

S. aureus COL Locus	Gene	t0 v t10 ¹	t0 v t40 ¹	t10 v t40 ¹	expr. ²	SigB ³	linoleic acid ⁴	functional gene annotation	cellular role category
SACOL0247	IrgA	8.64	-1.04	-8.99	C1		↓	holin-like protein IrgA	Cell envelope: Biosynthesis and degradation of murein sacculus and peptidoglycan
SACOL0248	IrgB	14.03	1.45	-9.69	C1			IrgB protein	Cell envelope: Biosynthesis and degradation of murein sacculus and peptidoglycan
SACOL0740	-	2.65	-1.24	-3.30	C1	☉	↑	decarboxylase family protein	Unknown function: Enzymes of unknown specificity
SACOL0741	-	3.19	1.30	-2.45	C1	☉	↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0742	-	3.43	1.29	-2.66	C1	☉		conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0866	-	5.43	1.98	-2.74	C1			hypothetical protein	-
SACOL1074	purK	2.31	-1.34	-3.09	C1			phosphoribosylaminoimidazole carboxylase, ATPase subunit	Purines, pyrimidines, nucleosides, and nucleotides: Purine ribonucleotide biosynthesis
SACOL1076	purS	2.22	-1.13	-2.50	C1			phosphoribosylformylglycinamide synthase, PurS protein	Purines, pyrimidines, nucleosides, and nucleotides: Purine ribonucleotide biosynthesis
SACOL1077	purQ	2.54	-1.86	-4.71	C1			phosphoribosylformylglycinamide synthase I	Purines, pyrimidines, nucleosides, and nucleotides: Purine ribonucleotide biosynthesis
SACOL1078	purL	2.10	-1.62	-3.41	C1			phosphoribosylformylglycinamide synthase II	Purines, pyrimidines, nucleosides, and nucleotides: Purine ribonucleotide biosynthesis
SACOL1080	purM	3.11	1.47	-2.12	C1			phosphoribosylformylglycinamide cyclo-ligase	Purines, pyrimidines, nucleosides, and nucleotides: Purine ribonucleotide biosynthesis
SACOL1090	-	2.35	-1.47	-3.45	C1	☉	↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1226	-	2.86	-1.06	-3.03	C1			conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1236	-	1.79	-1.54	-2.76	C1			thiamine pyrophosphokinase	Biosynthesis of cofactors, prosthetic groups, and carriers: Thiamine
SACOL1373	-	3.75	1.47	-2.55	C1			conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1398	-	1.89	-1.41	-2.67	C1			transcriptional regulator, putative	Regulatory functions: Other
SACOL1602	-	2.25	-1.61	-3.63	C1		↑	metallo-beta-lactamase family protein	Unknown function: Enzymes of unknown specificity
SACOL1647	-	1.96	-1.46	-2.86	C1			conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1735	coaE	2.09	-1.41	-2.95	C1			dephospho-CoA kinase	Biosynthesis of cofactors, prosthetic groups, and carriers: Pantothenate and coenzyme A
SACOL1745	pyk	2.67	-1.66	-4.42	C1			pyruvate kinase	Energy metabolism: Glycolysis/gluconeogenesis
SACOL1789	-	2.23	-1.34	-3.00	C1	☉		conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1895	-	3.11	1.17	-2.66	C1			conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1897	-	2.39	-1.06	-2.55	C1			protein export protein PrsA, putative	Protein fate: Protein and peptide secretion and trafficking
SACOL1898	cbf1	2.51	1.19	-2.11	C1			cmp-binding factor 1	Mobile and extrachromosomal element functions: Plasmid functions
SACOL1912	-	2.65	1.45	-1.82	C1	☉		glucosamine-6-phosphate isomerase, putative	Central intermediary metabolism: Amino sugars
SACOL1933	-	4.68	1.76	-2.66	C1	☉	↑	Thu/PrpI family protein	Unknown function: General
SACOL1934	-	3.37	1.50	-2.24	C1	☉		conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1941	yihY	2.95	-1.13	-3.34	C1	☉		YihY family protein	Unknown function: General
SACOL2091	fabZ	4.02	-1.02	-4.08	C1	☉	↑	beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabZ	Fatty acid and phospholipid metabolism: Biosynthesis
SACOL2132	-	2.50	1.46	-1.71	C1	☉		conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2136	-	4.11	1.38	-2.97	C1	☉	↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2174	-	5.38	1.74	-3.09	C1	☉	↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2175	-	5.70	1.29	-4.41	C1	☉	↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2242	-	2.32	-1.10	-2.55	C1			xanthine/uracil permease family protein	Transport and binding proteins: Nucleosides, purines and pyrimidines
SACOL2300	-	3.13	1.09	-2.87	C1	☉	↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2301	-	3.45	1.47	-2.35	C1	☉	↑	formate dehydrogenase, alpha subunit, putative	Energy metabolism: Anaerobic
SACOL2302	-	2.51	-1.19	-2.98	C1	☉	↑	transcriptional regulator, putative	Regulatory functions: Other
SACOL2321	-	3.42	1.58	-2.16	C1	☉	↑	oxidoreductase, short chain dehydrogenase/reductase family	Unknown function: Enzymes of unknown specificity
SACOL2327	hutG	2.57	-1.06	-2.74	C1	☉	↑	formiminoglutamate	Energy metabolism: Amino acids and amines
SACOL2329	rpiA	2.76	-1.40	-3.86	C1			ribose 5-phosphate isomerase	Energy metabolism: Pentose phosphate pathway
SACOL2379	-	3.36	1.32	-2.55	C1	☉	↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2394	narH	3.26	1.20	-2.73	C1		↑	respiratory nitrate reductase, beta subunit	Energy metabolism: Anaerobic; Energy metabolism: Electron transport; Central intermediary metabolism: Nitrogen metabolism
SACOL2395	narG	3.49	1.17	-2.98	C1		↑	respiratory nitrate reductase, alpha subunit	Energy metabolism: Anaerobic; Energy metabolism: Electron transport; Central intermediary metabolism: Nitrogen metabolism
SACOL2563	clpL	2.53	1.08	-2.34	C1	☉	↑	ATP-dependent Clp protease, putative	Protein fate: Degradation of proteins, peptides, and glycopeptides
SACOL2578	-	1.88	-1.37	-2.59	C1	☉	↑	glycosyl transferase, group 2 family protein	Cell envelope: Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides
SACOL2596	-	2.89	1.14	-2.53	C1	☉	↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2597	-	3.50	1.39	-2.52	C1	☉	↑	hydrolase, alpha/beta hydrolase fold family	Unknown function: Enzymes of unknown specificity
SACOL2609	-	2.31	-1.79	-4.14	C1	☉	↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2621	-	2.94	1.03	-2.86	C1			hypothetical protein	-
SACOL2625	-	3.33	1.18	-2.83	C1	☉	↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2681	-	2.90	1.54	-1.88	C1	☉	↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2717	-	2.83	-1.21	-3.42	C1			hypothetical protein	-
SACOL0012	-	1.06	2.84	2.69	C2			homoserine O-acetyltransferase, putative	Amino acid biosynthesis: Aspartate family
SACOL0184	-	1.25	4.03	3.23	C2			peptide ABC transporter, ATP-binding protein	Transport and binding proteins: Amino acids, peptides and amines
SACOL0263	lytM	1.12	3.86	3.43	C2			peptidoglycan hydrolase	Cell envelope: Biosynthesis and degradation of murein sacculus and peptidoglycan
SACOL0428	metE	1.18	2.80	2.38	C2			5-methyltetrahydropteroyltryptophan-homocysteine methyltransferase	Amino acid biosynthesis: Aspartate family
SACOL0504	-	-1.19	4.44	5.29	C2			ABC transporter, ATP-binding protein	Transport and binding proteins: Unknown substrate
SACOL0505	-	1.33	6.67	5.00	C2			ABC transporter, permease protein	Transport and binding proteins: Unknown substrate
SACOL0514	gltB	-1.03	3.48	3.57	C2			glutamate synthase, large subunit	Amino acid biosynthesis: Glutamate family
SACOL0515	gltD	1.21	3.87	3.19	C2			glutamate synthase, small subunit	Amino acid biosynthesis: Glutamate family
SACOL0517	treC	1.18	3.23	2.74	C2			alpha,alpha-phosphotrehalase	Energy metabolism: Biosynthesis and degradation of polysaccharides
SACOL0641	-	1.11	2.62	2.37	C2		↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0712	-	-1.16	3.11	3.60	C2			lipase/esterase	Fatty acid and phospholipid metabolism: Degradation
SACOL0770	-	1.21	4.81	3.96	C2			radical activating enzyme family protein	Unknown function: Enzymes of unknown specificity
SACOL0771	-	1.30	5.31	4.09	C2		↑	6-pyruvoyl tetrahydrobiopterin synthase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers: Other
SACOL0772	-	1.01	4.29	4.25	C2			exsB protein	Unknown function: General
SACOL0802	-	-1.17	3.77	4.43	C2		↓	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0813	-	1.26	3.07	2.43	C2			comF operon protein 1, putative	Cellular processes: DNA transformation
SACOL0845	est	1.26	3.31	2.63	C2			carboxylesterase	Cellular processes: Detoxification; Fatty acid and phospholipid metabolism: Degradation
SACOL0870	-	1.20	2.66	2.22	C2			LysE/YgaA family protein	Unknown function: General
SACOL0882	-	-1.21	4.53	5.49	C2			ABC transporter, ATP-binding protein	Transport and binding proteins: Unknown substrate
SACOL0883	-	-1.06	5.19	5.50	C2			ABC transporter, permease protein	Transport and binding proteins: Unknown substrate
SACOL0884	-	1.10	4.39	3.98	C2			ABC transporter, substrate-binding protein	Transport and binding proteins: Unknown substrate
SACOL1032	-	-1.15	3.87	4.44	C2			ComK family protein	Unknown function: General
SACOL1268	gid	1.09	2.60	2.39	C2		↑	Gid protein	Unknown function: General
SACOL1375	-	1.18	3.67	3.11	C2			conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1414	-	1.19	3.08	2.59	C2			peptide ABC transporter, ATP-binding protein	Transport and binding proteins: Amino acids, peptides and amines
SACOL1415	-	1.09	3.06	2.80	C2			peptide ABC transporter, ATP-binding protein	Transport and binding proteins: Amino acids, peptides and amines
SACOL1416	-	1.00	4.13	4.12	C2			peptide ABC transporter, permease protein, putative	Transport and binding proteins: Amino acids, peptides and amines
SACOL1417	-	1.26	5.78	4.60	C2			peptide ABC transporter, permease protein	Transport and binding proteins: Amino acids, peptides and amines
SACOL1442	-	1.14	2.66	2.33	C2			peptide ABC transporter, permease protein	Transport and binding proteins: Amino acids, peptides and amines
SACOL1468	-	1.24	2.89	2.33	C2			IS1272-related, transposase, degenerate	Mobile and extrachromosomal element functions: Transposon functions; Disrupted reading frame
SACOL1490	pbp2	1.17	2.59	2.21	C2			membrane protein, putative	Cell envelope: Other
SACOL1541	-	1.34	4.01	3.00	C2		↓	penicillin-binding protein 2	Cell envelope: Biosynthesis and degradation of murein sacculus and peptidoglycan
SACOL1724	-	1.14	3.14	2.75	C2			transcriptional regulator, Fur family	Transport and binding proteins: Cations and iron carrying compounds; Regulatory functions: DNA interactions
								MutT/nudix family protein	DNA metabolism: DNA replication, recombination, and repair

SACOL1830	-	-1.13	2.41	2.73	C2	abortive infection protein family	Unknown function: General
SACOL1870	-	1.02	3.18	3.12	C2	hypothetical protein	-
SACOL1880	lukD	1.15	2.78	2.42	C2	leukotoxin LukD	Cellular processes: Toxin production and resistance; Cellular processes: Pathogenesis
SACOL1881	lukE	-1.17	2.82	3.29	C2	leukotoxin LukE	Cellular processes: Toxin production and resistance; Cellular processes: Pathogenesis
SACOL1954	-	1.07	3.24	3.04	C2	exonuclease	Unknown function: Enzymes of unknown specificity
SACOL2020	-	-1.05	3.47	3.66	C2	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2033	-	-1.03	4.20	4.32	C2	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2034	-	-1.01	4.54	4.60	C2	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2066	kdjC	1.24	3.59	2.89	C2	K ⁺ -transporting ATPase, C subunit	Transport and binding proteins: Cations and iron carrying compounds
SACOL2081	-	-1.03	4.59	4.75	C2	hypothetical protein	-
SACOL2322	-	1.28	3.49	2.72	C2	peptidase, M20/M25/M40 family	Protein fate: Degradation of proteins, peptides, and glycopeptides
SACOL2458	-	1.06	4.25	3.99	C2	amino acid permease	Transport and binding proteins: Amino acids, peptides and amines
SACOL2466	-	1.16	5.43	4.69	C2	hypothetical protein	-
SACOL2483	-	1.26	3.07	2.43	C2	transporter, putative	Transport and binding proteins: Unknown substrate
SACOL2544	sdaAA	1.11	4.00	3.62	C2	L-serine dehydratase, iron-sulfur-dependent, alpha subunit	Energy metabolism: Amino acids and amines
SACOL2545	sdaAB	1.07	6.96	6.53	C2	L-serine dehydratase, iron-sulfur-dependent, beta subunit	Energy metabolism: Amino acids and amines
SACOL2546	-	1.06	6.29	5.91	C2	perfringolysin O regulator protein, putative	Regulatory functions: Other
SACOL2588	-	1.03	2.90	2.82	C2	hypothetical protein	-
SACOL2615	panB	1.03	2.97	2.88	C2	3-methyl-2-oxobutanoate hydroxymethyltransferase	Biosynthesis of cofactors, prosthetic groups, and carriers: Pantothenate and coenzyme A
SACOL0007	-	1.55	2.74	1.76	C3	YjeF-related protein	Unknown function: General
SACOL0061	-	1.55	2.61	1.68	C3	conserved domain protein	Hypothetical proteins: Domain
SACOL0129	-	1.36	2.79	2.05	C3	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0178	-	1.78	2.74	1.54	C3	PTS system, IIBC components	Transport and binding proteins: Carbohydrates, organic alcohols, and acids; Signal transduction: PTS
SACOL0210	-	1.57	3.08	1.97	C3	hypothetical protein	-
SACOL0212	-	1.61	3.13	1.95	C3	3-hydroxyacyl-CoA dehydrogenase protein	Fatty acid and phospholipid metabolism: Degradation
SACOL0231	-	1.62	3.27	2.02	C3	hypothetical protein	-
SACOL0308	-	1.44	2.71	1.89	C3	carbohydrate kinase, PfkB family	Energy metabolism: Sugars
SACOL0309	-	1.64	3.82	2.33	C3	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0310	-	2.29	4.54	1.99	C3	nucleoside permease NupC, putative	Transport and binding proteins: Nucleosides, purines and pyrimidines
SACOL0324	-	1.51	2.74	1.81	C3	hypothetical protein	-
SACOL0333	-	1.60	2.50	1.56	C3	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0334	-	1.57	2.56	1.63	C3	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0413	-	1.57	2.65	1.68	C3	ribosomal-protein-serine acetyltransferase, putative	Protein synthesis: Ribosomal proteins: synthesis and modification
SACOL0414	-	1.57	3.53	2.25	C3	lipoprotein, putative	Cell envelope: Other
SACOL0415	-	1.31	2.75	2.10	C3	Dyp-type peroxidase family protein	Unknown function: Enzymes of unknown specificity
SACOL0442	-	1.64	2.59	1.58	C3	staphylococcal enterotoxin, putative	Cellular processes: Toxin production and resistance
SACOL0462	-	1.47	2.62	1.78	C3	hypothetical protein	-
SACOL0754	norA	1.64	3.62	2.20	C3	multi drug resistance protein (norA)	Cellular processes: Toxin production and resistance; Transport and binding proteins: Other
SACOL0757	-	1.59	3.79	2.38	C3	transcriptional regulator, DeoR family	Regulatory functions: DNA interactions
SACOL0758	fruK	1.69	4.58	2.70	C3	↓ 1-phosphofruktokinase	Energy metabolism: Glycolysis/gluconeogenesis
SACOL0804	-	2.05	3.45	1.69	C3	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0814	-	1.43	2.95	2.06	C3	competence protein F	Cellular processes: DNA transformation
SACOL0820	-	1.31	2.68	2.05	C3	LysM domain protein	Unknown function: General
SACOL0846	-	2.07	4.05	1.96	C3	↑ exoribonuclease, VacB/RNase II family	Transcription: Degradation of RNA
SACOL0847	smfB	2.09	4.17	2.00	C3	↑ SsrA-binding protein	Protein synthesis: Other
SACOL0855	-	1.96	4.32	2.20	C3	↑ acetyltransferase, GNAT family	Unknown function: Enzymes of unknown specificity
SACOL0865	-	1.68	2.79	1.66	C3	↑ hypothetical protein	-
SACOL0998	-	1.51	2.89	1.91	C3	oligopeptide ABC transporter, ATP-binding protein	Transport and binding proteins: Amino acids, peptides and amines
SACOL1107	-	1.81	3.22	1.78	C3	transcriptional regulator, Cro/Ci family	Regulatory functions: DNA interactions
SACOL1182	arcC1	1.74	2.62	1.51	C3	↓ carbamate kinase	Energy metabolism: Amino acids and amines
SACOL1238	rpmB	1.66	2.73	1.64	C3	ribosomal protein L28	Protein synthesis: Ribosomal proteins: synthesis and modification
SACOL1362	hom	1.40	4.65	3.32	C3	homoserine dehydrogenase	Amino acid biosynthesis: Aspartate family
SACOL1363	thrC	1.33	3.44	2.59	C3	threonine synthase	Amino acid biosynthesis: Aspartate family
SACOL1400	-	1.32	2.94	2.22	C3	ImpB/MucB/Samb family protein	DNA metabolism: DNA replication, recombination, and repair
SACOL1488	-	1.35	2.88	2.13	C3	hypothetical protein	-
SACOL1489	recU	1.57	3.60	2.29	C3	recombination protein U	DNA metabolism: DNA replication, recombination, and repair
SACOL1525	fer	1.54	4.66	3.03	C3	ferredoxin	Energy metabolism: Electron transport
SACOL1540	xerD	1.39	4.28	3.08	C3	tyrosine recombinase XerD	DNA metabolism: DNA replication, recombination, and repair
SACOL1696	ruvB	1.52	2.55	1.68	C3	Holliday junction DNA helicase RuvB	DNA metabolism: DNA replication, recombination, and repair
SACOL1698	-	1.96	3.08	1.57	C3	ACT domain protein	Unknown function: General
SACOL1699	-	1.83	2.82	1.54	C3	GTP-binding protein, GTP1/OBG family	Unknown function: General
SACOL1702	rplU	1.70	2.76	1.62	C3	ribosomal protein L21	Protein synthesis: Ribosomal proteins: synthesis and modification
SACOL1723	-	1.54	3.28	2.13	C3	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1822	arsR	1.45	4.93	3.41	C3	arsenical resistance operon repressor	Cellular processes: Detoxification; Regulatory functions: DNA interactions
SACOL1823	arsB	1.70	4.60	2.71	C3	arsenic pump membrane protein	Cellular processes: Detoxification; Transport and binding proteins: Other
SACOL1824	arsC	1.51	3.27	2.17	C3	arsenate reductase (thioredoxin)	Cellular processes: Detoxification
SACOL1825	-	1.58	2.99	1.89	C3	N-acetylmuramoyl-L-alanine amidase, family 4	Cell envelope: Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides
SACOL2088	sceD	2.38	11.30	4.75	C3	↑ sceD protein, putative	Unknown function: General
SACOL2215	rpsM	1.37	2.73	1.99	C3	↑ ribosomal protein S13/S18	Protein synthesis: Ribosomal proteins: synthesis and modification
SACOL2256	-	1.77	2.78	1.58	C3	transcriptional regulator, MarR family	Cellular processes: Toxin production and resistance; Regulatory functions: DNA interactions
SACOL2291	-	1.59	3.57	2.24	C3	staphyloxanthin biosynthesis protein	Cellular processes: Pathogenesis
SACOL2353	tcaR	1.95	5.71	2.93	C3	↑ transcriptional regulator TcaR	Cell envelope: Biosynthesis and degradation of murein sacculus and peptidoglycan; Toxin production and resistance; Regulatory functions: DNA interactions
SACOL2416	-	1.28	2.78	2.17	C3	cation efflux family protein	Transport and binding proteins: Cations and iron carrying compounds
SACOL2441	-	1.39	3.41	2.44	C3	amino acid permease	Transport and binding proteins: Amino acids, peptides and amines
SACOL2464	-	2.34	5.64	2.41	C3	addiction module toxin, Txe/YoeB family	Cellular processes: Toxin production and resistance; Mobile and extrachromosomal element functions: Other
SACOL2465	-	2.28	4.96	2.17	C3	addiction module antitoxin, Axe family	Cellular processes: Toxin production and resistance; Mobile and extrachromosomal element functions: Other
SACOL2614	panC	1.39	3.09	2.22	C3	pantoate-beta-alanine ligase	Biosynthesis of cofactors, prosthetic groups, and carriers: Pantothenate and coenzyme A
SACOL2632	cuoT	1.32	2.85	2.15	C3	osmoprotectant transporter, BCCT family	Transport and binding proteins: Amino acids, peptides and amines
SACOL2710	-	1.37	2.72	1.99	C3	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2713	-	2.39	4.93	2.06	C3	rhodanese-like domain protein	Unknown function: General
SACOL2714	pcp	1.33	3.61	2.72	C3	pyrrolidone-carboxylate peptidase	Protein fate: Degradation of proteins, peptides, and glycopeptides
SACOL0008	hutH	3.87	4.16	1.08	C4	histidine ammonia-lyase	Energy metabolism: Amino acids and amines
SACOL0065	-	3.41	2.83	-1.20	C4	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0073	-	2.41	2.59	1.08	C4	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0122	-	2.10	2.61	1.24	C4	↑ tetracycline resistance protein, putative	Cellular processes: Toxin production and resistance; Transport and binding proteins: Other
SACOL0136	cap5A	3.80	2.67	-1.43	C4	↑ capsular polysaccharide biosynthesis protein Cap5A	Cell envelope: Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides; Transport and binding proteins: Carbohydrates, organic alcohols, and acids

SACOL0137	cap5B	3.01	2.30	-1.31	C4	♂	capsular polysaccharide biosynthesis protein Cap5B	Cell envelope: Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	
SACOL0138	cap5C	3.37	1.99	-1.69	C4	♂	capsular polysaccharide biosynthesis protein Cap5C	Cell envelope: Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	
SACOL0264	-	3.93	4.44	1.13	C4		ABC transporter, ATP-binding protein	Transport and binding proteins: Unknown substrate	
SACOL0265	-	3.13	4.97	1.59	C4		hypothetical protein	-	
SACOL0317	-	2.37	3.79	1.60	C4		lipase precursor, interruption-N	Fatty acid and phospholipid metabolism: Degradation; Disrupted reading frame	
SACOL0342	-	1.95	2.73	1.40	C4		hypothetical protein	-	
SACOL0343	-	1.98	2.61	1.32	C4		prophage L54a, replicative DNA helicase, putative	DNA metabolism: DNA replication, recombination, and repair; Mobile and extrachromosomal element functions: Prophage functions	
SACOL0399	-	4.30	1.99	-2.16	C4	♂	↑	oxidoreductase, putative	Unknown function: Enzymes of unknown specificity
SACOL0437	rpsF	2.12	2.67	1.26	C4		ribosomal protein S6	Protein synthesis: Ribosomal proteins: synthesis and modification	
SACOL0438	ssb2	2.05	2.75	1.34	C4		↑	single-stranded DNA-binding protein	DNA metabolism: DNA replication, recombination, and repair
SACOL0446	-	2.54	1.79	-1.42	C4	♂	↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0447	-	2.59	2.65	1.02	C4		phosphoglycerate mutase family protein	Unknown function: General	
SACOL0585	rplJ	4.41	6.46	1.46	C4		ribosomal protein L10	Protein synthesis: Ribosomal proteins: synthesis and modification	
SACOL0620	proP	2.74	3.43	1.25	C4		osmoprotectant proline transporter	Transport and binding proteins: Amino acids, peptides and amines	
SACOL0630	-	2.91	1.93	-1.51	C4	♂	↑	amino acid permease	Transport and binding proteins: Amino acids, peptides and amines
SACOL0671	-	3.86	2.25	-1.72	C4	♂	↑	hydrolase, alpha/beta hydrolase fold family	Unknown function: Enzymes of unknown specificity
SACOL0673	-	3.11	4.24	1.36	C4		hypothetical protein	-	
SACOL0678	-	4.16	3.04	-1.37	C4	♂		integrase/recombinase, phage integrase family	DNA metabolism: DNA replication, recombination, and repair
SACOL0679	-	3.11	2.78	-1.12	C4	♂		Na ⁺ /H ⁺ antiporter, MnhA component, putative	Transport and binding proteins: Cations and iron carrying compounds
SACOL0680	-	2.95	3.08	1.04	C4	♂		Na ⁺ /H ⁺ antiporter, MnhB component, putative	Transport and binding proteins: Cations and iron carrying compounds
SACOL0681	-	3.33	3.50	1.05	C4	♂		Na ⁺ /H ⁺ antiporter, MnhC component, putative	Transport and binding proteins: Cations and iron carrying compounds
SACOL0682	-	3.03	3.13	1.03	C4	♂		Na ⁺ /H ⁺ antiporter, MnhD component, putative	Transport and binding proteins: Cations and iron carrying compounds
SACOL0684	-	2.62	2.84	1.08	C4	♂		Na ⁺ /H ⁺ antiporter, MnhE component, putative	Transport and binding proteins: Cations and iron carrying compounds
SACOL0685	-	2.46	2.87	1.17	C4	♂		Na ⁺ /H ⁺ antiporter, MnhF component, putative	Transport and binding proteins: Cations and iron carrying compounds
SACOL0686	-	2.42	2.62	1.08	C4	♂		Na ⁺ /H ⁺ antiporter, MnhG component, putative	Transport and binding proteins: Cations and iron carrying compounds
SACOL0756	-	2.70	4.93	1.83	C4		ebcS protein	Unknown function: General	
SACOL0768	-	3.39	2.55	-1.33	C4		↓	lipoprotein, putative	Hypothetical proteins: Conserved
SACOL0789	-	3.06	3.09	1.01	C4		↑	GTP cyclohydrolase I family protein	Unknown function: Enzymes of unknown specificity
SACOL0790	-	1.77	2.51	1.41	C4		↑	integral membrane domain protein	Unknown function: General
SACOL0854	-	3.56	5.14	1.44	C4		↑	hypothetical protein	-
SACOL0856	clfA	3.30	3.01	-1.09	C4	♂	↑	clumping factor A	Cellular processes: Pathogenesis
SACOL0871	-	3.28	6.21	1.89	C4		↑	acetyltransferase, putative	Unknown function: Enzymes of unknown specificity
SACOL0872	-	3.61	3.26	-1.11	C4		↑	OsmC/Ohr family protein	Unknown function: General
SACOL1033	-	3.28	4.19	1.28	C4		↑	hypothetical protein	-
SACOL1062	atl	3.94	4.05	1.03	C4		↑	bifunctional autolysin	Cell envelope: Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides
SACOL1081	purN	2.91	1.70	-1.71	C4		↑	phosphoribosylglycinamide formyltransferase	Purines, pyrimidines, nucleosides, and nucleotides: Purine ribonucleotide biosynthesis
SACOL1082	purH	2.52	1.68	-1.50	C4		↑	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	Purines, pyrimidines, nucleosides, and nucleotides: Purine ribonucleotide biosynthesis
SACOL1108	-	2.53	3.76	1.49	C4		↑	spermidine/putrescine ABC transporter, ATP-binding protein	Transport and binding proteins: Amino acids, peptides and amines
SACOL1109	-	2.82	4.07	1.44	C4		↑	spermidine/putrescine ABC transporter, permease protein	Transport and binding proteins: Amino acids, peptides and amines
SACOL1110	-	2.62	3.53	1.35	C4		↑	spermidine/putrescine ABC transporter, permease protein	Transport and binding proteins: Amino acids, peptides and amines
SACOL1111	-	2.58	3.35	1.30	C4		↑	spermidine/putrescine ABC transporter, spermidine/putrescine-binding protein	Transport and binding proteins: Amino acids, peptides and amines
SACOL1183	-	2.84	3.24	1.14	C4		↑	membrane protein, putative	Cell envelope: Other
SACOL1254	rpsP	3.84	3.34	-1.15	C4		↑	ribosomal protein S16	Protein synthesis: Ribosomal proteins: synthesis and modification
SACOL1255	rimM	3.51	3.99	1.14	C4		↑	16S rRNA processing protein RimM	Transcription: RNA processing
SACOL1256	trmD	3.42	3.96	1.16	C4		↑	tRNA [guanine-N1]-methyltransferase	Protein synthesis: tRNA and rRNA base modification
SACOL1292	rpsO	2.27	2.61	1.15	C4		↑	ribosomal protein S15	Protein synthesis: Ribosomal proteins: synthesis and modification
SACOL1371	guaC	4.01	1.95	-2.06	C4		↑	GMP reductase	Purines, pyrimidines, nucleosides, and nucleotides: Nucleotide and nucleoside interconversions
SACOL1418	-	2.78	1.66	-1.68	C4		↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1420	-	2.52	2.72	1.08	C4		↑	phosphate transport system protein PhoU, putative	Transport and binding proteins: Anions
SACOL1421	-	2.86	2.75	-1.04	C4		↑	phosphate ABC transporter, ATP-binding protein	Transport and binding proteins: Anions
SACOL1422	-	3.14	3.67	1.17	C4		↑	phosphate ABC transporter, permease protein	Transport and binding proteins: Anions
SACOL1451	arlR	1.95	2.62	1.34	C4		↑	DNA-binding response regulator ArlR	Cellular processes: Pathogenesis; Regulatory functions: DNA interactions; Regulatory functions: Protein interactions; Signal transduction: Two-component systems
SACOL1453	murG	2.88	1.80	-1.60	C4		↑	UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl transferase	Cell envelope: Biosynthesis and degradation of murein sacculus and peptidoglycan
SACOL1550	-	3.69	2.66	-1.38	C4		↑	transcriptional regulator, AraC family	Regulatory functions: DNA interactions
SACOL1576	-	2.05	2.64	1.28	C4		↑	traG protein, putative	Mobile and extrachromosomal element functions: Plasmid functions
SACOL1577	-	2.15	2.71	1.27	C4		↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1700	rpmA	2.07	2.92	1.41	C4		↑	ribosomal protein L27	Protein synthesis: Ribosomal proteins: synthesis and modification
SACOL1701	-	2.14	3.02	1.41	C4		↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1769	rpsD	3.54	2.57	-1.37	C4		↑	ribosomal protein S4	Protein synthesis: Ribosomal proteins: synthesis and modification
SACOL1778	tyrS	2.70	1.59	-1.70	C4		↑	tyrosyl-tRNA synthetase	Protein synthesis: tRNA aminoacylation
SACOL1871	epiG	3.69	1.91	-1.93	C4	♂	↑	epidermin immunity protein F	Cellular processes: Toxin production and resistance
SACOL1872	epiE	3.32	2.24	-1.48	C4	♂	↑	epidermin immunity protein F	Cellular processes: Toxin production and resistance
SACOL1882	-	2.02	2.59	1.28	C4		↑	hypothetical protein	-
SACOL1903	-	2.02	2.61	1.29	C4		↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1935	-	2.56	2.32	-1.10	C4		↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1939	-	2.50	2.44	-1.02	C4		↑	phosphotyrosine protein phosphatase	Regulatory functions: Protein interactions
SACOL1952	-	3.71	6.34	1.71	C4		↓	ferritin family protein	Transport and binding proteins: Cations and iron carrying compounds
SACOL2012	-	3.76	2.74	-1.38	C4		↓	acetyltransferase, GNAT family	Unknown function: Enzymes of unknown specificity
SACOL2013	-	3.66	2.73	-1.34	C4		↓	hypothetical protein	-
SACOL2019	-	3.81	3.27	-1.17	C4		↓	sdhH protein, putative	Cell envelope: Other
SACOL2067	kdpB	2.78	3.86	1.39	C4		↓	K ⁺ -transporting ATPase, B subunit	Transport and binding proteins: Cations and iron carrying compounds
SACOL2131	-	3.48	6.44	1.85	C4		↓	Dps family protein	Cellular processes: Adaptations to atypical conditions
SACOL2137	czrA	6.47	7.32	1.13	C4		↓	transcriptional regulator CzrA	Regulatory functions: DNA interactions
SACOL2138	-	6.73	7.85	1.17	C4		↓	cation efflux family protein	Transport and binding proteins: Cations and iron carrying compounds
SACOL2176	opuD2	3.84	2.21	-1.74	C4	♂	↑	osmoprotectant transporter, BCCT family	Transport and binding proteins: Amino acids, peptides and amines
SACOL2197	-	9.21	11.87	1.29	C4	♂	↑	surface protein, putative	Cell envelope: Other
SACOL2287	sarR	2.19	2.54	1.16	C4		↑	staphylococcal accessory regulator R	Cellular processes: Toxin production and resistance; Regulatory functions: Other; Cellular processes: Pathogenesis; Regulatory functions: DNA interactions
SACOL2295	-	5.46	7.21	1.32	C4		↑	staphyloxanthin biosynthesis protein, putative	Cellular processes: Pathogenesis
SACOL2398	nirB	2.76	2.37	-1.16	C4		↑	nitrite reductase [NAD(P)H], large subunit	Central intermediary metabolism: Nitrogen metabolism
SACOL2434	-	3.04	3.17	1.04	C4	♂	↑	membrane protein, putative	Cell envelope: Other
SACOL2477	-	2.58	1.79	-1.44	C4		↑	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2481	-	3.38	2.24	-1.51	C4		↑	hypothetical protein	-
SACOL2510	-	1.91	2.77	1.45	C4		↑	hypothetical protein	-
SACOL2511	fnbA	2.97	5.44	1.83	C4		↑	fibronectin-binding protein A	Cell envelope: Other; Cellular processes: Pathogenesis
SACOL2554	-	2.82	1.74	-1.62	C4	♂	↑	membrane protein, putative	Cell envelope: Other
SACOL2557	-	4.33	2.64	-1.64	C4	♂	↑	conserved domain protein	Hypothetical proteins: Domain

SACOL2631	-	2.50	2.53	1.01	C4	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2735	-	4.15	4.75	1.14	C4	chromosome partitioning protein, ParB family	Cellular processes: Cell division
SACOL2736	gidB	3.18	4.03	1.27	C4	glucose-inhibited division protein B	Unknown function: General
SACOL2737	gidA	3.57	4.33	1.21	C4	glucose inhibited division protein A	Unknown function: General
SACOL2738	trmE	3.56	4.00	1.13	C4	rRNA modification GTPase TrmE	Cellular processes: Detoxification
SACOL2739	rnpA	3.52	4.50	1.28	C4	ribonuclease P protein component	Transcription: RNA processing
SACOL2740	rpmH	2.44	2.85	1.17	C4	ribosomal protein L34	Protein synthesis: Ribosomal proteins: synthesis and modification
SACOL0024	sasH	-3.45	-4.89	-1.42	C5	5-nucleotidase family protein	Purines, pyrimidines, nucleosides, and nucleotides: Other
SACOL0032	maoC	-1.95	-2.49	-1.28	C5	MAoC domain protein	Unknown function: General
SACOL0052	-	-1.86	-2.63	-1.41	C5	glycosyl transferase, group 1 family protein	Cell envelope: Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides
SACOL0058	-	-2.78	-3.05	-1.10	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0099	sirA	-3.24	-2.47	1.31	C5	iron compound ABC transporter, iron compound-binding protein SirA	Cell envelope: Other; Transport and binding proteins: Cations and iron carrying compounds
SACOL0109	-	-1.83	-2.60	-1.42	C5	hypothetical protein	-
SACOL0110	-	-2.20	-3.58	-1.63	C5	hypothetical protein	-
SACOL0192	-	-4.90	-3.19	1.54	C5	maltose ABC transporter, ATP-binding protein, putative	Transport and binding proteins: Carbohydrates, organic alcohols, and acids
SACOL0218	-	-2.46	-4.44	-1.80	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0236	-	-2.17	-3.44	-1.58	C5	4-diphosphocytidyl-2C-methyl-D-erythritol synthase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers: Other
SACOL0246	lytR	-2.19	-2.86	-1.30	C5	response regulator LytR	Cell envelope: Biosynthesis and degradation of murein sacculus and peptidoglycan: Pathogenesis; Regulatory functions; Signal transduction: Two-component systems
SACOL0284	-	-3.08	-4.38	-1.42	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0297	-	-1.94	-2.67	-1.38	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0302	brnQ2	-3.68	-2.70	1.36	C5	branched-chain amino acid transport system II carrier protein	Transport and binding proteins: Amino acids, peptides and amines
SACOL0303	-	-5.88	-14.78	-2.51	C5	acid phosphatase5-nucleotidase, lipoprotein (P4) family	Transport and binding proteins: Other; Biosynthesis of cofactors, prosthetic groups, and carriers: Pyridine nucleotides
SACOL0417	-	-4.54	-2.67	1.70	C5	MtbB family protein	Protein fate: Protein and peptide secretion and trafficking
SACOL0418	-	-4.15	-2.46	1.69	C5	mttA/Hcf106 family protein	Protein fate: Protein and peptide secretion and trafficking
SACOL0419	-	-5.67	-2.79	2.03	C5	hypothetical protein	-
SACOL0512	-	-3.72	-2.12	1.75	C5	conserved hypothetical protein	-
SACOL0553	tlpS	-2.53	-1.74	1.46	C5	trNA(ile)-lysine synthetase	Hypothetical proteins: Conserved
SACOL0566	nupC	-2.75	-3.30	-1.20	C5	nucleoside permease NupC	Protein synthesis: tRNA and rRNA base modification
SACOL0604	-	-2.74	-2.50	1.09	C5	deoxynucleoside kinase family protein	Transport and binding proteins: Nucleosides, purines and pyrimidines
SACOL0649	-	-2.65	-1.87	1.41	C5	conserved hypothetical protein	Purines, pyrimidines, nucleosides, and nucleotides: Nucleotide and nucleoside interconversions
SACOL0650	-	-2.51	-1.84	1.36	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0651	-	-4.20	-2.18	1.93	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0653	-	-2.91	-1.70	1.71	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0688	-	-4.65	-9.59	-2.06	C5	ABC transporter, substrate-binding protein	Transport and binding proteins: Unknown substrate
SACOL0689	-	-7.06	-9.80	-1.39	C5	ABC transporter, permease protein	Transport and binding proteins: Unknown substrate
SACOL0690	-	-5.84	-10.93	-1.87	C5	ABC transporter, ATP-binding protein	Transport and binding proteins: Unknown substrate
SACOL0693	tagA	-2.91	-2.37	1.23	C5	UDP-N-acetyl-D-mannosamine transferase	Cell envelope: Biosynthesis and degradation of murein sacculus and peptidoglycan
SACOL0815	-	-3.34	-6.41	-1.92	C5	ribosomal subunit interface protein	Protein synthesis: Translation factors
SACOL0860	nuc	-5.73	-14.78	-2.58	C5	thermonuclease precursor	DNA metabolism: Degradation of DNA
SACOL0887	sei	-1.98	-3.12	-1.58	C5	staphylococcal enterotoxin type I	Cellular processes: Toxin production and resistance; Cellular processes: Pathogenesis
SACOL0889	-	-2.24	-2.59	-1.16	C5	pathogenicity island protein	Cellular processes: Pathogenesis
SACOL0922	-	-2.85	-3.10	-1.09	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0924	-	-2.73	-2.96	-1.08	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0930	-	-2.62	-2.79	-1.07	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0959	-	-4.22	-3.21	1.31	C5	NADH-dependent flavin oxidoreductase, Oye family	Unknown function: Enzymes of unknown specificity
SACOL0975	cdr	-2.15	-3.38	-1.57	C5	CoA-disulfide reductase	Energy metabolism: Electron transport
SACOL0976	-	-2.44	-3.45	-1.41	C5	hydrolase, haloacid dehalogenase-like family	Unknown function: Enzymes of unknown specificity
SACOL1005	pepF	-2.88	-3.03	-1.05	C5	oligoendopeptidase F	Protein fate: Degradation of proteins, peptides, and glycopeptides
SACOL1028	htrA	-1.76	-2.58	-1.46	C5	serine protease	Protein fate: Degradation of proteins, peptides, and glycopeptides; Cellular processes: Pathogenesis
SACOL1034	-	-2.90	-4.32	-1.49	C5	lipote-protein ligase A family protein	Protein fate: Protein modification and repair
SACOL1048	-	-3.30	-2.58	1.28	C5	acetyltransferase, GNAT family	Unknown function: Enzymes of unknown specificity
SACOL1094	cydA	-2.81	-2.19	1.28	C5	cytochrome d ubiquinol oxidase, subunit I	Energy metabolism: Electron transport
SACOL1095	cydB	-2.75	-2.15	1.28	C5	cytochrome d ubiquinol oxidase, subunit II	Energy metabolism: Electron transport
SACOL1115	-	-2.32	-3.53	-1.52	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1140	sasE	-5.88	-5.72	1.03	C5	LPXTG cell wall surface anchor protein	Cell envelope: Other
SACOL1142	isdD	-2.74	-1.71	1.60	C5	hypothetical protein	-
SACOL1143	-	-2.78	-1.73	1.60	C5	iron compound ABC transporter, iron compound-binding protein, putative	Cell envelope: Other; Transport and binding proteins: Cations and iron carrying compounds
SACOL1145	srtB	-2.56	-2.78	-1.09	C5	sortase B	Cell envelope: Other
SACOL1150	rmhC	-2.20	-2.49	-1.13	C5	ribonuclease HIII	DNA metabolism: DNA replication, recombination, and repair
SACOL1206	ileS	-2.46	-3.72	-1.52	C5	isoleucyl-tRNA synthetase	Protein synthesis: tRNA aminoacylation
SACOL1296	-	-3.37	-2.77	1.22	C5	transcriptional regulator, GntR family, putative	Regulatory functions: DNA interactions
SACOL1297	-	-5.26	-3.06	1.72	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1298	-	-3.04	-4.03	-1.33	C5	peptidase, M16 family	Protein fate: Degradation of proteins, peptides, and glycopeptides
SACOL1299	-	-2.85	-4.16	-1.46	C5	acetoacetyl-CoA reductase, putative	Fatty acid and phospholipid metabolism: Biosynthesis
SACOL1300	-	-2.34	-3.87	-1.65	C5	ACT domain protein	Unknown function: General
SACOL1321	glpD	-2.05	-3.90	-1.42	C5	aerobic glycerol-3-phosphate dehydrogenase	Energy metabolism: Other
SACOL1328	glmR	-2.34	-2.00	-1.28	C5	glutamine synthetase repressor	Cellular processes: Toxin production and resistance; Regulatory functions: DNA interactions
SACOL1419	-	-10.64	-11.53	-1.08	C5	oligoendopeptidase F, putative	Protein fate: Degradation of proteins, peptides, and glycopeptides
SACOL1438	-	-5.99	-5.02	1.19	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1471	-	-2.77	-1.77	1.56	C5	cell wall enzyme EbsB, putative	Cell envelope: Other; Protein fate: Degradation of proteins, peptides, and glycopeptides
SACOL1481	-	-3.88	-4.73	-1.22	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1495	-	-2.06	-3.14	-1.52	C5	DNA polymerase III, epsilon subunit/ATP-dependent helicase DinG	DNA metabolism: DNA replication, recombination, and repair
SACOL1496	birA	-2.28	-2.57	-1.13	C5	birA bifunctional protein	Biosynthesis of cofactors, prosthetic groups, and carriers: Biotin; Protein fate: Protein modification and repair; Regulatory functions: DNA interactions
SACOL1530	-	-2.16	-2.54	-1.17	C5	lipoprotein, putative	Cell envelope: Other
SACOL1552	malR	-3.46	-2.28	1.51	C5	maltose operon repressor	Regulatory functions: DNA interactions
SACOL1564	recN	-2.71	-3.76	-1.39	C5	DNA repair protein RecN	DNA metabolism: DNA replication, recombination, and repair
SACOL1565	argR	-3.99	-3.93	1.02	C5	arginine repressor	Amino acid biosynthesis: Glutamate family; Regulatory functions: DNA interactions
SACOL1674	-	-2.47	-1.94	1.27	C5	helicase, putative, RecD/TraA family	Unknown function: Enzymes of unknown specificity
SACOL1743	-	-2.17	-2.89	-1.33	C5	amino acid permease	Transport and binding proteins: Amino acids, peptides and amines
SACOL1771	-	-2.38	-3.39	-1.42	C5	OsmC/Ohr family protein	Unknown function: General
SACOL1777	-	-3.69	-4.74	-1.29	C5	serine protease HtrA, putative	Protein fate: Degradation of proteins, peptides, and glycopeptides
SACOL1816	putA	-4.11	-2.21	1.86	C5	proline dehydrogenase	Energy metabolism: Amino acids and amines
SACOL1818	ribBA	-3.15	-2.12	1.48	C5	3,4-dihydroxy-2-butanone-4-phosphate synthase/GTP cyclohydrolase II	Biosynthesis of cofactors, prosthetic groups, and carriers: Riboflavin, FMN, and FAD
SACOL1819	ribE	-3.59	-1.96	1.83	C5	riboflavin synthase, alpha subunit	Biosynthesis of cofactors, prosthetic groups, and carriers: Riboflavin, FMN, and FAD
SACOL1820	ribD	-3.41	-1.94	1.76	C5	riboflavin biosynthesis protein RibD	Biosynthesis of cofactors, prosthetic groups, and carriers: Riboflavin, FMN, and FAD
SACOL1833	-	-2.96	-2.09	1.42	C5	crbB family protein	Unknown function: General

SACOL1838	pckA	-3.24	-2.43	1.33	C5	phosphoenolpyruvate carboxykinase (ATP)	Energy metabolism: Glycolysis/gluconeogenesis
SACOL1840	-	-3.26	-5.42	-1.66	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1841	ytbD	-4.82	-5.30	-1.10	C5	nucleoside triphosphatase Ytd	DNA metabolism: DNA replication, recombination, and repair
SACOL1844	-	-3.47	-6.46	-1.86	C5	O-succinylbenzoyl acid-CoA ligase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers: Menaquinone and ubiquinone
SACOL1848	-	-4.91	-5.68	-1.16	C5	lipoprotein, putative	-
SACOL1851	-	-3.42	-3.39	1.01	C5	hypothetical protein	-
SACOL1893	-	-2.20	-3.67	-1.67	C5	ABC transporter, ATP-binding protein	Transport and binding proteins: Unknown substrate
SACOL1946	-	-3.35	-4.13	-1.23	C5	methionine aminopeptidase, type I	Protein fate: Protein modification and repair
SACOL1984	aldA2	-2.24	-3.14	-1.40	C5	aldehyde dehydrogenase	Energy metabolism: Fermentation
SACOL1992	-	-2.60	-2.19	1.19	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2017	groES	-2.11	-2.79	-1.32	C5	chaperonin, 10 kDa	Protein fate: Protein folding and stabilization
SACOL2075	ftsW	-2.53	-2.73	-1.08	C5	cell division protein, FtsW/RodA/SpoVE family	Cellular processes: Cell division
SACOL2130	deoD2	-2.24	-3.23	-1.44	C5	purine nucleoside phosphorylase	Purines, pyrimidines, nucleosides, and nucleotides: Salvage of nucleosides and nucleotides
SACOL2146	-	-3.42	-5.27	-1.54	C5	PTS system, manitol-specific IIBC components	Transport and binding proteins: Carbohydrates, organic alcohols, and acids; Signal transduction: PTS
SACOL2164	-	-4.24	-3.86	1.10	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2179	-	-2.05	-2.97	-1.44	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2193	-	-3.04	-4.85	-1.59	C5	transcriptional regulator, MerR family	Regulatory functions: DNA interactions
SACOL2273	fdhD	-3.30	-1.84	1.80	C5	formate dehydrogenase accessory protein FdhD	Energy metabolism: Anaerobic; Energy metabolism: Electron transport
SACOL2280	ureA	-2.95	-3.11	-1.05	C5	urease, gamma subunit	Central intermediary metabolism: Nitrogen metabolism
SACOL2281	ureB	-3.19	-2.88	1.11	C5	urease, beta subunit	Central intermediary metabolism: Nitrogen metabolism
SACOL2306	-	-4.23	-5.94	-1.41	C5	abortive infection protein family	Unknown function: General
SACOL2310	-	-2.36	-2.73	-1.16	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2311	-	-1.75	-2.49	-1.43	C5	hypothetical protein	-
SACOL2362	mqo1	-2.70	-5.06	-1.87	C5	malate:quinone oxidoreductase	Energy metabolism: TCA cycle
SACOL2470	-	-2.64	-3.35	-1.27	C5	hypothetical protein	-
SACOL2486	-	-2.34	-4.15	-1.77	C5	hypothetical protein	-
SACOL2487	-	-3.35	-3.47	-1.03	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2488	-	-2.81	-3.33	-1.18	C5	oxidoreductase, short-chain dehydrogenase/reductase family	Unknown function: Enzymes of unknown specificity
SACOL2491	-	-2.93	-4.08	-1.39	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2501	-	-2.63	-4.77	-1.81	C5	phosphoglucomutase/phosphomannomutase family protein	Energy metabolism: Sugars
SACOL2502	-	-4.45	-3.18	1.40	C5	hypothetical protein	-
SACOL2503	-	-3.47	-2.87	1.21	C5	hypothetical protein	-
SACOL2518	-	-3.77	-5.19	-1.38	C5	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2522	-	-3.05	-2.40	1.27	C5	DedA family protein	Unknown function: General
SACOL2551	-	-2.48	-2.53	-1.02	C5	conserved hypothetical protein TIGR00051	Hypothetical proteins: Conserved
SACOL2606	pyrD	-2.68	-1.97	1.36	C5	dihydroorotate dehydrogenase	Purines, pyrimidines, nucleosides, and nucleotides: Pyrimidine ribonucleotide biosynthesis
SACOL2660	isaB	-2.72	-4.70	-1.73	C5	immunodominant antigen B	Unknown function: General
SACOL0003	-	-1.49	-2.80	-1.88	C6	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0004	-	-1.61	-2.68	-1.66	C6	recF protein	DNA metabolism: DNA replication, recombination, and repair
SACOL0005	gyrB	-1.57	-2.59	-1.65	C6	DNA gyrase, B subunit	DNA metabolism: DNA replication, recombination, and repair
SACOL0006	gyrA	-1.76	-3.93	-2.23	C6	DNA gyrase, A subunit	DNA metabolism: DNA replication, recombination, and repair
SACOL0009	serS	-2.11	-3.72	-1.77	C6	seryl-tRNA synthetase	Protein synthesis: tRNA aminoacylation
SACOL0023	yycJ	-1.47	-3.01	-2.04	C6	metallo-beta-lactamase family protein YycJ	Unknown function: General
SACOL0025	-	-1.45	-3.22	-2.23	C6	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0173	ipdC	-1.35	-3.80	-2.80	C6	indole-3-pyruvate decarboxylase	Central intermediary metabolism: Other
SACOL0181	-	-1.62	-3.09	-1.90	C6	conserved domain protein	Hypothetical proteins: Domain
SACOL0182	-	-2.13	-4.50	-2.11	C6	hypothetical protein	-
SACOL0183	-	-1.57	-2.65	-1.69	C6	hypothetical protein	-
SACOL0219	-	-2.38	-9.53	-4.00	C6	hypothetical protein	-
SACOL0220	-	-1.74	-3.62	-2.08	C6	flavoheomprotein, putative	Unknown function: General
SACOL0225	-	-2.50	-4.95	-1.98	C6	inosine-uridine preferring nucleoside hydrolase	Purines, pyrimidines, nucleosides, and nucleotides: Salvage of nucleosides and nucleotides
SACOL0274	-	-1.71	-6.28	-3.68	C6	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0275	-	-1.60	-6.37	-3.98	C6	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0299	-	-1.30	-2.69	-2.07	C6	lipoprotein, putative	-
SACOL0477	-	-1.72	-3.55	-2.06	C6	type I restriction-modification system, S subunit, EcoA family, putative	DNA metabolism: Restriction/modification
SACOL0478	-	-2.39	-4.32	-1.80	C6	exotoxin 3, putative	Cellular processes: Toxin production and resistance
SACOL0536	ksgA	-1.50	-2.54	-1.69	C6	dimethyladenosine transferase	Cellular processes: Toxin production and resistance; Protein synthesis: tRNA and rRNA base modification
SACOL0558	folP	-1.96	-4.08	-2.08	C6	dihydropteroteate synthase	Biosynthesis of cofactors, prosthetic groups, and carriers: Folic acid
SACOL0564	-	-1.37	-4.28	-3.11	C6	pyridoxine biosynthesis protein	Biosynthesis of cofactors, prosthetic groups, and carriers: Pyridoxine
SACOL0567	ctsR	-1.68	-2.63	-1.57	C6	transcriptional regulator CtsR	Regulatory functions: DNA interactions
SACOL0602	-	-1.35	-2.48	-1.83	C6	hydrolase, haloacid dehalogenase-like family	Unknown function: Enzymes of unknown specificity
SACOL0633	-	-1.71	-5.11	-3.00	C6	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0714	-	-1.64	-2.84	-1.73	C6	acetyltransferase, GNAT family	Unknown function: Enzymes of unknown specificity
SACOL0739	-	-1.49	-3.61	-2.42	C6	acetyltransferase, GNAT family	Unknown function: Enzymes of unknown specificity
SACOL0781	-	-1.37	-2.82	-2.07	C6	osmoprotectant ABC transporter, ATP-binding protein, putative	Transport and binding proteins: Amino acids, peptides and amines
SACOL0799	-	-1.41	-2.74	-1.94	C6	transferrin receptor	Cell envelope: Other; Transport and binding proteins: Cations and iron carrying compounds
SACOL0833	clpP	-1.35	-3.35	-2.48	C6	ATP-dependent Clp protease, proteolytic subunit ClpP	Protein fate: Degradation of proteins, peptides, and glycopeptides
SACOL0849	-	-1.30	-4.61	-3.55	C6	hypothetical protein	-
SACOL0850	-	-1.49	-3.03	-2.03	C6	hypothetical protein	-
SACOL0851	-	-2.35	-4.89	-2.08	C6	lipoprotein, putative	-
SACOL0859	-	-1.88	-3.11	-1.65	C6	hypothetical protein	-
SACOL0875	-	-1.24	-3.21	-2.59	C6	thioredoxin, putative	Energy metabolism: Electron transport
SACOL0876	-	-1.56	-3.80	-2.44	C6	arsenate reductase, putative	Cellular processes: Detoxification
SACOL0877	gcvH	-1.35	-2.90	-2.16	C6	glycine cleavage system H protein	Energy metabolism: Amino acids and amines
SACOL0888	-	-1.91	-3.39	-1.78	C6	pathogenicity island, lipoprotein, putative	Cell envelope: Other; Cellular processes: Pathogenesis
SACOL0925	-	-1.66	-2.69	-1.63	C6	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0926	-	-1.43	-2.98	-2.08	C6	5-nucleotidase family protein	Purines, pyrimidines, nucleosides, and nucleotides: Other
SACOL0931	-	-1.62	-2.74	-1.70	C6	hydrolase, haloacid dehalogenase-like family	Unknown function: Enzymes of unknown specificity
SACOL0944	-	-1.52	-3.49	-2.30	C6	NADH dehydrogenase, putative	Energy metabolism: Electron transport
SACOL0977	-	-1.52	-2.88	-1.89	C6	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0987	fabH	-2.19	-4.48	-2.04	C6	3-oxoacyl-(acyl-carrier-protein) synthase III	Fatty acid and phospholipid metabolism: Biosynthesis
SACOL0988	fabF	-1.53	-3.31	-2.16	C6	3-oxoacyl-(acyl-carrier-protein) synthase II	Fatty acid and phospholipid metabolism: Biosynthesis
SACOL1168	efb	-1.36	-4.43	-3.25	C6	fibronin-binding protein	Cell envelope: Other
SACOL1301	-	-1.77	-3.23	-1.82	C6	transcriptional regulator, putative	Regulatory functions: Other
SACOL1302	pgsA	-1.72	-3.66	-2.13	C6	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	Fatty acid and phospholipid metabolism: Biosynthesis
SACOL1325	gpxA1	-1.46	-2.58	-1.77	C6	glutathione peroxidase	Biosynthesis of cofactors, prosthetic groups, and carriers: Glutathione and analogs; Cellular processes: Detoxification

SACOL1365	-	-1.23	-2.58	-2.09	C6	hydrolase, haloacid dehalogenase-like family	Unknown function: Enzymes of unknown specificity
SACOL1377	tkf	-1.69	-2.54	-1.50	C6	transketolase	Energy metabolism: Pentose phosphate pathway
SACOL1439	-	-1.58	-3.16	-2.01	C6	acylphosphatase	Fatty acid and phospholipid metabolism: Other
SACOL1440	-	-1.23	-3.26	-2.65	C6	ypaC protein, putative	Cellular processes: Other
SACOL1516	rpsA	-1.40	-2.92	-2.08	C6	ribosomal protein S1	Protein synthesis: Ribosomal proteins: synthesis and modification
SACOL1520	-	-1.82	-2.94	-1.62	C6	pyridine nucleotide-disulfide oxidoreductase	Unknown function: Enzymes of unknown specificity
SACOL1554	gnd	-1.44	-2.89	-2.01	C6	6-phosphogluconate dehydrogenase, decarboxylating	Energy metabolism: Pentose phosphate pathway
SACOL1562	-	-1.43	-2.62	-1.83	C6	2-oxoisovalerate dehydrogenase, E1 component, alpha subunit	Energy metabolism: Amino acids and amines
SACOL1563	lpdA	-1.52	-2.53	-1.66	C6	2-oxoisovalerate dehydrogenase, E3 component, lipamide dehydrogenase	Energy metabolism: Amino acids and amines
SACOL1566	ispA	-1.45	-2.80	-1.94	C6	geranyltranstransferase	Biosynthesis of cofactors, prosthetic groups, and carriers: Menaquinone and ubiquinone
SACOL1568	xseA	-1.45	-2.85	-1.97	C6	exodeoxyribonuclease VII, large subunit	DNA metabolism: Degradation of DNA
SACOL1588	-	-1.31	-3.00	-2.28	C6	proline dipeptidase	Protein fate: Degradation of proteins, peptides, and glycopeptides
SACOL1629	-	-1.22	-2.49	-2.04	C6	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1630	-	-1.58	-2.55	-1.62	C6	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1631	-	-1.71	-2.82	-1.65	C6	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1714	hemL1	-1.28	-3.26	-2.55	C6	glutamate-1-semialdehyde-2,1-aminomutase	Biosynthesis of cofactors, prosthetic groups, and carriers: Heme, porphyrin, and cobalamin
SACOL1715	hemB	-1.49	-3.19	-2.14	C6	delta-aminolevulinic acid dehydratase	Biosynthesis of cofactors, prosthetic groups, and carriers: Heme, porphyrin, and cobalamin
SACOL1716	hemD	-1.75	-3.06	-1.75	C6	uroporphyrinogen-III synthase	Biosynthesis of cofactors, prosthetic groups, and carriers: Heme, porphyrin, and cobalamin
SACOL1782	fhs	-1.62	-5.16	-3.18	C6	formate-tetrahydrofolate ligase	Central intermediary metabolism: One-carbon metabolism
SACOL1835	-	-1.53	-2.61	-1.71	C6	oxidoreductase, aldo/keto reductase family	Unknown function: Enzymes of unknown specificity
SACOL1843	-	-1.94	-4.00	-2.06	C6	o-succinylbenzoic acid (OSB) synthetase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers: Menaquinone and ubiquinone
SACOL1892	-	-1.43	-3.36	-2.35	C6	membrane protein, putative	Cell envelope: Other
SACOL1893	vraS	-1.40	-2.68	-1.91	C6	sensor histidine kinase VraS	Cellular processes: Toxin production and resistance; Regulatory functions: Protein interactions; Signal transduction: Two-component systems
SACOL1961	gatA	-1.28	-2.64	-2.07	C6	glutamyl-tRNA(Gln) amidotransferase, A subunit	Protein synthesis: tRNA aminoacylation
SACOL1970	sspB2	-1.36	-2.56	-1.88	C6	cysteine protease precursor SspB	Protein fate: Degradation of proteins, peptides, and glycopeptides; Cellular processes: Pathogenesis
SACOL2018	-	-2.78	-6.45	-3.32	C6	abortive infection protein family	Unknown function: General
SACOL2126	luxS	-1.42	-2.82	-1.99	C6	autoinducer-2 production protein LuxS	Cellular processes: Other
SACOL2186	-	-1.28	-2.88	-2.24	C6	galactose-6-phosphate isomerase, LacA subunit	Energy metabolism: Biosynthesis and degradation of polysaccharides
SACOL2241	-	-2.84	-6.72	-2.37	C6	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2439	-	-2.36	-4.55	-1.93	C6	lipoprotein, putative	Cell envelope: Other
SACOL2534	frp	-1.74	-2.98	-1.71	C6	NAD(P)H-flavin oxidoreductase	Energy metabolism: Electron transport
SACOL2535	-	-1.71	-2.72	-1.59	C6	D-isomer specific 2-hydroxyacid dehydrogenase family protein	Central intermediary metabolism: Other
SACOL2592	-	-1.75	-3.54	-2.01	C6	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2593	-	-1.81	-3.30	-1.82	C6	transcriptional regulator, TetR family	Regulatory functions: DNA interactions
SACOL2618	ldh2	-1.95	-5.19	-2.67	C6	L-lactate dehydrogenase	Energy metabolism: Anaerobic; Energy metabolism: Glycolysis/gluconeogenesis
SACOL2688	icaR	-3.14	-8.59	-2.74	C6	intercellular adhesion regulator	Cellular processes: Pathogenesis; Regulatory functions: DNA interactions
SACOL2731	-	-2.58	-5.59	-2.17	C6	cold shock protein, CSD family	Cellular processes: Adaptations to atypical conditions
SACOL0170	rocD1	-1.48	2.42	3.57	C7	ornithine aminotransferase	Energy metabolism: Amino acids and amines
SACOL0430	-	-1.57	1.61	2.53	C7	trans-sulfuration enzyme family protein	Amino acid biosynthesis: Aspartate family
SACOL0494	nuoF	-2.82	-1.33	2.12	C7	NADH dehydrogenase I, F subunit	Energy metabolism: Electron transport
SACOL0501	-	-8.34	-2.18	3.83	C7	sodium-dependent transporter, putative	Transport and binding proteins: Unknown substrate; Transport and binding proteins: Cations and iron carrying compounds
SACOL0502	-	-2.26	2.98	6.74	C7	cysteine synthase/cystathionine beta-synthase family protein	Amino acid biosynthesis: Serine family
SACOL0506	-	-1.25	2.28	2.85	C7	ABC transporter, substrate-binding protein	Transport and binding proteins: Unknown substrate
SACOL0516	-	-2.04	1.38	2.83	C7	PTS system, IIBC components	Transport and binding proteins: Carbohydrates, organic alcohols, and acids; Signal transduction: PTS
SACOL0621	-	-1.76	1.74	3.06	C7	substrate-CoA ligase, putative	Fatty acid and phospholipid metabolism: Other
SACOL0652	-	-2.55	-1.25	2.05	C7	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0725	-	-2.57	1.26	3.23	C7	transcriptional regulator, AraC family	Regulatory functions: DNA interactions
SACOL0769	-	-1.84	1.61	2.95	C7	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1044	-	-2.54	-1.44	1.77	C7	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1141	isdC	-2.99	-1.45	2.06	C7	NPQTN cell wall surface anchor protein	Cell envelope: Other
SACOL1269	xerC	-2.24	1.18	2.64	C7	tyrosine recombinase XerC	DNA metabolism: DNA replication, recombination, and repair
SACOL1675	-	-2.73	-1.58	1.73	C7	TPR domain protein	Unknown function: General
SACOL1687	-	-2.68	-1.52	1.76	C7	N-acetylmuramoyl-L-alanine amidase, family 3	Cell envelope: Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides
SACOL1832	crbB	-2.50	-1.32	1.89	C7	crbB protein	Unknown function: General
SACOL1904	-	-1.48	1.79	2.65	C7	transcriptional regulator, putative	Regulatory functions: Other
SACOL2086	-	-2.77	1.37	3.81	C7	transcriptional regulator, TenA family	Regulatory functions: Other
SACOL2157	-	-1.35	1.87	2.52	C7	drug resistance transporter, EmrB/QacA subfamily	Cellular processes: Toxin production and resistance; Transport and binding proteins: Other
SACOL2158	-	-2.37	1.15	2.74	C7	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2159	-	-1.48	1.92	2.83	C7	drug transporter, putative	Cellular processes: Toxin production and resistance; Transport and binding proteins: Other
SACOL2163	-	-2.90	-1.39	2.09	C7	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2440	-	-2.73	-1.56	1.75	C7	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL2463	pepA2	-1.39	3.00	4.17	C7	glutamyl-aminopeptidase	Protein fate: Degradation of proteins, peptides, and glycopeptides
SACOL2509	fnbB	-2.01	2.90	5.83	C7	fibronectin binding protein B	Cell envelope: Other
SACOL2689	icaA	-1.42	2.53	3.60	C7	intercellular adhesion protein A	Cell envelope: Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides
SACOL2690	icaD	-1.47	2.14	3.13	C7	intercellular adhesion protein D	Cell envelope: Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides
SACOL0018	purA	1.87	-2.17	-4.06	C8	adenylosuccinate synthetase	Purines, pyrimidines, nucleosides, and nucleotides: Purine ribonucleotide biosynthesis
SACOL0226	-	-1.15	-3.07	-2.67	C8	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0331	mecA	1.26	-1.98	-2.49	C8	penicillin-binding protein 2	Cell envelope: Biosynthesis and degradation of murein sacculus and peptidoglycan
SACOL0335	-	1.77	-1.88	-3.33	C8	hypothetical protein	-
SACOL0992	-	1.61	-2.20	-3.55	C8	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0995	spa	1.10	-5.78	-6.35	C8	immunoglobulin G binding protein A precursor	Cellular processes: Pathogenesis
SACOL0111	-	-1.14	-2.57	-2.25	C8	acetoin reductase	Energy metabolism: Fermentation
SACOL0119	sasD	1.25	-2.24	-2.81	C8	cell wall surface anchor family protein	Cell envelope: Other
SACOL0276	yukA	1.02	-2.43	-2.48	C8	diarrheal toxin	Unknown function: General
SACOL0300	-	-1.06	-2.93	-2.75	C8	hypothetical protein	-
SACOL0565	-	-1.18	-2.86	-2.43	C8	conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL0617	-	1.02	-2.67	-2.72	C8	hexulose-6-phosphate synthase, putative	Energy metabolism: Sugars
SACOL0618	-	1.20	-2.20	-2.64	C8	SIS domain protein	Unknown function: General
SACOL0635	-	1.64	-1.64	-2.69	C8	lipotein-protein ligase A family protein	Protein fate: Protein modification and repair
SACOL0763	-	2.08	-2.74	-5.70	C8	oxidoreductase, aldo/keto reductase family	Unknown function: Enzymes of unknown specificity
SACOL0777	-	1.11	-2.39	-2.66	C8	urea amidolyase-related protein	Unknown function: General
SACOL0778	-	1.64	-1.51	-2.48	C8	sulfatase family protein	Unknown function: Enzymes of unknown specificity
SACOL0783	opuBB	1.26	-2.06	-2.59	C8	osmoprotectant ABC transporter, permease protein	Transport and binding proteins: Amino acids, peptides and amines
SACOL0957	-	1.61	-2.32	-3.74	C8	peptidyl-prolyl cis-trans isomerase, cyclophilin-type	Protein fate: Protein folding and stabilization
SACOL0985	-	1.42	-2.57	-3.65	C8	surface protein, putative	Cell envelope: Other
SACOL1123	pyc	1.13	-2.24	-2.53	C8	pyruvate carboxylase	Energy metabolism: Glycolysis/gluconeogenesis

SACOL1164	-	1.91	-3.35	-6.40	C8		fibrinogen binding-related protein	Unknown function: General
SACOL1169	-	-1.14	-4.32	-3.80	C8		fibrinogen-binding protein precursor-related protein	Unknown function: General
SACOL1317	gfpP	-1.07	-2.61	-2.44	C8		glycerol uptake operon antiterminator regulatory protein	Regulatory functions: RNA interactions
SACOL1329	femC	-1.05	-3.56	-3.38	C8		glutamine synthetase FemC	Cell envelope: Biosynthesis and degradation of murein sacculus and peptidoglycan
SACOL1351	cls1	-1.05	-2.58	-2.45	C8		cardiolipin synthetase	Fatty acid and phospholipid metabolism: Biosynthesis
SACOL1441	-	1.16	-3.30	-3.81	C8		tellurite resistance protein, putative	Cellular processes: Toxin production and resistance
SACOL1456	-	1.86	-2.14	-3.97	C8		conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1457	-	1.66	-2.83	-4.70	C8		PTS system, IIA component	Transport and binding proteins: Carbohydrates, organic alcohols, and acids; Signal transduction: PTS
SACOL1623	-	1.20	-2.45	-2.95	C8		DNA repair protein RecO family	DNA metabolism: DNA replication, recombination, and repair
SACOL1670	-	1.67	-1.55	-2.60	C8		conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1753	-	1.22	-2.81	-3.42	C8		universal stress protein family	Cellular processes: Adaptations to atypical conditions
SACOL1759	-	-1.11	-3.64	-3.28	C8		universal stress protein family	Cellular processes: Adaptations to atypical conditions
SACOL1760	ackA	1.14	-3.37	-3.83	C8	↓	acetate kinase	Central intermediary metabolism: Other; Energy metabolism: Fermentation
SACOL1796	-	1.70	-1.89	-3.21	C8		conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1831	tal	-1.18	-5.26	-4.46	C8		transaldolase	Energy metabolism: Pentose phosphate pathway
SACOL1942	vraR	-1.16	-2.69	-2.31	C8		DNA-binding response regulator VraR	Cellular processes: Toxin production and resistance; Regulatory functions: DNA interactions; Regulatory functions; Signal transduction: Two-component systems
SACOL1960	gatB	1.03	-2.44	-2.50	C8		glutamyl-tRNA(Gln) amidotransferase, B subunit	Protein synthesis: tRNA aminoacylation
SACOL1964	camS	-1.03	-2.60	-2.53	C8		Staphylococcus aureus sex pheromone	Cellular processes: Other; Cellular processes: Cell adhesion
SACOL1965	lga	-1.01	-2.57	-2.54	C8		DNA ligase, NAD-dependent	DNA metabolism: DNA replication, recombination, and repair
SACOL1966	pcrA	1.04	-2.38	-2.49	C8		ATP-dependent DNA helicase PcrA	DNA metabolism: DNA replication, recombination, and repair
SACOL1968	-	1.05	-3.20	-3.34	C8		conserved hypothetical protein	Hypothetical proteins: Conserved
SACOL1969	purB	1.24	-2.94	-3.65	C8		adenylosuccinate lyase	Purines, pyrimidines, nucleosides, and nucleotides: Purine ribonucleotide biosynthesis
SACOL2006	-	1.61	-1.64	-2.64	C8		Aerolysin/Leukocidin family protein	Cellular processes: Toxin production and resistance; Cellular processes: Pathogenesis
SACOL2006	-	1.61	-1.64	-2.64	C8		Aerolysin/Leukocidin family protein	Cellular processes: Toxin production and resistance; Cellular processes: Pathogenesis
SACOL2117	fbaA	-1.21	-4.13	-3.41	C8	↓	fructose-bisphosphate aldolase, class II	Energy metabolism: Glycolysis/gluconeogenesis
SACOL2192	-	1.07	-3.06	-3.28	C8		oxidoreductase, aldo/keto reductase family	Unknown function: Enzymes of unknown specificity
SACOL2415	gpm	1.19	-2.53	-3.01	C8	↑	phosphoglycerate mutase	Energy metabolism: Glycolysis/gluconeogenesis
SACOL2418	-	-1.13	-4.54	-4.03	C8		IgG-binding protein SBI	Cellular processes: Pathogenesis
SACOL2467	-	1.74	-1.74	-3.02	C8	↓	lipoprotein, putative	Cell envelope: Other
SACOL2576	crtN	1.67	-1.58	-2.65	C8	↑	dehydroqualene desaturase	Central intermediary metabolism: Other
SACOL2622	fdaB	-1.09	-8.52	-7.83	C8	↑	fructose-bisphosphate aldolase, class I	Energy metabolism: Glycolysis/gluconeogenesis
SACOL2667	-	1.17	-2.39	-2.81	C8	↑	isochorismatase family protein	Unknown function: Enzymes of unknown specificity

1) Fold change: genes that passed the significance test (see materials and methods section) are shown in bold. Red: at least 2.5 fold up-regulation. Green: at least -2.5 fold down regulation.

2) Genes grouped based on expression kinetics. **C1**: up-regulated at 10 min and down regulated at 40 min; **C2**: unchanged at 10 min and up-regulated at 40 min; **C3**: up-regulated at 10 min and further up-regulated at 40 min; **C4**:

up-regulated at 10 min and remains up-regulated at a similar level at 40 min; **C5**: down-regulated at 10 min and remains down-regulated at a similar level at 40 min;

regulated at 10 min and up-regulated at 40 min; **C8**: unchanged at 10 min and down-regulated at 40 min

3) Genes positively regulated by SigB as identified by Bischoff et al. 2004 and Pané-Farré et al. 2006 (overlap between both studies). Genes organized in transcription units that are transcribed from an experimentally confirmed SigB-dependent promoter are shaded gray (Bischoff et al. 2004, Pané-Farré et al. 2006, Homerova et al. 2004).

4) Upward and downward arrows show genes induced or repressed in response to linoleic acid based on Kenny et al. 2009.

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