

Table S2: RNA-Seq transcriptome analysis of gene expression changes in *S. aureus* COL wild type and the *mhgR* deletion mutant before and after MHQ stress.

Gene name	Region	Locus	Operon	log2 fold change (M-value)				Fold changes				Function	
				WT MHO		ΔmhgR MHO		WT MHO		ΔmhgR MHO			
				WT co	MHO	ΔmhgR co	MHO	WT co	MHO	ΔmhgR co	MHO		
Amino acid biosynthesis	CodY	SACOL0302	bem2	1.31	1.02	0.94	0.65	2.48	2.03	0.52	0.64	branched-chain amino acid transport system I carrier protein	
Amino acid biosynthesis	CodY	SACOL2574	tdh	-1.70	-0.45	0.88	-0.37	0.31	0.73	1.84	0.77	D-isomer specific 2-hydroxyacid dehydrogenase family protein	
Amino acid biosynthesis	CodY	SACOL2575	tdh	-1.96	-0.11	0.62	-0.22	0.52	0.93	1.54	0.86	N-succinylamino acid aminotransferase	
Amino acid biosynthesis	CodY	SACOL2511	trpE	2.75	1.40	1.17	0.20	0.28	0.78	2.64	0.38	lysine-binding protein	
Amino acid biosynthesis	CodY	SACOL1362	hom	-1.17	-0.28	0.63	0.03	0.44	0.67	1.55	1.02	homoserine dehydrogenase	
Amino acid biosynthesis	CodY	SACOL1363	hom	-1.03	-0.56	0.19	0.39	0.98	0.84	1.14	1.31	threonine synthase	
Amino acid biosynthesis	CodY	SACOL1429	tyrC	0.19	0.13	0.21	0.40	0.61	0.41	0.99	1.17	tyrosine aminotransferase	
Amino acid biosynthesis	CodY	SACOL2584	isaA	-1.32	-0.43	0.77	0.12	0.40	0.74	1.71	0.92	immunodominant antigen A	
Amino acid biosynthesis	CodY	SACOL1428	lycC	-2.49	-0.47	0.65	-1.22	0.18	0.72	1.57	0.43	aspartate kinase	
Amino acid biosynthesis	CodY	SACOL1429	lycC	-2.59	-0.33	0.18	-0.09	0.93	0.80	1.13	0.50	aspartate semialdehyde dehydrogenase	
Amino acid biosynthesis	CodY	SACOL1430	lycC	-1.31	-0.08	0.12	-1.03	0.40	0.95	1.09	0.49	dihydrodipicolinate synthase	
Amino acid biosynthesis	CodY	SACOL1431	lycC	-0.71	0.05	0.02	-0.72	0.61	1.04	1.03	0.61	dihydrodipicolinate synthase	
Amino acid biosynthesis	CodY	SACOL1432	phoD	-0.40	-1.13	-0.11	-0.61	0.76	1.09	0.99	0.93	high affinity proline permease	
Amino acid biosynthesis	CodY	SACOL1363	trpE	1.26	0.39	0.42	0.44	0.42	0.75	1.34	0.74	high affinity proline permease	
Amino acid biosynthesis	CodY	SACOL1817	rhlB	2.54	1.24	-1.40	0.11	5.81	2.36	0.38	0.99	rhlB/aiiA synthase beta subunit	
Amino acid biosynthesis	CodY	SACOL1818	rhlB	2.42	1.39	-1.31	-0.28	5.33	2.62	0.40	0.82	difluoromethyl 3,4-dihydroxy-2-butanone-4-phosphate synthase/GTP cyclohydrolase II	
Amino acid biosynthesis	CodY	SACOL1820	rhlB	2.59	1.37	-1.32	0.11	6.01	2.58	0.40	0.93	rhlB/aiiA synthase alpha subunit	
Amino acid biosynthesis	CodY	SACOL1820	rhlB	2.58	1.28	-1.46	0.18	5.96	2.43	0.36	0.88	diaminohydroxyphosphoribosylaminoimidazole deaminase	
Amino acid biosynthesis	CodY	SACOL0924	SACOL0924	-0.05	-0.04	-0.32	-0.31	0.97	0.97	0.80	0.81	hypothetical protein	
Amino acid biosynthesis	CodY	SACOL0925	SACOL0925	0.49	0.37	0.38	0.16	1.4	1.21	1.20	1.20	hypothetical protein	
Amino acid biosynthesis	CodY	SACOL0926	SACOL0926	0.81	0.36	-0.52	0.08	1.75	1.28	0.70	0.95	5'-nucleotidase	
Amino acid biosynthesis	CodY	SACOL1365	SACOL1365	0.71	0.55	0.02	0.13	1.64	1.46	0.99	1.09	HAD superfamily hydrolase	
Amino acid biosynthesis	CodY	SACOL1374	SACOL1374	1.24	0.23	0.23	0.26	1.96	1.86	0.85	0.86	HAD superfamily hydrolase	
Amino acid biosynthesis	CodY	SACOL1775	ptaA	-1.44	-0.64	0.81	0.01	0.37	0.64	1.75	1.01	PTS system, IIBC components	
Amino acid biosynthesis	CodY	SACOL2318	SACOL2318	1.17	-0.14	1.29	0.00	2.25	0.91	0.41	1.00	hypothetical protein	
Amino acid biosynthesis	CodY	SACOL0919	isaA	1.82	0.45	0.82	0.58	1.28	1.63	0.73	1.67	amino acid permease	
Amino acid biosynthesis	CodY	SACOL2295	isaA	1.19	1.55	0.55	0.22	2.27	2.93	1.46	1.16	secretory antigen Saa	
Amino acid biosynthesis	CodY	SACOL1477	ivaI	-0.36	0.48	0.62	-0.20	0.78	1.39	1.54	0.87	threonine ammonia-lyase	
Amino acid biosynthesis	CodY	SACOL1478	ivaI	-0.47	0.17	0.72	0.50	0.55	0.66	0.66	1.00	amine dehydrogenase	
Amino acid biosynthesis	CodY	SACOL1403	trpE	1.62	1.09	0.02	0.38	3.08	2.13	0.99	1.30	anthranilate synthase component 1	
Amino acid biosynthesis	CodY	SACOL1404	trpE	0.91	1.15	0.22	0.05	1.88	2.22	1.16	0.97	anthranilate synthase component II	
Amino acid biosynthesis	CodY	SACOL1405	trpE	1.17	0.67	0.17	0.24	2.32	1.66	1.18	anthranilate phosphoribosyltransferase		
Amino acid biosynthesis	CodY	SACOL1406	trpE	1.03	0.76	0.11	0.12	2.04	1.69	0.93	indole-3-pyruvate synthase		
Amino acid biosynthesis	CodY	SACOL1407	trpE	1.89	0.69	0.41	0.57	3.71	1.61	0.75	1.48	N ⁵ -phosphoribosylanthranilate isomerase	
Amino acid biosynthesis	CodY	SACOL1408	trpE	1.29	0.59	-0.21	0.02	2.02	1.83	1.09	1.09	tryptophan synthase subunit beta	
Amino acid biosynthesis	CodY	SACOL1409	trpA	1.29	0.49	-0.54	0.22	2.45	1.40	0.69	1.16	tryptophan synthase subunit alpha	
Amino acid biosynthesis	CodY	SACOL1401	trpA	1.26	1.19	0.13	0.17	2.40	2.28	1.09	1.11	phenylalanine dehydrogenase	
Amino acid biosynthesis	CodY	SACOL1402	trpA	0.68	0.31	-0.48	0.24	1.60	1.44	0.71	1.17	metallo-beta-lactamase	
Amino acid biosynthesis	CodY	SACOL0928	trpE	1.27	0.63	0.84	0.56	1.93	1.49	1.13	1.13	tryptophan synthase alpha subunit	
Amino acid utilization	ArcA	SACOL0786	arcA	1.43	0.93	0.61	0.61	2.09	1.49	0.83	0.83	phosphoenolpyruvate carboxyltransferase	
Ammonium biosynthesis	ArcR	SACOL2654	arcC	-1.64	-0.87	0.00	0.13	0.32	0.55	1.87	1.09	carbamate kinase	
Ammonium biosynthesis	ArcR	SACOL2655	arcC	-0.94	-0.48	0.86	0.12	0.52	0.74	1.28	0.92	AHC family amino acid polyamine-ornithine transporter	
Ammonium biosynthesis	ArcR	SACOL2656	arcC	-0.94	-0.86	0.75	0.60	1.60	1.02	1.66	1.00	hydroxyethylamine dehydrogenase	
Ammonium biosynthesis	ArcR	SACOL2657	arcC	-1.38	-0.94	1.30	0.95	0.10	0.52	2.46	0.52	arginase deaminase	
Ammonium biosynthesis	ArcR	SACOL2653	arcR	-1.72	-0.51	0.96	0.90	0.50	0.57	1.96	1.04	Ctp/Trk family transcriptional regulator	
Ammonium biosynthesis	ArcR	SACOL0167	argB	0.58	0.07	0.47	0.16	0.67	1.05	1.39	1.90	acetylglutamate kinase	
Ammonium biosynthesis	ArcR	SACOL0168	argB	0.88	-0.04	0.36	0.45	0.54	0.97	1.28	0.73	glutamate N acetyltransferase	
Ammonium biosynthesis	ArcR	SACOL0169	argB	-1.48	-0.10	0.79	-0.48	0.36	0.93	1.73	0.72	N acetyl-gamma-glutamyl phosphate reductase	
Ammonium biosynthesis	ArcR	SACOL0170	argB	-1.49	-0.35	0.93	0.57	0.88	1.14	1.43	1.43	glutamate-oxaloacetate transaminase	
Ammonium biosynthesis	ArcR	SACOL0963	argH	-4.94	-2.24	0.04	0.54	0.07	0.21	1.03	0.69	argininosuccinate lyase	
Ammonium biosynthesis	ArcR	SACOL0964	argH	-4.95	-2.48	0.19	0.38	0.03	0.16	0.88	0.47	argininosuccinate synthase	
Ammonium biosynthesis	ArcR	SACOL1915	argH	-1.95	-0.88	0.97	0.17	0.64	1.56	0.24	1.84	glutamate ABC transporter, ATP-binding protein	
Ammonium biosynthesis	ArcR	SACOL1916	argM	-2.93	-0.91	0.97	0.43	0.13	0.53	1.96	0.74	amino acid ABC transporter, membrane protein	
Ammonium biosynthesis	ArcR	SACOL2632	argT	-2.52	-1.84	1.58	0.08	0.09	0.28	2.99	0.95	BCT1 family beta-caranine/choline transporter	
Ammonium metabolism	FruR	SACOL0787	fruA	0.22	0.07	0.24	0.23	1.05	1.18	1.07	1.07	DexA family transcriptional regulator	
Ammonium metabolism	FruR	SACOL0788	fruA	0.18	-0.43	0.04	0.57	2.08	1.35	1.03	1.48	1-phosphoglucohydrolase	
Ammonium metabolism	FruR	SACOL1328	glpA	-0.77	-0.61	-0.21	-0.37	0.59	0.66	0.86	0.71	glutamate-ammonia lyase repressor	
Ammonium metabolism	FruR	SACOL1329	glpA	-0.68	-0.26	0.31	0.63	0.89	0.66	1.07	1.07	glutamate-ammonia lyase	
Antibiotics resistance	VraSR	SACOL2485	vraS	-1.15	-0.51	0.54	0.11	0.45	0.70	1.45	0.93	glycerate kinase	
Antibiotics resistance	VraSR	SACOL2486	vraS	-1.05	-0.54	0.47	0.10	0.48	0.69	1.39	0.97	hypothetical protein	
Antibiotics resistance	VraSR	SACOL1894	vraS	-0.59	-0.29	0.45	0.46	0.65	1.17	1.75	1.07	phosphorylase isomerase	
Antibiotics resistance	VraSR	SACOL1932	vraS	-1.36	-0.59	0.70	0.06	0.39	0.66	1.62	0.96	monofunctional glycosyltransferase	
Antibiotics resistance	VraSR	SACOL1942	vraS	1.46	0.73	-0.64	0.07	2.75	1.66	0.64	1.05	response regulator VraR	
Antibiotics resistance	VraSR	SACOL1943	vraS	1.65	0.65	-0.61	0.67	0.66	0.67	1.02	1.05	phosphonate kinase VraS	
Antibiotics resistance	VraSR	SACOL1944	vraS	1.05	0.62	-0.39	0.03	2.08	1.54	0.76	1.02	hypothetical membrane protein	
Antibiotics resistance	VraSR	SACOL1945	vraS	0.93	0.49	-0.37	0.06	1.91	1.40	0.77	1.04	hypothetical protein	
Cell wall biosynthesis	CitR	SACOL2198	budA1	2.77	1.61	1.68	0.88	6.83	2.41	0.48	1.80	antibiotec deacetylase	
Cell wall biosynthesis	CitR	SACOL2199	budA1	2.75	1.35	1.72	0.10	1.57	2.55	0.65	0.65	1.07	phosphorylase isomerase
Cell wall biosynthesis	CitR	SACOL2533	cidC	2.00	0.62	-1.02	0.58	1.58	1.33	0.48	1.46	pyruvate oxidase	
Cell wall biosynthesis	CitR	SACOL2534	cidC	2.77	0.77	-0.29	0.80	0.84	0.80	0.72	0.72	1.45	hypothetical membrane protein
Cell wall biosynthesis	GrxR	SACOL0921	igppQ	1.47	0.77	0.73	0.93	1.78	1.78	0.77	0.77	acetylphosphotransferase/phenolphosphatase	
Cell wall biosynthesis	GrxR	SACOL2129	docE2	1.40	2.32	1.19	0.26	2.65	4.99	2.28	1.20	tyrosine phosphatase aldolase	
Cell wall biosynthesis	GrxR	SACOL1743	zapa	-0.84	-0.05	0.55	-0.24	0.56	0.97	1.46	0.85	AHC family amino acid polyamine-ornithine transporter	
Cell wall biosynthesis	GrxR	SACOL1744	zapa	-0.84	-0.05	0.55	-0.24	0.56	0.97	1.46	0.85	AHC family amino acid polyamine-ornithine transporter	
Cell wall biosynthesis	GrxR	SACOL1761	ackA	2.28	1.75	-1.14	-0.58	4.85	3.36	0.45	0.67	hypothetical protein	
Cell wall biosynthesis	GrxR	SACOL0190	aqdD	7.79	5.38	-1.31	1.05	221.15	41.64	4.60	2.07	zinc oxidase	
Cell wall biosynthesis	GrxR	SACOL0191	aqdD	6.95	4.97	-1.57	0.95	21.52	3.95	0.96	1.66	alcohol dehydrogenase	
Cell wall biosynthesis	GrxR	SACOL2192	alrSf	1.78	0.66	-1.11	-0.01	3.43	1.58	0.46	0.99	oxidoreductase, aldo/keto reductase	
Cell wall biosynthesis	GrxR	SACOL2094	atpC	-0.86	-0.82	0.25	0.01	0.55	0.65	1.19	1.01	proton-translocating F ₁ F ₀ ATPase epsilon subunit	
Cell wall biosynthesis	GrxR	SACOL2095	atpC	-0.86	-0.82	0.25	0.01	0.55	0.65	1.19	1.01	proton-translocating F ₁ F ₀ ATPase epsilon subunit	
Cell wall biosynthesis	GrxR	SACOL2096	atpG	-1.14	-0.80	0.54	0.19	0.45	0.57	1.45	1.14	proton-translocating F ₁ F ₀ ATPase alpha subunit	
Cell wall biosynthesis	GrxR	SACOL2097	atpA	-1.13	-0.59	0.61	0.06	0.46	0.66	1.53	1.04	proton-translocating F ₁ F ₀ ATPase alpha subunit	
Cell wall biosynthesis	GrxR	SACOL2098	atpA	-1.13	-0.59	0.61	0.06	0.46	0.66	1.53	1.04	proton-translocating F ₁ F ₀ ATPase alpha subunit	
Cell wall biosynthesis	GrxR	SACOL2099	atpF	-1.03	-0.72	0.47	0.16	0.49	0.61	1.39	1.12	proton-translocating F ₁ F ₀ ATPase subunit B	
Cell wall biosynthesis	GrxR	SACOL2100	atpE	-0.99	-0.86	0.40	0.26	0.50	0.55	1.32	1.20	proton-translocating F ₁ F ₀ ATPase epsilon subunit C	

Function	Region	Gene	Dysregulation	Gene symbol	log2-fold change (M-value)				Fold changes				Function
					WT MND3 / WT co	Δmsh2 MND3 / Δmsh2 co	Δmsh2 MND3 / WT MND3	Δmsh2 co / WT co	WT MND3 / WT co	Δmsh2 MND3 / Δmsh2 co	Δmsh2 MND3 / WT MND3	Δmsh2 co / WT co	
Cell wall biosynthesis	GraRS	SACOL2451	opuCD opuCC opuCB opuCA	opuCC	2.16	1.59	-1.37	-0.77	4.46	3.01	0.39	0.59	glycine betaine/L-proline ABC transporter, binding protein
Cell wall biosynthesis	GraRS	SACOL2452	opuCD opuCC opuCB opuCA	opuCB	2.17	1.32	-1.45	-0.58	4.50	2.50	0.37	0.67	glycine betaine/choline ABC transporter, membrane protein
Cell wall biosynthesis	GraRS	SACOL2453	opuCD opuCC opuCB opuCA	opuCA	1.78	1.38	-1.14	-0.71	3.44	2.60	0.40	0.61	glycine betaine/choline ABC transporter, ATP-binding protein
Cell wall biosynthesis	GraRS	SACOL2454	opuCD opuCC opuCB opuCA	opuB	1.12	0.93	-0.95	-0.25	0.25	0.85	1.27	0.85	NCS1 family nucleobase/uracil transporter 2
Cell wall biosynthesis	GraRS	SACOL2128	pdp	pdp	1.30	1.81	0.80	0.28	2.46	3.51	1.74	1.21	pyrimidine nucleoside phosphorylase
Cell wall biosynthesis	GraRS	SACOL0125	phnE1 phnE2 phnC phnD	phnE1	-0.42	-0.12	-0.25	-0.41	0.75	0.92	0.84	0.75	phosphonate ABC transporter, permease
Cell wall biosynthesis	GraRS	SACOL0126	phnE1 phnE2 phnC phnD	phnE2	0.61	0.63	-0.56	-0.34	0.56	0.86	0.96	0.69	phosphonate ABC transporter, permease
Cell wall biosynthesis	GraRS	SACOL0127	phnE1 phnE2 phnC phnD	phnC	-0.79	-0.16	-0.55	-0.04	0.58	0.90	1.46	0.97	phosphonate ABC transporter, ATP-binding protein
Cell wall biosynthesis	GraRS	SACOL0128	phnE1 phnE2 phnC phnD	phnD	-2.00	-0.46	-1.04	-0.37	0.25	0.73	2.06	0.77	phosphonate ABC transporter, phosphate-binding protein
Cell wall biosynthesis	GraRS	SACOL0272	ptaA	ptaA	1.72	0.12	-0.13	-0.55	3.30	1.59	0.29	1.68	DNA repair protein RecA
Cell wall biosynthesis	GraRS	SACOL0573	ptaP	ptaP	0.86	-0.17	-1.95	-0.93	1.82	0.89	0.76	0.52	intralumenal membrane protein (PIN domain superfamily)
Cell wall biosynthesis	GraRS	SACOL2518	repE	repE	-0.85	0.34	-0.17	-1.33	0.55	1.27	0.89	0.40	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL0077	SACOL0077	SACOL0077	0.72	-0.30	-0.52	-0.51	0.61	0.81	1.01	1.01	hypothetical membrane protein
Cell wall biosynthesis	GraRS	SACOL0259	SACOL0259	SACOL0259	-1.01	-1.27	-0.09	-0.16	0.50	0.41	0.94	1.12	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL0283	SACOL0283	SACOL0283	-2.06	-0.84	0.55	-0.63	0.24	0.56	1.46	0.65	hypothetical membrane protein
Cell wall biosynthesis	GraRS	SACOL0300	SACOL0300	SACOL0300	1.77	-1.51	0.20	-0.66	0.29	0.35	1.25	0.96	hypothetical membrane protein
Cell wall biosynthesis	GraRS	SACOL0466	SACOL0466 SACOL0467	SACOL0466	1.52	0.91	-2.30	0.20	11.44	1.88	0.20	1.15	hypothetical membrane protein
Cell wall biosynthesis	GraRS	SACOL0467	SACOL0466 SACOL0467	SACOL0467	3.35	0.74	-2.40	-0.12	10.22	1.67	0.19	1.09	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL0551	SACOL0551 SACOL0552	SACOL0551	1.29	0.34	-0.59	0.08	2.02	1.27	0.66	1.06	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL0552	SACOL0551 SACOL0552	SACOL0552	0.98	0.74	0.47	-0.21	1.97	1.67	0.72	0.86	hypothetical membrane protein
Cell wall biosynthesis	GraRS	SACOL0606	SACOL0606 aot1	SACOL0606	0.08	1.49	0.27	0.55	1.25	2.81	2.60	0.50	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL0607	SACOL0606 aot1	aot1	0.60	1.49	1.07	0.21	1.52	2.81	2.10	1.16	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL0849	SACOL0849 SACOL0850	SACOL0849	-1.91	-0.53	-0.19	-1.49	0.27	0.69	0.88	0.36	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL0850	SACOL0849 SACOL0850	SACOL0850	1.20	0.34	-0.59	0.08	2.02	1.27	0.66	1.06	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL0851	SACOL0851	SACOL0851	-2.51	-0.61	-0.56	-2.82	0.18	0.66	0.68	0.19	hypothetical lipoprotein
Cell wall biosynthesis	GraRS	SACOL1005	SACOL1004 pepF	pepF	1.37	1.76	0.01	-0.37	2.58	3.39	0.99	0.77	M03 family oligopeptidase F
Cell wall biosynthesis	GraRS	SACOL1225	SACOL1225	SACOL1225	-1.06	0.50	-0.49	-1.26	0.48	1.41	1.14	0.42	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL1333	SACOL1333	SACOL1333	1.93	0.92	-0.12	-0.37	3.19	0.71	1.38	0.97	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL1456	SACOL1456 err	err	1.97	0.48	-0.98	0.44	3.92	1.39	0.49	1.36	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL1457	SACOL1456 err	err	1.88	0.47	-0.98	0.42	3.69	1.39	0.51	1.34	PTS family glucose/glucose 6-phosphate porter component BA
Cell wall biosynthesis	GraRS	SACOL1902	SACOL1902 SACOL1903	SACOL1902	1.93	0.91	-0.20	-0.20	3.20	1.42	0.90	1.02	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL1903	SACOL1902 SACOL1903	SACOL1903	0.63	-0.13	0.61	0.09	0.64	0.91	1.53	1.06	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL2127	SACOL2127	SACOL2127	0.99	-1.27	0.62	0.33	1.98	2.41	1.54	1.26	hypothetical membrane protein
Cell wall biosynthesis	GraRS	SACOL2252	SACOL2252	SACOL2252	1.31	0.25	-0.75	-0.40	2.40	0.90	0.80	0.57	possible H4D superfamily hydrolase
Cell wall biosynthesis	GraRS	SACOL2252	SACOL2252 hemK	hemK	0.81	-0.11	-0.78	0.12	1.75	0.93	0.58	1.09	RND resistance-nucleation-cell division acriflavine/proton antiporter
Cell wall biosynthesis	GraRS	SACOL2253	SACOL2252 hemK	hemK	0.26	-0.25	-0.53	-0.03	1.20	0.84	0.69	0.98	peptidoglycan pentapeptide interdivisive biosynthesis protein FmB8
Cell wall biosynthesis	GraRS	SACOL2344	SACOL2343 SACOL2344	SACOL2343	1.53	0.29	-1.93	-1.48	1.34	1.87	1.08	1.13	RND resistance-nucleation-cell division acriflavine/proton antiporter
Cell wall biosynthesis	GraRS	SACOL2344	SACOL2343 SACOL2344	SACOL2344	1.32	0.33	-1.09	-1.10	2.49	1.26	0.47	0.93	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL2430	SACOL2430 mshA3	mshA3	0.59	0.91	-0.10	-0.35	1.51	1.88	0.93	0.78	ABC transporter, ATP-binding protein
Cell wall biosynthesis	GraRS	SACOL2431	SACOL2430 mshA3	mshA3	1.09	0.32	0.58	0.44	1.64	1.17	0.84	0.61	ABC transporter, ATP-binding protein
Cell wall biosynthesis	GraRS	SACOL2477	SACOL2477 hmo dafP	SACOL2477	1.62	2.11	-1.11	-0.77	12.33	4.32	0.46	1.29	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL2478	SACOL2477 hmo dafP	hmoD	4.64	1.88	-1.88	-0.68	26.97	3.68	0.27	1.40	rRNA methyltransferase FmO
Cell wall biosynthesis	GraRS	SACOL2479	SACOL2477 hmo dafP	dafP	4.08	2.16	-1.82	-0.90	25.90	4.67	0.31	1.46	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL2522	SACOL2522	SACOL2522	1.71	0.54	-2.00	-1.46	3.27	1.45	0.14	0.36	alkaline phosphatase
Cell wall biosynthesis	GraRS	SACOL2582	SACOL2582	SACOL2582	-1.23	0.12	1.62	0.28	0.43	1.09	1.07	1.21	possible acetyltransferase
Cell wall biosynthesis	GraRS	SACOL2584	SCN 2	SCN 2	0.75	-0.91	0.17	0.33	0.93	1.33	1.24	1.34	Mark3/4 family transcriptional regulator
Cell wall biosynthesis	GraRS	SACOL2608	SCN 2	SCN 2	-1.05	-1.04	-0.14	-0.59	0.48	0.49	0.91	0.94	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL0816	SecA	SecA	0.98	0.00	-0.40	-0.19	1.98	1.29	0.57	0.88	Sec Type 1 general secretory pathway prepore translocase SecA
