	genes_P0.05Fold2_mrna_trT_set02_StcNasMgh_S_baseNa_Exp_noFilter_p1Sf_noNormMg_mM_Levels_kegg	
Ribosome _ padj:0.00000 N(-44/ +0/ 77)	rpaS ppIW rpIV rpimC rpIP rpsA rpimI rpsC rpII rpsC rpII rpsC rpIII rpsC rpSC rpIII rpsC rpSC rpIII rpsC rpSC rpSC rpSC rpSC rpSC rpSC rpSC rpS	
ABC transporters	feeD feeE feeC cysP cysW cysA cysU nlpA livW livF dippB dppC medF touB livJ sampC feeB dppF dppD oppC tauC	ugpA alsC pstC ssuB proX alsA ssuA proW ssuC alsB modA pstS
Oxidative phosphorylation padj:0.00000 N(-13/ +0/ 41)	nuou nuot eyoA nuok ppa atpG eyoB ndn aspA	
enylalanine, tyrosine and tryptophan biosynthesis padj:0.00000 N(-10/ +0/ 21)	trpC trpE trpB pheA avoG aroE aspC avoA avoF	
Valine, leucine and isoleucine biosynthesis	INH INA IIVO IIVE INUD IIVC IINS	
Sulfur metabolism	oyal oyaM oyaM oyaM oyaM oyaM oyaM	
Purine metabolism	cysD cysN cysC purD pnp rpoC rpoB rpoA pysF add purL gusA dnaE purC holB	nrdE
Flagellar assembly	FINA figit figis figis figis figis figis	
Two-component system _ padj:0.00029 N(-12/ +5/ 115)	back trpC trpE trpD trpB phoQ cusC ompF cusB fthC cusA ginA	narl narG narH narJ pstS
Nitrogen metabolism padj:0.00039 N(-4/ +5/ 33)	BENA 9DNA 9ID 9NA	narl narG tnaA narH narJ
Aminoacyl-tRNA biosynthesis padj:0.00041 N(-8/ +0/ 25)	pheT pheS valS lyaS giX alas leS glyS	
Fatty acid biosynthesis	fabG fabH accA fabF	
Alanine, aspartate and glutamate metabolism padj:0.00088 N(-6/ +2/ 28)	asnA gimS gdhA aspC gitto glhA	pyrl putA
Glycine, serine and threonine metabolism padj:0.00173 N(-8/ +0/ 30)	th/B thr/A th/C liv/A trpB and ser/C ser/A	
Pyrimidine metabolism _ padj:0.00840 N(-7/ +2/ 52)	pyH prop rpoC rpoB rpoA druE holis	pyrl nrdE
Selenoamino acid metabolism padj:0.01940 N(–5/ +0/ 14)	cysib cysiM cysiC cysiK	
RNA degradation	rne pnp rnr deelD rhIE	
Cysteine and methionine metabolism padj:0.04465 N(-6/ +0/ 23)	cysM dvA asd supC cysK speD	
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