

TABLE S1. Differential expression of genes in COL induced with 1 mM diamide

Gene/locus	Function	Fold change (Diamide/TSB)
Transporters		
<i>aapA</i>	D-serine/D-alanine/glycine transporter	-4.07
<i>brnQ1</i>	Branched-chain amino acid transport system II carrier	-8.00
<i>copA</i>	Copper-transporting ATPase	4.40
<i>cycA</i>	D-serine/D-alanine/glycine transporter	-4.09
<i>feoA</i>	Ferrous iron transport protein A	-2.76
<i>fhuA</i>	Ferrichrome transport ATP-binding protein	2.50
<i>fhuB</i>	Ferrichrome transport permease	2.61
<i>fhuD</i>	Ferrichrome transport permease	3.15
<i>glpT</i>	Glycerol-3-phosphate transporter	-5.74
<i>nhaC</i>	Na ⁺ /H ⁺ antiporter	-2.33
<i>nixA</i>	High-affinity nickel-transport protein	3.06
<i>nupC</i>	Nucleoside permease	-10.83
<i>opp-2C</i>	Peptide ABC transporter, permease protein	2.67
<i>opp-2D</i>	Peptide ABC transporter, ATP-binding protein	3.16
<i>opuBB</i>	Osmoprotectant ABC transporter, permease protein	3.44
<i>opuD</i>	Glycine betaine transporter	-3.12
<i>putP</i>	High affinity proline permease	-3.00
<i>rarD</i>	Superfamily drug/metabolite transporter	4.58
SACOL0261	Putative drug transporter	4.85
SACOL0305	Permease; Putative	-3.35
SACOL0665	Iron compound-binding ABC transporter; Putative	-4.79
SACOL0687	Na ⁺ /H ⁺ antiporter; Putative	3.56
SACOL0688	ABC transporter, substrate-binding protein	-9.11
SACOL0701	Nucleoside permease	-3.50
SACOL0722	Inorganic phosphate transporter	-2.21
SACOL0733	Sugar efflux transporter; Putative	2.62
SACOL0744	ABC transporter ATP-binding protein	3.41
SACOL0745	ABC transporter ATP-binding protein	3.39
SACOL0781	Osmoprotectant ABC transporter, ATP-binding protein; Putative	2.94

SACOL0788	Proton-dependent oligopeptide transporter family protein	-3.95
SACOL1367	Amino acid permease	-5.78
SACOL1743	Amino acid permease	-4.03
SACOL2011	Sodium transport family protein	2.32
SACOL2170	Transporter; Putative	7.37
SACOL2242	Xanthine/uracil permease family protein	-2.72
SACOL2279	Transporter; Putative	4.03
SACOL2335	ABC transporter, ATP-binding protein; Putative	-6.05
SACOL2401	Formate/nitrite transporter family protein	-4.04
SACOL2403	ABC transporter, substrate-binding protein; Putative	-3.00
SACOL2416	Cation efflux family protein; Putative	2.30
SACOL2430	ABC transporter permease; Putative	2.58
SACOL2718	Anion transporter family protein	-2.26
<i>sirA</i>	Iron compound ABC transporter	-3.25
<i>tagH</i>	Teichoic acids export protein ATP-binding subunit	3.54
<i>vraD</i>	ABC transporter ATP-binding protein	2.99
<i>vraE</i>	ABC transporter, permease protein	2.29

PTS system

<i>glcA</i>	Glucose-specific PTS transporter protein, IIABC component	-10.93
<i>nagE</i>	N-acetylglucosamine-specific IIBC component	-3.53
<i>ptaA</i>	N-acetylglucosamine-specific IIABC component	-3.64
<i>ptsG</i>	PTS system glucose-specific IIBC subunit	-10.93
<i>treP</i>	phosphoenolpyruvate-dependent, trehalose-specific	-4.91

Amino Acid Metabolism and Biosynthesis

<i>femC</i>	Glutamine synthetase	-8.36
<i>glnA</i>	Glutamine-ammonia ligase	-8.20
<i>glnR</i>	Glutamine synthetase repressor	-9.50
<i>glyA</i>	Serine hydroxymethyltransferase	-2.25
<i>hisC</i>	Histidinol-phosphate aminotransferase	3.37
<i>hutG</i>	Formimidoylglutamase	-2.36
<i>ipdC</i>	Indole-3-pyruvate decarboxylase	2.36

<i>murl</i>	Glutamate racemase	5.14
<i>purB</i>	Adenylosuccinate lyase	-5.68
<i>rocA</i>	1-pyrroline-5-carboxylate dehydrogenase	6.02
<i>rocD</i>	Ornithine-oxo-acid transaminase	2.54
SACOL1801	Dipeptidase PepV	-3.84
SACOL2114	Aldehyde dehydrogenase (NAD ⁺)	4.08

Carbohydrate Metabolism and TCA cycle

<i>ccpA</i>	Catabolite control protein	2.41
<i>cidC</i>	Pyruvate oxidase	2.52
<i>manA1</i>	Mannose-6-phosphate isomerase	-4.40
<i>manA2</i>	Mannose-6-phosphate isomerase	-3.86
<i>mnaA</i>	UDP-GlcNAc 2-epimerase	-2.58
<i>panB</i>	3-methyl-2-oxobutanoate hydroxymethyltransferase	2.70
<i>panC</i>	Pantoate-beta-alanine ligase	2.67
<i>panD</i>	Aspartate alpha-decarboxylase	2.84
<i>pflB</i>	Formate acetyltransferase	-2.49
SACOL1439	Acylphosphatase	2.40
SACOL2103	UDP-GlcNAc 2-epimerase	-2.61
<i>sdhA</i>	Succinate dehydrogenase flavoprotein subunit	-4.00
<i>sdhB</i>	Succinate dehydrogenase iron-sulfur subunit	-3.56
<i>sdhC</i>	Succinate dehydrogenase cytochrome b-558	-3.38
<i>sucA</i>	2-oxoglutarate dehydrogenase E1 component	-3.05

Nucleotide Excision and Repair

<i>mutS2</i>	Recombination and DNA strand exchange inhibitor protein	2.71
<i>radA</i>	DNA repair	4.69
<i>radC</i>	DNA repair protein	4.68
SACOL1954	Exonuclease	-3.47
<i>uvrA</i>	Excinuclease ABC subunit A	2.67
<i>uvrB</i>	Excinuclease ABC subunit B	2.97
<i>uvrC</i>	Excinuclease ABC subunit C	3.37

Virulence Factors

<i>capC</i>	Capsular polysaccharide biosynthesis protein	-4.47
<i>capD</i>	Capsular polysaccharide biosynthesis protein	-4.82
<i>capF</i>	Capsular polysaccharide biosynthesis protein	-2.20
<i>capG</i>	Capsular polysaccharide biosynthesis protein	-2.56
<i>crtM</i>	Squalene desaturase	-3.50
<i>crtN</i>	Squalene synthase	-3.87
<i>crtQ</i>	Glycosyl transferase	-3.65
<i>ebh</i>	Cell wall associated fibronectin-binding protein	5.99
<i>fntA</i>	Autolysis and methicillin resistant-related protein	-3.16
<i>geh</i>	Glycerol ester hydrolase, lipase precursor	-3.25
<i>hla</i>	Alpha-hemolysin precursor	-6.37
<i>isdA</i>	Iron-regulated heme-iron binding protein	-5.11
<i>mntC</i>	Iron-repressed lipoprotein	-9.11
<i>plc</i>	1-phosphatidylinositol phosphodiesterase precursor	-4.17
SACOL1220	Fibronectin/fibrinogen binding-related protein	3.47
<i>spa</i>	Immunoglobulin G binding protein A precursor	-3.56
<i>sspA</i>	Serine protease	-2.28

Transcriptional Regulators

<i>arsR</i>	Transcriptional regulator	4.75
<i>czrA</i>	Transcriptional regulator	4.76
<i>nirR</i>	Transcriptional regulator	-5.67
<i>norR</i>	MarR family transcriptional regulator	-2.25
SACOL0980	LysR family transcriptional regulator	3.75
SACOL1296	GntR family transcriptional regulator	-2.24
SACOL1550	AraC family transcriptional regulator	2.52
SACOL2325	LysR family transcriptional regulator	-2.21
<i>spxA</i>	Transcriptional regulator	-2.33

Other

<i>acpD</i>	Azoreductase	22.28
<i>adaB</i>	Methylated DNA-protein cysteine methyltransferase	2.33

<i>atpA</i>	F0F1 ATP synthase subunit alpha	-3.15
<i>atpB</i>	F0F1 ATP synthase subunit A	-3.34
<i>atpC</i>	F0F1 ATP synthase subunit epsilon	-2.43
<i>atpD</i>	F0F1 ATP synthase subunit beta	-2.62
<i>atpE</i>	F0F1 ATP synthase subunit C	-2.91
<i>atpF</i>	F0F1 ATP synthase subunit B	-3.05
<i>atpG</i>	F0F1 ATP synthase subunit gamma	-2.86
<i>atpH</i>	F0F1 ATP synthase subunit delta	-2.98
<i>bshA</i>	Glycosyl transferase involved in bacillithiol biosynthesis	2.31
<i>bshC</i>	Bacillithiol synthase	5.20
<i>cinA</i>	Competence/damage-inducible protein	2.67
<i>clpB</i>	ClpB chaperone-like protein	34.39
<i>clpP</i>	ATP-dependent Clp protease, proteolytic subunit	5.35
<i>ctaA</i>	Cytochrome oxidase assembly protein	-2.38
<i>ctaB</i>	Protoheme IX farnesyltransferase	-2.50
<i>cysE</i>	Serine acetyltransferase-like protein	2.62
<i>cysJ</i>	Sulfite reductase (NADPH) flavoprotein alpha-component	2.72
<i>def</i>	Peptide deformylase	2.39
<i>dfrA/foIA</i>	Dihydrofolate reductase	-3.00
<i>dnaK</i>	Molecular chaperone	7.93
<i>ezrA</i>	Septation ring formation regulator	-2.37
<i>fdhD</i>	Formate dehydrogenase accessory protein	3.76
<i>fer</i>	Ferredoxin	2.91
<i>ftn</i>	Ferritin	-5.00
<i>fumC</i>	Fumarate hydratase	-3.44
<i>gatA</i>	Aspartyl/glutamyl-tRNA amidotransferase subunit A	-2.99
<i>gatB</i>	Aspartyl/glutamyl-tRNA amidotransferase subunit B	-2.61
<i>gatC</i>	Aspartyl/glutamyl-tRNA amidotransferase subunit C	5.33
<i>glcT</i>	Transcription antiterminator	2.67
<i>glpQ</i>	Glycerophosphoryl diester phosphodiesterase	-2.77
<i>groEL</i>	Chaperonin	7.17
<i>groES</i>	Co-chaperonin	7.25
<i>grpE</i>	Heat shock protein	6.76

<i>guaC</i>	Guanosine 5'-monophosphate oxidoreductase	-3.91
<i>hsIO</i>	Hsp33-like chaperonin	3.92
<i>lytH</i>	N-acetylmuramoyl-L-alanine amidase	-3.31
<i>metG</i>	Methionyl-tRNA synthetase	-2.30
<i>mnmA</i>	tRNA-specific 2-thiouridylase	2.67
<i>moaA</i>	Molybdenum cofactor biosynthesis protein A	2.34
<i>moaD</i>	Molybdopterin converting factor, subunit 1	2.40
<i>mobA</i>	Molybdopterin-guanine dinucleotide biosynthesis protein A	2.42
<i>modA</i>	Molybdate-binding protein	-2.49
<i>mraY</i>	Phospho-N-acetylmuramoyl-pentapeptide-transferase	-2.93
<i>nth</i>	Endonuclease-like protein; Base excision repair	2.65
<i>nuc</i>	Thermonuclease precursor	-35.53
<i>pbp4</i>	Penicillin-binding protein 4	-2.41
<i>pepA1</i>	Glutamyl aminopeptidase	2.42
<i>pepF</i>	Oligoendopeptidase F	-6.38
<i>prmA</i>	Ribosomal protein L11 methyltransferase	5.79
<i>purC</i>	Phosphoribosylaminoimidazole carboxylase, catalytic subunit	-2.56
<i>purE</i>	Phosphoribosylaminoimidazole carboxylase, catalytic subunit	-6.55
<i>purK</i>	Phosphoribosylaminoimidazole carboxylase ATPase subunit	-6.55
<i>purQ</i>	Phosphoribosylformylglycinamide synthase I	-11.12
<i>purS</i>	Phosphoribosylformylglycinamide synthase	-7.22
<i>pyrH</i>	Uridylate kinase	-2.70
<i>qoxA</i>	Quinol oxidase, subunit I	-2.63
<i>qoxB</i>	Quinol oxidase, subunit II	-2.77
<i>qoxC</i>	Quinol oxidase polypeptide III	-2.74
<i>qoxD</i>	Quinol oxidase polypeptide IV	-3.72
<i>recJ</i>	Single-stranded-DNA-specific exonuclease	2.52
<i>recX</i>	Recombination regulator	2.33
<i>rexA</i>	Exonuclease	2.51
<i>ribAB</i>	Riboflavin biosynthesis protein	4.88
<i>ribE</i>	Riboflavin synthase subunit alpha	4.61
<i>ribF</i>	Riboflavin biosynthesis protein	2.52
<i>ribH</i>	6,7-dimethyl-8-ribityllumazine synthase	3.91

<i>sigB</i>	RNA polymerase sigma factor SigB	-3.29
<i>rsbV</i>	Anti-sigma-B factor	-2.30
<i>rsbW</i>	Serine-protein kinase	-3.29
<i>sasF</i>	Fatty-acid responsive surface-anchored protein	2.33
<i>smbA</i>	Uridylate kinase	-2.66
<i>srrA</i>	Staphylococcal respiratory response protein	-2.46
<i>thiD</i>	Phosphomethylpyrimidine kinase	2.57
<i>truB</i>	tRNA pseudouridine 5s synthase	2.50
<i>ung</i>	Uracil-DNA glycosylase	-2.98
<i>upp</i>	Uracil phosphoribosyltransferase	-2.65
<i>ureA</i>	Urease subunit gamma	3.89
<i>ureC</i>	Urease subunit alpha	2.77
<i>ureD</i>	Urease accessory protein	2.39
<i>ureE</i>	Urease accessory protein	2.38
<i>ypfP</i>	Diacylglycerol glucosyltransferase	2.62
<i>zwf</i>	Glucose-6-phosphate 1-dehydrogenase	3.38

Hypothetical and Putative Proteins

SACOL1440	Hypothetical protein	2.48
SACOL1444	Hypothetical protein	2.29
SACOL1491	Hypothetical protein	3.07
SACOL1493	DNA replication protein; Putative	2.91
SACOL1501	Hypothetical protein	2.30
SACOL1520	Pyridine nucleotide-disulfide oxidoreductase	4.24
SACOL1526	Hypothetical protein	4.01
SACOL1553	Glyoxalase family protein	2.46
SACOL1555	M20/M25/M40 family peptidase	3.85
SACOL1557	Hypothetical protein	2.79
SACOL1607	5-formyltetrahydrofolate cyclo-ligase family protein	-2.80
SACOL1634	16S ribosomal RNA methyltransferase	2.79
SACOL1677	Aminotransferase, class V	3.21
SACOL1678	Luciferase family protein	22.17
SACOL1705	Hypothetical protein	-3.05

SACOL1749	NADP-dependent malic enzyme; Putative	-2.20
SACOL1753	Universal stress protein	-2.92
SACOL1768	GAF domain-containing protein	2.79
SACOL1770	Glycerophosphoryl diester phosphodiesterase; Putative	-2.82
SACOL1771	OsmC/Ohr family protein	5.09
SACOL1776	1-acyl-sn-glycerol-3-phosphate acyltransferase; Putative	-5.45
SACOL1826	Hypothetical protein	2.57
SACOL1827	RNA polymerase sigma-70 family protein	2.35
SACOL1835	Aldo/keto reductase family oxidoreductase	2.42
SACOL1846	Hypothetical protein	-4.49
SACOL1846	Hypothetical protein	-4.49
SACOL1939	Phosphotyrosine protein phosphatase	-2.38
SACOL1941	Ribonuclease; Putative	-8.10
SACOL1952	Ferritins family protein	-5.12
SACOL1976	Nitric-oxide synthase, oxygenase subunit	-3.43
SACOL1983	Hypothetical protein	4.30
SACOL1998	Hypothetical protein	3.89
SACOL2020	Hypothetical protein	10.21
SACOL2021	Carbon-nitrogen family hydrolase	5.57
SACOL2037	Hypothetical protein	-4.11
SACOL2102	Hypothetical protein	-3.01
SACOL2106	Hypothetical protein	-2.53
SACOL2107	Phosphotyrosine protein phosphatase	-2.35
SACOL2134	Hypothetical protein	-3.56
SACOL2136	Hypothetical protein	-2.73
SACOL2168	Hypothetical protein	2.78
SACOL2169	Aerobactin biosynthesis protein	3.58
SACOL2174	Hypothetical protein	-3.80
SACOL2175	Hypothetical protein	-4.13
SACOL2177	Alcohol dehydrogenase; Putative	3.48
SACOL2178	Alcohol dehydrogenase; Putative	4.20
SACOL2179	Hypothetical protein	4.55
SACOL2193	MerR family transcriptional regulator	4.02

SACOL2241	Hypothetical protein	3.80
SACOL2247	Hypothetical protein	7.63
SACOL2293	NAD/NADP octopine/nopaline dehydrogenase family protein	-3.21
SACOL2294	Hypothetical protein	-2.70
SACOL2300	Hypothetical protein	-4.90
SACOL2330	Hypothetical protein	2.39
SACOL2334	Hypothetical protein	-3.09
SACOL2344	Hypothetical protein	2.66
SACOL2368	Acetyltransferase; Putative	5.24
SACOL2369	Pyridine nucleotide-disulfide oxidoreductase	4.26
SACOL2391	Hypothetical protein	-2.55
SACOL2400	Acetyltransferase; Putative	2.98
SACOL2439	Hypothetical protein	6.06
SACOL2440	Hypothetical protein	7.25
SACOL2446	Epimerase/dehydratase; Putative	2.55
SACOL2520	Hypothetical protein	2.57
SACOL2549	Hypothetical protein	4.56
SACOL2550	Hypothetical protein	6.58
SACOL2551	Hypothetical protein	7.30
SACOL2554	Hypothetical protein	2.31
SACOL2554.1	Holin-like protein	2.40
SACOL2570	Galactoside O-acetyltransferase	12.67
SACOL2573	Copper ion binding protein; Putative	11.39
SACOL2579	Phytoene dehydrogenase; Putative	-4.33
SACOL2580	Hypothetical protein	-4.29
SACOL2588	Hypothetical protein	6.62
SACOL2589	Hypothetical protein	5.99
SACOL2598	Cobalamin synthesis protein; Putative	2.65
SACOL2599	Hypothetical protein	2.53
SACOL2638	Precorrin-2 dehydrogenase; Putative	2.58
SACOL2717	Hypothetical protein	-4.03
SACOL2733	Hypothetical protein	-2.45
sarV	Hypothetical protein	2.42

<i>tal</i>	Transaldolase; Putative	4.47
<i>tpx</i>	Thiol peroxidase; Putative	2.34
<i>veg</i>	Hypothetical protein	-2.46

Fold change determined for expression of genes in COL grown in TSB with diamide over expression in COL grown in TSB alone