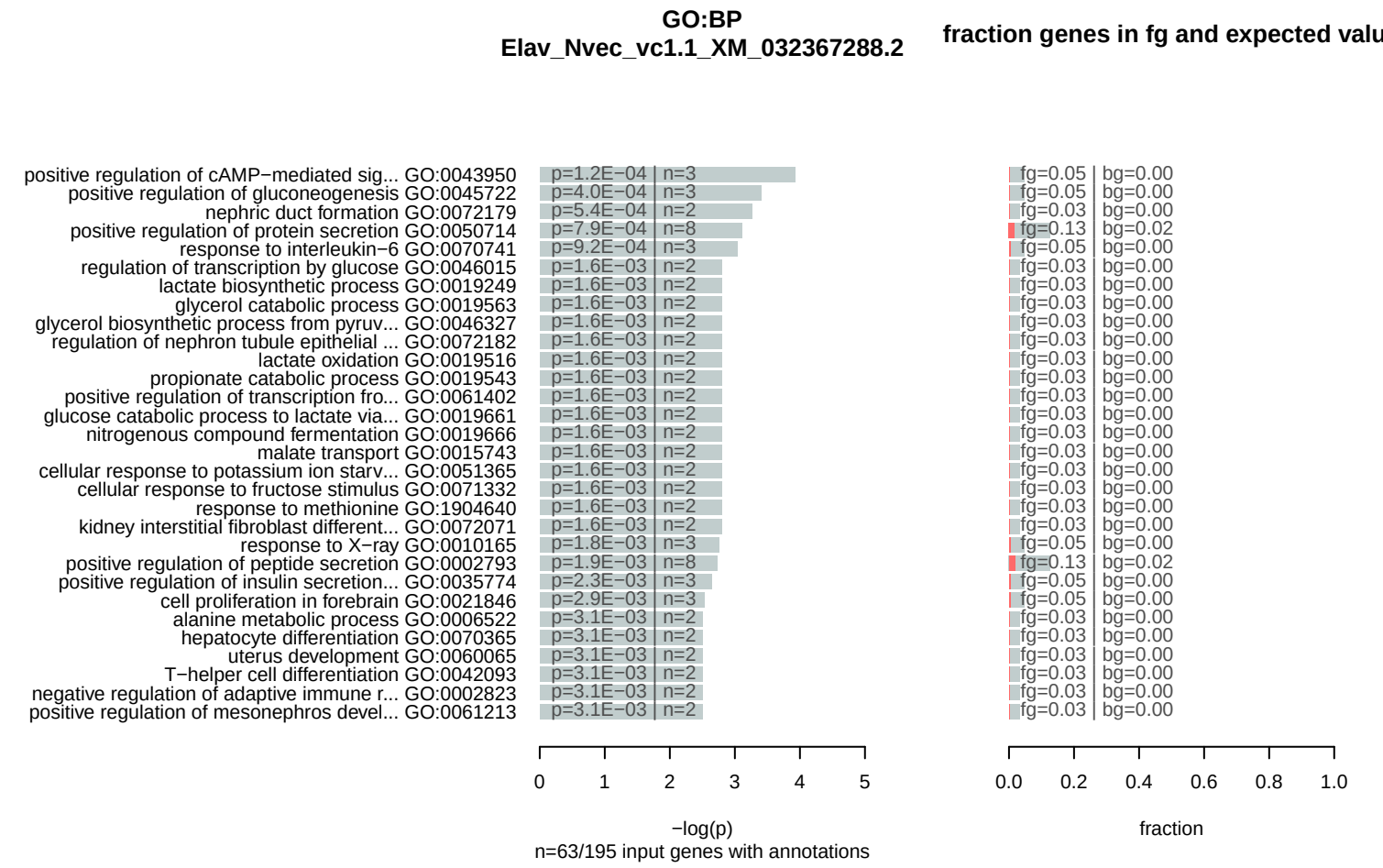
GO:BP
Elav_Nvec_vc1.1_XM_032367288.2
fraction genes in fg and expected valu
positive regulation of cAMP−mediated sig... GO:0043950 p=1.2E−04 n=3 fg=0.05 bg=0.00
positive regulation of gluconeogenesis GO:0045722 p=4.0E−04 n=3 fg=0.05 bg=0.00
nephric duct formation GO:0072179 p=5.4E−04 n=2 fg=0.03 bg=0.00
positive regulation of protein secretion GO:0050714 p=7.9E−04 n=8 fg=0.13 bg=0.02
response to interleukin−6 GO:0070741 p=9.2E−04 n=3 fg=0.05 bg=0.00
regulation of transcription by glucose GO:0046015 p=1.6E−03 n=2 fg=0.03 bg=0.00
lactate biosynthetic process GO:0019249 p=1.6E−03 n=2 fg=0.03 bg=0.00
glycerol catabolic process GO:0019563 p=1.6E−03 n=2 fg=0.03 bg=0.00
glycerol biosynthetic process from pyruv... GO:0046327 p=1.6E−03 n=2 fg=0.03 bg=0.00
regulation of nephron tubule epithelial ... GO:0072182 p=1.6E−03 n=2 fg=0.03 bg=0.00
lactate oxidation GO:0019516 p=1.6E−03 n=2 fg=0.03 bg=0.00
propionate catabolic process GO:0019543 p=1.6E−03 n=2 fg=0.03 bg=0.00
positive regulation of transcription fro... GO:0061402 p=1.6E−03 n=2 fg=0.03 bg=0.00
glucose catabolic process to lactate via... GO:0019661 p=1.6E−03 n=2 fg=0.03 bg=0.00
nitrogenous compound fermentation GO:0019666 p=1.6E−03 n=2 fg=0.03 bg=0.00
malate transport GO:0015743 p=1.6E−03 n=2 fg=0.03 bg=0.00
cellular response to potassium ion starv... GO:0051365 p=1.6E−03 n=2 fg=0.03 bg=0.00
cellular response to fructose stimulus GO:0071332 p=1.6E−03 n=2 fg=0.03 bg=0.00
response to methionine GO:1904640 p=1.6E−03 n=2 fg=0.03 bg=0.00
kidney interstitial fibroblast different... GO:0072071 p=1.6E−03 n=2 fg=0.03 bg=0.00
response to X−ray GO:0010165 p=1.8E−03 n=3 fg=0.05 bg=0.00
positive regulation of peptide secretion GO:0002793 p=1.9E−03 n=8 fg=0.13 bg=0.02
positive regulation of insulin secretion... GO:0035774 p=2.3E−03 n=3 fg=0.05 bg=0.00
cell proliferation in forebrain GO:0021846 p=2.9E−03 n=3 fg=0.05 bg=0.00
alanine metabolic process GO:0006522 p=3.1E−03 n=2 fg=0.03 bg=0.00
hepatocyte differentiation GO:0070365 p=3.1E−03 n=2 fg=0.03 bg=0.00
uterus development GO:0060065 p=3.1E−03 n=2 fg=0.03 bg=0.00
T−helper cell differentiation GO:0042093 p=3.1E−03 n=2 fg=0.03 bg=0.00
negative regulation of adaptive immune r... GO:0002823 p=3.1E−03 n=2 fg=0.03 bg=0.00
positive regulation of mesonephros devel... GO:0061213 p=3.1E−03 n=2 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=63/195 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=9.7E−05 n=3 fg=0.06 bg=0.00
oxidoreductase activity, acting on the C... GO:0016899 p=1.4E−03 n=2 fg=0.04 bg=0.00
phosphoenolpyruvate carboxykinase (GTP) ... GO:0004613 p=1.4E−03 n=2 fg=0.04 bg=0.00
inosine kinase activity GO:0008906 p=1.4E−03 n=2 fg=0.04 bg=0.00
amyloid−beta binding GO:0001540 p=2.4E−03 n=3 fg=0.06 bg=0.01
DNA binding domain binding GO:0050692 p=2.8E−03 n=2 fg=0.04 bg=0.00
ubiquitin−dependent protein binding GO:0140036 p=2.8E−03 n=2 fg=0.04 bg=0.00
lactate dehydrogenase activity GO:0004457 p=2.8E−03 n=2 fg=0.04 bg=0.00
nucleoside diphosphate kinase activity GO:0004550 p=4.5E−03 n=2 fg=0.04 bg=0.00
G protein−coupled amine receptor activit... GO:0008227 p=4.5E−03 n=2 fg=0.04 bg=0.00
HMG box domain binding GO:0071837 p=9.2E−03 n=2 fg=0.04 bg=0.00
manganese ion binding GO:0030145 p=1.0E−02 n=3 fg=0.06 bg=0.01
GTP binding GO:0005525 p=1.5E−02 n=4 fg=0.08 bg=0.02
protein−disulfide reductase (NAD(P)) act... GO:0047134 p=1.5E−02 n=2 fg=0.04 bg=0.00
purine ribonucleoside binding GO:0032550 p=1.7E−02 n=4 fg=0.08 bg=0.02
ribonucleoside binding GO:0032549 p=1.7E−02 n=4 fg=0.08 bg=0.02
oxidoreductase activity, acting on a sul... GO:0016668 p=1.9E−02 n=2 fg=0.04 bg=0.00
purine nucleoside binding GO:0001883 p=2.0E−02 n=4 fg=0.08 bg=0.02
guanyl nucleotide binding GO:0019001 p=2.1E−02 n=4 fg=0.08 bg=0.02
guanyl ribonucleotide binding GO:0032561 p=2.1E−02 n=4 fg=0.08 bg=0.02
nucleoside binding GO:0001882 p=2.1E−02 n=4 fg=0.08 bg=0.02
1−phosphatidylinositol−3−phosphate 4−kin... GO:0052811 p=2.2E−02 n=1 fg=0.02 bg=0.00
bradykinin receptor binding GO:0031711 p=2.2E−02 n=1 fg=0.02 bg=0.00
B2 bradykinin receptor binding GO:0031713 p=2.2E−02 n=1 fg=0.02 bg=0.00
phosphatidylinositol phosphate kinase ac... GO:0016307 p=2.2E−02 n=1 fg=0.02 bg=0.00
1−phosphatidylinositol−4−phosphate 5−kin... GO:0016308 p=2.2E−02 n=1 fg=0.02 bg=0.00
1−phosphatidylinositol−5−phosphate 4−kin... GO:0016309 p=2.2E−02 n=1 fg=0.02 bg=0.00
retromer complex binding GO:1905394 p=2.2E−02 n=1 fg=0.02 bg=0.00
beta−endorphin binding GO:0031626 p=2.2E−02 n=1 fg=0.02 bg=0.00
phosphopantetheine−dependent carrier act... GO:0140414 p=2.2E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=52/195 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
growth cone lamellipodium GO:1990761 p=2.8E−03 n=2 fg=0.03 bg=0.00
protein serine/threonine phosphatase com... GO:0008287 p=4.8E−03 n=3 fg=0.05 bg=0.01
dendritic spine GO:0043197 p=5.3E−03 n=5 fg=0.08 bg=0.02
U5 snRNP GO:0005682 p=1.3E−02 n=2 fg=0.03 bg=0.00
magnesium−dependent protein serine/threo... GO:0005963 p=1.3E−02 n=2 fg=0.03 bg=0.00
plasma membrane GO:0005886 p=1.4E−02 n=22 fg=0.37 bg=0.23
cell periphery GO:0071944 p=1.8E−02 n=23 fg=0.38 bg=0.25
cell surface GO:0009986 p=1.8E−02 n=6 fg=0.10 bg=0.04
stress fiber GO:0001725 p=1.9E−02 n=2 fg=0.03 bg=0.00
contractile actin filament bundle GO:0097517 p=1.9E−02 n=2 fg=0.03 bg=0.00
membrane GO:0016020 p=2.1E−02 n=33 fg=0.55 bg=0.41
sarcolemma GO:0042383 p=2.1E−02 n=3 fg=0.05 bg=0.01
protein phosphatase 4 complex GO:0030289 p=2.2E−02 n=1 fg=0.02 bg=0.00
spectrin−associated cytoskeleton GO:0014731 p=2.2E−02 n=1 fg=0.02 bg=0.00
dendritic spine head GO:0044327 p=2.2E−02 n=1 fg=0.02 bg=0.00
septin collar GO:0032173 p=2.2E−02 n=1 fg=0.02 bg=0.00
cytoplasmic side of dendritic spine plas... GO:1990780 p=2.2E−02 n=1 fg=0.02 bg=0.00
actin filament bundle GO:0032432 p=2.4E−02 n=2 fg=0.03 bg=0.00
autophagosome GO:0005776 p=2.5E−02 n=3 fg=0.05 bg=0.01
precatalytic spliceosome GO:0071011 p=2.8E−02 n=2 fg=0.03 bg=0.00
T−tubule GO:0030315 p=3.2E−02 n=2 fg=0.03 bg=0.00
growth cone filopodium GO:1990812 p=4.4E−02 n=1 fg=0.02 bg=0.00
node of Ranvier GO:0033268 p=4.4E−02 n=1 fg=0.02 bg=0.00
interphase microtubule organizing center GO:0031021 p=4.4E−02 n=1 fg=0.02 bg=0.00
DNA replication preinitiation complex GO:0031261 p=4.4E−02 n=1 fg=0.02 bg=0.00
Elg1 RFC−like complex GO:0031391 p=4.4E−02 n=1 fg=0.02 bg=0.00
cytoplasmic cyclin−dependent protein kin... GO:0000308 p=4.4E−02 n=1 fg=0.02 bg=0.00
GINS complex GO:0000811 p=4.4E−02 n=1 fg=0.02 bg=0.00
dendritic spine neck GO:0044326 p=4.4E−02 n=1 fg=0.02 bg=0.00
calcineurin complex GO:0005955 p=4.4E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=60/195 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction