

TABLE S2. Differential expression of genes in isogenic strains induced with 1 mM diamide

Gene/locus	Function	Fold Change ($\Delta bshA/COL$)
Transporters		
<i>feoA</i>	Ferrous iron transport protein A	3.33
<i>feoB</i>	Ferrous iron transport protein B	4.00
SACOL0195	Maltose ABC transporter	2.63
SACOL0688	ABC transporter; Putative	2.86
<i>trkA</i>	Potassium uptake protein	2.17
<i>uhpT</i>	Hexose phosphate transport protein	4.76
Amino Acid Metabolism and Biosynthesis		
<i>ipdC</i>	Indole-3-pyruvate decarboxylase	2.38
SACOL1976	Nitric-oxide synthase, oxygenase subunit	2.56
Carbohydrate Metabolism and TCA cycle		
<i>folA</i>	Dihydrofolate reductase	2.38
<i>ldh1</i>	L-lactate dehydrogenase	2.22
<i>pckA</i>	Phosphoenolpyruvate carboxykinase	2.17
<i>pflA</i>	Formate acetyltransferase	3.57
<i>pflB</i>	Formate acetyltransferase	6.25
<i>sdhC</i>	Succinate dehydrogenase cytochrome B-558	2.33
<i>treP</i>	PTS system, trehalose-specific IIBC component	2.44
<i>gpm</i>	Phosphoglycerate mutase	2.33
Virulence Factors		
<i>cidA</i>	Holin-like protein	3.70
<i>coa</i>	Staphylocoagulase precursor	6.25
<i>hla</i>	Alpha-hemolysin precursor	3.13
<i>isdA</i>	LPXTG cell wall surface anchor protein	-2.99
<i>isdC</i>	Iron-regulated cell surface protein	-3.68
Transcriptional Regulators		
<i>nirR</i>	Transcriptional regulator	2.27
SACOL1296	GntR family transcriptional regulator	-2.01

SACOL0218	MarR family member	3.23
SACOL1242	Fatty acid biosynthesis transcriptional regulator; Putative	2.17

Hypothetical & Putative Proteins

<i>bshA</i>	Glycosyl transferase involved in BSH biosynthesis	-137.14
<i>crtM</i>	Squalene desaturase	2.63
<i>crtN</i>	Squalene synthase	2.08
<i>crtQ</i>	Glycosyl transferase, group 2 family protein	2.50
<i>cydA</i>	Cytochrome d ubiquinol oxidase, subunit I	2.63
<i>deoD</i>	Purine nucleoside phosphorylase	3.23
<i>fntB</i>	Cell wall-associated protein	2.27
<i>groEL</i>	Chaperonin	-2.31
<i>groES</i>	Co-chaperonin	-2.65
<i>lytH</i>	N-acetylmuramoyl-L-alanine amidase	-2.19
<i>mntC</i>	Iron-repressed lipoprotein	2.94
<i>mraY</i>	Phospho-N-acetylmuramoyl-pentapeptide-transferase	2.17
<i>nanA</i>	N-acetylneuraminatase lyase	2.17
<i>nuc</i>	Thermonuclease precursor	-2.67
<i>purE</i>	Phosphoribosylaminoimidazole carboxylase, catalytic subunit	2.13
<i>sodA</i>	Superoxide dismutase	-2.00
<i>sodM</i>	Manganese/iron superoxide dismutase	-2.00
<i>srrA</i>	Staphylococcal respiratory response protein	2.38
<i>sucA</i>	2-oxoglutarate dehydrogenase E1 component	2.13

Other

<i>cidB</i>	Unknown function	2.70
<i>plsX</i>	Glycerol-3-phosphate acyltransferase; Putative	2.17
SACOL0223	Unknown function	2.27
SACOL0606	HAD superfamily hydrolase	-2.02
SACOL0851	Lipoprotein; Putative	-2.31
SACOL0871	GNAT family acetyltransferase	-2.08
SACOL1502	IDEAL family protein	2.04
SACOL1503	Tetratricopeptide repeat family protein	2.13
SACOL1846	Excalibur calcium-binding domain protein	3.70
SACOL2402	S-transferase; Putative	-2.04

SACOL2425	8-amino-7-oxononanoate synthase; Putative	2.13
SACOL2491	Unknown function	3.33
SACOL2579	Phytoene dehydrogenase; Putative	2.63
SACOL2676	LPXTG-containing protein	2.00

*Change in *bshA* mutant induced with 1 mM diamide relative to wild type induced in 1 mM diamide.