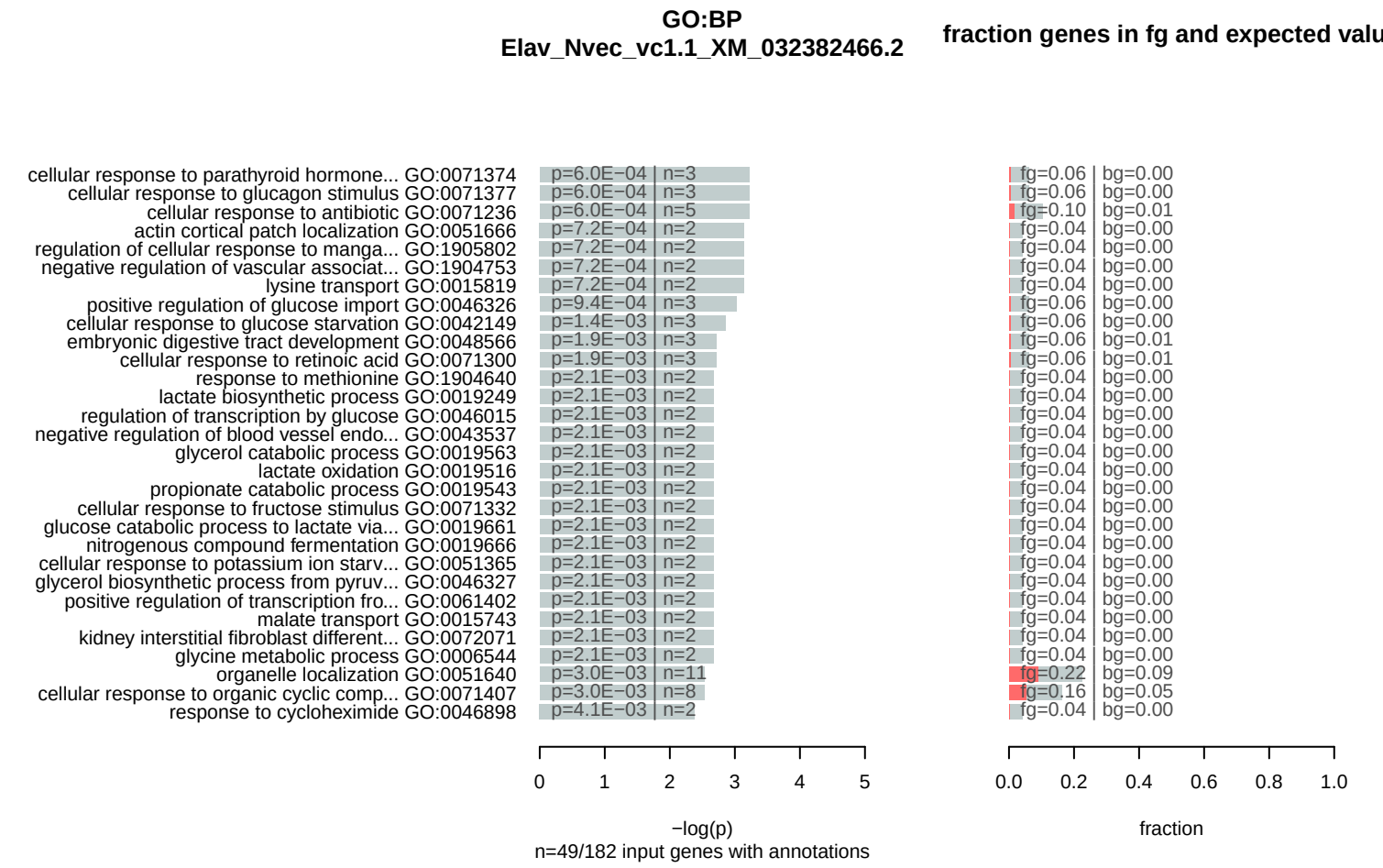
GO:BP
Elav_Nvec_vc1.1_XM_032382466.2
fraction genes in fg and expected valu
cellular response to parathyroid hormone... GO:0071374 p=6.0E−04 n=3 fg=0.06 bg=0.00
cellular response to glucagon stimulus GO:0071377 p=6.0E−04 n=3 fg=0.06 bg=0.00
cellular response to antibiotic GO:0071236 p=6.0E−04 n=5 fg=0.10 bg=0.01
actin cortical patch localization GO:0051666 p=7.2E−04 n=2 fg=0.04 bg=0.00
regulation of cellular response to manga... GO:1905802 p=7.2E−04 n=2 fg=0.04 bg=0.00
negative regulation of vascular associat... GO:1904753 p=7.2E−04 n=2 fg=0.04 bg=0.00
lysine transport GO:0015819 p=7.2E−04 n=2 fg=0.04 bg=0.00
positive regulation of glucose import GO:0046326 p=9.4E−04 n=3 fg=0.06 bg=0.00
cellular response to glucose starvation GO:0042149 p=1.4E−03 n=3 fg=0.06 bg=0.00
embryonic digestive tract development GO:0048566 p=1.9E−03 n=3 fg=0.06 bg=0.01
cellular response to retinoic acid GO:0071300 p=1.9E−03 n=3 fg=0.06 bg=0.01
response to methionine GO:1904640 p=2.1E−03 n=2 fg=0.04 bg=0.00
lactate biosynthetic process GO:0019249 p=2.1E−03 n=2 fg=0.04 bg=0.00
regulation of transcription by glucose GO:0046015 p=2.1E−03 n=2 fg=0.04 bg=0.00
negative regulation of blood vessel endo... GO:0043537 p=2.1E−03 n=2 fg=0.04 bg=0.00
glycerol catabolic process GO:0019563 p=2.1E−03 n=2 fg=0.04 bg=0.00
lactate oxidation GO:0019516 p=2.1E−03 n=2 fg=0.04 bg=0.00
propionate catabolic process GO:0019543 p=2.1E−03 n=2 fg=0.04 bg=0.00
cellular response to fructose stimulus GO:0071332 p=2.1E−03 n=2 fg=0.04 bg=0.00
glucose catabolic process to lactate via... GO:0019661 p=2.1E−03 n=2 fg=0.04 bg=0.00
nitrogenous compound fermentation GO:0019666 p=2.1E−03 n=2 fg=0.04 bg=0.00
cellular response to potassium ion starv... GO:0051365 p=2.1E−03 n=2 fg=0.04 bg=0.00
glycerol biosynthetic process from pyruv... GO:0046327 p=2.1E−03 n=2 fg=0.04 bg=0.00
positive regulation of transcription fro... GO:0061402 p=2.1E−03 n=2 fg=0.04 bg=0.00
malate transport GO:0015743 p=2.1E−03 n=2 fg=0.04 bg=0.00
kidney interstitial fibroblast different... GO:0072071 p=2.1E−03 n=2 fg=0.04 bg=0.00
glycine metabolic process GO:0006544 p=2.1E−03 n=2 fg=0.04 bg=0.00
organelle localization GO:0051640 p=3.0E−03 n=11 fg=0.22 bg=0.09
cellular response to organic cyclic comp... GO:0071407 p=3.0E−03 n=8 fg=0.16 bg=0.05
response to cycloheximide GO:0046898 p=4.1E−03 n=2 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=49/182 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032382466.2
fraction genes in fg and expected valu
phosphoenolpyruvate carboxykinase (GTP) ... GO:0004613 p=2.1E−03 n=2 fg=0.05 bg=0.00
lactate dehydrogenase activity GO:0004457 p=2.1E−03 n=2 fg=0.05 bg=0.00
inosine kinase activity GO:0008906 p=2.1E−03 n=2 fg=0.05 bg=0.00
DNA binding domain binding GO:0050692 p=2.1E−03 n=2 fg=0.05 bg=0.00
oxidoreductase activity, acting on the C... GO:0016899 p=2.1E−03 n=2 fg=0.05 bg=0.00
nucleoside diphosphate kinase activity GO:0004550 p=4.1E−03 n=2 fg=0.05 bg=0.00
epinephrine binding GO:0051379 p=6.8E−03 n=2 fg=0.05 bg=0.00
protein−disulfide reductase (NAD(P)) act... GO:0047134 p=1.4E−02 n=2 fg=0.05 bg=0.00
oxidoreductase activity, acting on a sul... GO:0016668 p=1.4E−02 n=2 fg=0.05 bg=0.00
cis−regulatory region sequence−specific ... GO:0000987 p=1.7E−02 n=5 fg=0.12 bg=0.04
RNA polymerase II cis−regulatory region ... GO:0000978 p=1.7E−02 n=5 fg=0.12 bg=0.04
carbohydrate derivative binding GO:0097367 p=1.8E−02 n=8 fg=0.19 bg=0.08
ribonucleotide binding GO:0032553 p=2.2E−02 n=7 fg=0.16 bg=0.07
purine ribonucleotide binding GO:0032555 p=2.2E−02 n=7 fg=0.16 bg=0.07
DNA−binding transcription activator acti... GO:0001228 p=2.2E−02 n=5 fg=0.12 bg=0.04
DNA−binding transcription activator acti... GO:0001216 p=2.2E−02 n=5 fg=0.12 bg=0.04
protein−disulfide reductase activity GO:0015035 p=2.3E−02 n=2 fg=0.05 bg=0.01
purine nucleotide binding GO:0017076 p=2.5E−02 n=7 fg=0.16 bg=0.07
ribonuclease inhibitor activity GO:0008428 p=2.7E−02 n=1 fg=0.02 bg=0.00
4−hydroxy−2−oxoglutarate aldolase activi... GO:0008700 p=2.7E−02 n=1 fg=0.02 bg=0.00
nuclease inhibitor activity GO:0140721 p=2.7E−02 n=1 fg=0.02 bg=0.00
sulfate transmembrane transporter activi... GO:0015116 p=2.7E−02 n=1 fg=0.02 bg=0.00
adenosine−phosphate deaminase activity GO:0047623 p=2.7E−02 n=1 fg=0.02 bg=0.00
adipokinetic hormone receptor activity GO:0097003 p=2.7E−02 n=1 fg=0.02 bg=0.00
aldehyde−lyase activity GO:0016832 p=2.7E−02 n=1 fg=0.02 bg=0.00
oxalate transmembrane transporter activi... GO:0019531 p=2.7E−02 n=1 fg=0.02 bg=0.00
exon−exon junction complex binding GO:1990448 p=2.7E−02 n=1 fg=0.02 bg=0.00
GMP binding GO:0019002 p=2.7E−02 n=1 fg=0.02 bg=0.00
JUN kinase activity GO:0004705 p=2.7E−02 n=1 fg=0.02 bg=0.00
AMP deaminase activity GO:0003876 p=2.7E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=43/182 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032382466.2
fraction genes in fg and expected valu
fungal−type vacuole membrane GO:0000329 p=4.0E−03 n=2 fg=0.04 bg=0.00
cell tip GO:0051286 p=4.0E−03 n=2 fg=0.04 bg=0.00
dendrite cytoplasm GO:0032839 p=4.0E−03 n=2 fg=0.04 bg=0.00
intrinsic component of endoplasmic retic... GO:0031227 p=2.2E−02 n=4 fg=0.08 bg=0.02
integral component of endoplasmic reticu... GO:0030176 p=2.2E−02 n=4 fg=0.08 bg=0.02
neuronal ribonucleoprotein granule GO:0071598 p=2.7E−02 n=1 fg=0.02 bg=0.00
FACT complex GO:0035101 p=2.7E−02 n=1 fg=0.02 bg=0.00
lytic vacuole GO:0000323 p=3.2E−02 n=8 fg=0.17 bg=0.06
ciliary base GO:0097546 p=3.3E−02 n=2 fg=0.04 bg=0.01
lysosome GO:0005764 p=3.8E−02 n=6 fg=0.12 bg=0.05
preribosome, small subunit precursor GO:0030688 p=5.2E−02 n=1 fg=0.02 bg=0.00
outer kinetochore GO:0000940 p=5.2E−02 n=1 fg=0.02 bg=0.00
nuclear stress granule GO:0097165 p=5.2E−02 n=1 fg=0.02 bg=0.00
U2AF complex GO:0089701 p=5.2E−02 n=1 fg=0.02 bg=0.00
cell division site GO:0032153 p=5.8E−02 n=2 fg=0.04 bg=0.01
endoplasmic reticulum membrane GO:0005789 p=7.0E−02 n=7 fg=0.15 bg=0.08
nuclear outer membrane−endoplasmic retic... GO:0042175 p=7.4E−02 n=7 fg=0.15 bg=0.08
nucleotide−activated protein kinase comp... GO:0031588 p=7.8E−02 n=1 fg=0.02 bg=0.00
U1 snRNP GO:0005685 p=7.8E−02 n=1 fg=0.02 bg=0.00
exon−exon junction complex GO:0035145 p=7.8E−02 n=1 fg=0.02 bg=0.00
endoplasmic reticulum exit site GO:0070971 p=7.8E−02 n=1 fg=0.02 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=7.8E−02 n=1 fg=0.02 bg=0.00
U2−type prespliceosome GO:0071004 p=7.8E−02 n=1 fg=0.02 bg=0.00
podosome GO:0002102 p=7.8E−02 n=1 fg=0.02 bg=0.00
commitment complex GO:0000243 p=7.8E−02 n=1 fg=0.02 bg=0.00
perinuclear endoplasmic reticulum GO:0097038 p=7.8E−02 n=1 fg=0.02 bg=0.00
Hrd1p ubiquitin ligase ERAD−L complex GO:0000839 p=7.8E−02 n=1 fg=0.02 bg=0.00
endoplasmic reticulum subcompartment GO:0098827 p=8.1E−02 n=7 fg=0.15 bg=0.08
vacuole GO:0005773 p=8.5E−02 n=8 fg=0.17 bg=0.07
endoplasmic reticulum−Golgi intermediate... GO:0005793 p=9.7E−02 n=2 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=48/182 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction