genes_P0.05Fold2_mrna_trT_set02_StcYtcNasMgh_SY_baseMg_baseNa_Exp_noFilter_p1Sf_noNorm__carbonSource_kegg
Ribosome
padj:0.00000 N(−50/ +0/ 77)
Purine metabolism
padj:0.00000 N(−23/ +1/ 76)
ABC transporters
padj:0.00000 N(−22/ +8/ 153)
Aminoacyl−tRNA biosynthesis
padj:0.00001 N(−10/ +0/ 25)
Pyrimidine metabolism
padj:0.00009 N(−12/ +0/ 52)
Selenoamino acid metabolism
padj:0.00014 N(−7/ +0/ 14)
Glycine, serine and threonine metabolism
padj:0.00042 N(−9/ +0/ 30)
One carbon pool by folate
padj:0.00156 N(−6/ +0/ 12)
Pantothenate and CoA biosynthesis
padj:0.00201 N(−5/ +2/ 16)
Valine, leucine and isoleucine biosynthesis
padj:0.00201 N(−5/ +2/ 19)
Protein export
padj:0.00879 N(−6/ +0/ 16)
Cysteine and methionine metabolism
padj:0.01101 N(−7/ +0/ 23)
Biosynthesis of siderophore group nonribosomal peptides
padj:0.01862 N(−4/ +0/ 6)
Sulfur metabolism
padj:0.02148 N(−5/ +0/ 13)
Arginine and proline metabolism
padj:0.02230 N(−5/ +3/ 35)
C5−Branched dibasic acid metabolism
padj:0.03144 N(−2/ +2/ 7)
Nitrogen metabolism
padj:0.03710 N(−5/ +2/ 33)
rank
−sign(cor)*P_log10
−3
0
3