genes_P0.05Fold2_mrna_trT_set02_StcNasMglMgh_S_baseMglowMg_baseNa_Exp_noFilter_p1Sf_noNorm__Mg_mM_Levels_kegg
Ribosome
padj:0.00000 N(−47/ +1/ 77)
Purine metabolism
padj:0.00000 N(−36/ +0/ 76)
ABC transporters
padj:0.00000 N(−47/ +3/ 153)
Pyrimidine metabolism
padj:0.00000 N(−27/ +0/ 52)
Aminoacyl−tRNA biosynthesis
padj:0.00000 N(−17/ +0/ 25)
Homologous recombination
padj:0.00000 N(−14/ +0/ 27)
Valine, leucine and isoleucine biosynthesis
padj:0.00000 N(−10/ +2/ 19)
Thiamine metabolism
padj:0.00000 N(−5/ +5/ 12)
Peptidoglycan biosynthesis
padj:0.00000 N(−12/ +0/ 19)
Fatty acid biosynthesis
padj:0.00000 N(−9/ +0/ 12)
Phenylalanine, tyrosine and tryptophan biosynthesis
padj:0.00000 N(−11/ +0/ 21)
Glycine, serine and threonine metabolism
padj:0.00003 N(−12/ +0/ 30)
Oxidative phosphorylation
padj:0.00006 N(−13/ +0/ 41)
One carbon pool by folate
padj:0.00006 N(−8/ +0/ 12)
Sulfur metabolism
padj:0.00006 N(−8/ +0/ 13)
Alanine, aspartate and glutamate metabolism
padj:0.00007 N(−10/ +1/ 28)
RNA degradation
padj:0.00021 N(−8/ +0/ 13)
Cysteine and methionine metabolism
padj:0.00044 N(−10/ +0/ 23)
Mismatch repair
padj:0.00045 N(−9/ +0/ 21)
DNA replication
padj:0.00057 N(−8/ +0/ 16)
Ubiquinone and other terpenoid−quinone biosynthesis
padj:0.00057 N(−8/ +0/ 17)
Arginine and proline metabolism
padj:0.00062 N(−11/ +1/ 35)
Vitamin B6 metabolism
padj:0.00143 N(−6/ +0/ 9)
Selenoamino acid metabolism
padj:0.00165 N(−7/ +0/ 14)
Bacterial secretion system
padj:0.00680 N(−9/ +0/ 30)
Nicotinate and nicotinamide metabolism
padj:0.00824 N(−7/ +0/ 16)
Protein export
padj:0.00824 N(−7/ +0/ 16)
Terpenoid backbone biosynthesis
padj:0.01183 N(−6/ +0/ 11)
Base excision repair
padj:0.01744 N(−6/ +0/ 12)
Lysine biosynthesis
padj:0.03411 N(−6/ +0/ 14)
rpsK
cysP
ykgM
malE
malF
modA
ilvB
ilvN
thiH
thiF
thiC
thiE
thiG
putA
putA
−47
−23
−22
−21
−20
−19
rank
−sign(cor)*P_log10
−20
−10
0
10
20