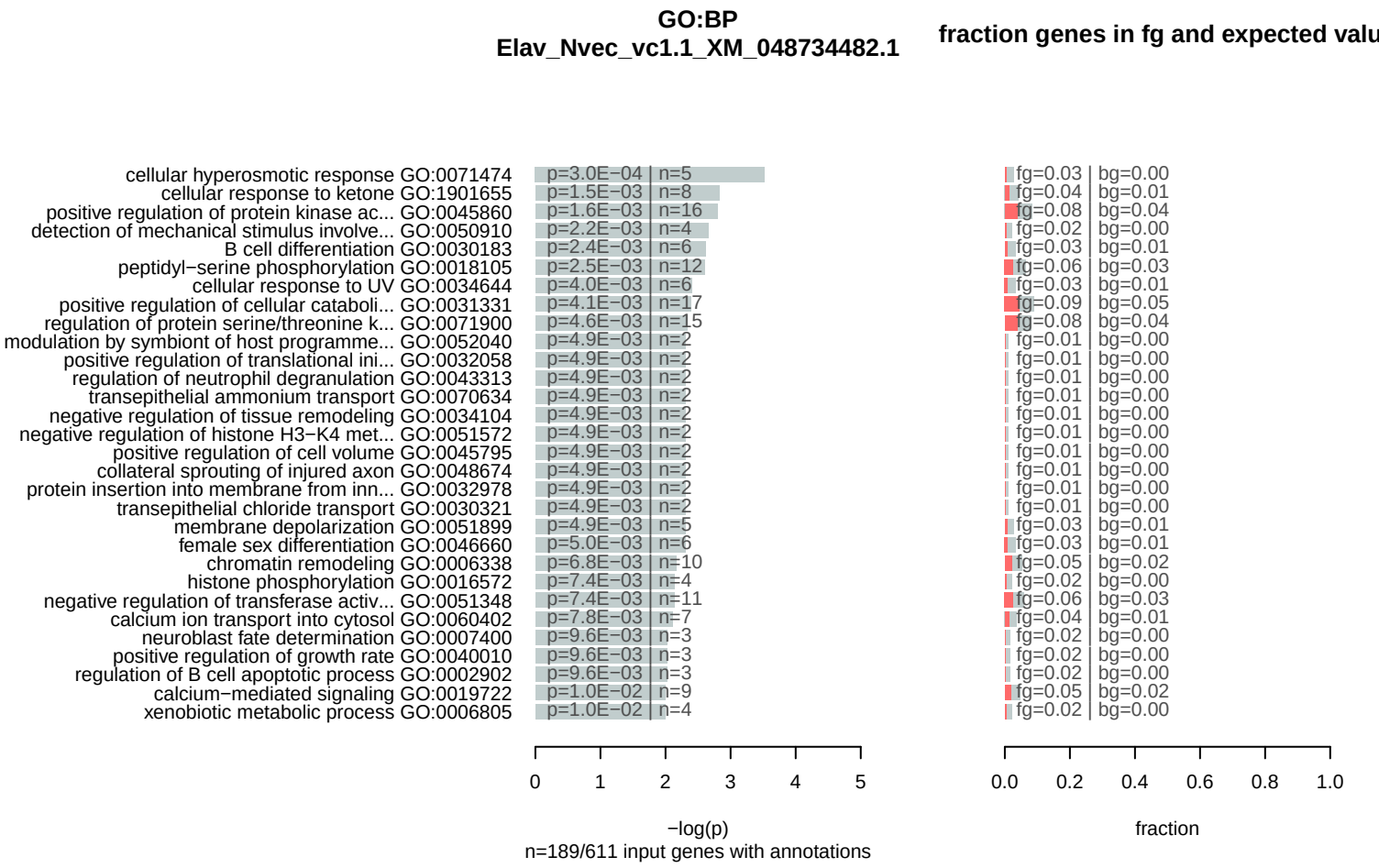
GO:BP
Elav_Nvec_vc1.1_XM_048734482.1
fraction genes in fg and expected valu
cellular hyperosmotic response GO:0071474 p=3.0E−04 n=5 fg=0.03 bg=0.00
cellular response to ketone GO:1901655 p=1.5E−03 n=8 fg=0.04 bg=0.01
positive regulation of protein kinase ac... GO:0045860 p=1.6E−03 n=16 fg=0.08 bg=0.04
detection of mechanical stimulus involve... GO:0050910 p=2.2E−03 n=4 fg=0.02 bg=0.00
B cell differentiation GO:0030183 p=2.4E−03 n=6 fg=0.03 bg=0.01
peptidyl−serine phosphorylation GO:0018105 p=2.5E−03 n=12 fg=0.06 bg=0.03
cellular response to UV GO:0034644 p=4.0E−03 n=6 fg=0.03 bg=0.01
positive regulation of cellular cataboli... GO:0031331 p=4.1E−03 n=17 fg=0.09 bg=0.05
regulation of protein serine/threonine k... GO:0071900 p=4.6E−03 n=15 fg=0.08 bg=0.04
modulation by symbiont of host programme... GO:0052040 p=4.9E−03 n=2 fg=0.01 bg=0.00
positive regulation of translational ini... GO:0032058 p=4.9E−03 n=2 fg=0.01 bg=0.00
regulation of neutrophil degranulation GO:0043313 p=4.9E−03 n=2 fg=0.01 bg=0.00
transepithelial ammonium transport GO:0070634 p=4.9E−03 n=2 fg=0.01 bg=0.00
negative regulation of tissue remodeling GO:0034104 p=4.9E−03 n=2 fg=0.01 bg=0.00
negative regulation of histone H3−K4 met... GO:0051572 p=4.9E−03 n=2 fg=0.01 bg=0.00
positive regulation of cell volume GO:0045795 p=4.9E−03 n=2 fg=0.01 bg=0.00
collateral sprouting of injured axon GO:0048674 p=4.9E−03 n=2 fg=0.01 bg=0.00
protein insertion into membrane from inn... GO:0032978 p=4.9E−03 n=2 fg=0.01 bg=0.00
transepithelial chloride transport GO:0030321 p=4.9E−03 n=2 fg=0.01 bg=0.00
membrane depolarization GO:0051899 p=4.9E−03 n=5 fg=0.03 bg=0.01
female sex differentiation GO:0046660 p=5.0E−03 n=6 fg=0.03 bg=0.01
chromatin remodeling GO:0006338 p=6.8E−03 n=10 fg=0.05 bg=0.02
histone phosphorylation GO:0016572 p=7.4E−03 n=4 fg=0.02 bg=0.00
negative regulation of transferase activ... GO:0051348 p=7.4E−03 n=11 fg=0.06 bg=0.03
calcium ion transport into cytosol GO:0060402 p=7.8E−03 n=7 fg=0.04 bg=0.01
neuroblast fate determination GO:0007400 p=9.6E−03 n=3 fg=0.02 bg=0.00
positive regulation of growth rate GO:0040010 p=9.6E−03 n=3 fg=0.02 bg=0.00
regulation of B cell apoptotic process GO:0002902 p=9.6E−03 n=3 fg=0.02 bg=0.00
calcium−mediated signaling GO:0019722 p=1.0E−02 n=9 fg=0.05 bg=0.02
xenobiotic metabolic process GO:0006805 p=1.0E−02 n=4 fg=0.02 bg=0.00
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−log(p)
n=189/611 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_048734482.1
fraction genes in fg and expected valu
enzyme inhibitor activity GO:0004857 p=2.4E−03 n=10 fg=0.06 bg=0.02
transcription coactivator activity GO:0003713 p=4.2E−03 n=12 fg=0.08 bg=0.03
sodium:potassium:chloride symporter acti... GO:0008511 p=4.4E−03 n=2 fg=0.01 bg=0.00
acid−ammonia (or amide) ligase activity GO:0016880 p=4.4E−03 n=2 fg=0.01 bg=0.00
nucleosomal DNA binding GO:0031492 p=4.4E−03 n=2 fg=0.01 bg=0.00
low voltage−gated calcium channel activi... GO:0008332 p=4.4E−03 n=2 fg=0.01 bg=0.00
protein serine/threonine kinase activity GO:0004674 p=4.6E−03 n=14 fg=0.09 bg=0.04
MAP kinase kinase activity GO:0004708 p=5.0E−03 n=3 fg=0.02 bg=0.00
hydrolase activity, acting on carbon−nit... GO:0016814 p=8.3E−03 n=3 fg=0.02 bg=0.00
protein kinase binding GO:0019901 p=1.1E−02 n=19 fg=0.12 bg=0.07
Wnt−activated receptor activity GO:0042813 p=1.3E−02 n=2 fg=0.01 bg=0.00
ammonium transmembrane transporter activ... GO:0008519 p=1.3E−02 n=3 fg=0.02 bg=0.00
kinase binding GO:0019900 p=2.2E−02 n=19 fg=0.12 bg=0.07
p53 binding GO:0002039 p=2.3E−02 n=4 fg=0.03 bg=0.01
protein kinase A catalytic subunit bindi... GO:0034236 p=2.4E−02 n=2 fg=0.01 bg=0.00
bHLH transcription factor binding GO:0043425 p=2.4E−02 n=2 fg=0.01 bg=0.00
cis−regulatory region sequence−specific ... GO:0000987 p=2.5E−02 n=10 fg=0.06 bg=0.03
RNA polymerase II cis−regulatory region ... GO:0000978 p=2.5E−02 n=10 fg=0.06 bg=0.03
protein kinase inhibitor activity GO:0004860 p=2.8E−02 n=4 fg=0.03 bg=0.01
kinase inhibitor activity GO:0019210 p=2.8E−02 n=4 fg=0.03 bg=0.01
RNA polymerase II transcription regulato... GO:0000977 p=2.9E−02 n=12 fg=0.08 bg=0.04
UDP−glycosyltransferase activity GO:0008194 p=3.0E−02 n=5 fg=0.03 bg=0.01
protein kinase A binding GO:0051018 p=3.2E−02 n=3 fg=0.02 bg=0.00
ATP binding GO:0005524 p=3.6E−02 n=12 fg=0.08 bg=0.04
TFIID−class transcription factor complex... GO:0001094 p=3.9E−02 n=2 fg=0.01 bg=0.00
misfolded protein binding GO:0051787 p=3.9E−02 n=2 fg=0.01 bg=0.00
eukaryotic initiation factor eIF2 bindin... GO:0071074 p=3.9E−02 n=2 fg=0.01 bg=0.00
deaminase activity GO:0019239 p=3.9E−02 n=2 fg=0.01 bg=0.00
microtubule binding GO:0008017 p=3.9E−02 n=8 fg=0.05 bg=0.02
nuclear receptor coactivator activity GO:0030374 p=4.1E−02 n=3 fg=0.02 bg=0.01
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−log(p)
n=158/611 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048734482.1
fraction genes in fg and expected valu
presynaptic periactive zone GO:0036062 p=2.8E−03 n=3 fg=0.02 bg=0.00
Barr body GO:0001740 p=4.6E−03 n=2 fg=0.01 bg=0.00
mitotic spindle midzone GO:1990023 p=5.3E−03 n=3 fg=0.02 bg=0.00
chromosome, centromeric region GO:0000775 p=1.3E−02 n=8 fg=0.04 bg=0.02
sperm principal piece GO:0097228 p=1.9E−02 n=3 fg=0.02 bg=0.00
dendritic spine membrane GO:0032591 p=2.5E−02 n=2 fg=0.01 bg=0.00
kinetochore microtubule GO:0005828 p=4.0E−02 n=2 fg=0.01 bg=0.00
outer kinetochore GO:0000940 p=4.0E−02 n=2 fg=0.01 bg=0.00
M band GO:0031430 p=4.3E−02 n=3 fg=0.02 bg=0.00
lateral plasma membrane GO:0016328 p=4.3E−02 n=3 fg=0.02 bg=0.00
P−body GO:0000932 p=5.0E−02 n=4 fg=0.02 bg=0.01
mitochondrial membrane GO:0031966 p=5.3E−02 n=16 fg=0.09 bg=0.06
voltage−gated calcium channel complex GO:0005891 p=5.8E−02 n=2 fg=0.01 bg=0.00
transcription factor TFTC complex GO:0033276 p=5.8E−02 n=2 fg=0.01 bg=0.00
nucleosome GO:0000786 p=5.8E−02 n=2 fg=0.01 bg=0.00
kinetochore GO:0000776 p=6.2E−02 n=5 fg=0.03 bg=0.01
cytoplasmic side of dendritic spine plas... GO:1990780 p=6.8E−02 n=1 fg=0.01 bg=0.00
spectrin GO:0008091 p=6.8E−02 n=1 fg=0.01 bg=0.00
spectrosome GO:0045170 p=6.8E−02 n=1 fg=0.01 bg=0.00
FACT complex GO:0035101 p=6.8E−02 n=1 fg=0.01 bg=0.00
autosome GO:0030849 p=6.8E−02 n=1 fg=0.01 bg=0.00
single−stranded DNA−dependent ATP−depend... GO:0017117 p=6.8E−02 n=1 fg=0.01 bg=0.00
RCAF complex GO:0035059 p=6.8E−02 n=1 fg=0.01 bg=0.00
dendritic spine head GO:0044327 p=6.8E−02 n=1 fg=0.01 bg=0.00
plus−end kinesin complex GO:0005873 p=6.8E−02 n=1 fg=0.01 bg=0.00
proton−transporting ATP synthase, cataly... GO:0045267 p=6.8E−02 n=1 fg=0.01 bg=0.00
Ndc80 complex GO:0031262 p=6.8E−02 n=1 fg=0.01 bg=0.00
cyclin A1−CDK2 complex GO:0097123 p=6.8E−02 n=1 fg=0.01 bg=0.00
cyclin A2−CDK2 complex GO:0097124 p=6.8E−02 n=1 fg=0.01 bg=0.00
Dbf4−dependent protein kinase complex GO:0031431 p=6.8E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=184/611 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction