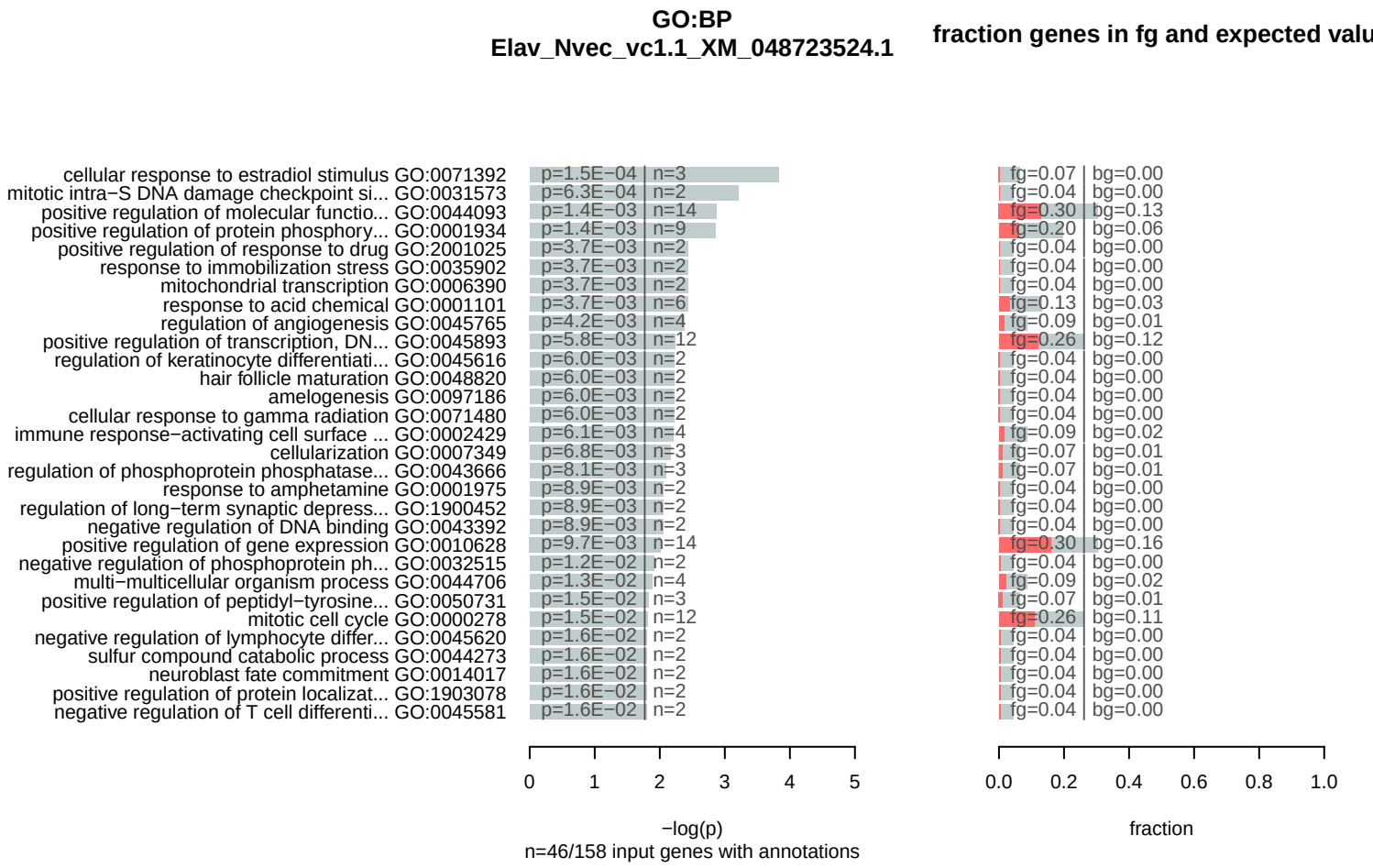
GO:BP
Elav_Nvec_vc1.1_XM_048723524.1
fraction genes in fg and expected valu
cellular response to estradiol stimulus GO:0071392 p=1.5E−04 n=3 fg=0.07 bg=0.00
mitotic intra−S DNA damage checkpoint si... GO:0031573 p=6.3E−04 n=2 fg=0.04 bg=0.00
positive regulation of molecular functio... GO:0044093 p=1.4E−03 n=14 fg=0.30 bg=0.13
positive regulation of protein phosphory... GO:0001934 p=1.4E−03 n=9 fg=0.20 bg=0.06
positive regulation of response to drug GO:2001025 p=3.7E−03 n=2 fg=0.04 bg=0.00
response to immobilization stress GO:0035902 p=3.7E−03 n=2 fg=0.04 bg=0.00
mitochondrial transcription GO:0006390 p=3.7E−03 n=2 fg=0.04 bg=0.00
response to acid chemical GO:0001101 p=3.7E−03 n=6 fg=0.13 bg=0.03
regulation of angiogenesis GO:0045765 p=4.2E−03 n=4 fg=0.09 bg=0.01
positive regulation of transcription, DN... GO:0045893 p=5.8E−03 n=12 fg=0.26 bg=0.12
regulation of keratinocyte differentiati... GO:0045616 p=6.0E−03 n=2 fg=0.04 bg=0.00
hair follicle maturation GO:0048820 p=6.0E−03 n=2 fg=0.04 bg=0.00
amelogenesis GO:0097186 p=6.0E−03 n=2 fg=0.04 bg=0.00
cellular response to gamma radiation GO:0071480 p=6.0E−03 n=2 fg=0.04 bg=0.00
immune response−activating cell surface ... GO:0002429 p=6.1E−03 n=4 fg=0.09 bg=0.02
cellularization GO:0007349 p=6.8E−03 n=3 fg=0.07 bg=0.01
regulation of phosphoprotein phosphatase... GO:0043666 p=8.1E−03 n=3 fg=0.07 bg=0.01
response to amphetamine GO:0001975 p=8.9E−03 n=2 fg=0.04 bg=0.00
regulation of long−term synaptic depress... GO:1900452 p=8.9E−03 n=2 fg=0.04 bg=0.00
negative regulation of DNA binding GO:0043392 p=8.9E−03 n=2 fg=0.04 bg=0.00
positive regulation of gene expression GO:0010628 p=9.7E−03 n=14 fg=0.30 bg=0.16
negative regulation of phosphoprotein ph... GO:0032515 p=1.2E−02 n=2 fg=0.04 bg=0.00
multi−multicellular organism process GO:0044706 p=1.3E−02 n=4 fg=0.09 bg=0.02
positive regulation of peptidyl−tyrosine... GO:0050731 p=1.5E−02 n=3 fg=0.07 bg=0.01
mitotic cell cycle GO:0000278 p=1.5E−02 n=12 fg=0.26 bg=0.11
negative regulation of lymphocyte differ... GO:0045620 p=1.6E−02 n=2 fg=0.04 bg=0.00
sulfur compound catabolic process GO:0044273 p=1.6E−02 n=2 fg=0.04 bg=0.00
neuroblast fate commitment GO:0014017 p=1.6E−02 n=2 fg=0.04 bg=0.00
positive regulation of protein localizat... GO:1903078 p=1.6E−02 n=2 fg=0.04 bg=0.00
negative regulation of T cell differenti... GO:0045581 p=1.6E−02 n=2 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=46/158 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_048723524.1
fraction genes in fg and expected valu
mRNA regulatory element binding translat... GO:0000900 p=2.4E−03 n=2 fg=0.04 bg=0.00
D2 dopamine receptor binding GO:0031749 p=2.4E−03 n=2 fg=0.04 bg=0.00
protein phosphatase inhibitor activity GO:0004864 p=4.7E−03 n=2 fg=0.04 bg=0.00
phosphatase binding GO:0019902 p=6.2E−03 n=5 fg=0.11 bg=0.03
protein tyrosine kinase activator activi... GO:0030296 p=7.7E−03 n=2 fg=0.04 bg=0.00
translation factor activity, RNA binding GO:0008135 p=9.7E−03 n=3 fg=0.07 bg=0.01
mRNA binding GO:0003729 p=1.2E−02 n=5 fg=0.11 bg=0.03
protein phosphatase 1 binding GO:0008157 p=2.1E−02 n=2 fg=0.04 bg=0.01
kinase binding GO:0019900 p=2.5E−02 n=8 fg=0.17 bg=0.08
heme binding GO:0020037 p=2.6E−02 n=2 fg=0.04 bg=0.01
nitrite reductase activity GO:0098809 p=2.9E−02 n=1 fg=0.02 bg=0.00
dynein light chain binding GO:0045503 p=2.9E−02 n=1 fg=0.02 bg=0.00
amino acid:cation symporter activity GO:0005416 p=2.9E−02 n=1 fg=0.02 bg=0.00
saccharopine dehydrogenase (NAD+, L−lysi... GO:0004754 p=2.9E−02 n=1 fg=0.02 bg=0.00
glycine transmembrane transporter activi... GO:0015187 p=2.9E−02 n=1 fg=0.02 bg=0.00
iron−responsive element binding GO:0030350 p=2.9E−02 n=1 fg=0.02 bg=0.00
transmembrane receptor protein phosphata... GO:0019198 p=2.9E−02 n=1 fg=0.02 bg=0.00
amino acid:proton symporter activity GO:0005280 p=2.9E−02 n=1 fg=0.02 bg=0.00
peroxisome targeting sequence binding GO:0000268 p=2.9E−02 n=1 fg=0.02 bg=0.00
ferrochelatase activity GO:0004325 p=2.9E−02 n=1 fg=0.02 bg=0.00
transmembrane receptor protein tyrosine ... GO:0005001 p=2.9E−02 n=1 fg=0.02 bg=0.00
selenocystathionine beta−synthase activi... GO:0098605 p=2.9E−02 n=1 fg=0.02 bg=0.00
translation elongation factor binding GO:0061770 p=2.9E−02 n=1 fg=0.02 bg=0.00
nitrite reductase (NO−forming) activity GO:0050421 p=2.9E−02 n=1 fg=0.02 bg=0.00
L−proline transmembrane transporter acti... GO:0015193 p=2.9E−02 n=1 fg=0.02 bg=0.00
L−tryptophan transmembrane transporter a... GO:0015196 p=2.9E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on other... GO:0016661 p=2.9E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on other... GO:0016662 p=2.9E−02 n=1 fg=0.02 bg=0.00
protein phosphatase 5 binding GO:1990634 p=2.9E−02 n=1 fg=0.02 bg=0.00
protein serine/threonine phosphatase inh... GO:0004865 p=2.9E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=46/158 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048723524.1
fraction genes in fg and expected valu
mitotic spindle pole GO:0097431 p=5.8E−03 n=2 fg=0.04 bg=0.00
protein phosphatase type 1 complex GO:0000164 p=5.8E−03 n=2 fg=0.04 bg=0.00
chromosomal region GO:0098687 p=6.4E−03 n=5 fg=0.11 bg=0.03
PML body GO:0016605 p=1.2E−02 n=2 fg=0.04 bg=0.00
condensed chromosome, centromeric region GO:0000779 p=1.4E−02 n=3 fg=0.07 bg=0.01
stress fiber GO:0001725 p=1.9E−02 n=2 fg=0.04 bg=0.00
contractile actin filament bundle GO:0097517 p=1.9E−02 n=2 fg=0.04 bg=0.00
actin filament bundle GO:0032432 p=1.9E−02 n=2 fg=0.04 bg=0.00
nuclear body GO:0016604 p=2.1E−02 n=7 fg=0.16 bg=0.06
nuclear mitotic cohesin complex GO:0034990 p=2.5E−02 n=1 fg=0.02 bg=0.00
mitochondrial DNA−directed RNA polymeras... GO:0034245 p=2.5E−02 n=1 fg=0.02 bg=0.00
dendritic spine neck GO:0044326 p=2.5E−02 n=1 fg=0.02 bg=0.00
dendritic spine head GO:0044327 p=2.5E−02 n=1 fg=0.02 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=2.5E−02 n=1 fg=0.02 bg=0.00
phenylalanine−tRNA ligase complex GO:0009328 p=2.5E−02 n=1 fg=0.02 bg=0.00
core−binding factor complex GO:0016513 p=2.5E−02 n=1 fg=0.02 bg=0.00
septin collar GO:0032173 p=2.5E−02 n=1 fg=0.02 bg=0.00
cytoplasmic side of dendritic spine plas... GO:1990780 p=2.5E−02 n=1 fg=0.02 bg=0.00
mitotic cohesin complex GO:0030892 p=2.5E−02 n=1 fg=0.02 bg=0.00
chromosome, centromeric region GO:0000775 p=3.0E−02 n=3 fg=0.07 bg=0.02
actomyosin GO:0042641 p=4.0E−02 n=2 fg=0.04 bg=0.01
condensed chromosome GO:0000793 p=4.0E−02 n=3 fg=0.07 bg=0.02
polytene chromosome GO:0005700 p=4.0E−02 n=3 fg=0.07 bg=0.02
nuclear cohesin complex GO:0000798 p=4.9E−02 n=1 fg=0.02 bg=0.00
eukaryotic translation initiation factor... GO:0005850 p=4.9E−02 n=1 fg=0.02 bg=0.00
RSF complex GO:0031213 p=4.9E−02 n=1 fg=0.02 bg=0.00
nuclear stress granule GO:0097165 p=4.9E−02 n=1 fg=0.02 bg=0.00
cohesin complex GO:0008278 p=4.9E−02 n=1 fg=0.02 bg=0.00
kinetochore GO:0000776 p=5.8E−02 n=2 fg=0.04 bg=0.01
filopodium GO:0030175 p=5.8E−02 n=2 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=45/158 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction