−03 n=2 fg=0.05 bg=0.00
positive regulation of transcription fro... GO:0061402 p=1.3E−03 n=2 fg=0.05 bg=0.00
malate transport GO:0015743 p=1.3E−03 n=2 fg=0.05 bg=0.00
kidney interstitial fibroblast different... GO:0072071 p=1.3E−03 n=2 fg=0.05 bg=0.00
glycine metabolic process GO:0006544 p=1.3E−03 n=2 fg=0.05 bg=0.00
regulation of phosphatidylinositol 3−kin... GO:0014066 p=2.1E−03 n=3 fg=0.08 bg=0.01
developmental growth GO:0048589 p=2.1E−03 n=11 fg=0.29 bg=0.11
regulation of neuron differentiation GO:0045664 p=2.5E−03 n=9 fg=0.24 bg=0.08
response to cycloheximide GO:0046898 p=2.5E−03 n=2 fg=0.05 bg=0.00
antibiotic catabolic process GO:0017001 p=2.5E−03 n=2 fg=0.05 bg=0.00
NADH oxidation GO:0006116 p=2.5E−03 n=2 fg=0.05 bg=0.00
uterus development GO:0060065 p=2.5E−03 n=2 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=38/126 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032367288.2
fraction genes in fg and expected valu
epinephrine binding GO:0051379 p=8.7E−05 n=3 fg=0.09 bg=0.00
amyloid−beta binding GO:0001540 p=1.3E−03 n=3 fg=0.09 bg=0.01
phosphoenolpyruvate carboxykinase (GTP) ... GO:0004613 p=1.3E−03 n=2 fg=0.06 bg=0.00
lactate dehydrogenase activity GO:0004457 p=1.3E−03 n=2 fg=0.06 bg=0.00
inosine kinase activity GO:0008906 p=1.3E−03 n=2 fg=0.06 bg=0.00
DNA binding domain binding GO:0050692 p=1.3E−03 n=2 fg=0.06 bg=0.00
oxidoreductase activity, acting on the C... GO:0016899 p=1.3E−03 n=2 fg=0.06 bg=0.00
nucleoside diphosphate kinase activity GO:0004550 p=2.6E−03 n=2 fg=0.06 bg=0.00
manganese ion binding GO:0030145 p=3.4E−03 n=3 fg=0.09 bg=0.01
G protein−coupled amine receptor activit... GO:0008227 p=4.3E−03 n=2 fg=0.06 bg=0.00
HMG box domain binding GO:0071837 p=6.3E−03 n=2 fg=0.06 bg=0.00
protein−disulfide reductase (NAD(P)) act... GO:0047134 p=8.7E−03 n=2 fg=0.06 bg=0.00
protein domain specific binding GO:0019904 p=1.4E−02 n=11 fg=0.32 bg=0.09
E−box binding GO:0070888 p=1.5E−02 n=2 fg=0.06 bg=0.01
GDP binding GO:0019003 p=1.8E−02 n=2 fg=0.06 bg=0.01
retromer complex binding GO:1905394 p=2.1E−02 n=1 fg=0.03 bg=0.00
interleukin−2 receptor binding GO:0005134 p=2.1E−02 n=1 fg=0.03 bg=0.00
beta−endorphin binding GO:0031626 p=2.1E−02 n=1 fg=0.03 bg=0.00
dopamine binding GO:0035240 p=2.1E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol phosphate kinase ac... GO:0016307 p=2.1E−02 n=1 fg=0.03 bg=0.00
1−phosphatidylinositol−4−phosphate 5−kin... GO:0016308 p=2.1E−02 n=1 fg=0.03 bg=0.00
1−phosphatidylinositol−5−phosphate 4−kin... GO:0016309 p=2.1E−02 n=1 fg=0.03 bg=0.00
ATPase−coupled inorganic anion transmemb... GO:0043225 p=2.1E−02 n=1 fg=0.03 bg=0.00
1−phosphatidylinositol−3−phosphate 4−kin... GO:0052811 p=2.1E−02 n=1 fg=0.03 bg=0.00
bradykinin receptor binding GO:0031711 p=2.1E−02 n=1 fg=0.03 bg=0.00
B2 bradykinin receptor binding GO:0031713 p=2.1E−02 n=1 fg=0.03 bg=0.00
insulin binding GO:0043559 p=2.1E−02 n=1 fg=0.03 bg=0.00
beta1−adrenergic receptor activity GO:0004940 p=2.1E−02 n=1 fg=0.03 bg=0.00
beta2−adrenergic receptor activity GO:0004941 p=2.1E−02 n=1 fg=0.03 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=2.1E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=34/126 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032367288.2
fraction genes in fg and expected valu
dendritic spine GO:0043197 p=1.1E−03 n=5 fg=0.14 bg=0.02
growth cone lamellipodium GO:1990761 p=1.2E−03 n=2 fg=0.05 bg=0.00
magnesium−dependent protein serine/threo... GO:0005963 p=8.0E−03 n=2 fg=0.05 bg=0.00
sarcolemma GO:0042383 p=8.1E−03 n=3 fg=0.08 bg=0.01
contractile actin filament bundle GO:0097517 p=1.3E−02 n=2 fg=0.05 bg=0.00
stress fiber GO:0001725 p=1.3E−02 n=2 fg=0.05 bg=0.00
actin filament bundle GO:0032432 p=1.3E−02 n=2 fg=0.05 bg=0.00
axon GO:0030424 p=1.4E−02 n=9 fg=0.24 bg=0.08
T−tubule GO:0030315 p=1.7E−02 n=2 fg=0.05 bg=0.01
Ctf18 RFC−like complex GO:0031390 p=2.1E−02 n=1 fg=0.03 bg=0.00
Elg1 RFC−like complex GO:0031391 p=2.1E−02 n=1 fg=0.03 bg=0.00
retromer complex GO:0030904 p=2.1E−02 n=1 fg=0.03 bg=0.00
spectrin−associated cytoskeleton GO:0014731 p=2.1E−02 n=1 fg=0.03 bg=0.00
cytoplasmic side of dendritic spine plas... GO:1990780 p=2.1E−02 n=1 fg=0.03 bg=0.00
protein phosphatase 4 complex GO:0030289 p=2.1E−02 n=1 fg=0.03 bg=0.00
calcineurin complex GO:0005955 p=2.1E−02 n=1 fg=0.03 bg=0.00
DNA replication factor C complex GO:0005663 p=2.1E−02 n=1 fg=0.03 bg=0.00
septin collar GO:0032173 p=2.1E−02 n=1 fg=0.03 bg=0.00
dendritic spine neck GO:0044326 p=2.1E−02 n=1 fg=0.03 bg=0.00
dendritic spine head GO:0044327 p=2.1E−02 n=1 fg=0.03 bg=0.00
actomyosin GO:0042641 p=2.8E−02 n=2 fg=0.05 bg=0.01
focal adhesion GO:0005925 p=3.6E−02 n=2 fg=0.05 bg=0.01
axon initial segment GO:0043194 p=4.1E−02 n=1 fg=0.03 bg=0.00
node of Ranvier GO:0033268 p=4.1E−02 n=1 fg=0.03 bg=0.00
growth cone filopodium GO:1990812 p=4.1E−02 n=1 fg=0.03 bg=0.00
cytoplasmic cyclin−dependent protein kin... GO:0000308 p=4.1E−02 n=1 fg=0.03 bg=0.00
cell−cell contact zone GO:0044291 p=4.1E−02 n=2 fg=0.05 bg=0.01
main axon GO:0044304 p=4.1E−02 n=2 fg=0.05 bg=0.01
filopodium GO:0030175 p=4.1E−02 n=2 fg=0.05 bg=0.01
plasma membrane GO:0005886 p=4.1E−02 n=17 fg=0.46 bg=0.27
0 1 2 3 4 5
−log(p)
n=37/126 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction