	genes_P0.05Fold2_mrna_trT_set02_StcYtcNasMgh_SY_baseMg_baseNa_Exp_noFilter_p1Sf_noNormcarbonSource_kegg	
Ribosome _ padj:0.00000 N(-50/ +0/ 77)	THE	
Purine metabolism	guals puriff purC purT purK gussA sapt purB cysD yjjG ads purH sapoT cysN purE rpcds cysC	ашв
ABC transporters	portA modiff feeC yfudZ feeD potB feeB saud fisE yfudY ffisiG nlpA tasiG feeE thisB saud fisE yfudY ffisiG	mglA xyIF glnH mglC mglB proX modA rbsB
Aminoacyl–tRNA biosynthesis	selA alaŭ argŭ aspŭ tyrš gliX kuS pheS metG lysS	
Pyrimidine metabolism _ padj:0.00009 N(-12/ +0/ 52)	cald pyrH pyrE tupp rpoA pyrF tirdA emk pyrG ygG pyrB rpoB	
Selenoamino acid metabolism padj:0.00014 N(-7/ +0/ 14)	sel/A melt/C cysM cysD cysN cysC	
Glycine, serine and threonine metabolism padj:0.00042 N(-9/ +0/ 30)	goviff sort glyA thrA ung thrib	
One carbon pool by folate padj:0.00156 N(-6/ +0/ 12)	geVT fold purt glyA meF purh	
Pantothenate and CoA biosynthesis padj:0.00201 N(-5/ +2/ 16)	NC coalE IN1 IV4 coalD	ilvB ilvN
Protein export padj:0.00879 N(-6/ +0/ 16)	sect secA test yid0 sect weef	IIVB IIVN
Cysteine and methionine metabolism padj:0.01101 N(-7/ +0/ 23)	upot medi med cyaM ninA ung	
Biosynthesis of siderophore group nonribosomal peptides padj:0.01862 N(-4/ +0/ 6)	entë entë entë entë	
Sulfur metabolism _ padj:0.02148 N(-5/ +0/ 13)	cycill cycl cynl cync	
Arginine and proline metabolism padj:0.02230 N(–5/ +3/ 35)	speE speO speB speC gdthA	glnA argl argA
C5-Branched dibasic acid metabolism padj:0.03144 N(-2/ +2/ 7)		ilvB ilvN
Nitrogen metabolism padj:0.03710 N(-5/ +2/ 33)	noth resp. gc.7 gdfs. rii0	glnA tnaA
	$-\sin(\operatorname{rco})^* P \log 10$	