Cell wall biosynthesis	GraRS	SACOL1005	SecY	SecY	2.35	-0.65	-0.23	-0.23	4.20	0.39	0.20	1.20	secretory antigen secretion factor SecY
Cell wall biosynthesis	GraRS	SACOL1891	TRAP	TRAP	2.85	1.68	-1.50	-0.31	7.19	3.10	0.35	0.81	RNAi-activating protein TRAP
Cell wall biosynthesis	GraRS	SACOL2550	traX 6 SACOL2551	traX 6	3.74	0.43	-2.07	-0.72	13.40	1.39	0.19	1.65	possible thiorodanin
Cell wall biosynthesis	GraRS	SACOL2551	traX 6 SACOL2551	SACOL2551	4.43	0.47	-2.07	-0.67	14.29	1.32	0.27	1.99	possible thiorodanin
Cell wall biosynthesis	GraRS	SACOL2280	ureABCDFG	ureA	1.97	0.29	-2.16	-0.36	3.93	1.22	0.22	0.78	urease gamma subunit
Cell wall biosynthesis	GraRS	SACOL2281	ureABCDFG	ureB	1.73	0.22	-2.12	-0.52	3.33	1.16	0.23	0.70	urease beta subunit
Cell wall biosynthesis	GraRS	SACOL2282	ureABCDFG	ureC	1.89	0.49	-2.05	-0.56	3.67	1.48	0.27	0.71	urease alpha subunit
Cell wall biosynthesis	GraRS	SACOL2283	ureABCDFG	ureE	1.70	0.36	-1.81	-0.44	3.35	1.28	0.29	0.74	urease accessory protein UreE
Cell wall biosynthesis	GraRS	SACOL2284	ureABCDFG	ureF	1.72	0.39	-1.75	-0.42	3.30	1.31	0.30	0.75	urease accessory protein UreF
Cell wall biosynthesis	GraRS	SACOL2285	ureABCDFG	ureG	1.81	0.38	-1.59	-0.16	3.52	1.30	0.63	0.90	urease accessory protein UreG
Cell wall biosynthesis	GraRS	SACOL2286	ureABCDFG	ureD	1.63	0.24	-1.84	-0.21	3.09	1.08	0.34	0.68	urease accessory protein UreD
Cell wall biosynthesis	GraRS	SACOL0019	waIRH	waIR	0.75	0.24	-0.69	-0.18	1.68	1.18	0.62	0.88	response regulator VcR
Cell wall biosynthesis	GraRS	SACOL0020	waRH	waR	0.84	0.20	-0.73	-0.10	1.79	1.15	0.60	0.93	sensor histidine kinase VcK
Cell wall biosynthesis	GraRS	SACOL0021	waRH	waR	0.92	0.21	-0.97	-0.14	1.90	1.13	0.63	0.94	hypothetical protein VcH
Cell wall biosynthesis	GraRS	SACOL0022	waRH	waR	1.02	0.22	-0.73	-0.09	1.98	1.27	0.60	0.94	hypothetical protein VcI
Cell wall biosynthesis	GraRS	SACOL1440	xpcA	xpcA	2.02	0.62	-1.29	-0.20	4.06	1.54	0.33	0.87	5-bromo-4-chlorouridine phosphate hydrolase
Cell wall biosynthesis	GraRS	SACOL1441	xpcA	xpcA	1.95	0.58	-1.36	-0.11	3.94	1.51	0.33	0.87	5-bromo-4-chlorouridine phosphate hydrolase
Cell wall biosynthesis	GraRS	SACOL2367	yHfP	yHfP	1.74	1.04	-1.26	-0.57	3.34	2.06	0.42	0.67	zinc-binding alcohol dehydrogenase
Cell wall biosynthesis	GraRS	SACOL0977	yWV	yWV	2.31	1.35	-1.10	-0.15	4.95	2.55	0.47	0.90	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL1006	yWV	yWV	1.09	0.16	-1.58	-0.33	2.13	1.88	0.91	1.02	hypothetical protein
Cell wall biosynthesis	GraRS	SACOL1007	yWV	yWV	0.76	0.35	-1.65	-0.55	1.70	0.78	0.32	0.68	globin family protein
Cell wall biosynthesis	GraRS	SACOL0656	yWV	yWV	0.99	-0.20	-1.07	-0.10	1.99	0.87	0.46	1.07	putative flavodoxin
Cell wall biosynthesis	GraRS	SACOL0657	yWV	yWV	1.54	0.34	-1.80	-0.26	3.16	0.76	0.42	1.01	glucose-6-phosphate 1-dehydrogenase
DNA damage	LnaA	SACOL1600	dnaB2	dnaB2	2.50	1.10	-1.22	-0.15	5.64	2.85	0.61	0.88	ImpB/Sam3/Sam8 family DNA-damage repair protein
DNA damage	LnaA	SACOL0789	zurF SACOL0790	zurF	-1.18	-0.36	0.93	0.10	0.44	0.78	1.93	1.59	7-Cyano-7-deazaadenine reductase
DNA damage	LnaA	SACOL0790	zurF SACOL0790	zurF	-1.02	-0.46	0.61	0.17	0.40	0.73	1.15	intracellular membrane domain-containing protein	
DNA damage	LnaA	SACOL1304	recA	recA	1.40	0.91	-0.66	-0.16	2.65	1.88	0.63	0.90	recombinase A
DNA damage	LnaA	SACOL0823	uvrB uvrA	uvrB	0.97	0.06	-0.94	-0.04	1.96	1.04	0.52	0.97	excinuclease ABC subunit B
DNA damage	LnaA	SACOL0824	uvrB uvrA	uvrA	1.73	0.51	-1.06	-0.48	3.25	1.62	0.43	0.92	excinuclease ABC subunit A
Energy metabolism	CagR	SACOL0837	znpR znpR TPA ppm eno	znpR	0.74	0.10	-0.47	-1.11	1.67	1.07	1.39	2.16	Deok family transcriptional regulator
Energy metabolism	CagR	SACOL0838	znpR znpR TPA ppm eno	znpR	1.10	-0.11	-0.44	-1.66	2.15	0.93	1.36	3.16	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)
Energy metabolism	CagR	SACOL0839	znpR znpR TPA ppm eno	znpR	1.48	0.04	-0.17	-1.57	2.71	1.03	1.13	2.97	phosphoglycerate kinase
Energy metabolism	CagR	SACOL0840	znpR znpR TPA ppm eno	znpR	1.41	0.03	-0.65	-1.49	2.68	1.08	1.09	1.71	triose-phosphate isomerase
Energy metabolism	CagR	SACOL0841	znpR znpR TPA ppm eno	znpR	1.41	0.04	-0.57	-1.47	2.66	0.97	1.04	2.77	bisphosphoglycerate mutase
Energy metabolism	CagR	SACOL0842	znpR znpR TPA ppm eno	eno	1.24	-0.05	-0.13	-1.07	2.47	1.68	0.91	2.10	phosphoenolpyruvate hydratase
Energy metabolism	PDH	SACOL1103	pdhA pdhB pdhC pdhD	pdhA	0.44	0.08	-0.43	-0.06	1.36	0.96	0.74	0.96	pyruvate dehydrogenase (acetyltransfering) alpha subunit
Energy metabolism	PDH	SACOL1103	pdhA pdhB pdhC pdhD	pdhB	0.53	-0.04	-0.53	0.03	1.44	0.97	0.69	1.02	pyruvate dehydrogenase (acetyltransfering) beta subunit
Energy metabolism	PDH	SACOL1104	pdhA pdhB pdhC pdhD	pdhC	0.60	0.00	-0.50	-0.09	1.52	1.00	0.71	1.08	hydroxylysine-residue acetyltransferase
Energy metabolism	PDH	SACOL1105	pdhA pdhB pdhC pdhD	pdhD	0.43	0.31	-0.38	0.17	1.13	0.97	0.71	1.13	hydroxylysine-lysine acetyltransferase
Fatty acid biosynthesis	FapR	SACOL0987	fapH	fapH	1.31	0.73	-1.33	-0.77	2.48	1.66	0.40	0.59	3-oxoacyl-[acyl-carrier-protein] synthase
Fatty acid biosynthesis	FapR	SACOL0988	fapH	fapH	1.40	0.65	-1.41	-0.67	2.65	1.57	0.38	0.63	3-oxoacyl-[acyl-carrier-protein] synthase (NADH)
Fatty acid biosynthesis	FapR	SACOL1242											

GeneSet	Regulon	Locus	Organ	Gene symbol	log ₂ -fold change (M-value)				Fold changes				Function
					WT MMEQ / WT co	ΔmtrA MMEQ / ΔmtrA co	ΔmtrG MMEQ / ΔmtrG co	ΔmtrH co / WT co	WT MMEQ / WT co	ΔmtrA MMEQ / ΔmtrA co	ΔmtrG MMEQ / ΔmtrG co	ΔmtrH co / WT co	
Stress and Starvation	StgB	SACOL0921	SACOL0921 fabK	SACOL0921	1.68	1.17	-0.34	0.13	3.19	2.25	0.79	1.09	CBS domain protein
Stress and Starvation	StgB	SACOL0922	SACOL0922 fabK	SACOL0922	1.51	1.51	-0.57	-0.18	3.75	2.85	0.67	0.88	2-nitropropane dioxygenase
Stress and Starvation	StgB	SACOL1046	SACOL1046	SACOL1046	1.34	0.23	-0.96	0.13	2.54	1.17	0.51	1.09	Hypothetical protein
Stress and Starvation	StgB	SACOL1788	SACOL1788 SACOL1789	SACOL1788	1.49	0.87	-0.22	0.18	2.42	1.83	0.96	1.13	Hypothetical protein
Stress and Starvation	StgB	SACOL1789	SACOL1788 SACOL1789	SACOL1789	0.99	0.78	-0.28	-0.07	1.99	1.72	0.82	0.95	possible general stress protein
Stress and Starvation	StgB	SACOL1802	SACOL1802 muA SACOL1804	SACOL1802	-0.38	-0.31	0.22	0.14	0.77	0.81	1.16	1.10	ribosomal small subunit pseudouridine synthase A
Stress and Starvation	StgB	SACOL1803	SACOL1802 muA SACOL1804	muA	0.56	0.40	0.20	0.40	0.68	0.76	1.23	1.10	ribosomal small subunit pseudouridine synthase A
Stress and Starvation	StgB	SACOL1804	SACOL1802 muA SACOL1804	muA	0.73	-0.47	0.40	0.13	0.60	0.72	1.32	1.09	polysaccharide biosynthesis protein
Stress and Starvation	StgB	SACOL1911	SACOL1911 SACOL1912	SACOL1911	0.97	0.37	-0.48	0.11	1.96	1.29	0.72	1.08	Hypothetical protein
Stress and Starvation	StgB	SACOL1912	SACOL1911 SACOL1912	SACOL1912	0.55	0.13	-0.22	0.11	1.47	0.73	1.22	1.10	glucosyltransferase
Stress and Starvation	StgB	SACOL2012	SACOL2012	SACOL2012	1.11	0.25	-0.72	0.12	2.15	1.19	0.61	1.09	GNAT family acetyltransferase
Stress and Starvation	StgB	SACOL2076	SACOL2076 SACOL2077 csoR	SACOL2076	-1.46	-1.08	0.83	0.43	0.36	0.47	1.78	1.35	Hypothetical protein
Stress and Starvation	StgB	SACOL2077	SACOL2076 SACOL2077 csoR	SACOL2077	0.73	-0.66	0.73	0.66	0.64	0.66	1.66	1.58	Hypothetical protein
Stress and Starvation	StgB	SACOL2078	SACOL2076 SACOL2077 csoR	csoR	0.86	0.54	0.55	0.55	0.55	0.69	1.89	1.47	Copper-sensing transcriptional repressor RcuR
Stress and Starvation	StgB	SACOL2114	SACOL2114	aldA	2.36	1.80	0.41	0.14	5.15	3.48	0.75	1.10	aldehyde dehydrogenase
Stress and Starvation	StgB	SACOL2132	SACOL2132	SACOL2132	2.29	0.98	-1.08	0.12	4.61	1.97	0.47	1.09	Hypothetical protein
Stress and Starvation	StgB	SACOL2168	SACOL2168 SACOL2169 SACOL2170	SACOL2168	2.50	1.56	-0.27	0.66	5.65	2.95	0.83	1.58	Hypothetical protein
Stress and Starvation	StgB	SACOL2169	SACOL2168 SACOL2169 SACOL2170	SACOL2169	1.75	1.01	-0.20	0.53	3.37	2.01	0.87	1.44	possible luciferase
Stress and Starvation	StgB	SACOL2170	SACOL2168 SACOL2169 SACOL2170	SACOL2170	2.24	1.14	-0.60	0.47	4.72	2.30	0.66	1.39	MFS family major facilitator transporter
Stress and Starvation	StgB	SACOL2519	SACOL2519	SACOL2519	1.88	1.50	-1.06	-0.67	3.68	2.83	0.48	0.63	Hypothetical protein
Stress and Starvation	StgB	SACOL2621	SACOL2621	SACOL2621	-1.92	-0.61	2.02	0.68	0.26	0.66	0.66	1.06	Hypothetical membrane protein
Stress and Starvation	StgB	SACOL2717	SACOL2717	SACOL2717	2.22	-1.07	0.97	0.21	4.98	2.56	0.48	0.86	possible metallo-beta-lactamase
Stress and Starvation	StgB	SACOL2717	SACOL2717	SACOL2717	-1.20	-0.75	0.71	0.25	0.43	0.59	1.64	1.19	Hypothetical protein
Stress and Starvation	StgB	SACOL0672	arpA	arpA	1.39	0.23	-1.14	-0.05	2.51	1.17	0.45	0.97	staphylococcal accessory regulator A
Stress and Starvation	StgB	SACOL2054	hfrB rnbW rnbU	hfrB	-1.58	-0.07	0.53	0.29	11.79	1.25	0.61	0.69	hypothetical accessory regulator 5
Stress and Starvation	StgB	SACOL2054	hfrB rnbW rnbU	hfrB	-0.59	0.12	0.75	0.05	0.67	1.09	1.68	1.04	DNA-directed RNA polymerase sigma subunit FliA
Stress and Starvation	StgB	SACOL2055	hfrB rnbW rnbU	rnbW	0.69	0.09	0.62	0.17	0.62	1.06	1.54	0.89	anti-sigma B factor
Stress and Starvation	StgB	SACOL2056	hfrB rnbW rnbU	hfrB	-0.71	-0.05	0.85	-0.18	0.61	0.97	1.80	1.13	anti-sigma B factor antagonist
Stress and Starvation	StgB	SACOL2057	hfrB rnbW rnbU	rnbU	0.05	0.57	0.10	0.00	2.69	1.07	1.49	1.01	sigma factor B regulator
Stress and Starvation	StgB	SACOL0118	hdhA1	hdhM	1.43	1.14	-0.59	-0.28	2.69	2.20	0.66	0.82	superoxide dismutase
Stress and Starvation	StgB	SACOL0118	hdhA1	hdhM	-1.11	-1.50	0.49	-0.39	0.49	0.45	1.22	1.56	ironical monophosphatase family protein
Stress and Starvation	StgB	SACOL2711	yeaE	yeaE	6.64	6.50	-0.47	1.66	100.06	22.43	0.72	1.16	Hypothetical protein
Stress and Starvation	StgB	SACOL2136	vibE	vibE	-0.79	-0.20	0.92	0.31	0.58	0.87	1.89	1.24	putative NAD dependent epimerase
Stress and Starvation	StgB	SACOL2300	yrbD yhbA	yrbD	-0.63	0.30	0.73	-0.19	0.65	1.23	1.66	0.88	Hypothetical protein
Stress and Starvation	StgB	SACOL2302	yrbD yhbA	yrbD	0.25	0.04	0.28	0.01	1.09	1.82	1.67	1.06	formate dehydrogenase alpha subunit
Sugar catabolism	CcpA	SACOL1048	SACOL1048	SACOL1048	2.45	0.21	-2.50	-0.22	5.48	1.16	0.18	0.86	acetyltransferase
Sugar catabolism	CcpA	SACOL1758	alg2	alg2	-1.58	-1.47	0.50	0.37	0.33	0.36	1.41	1.29	alanine dehydrogenase
Sugar catabolism	CcpA	SACOL1954	capD	capD	3.56	1.32	-2.59	0.33	2.79	1.25	1.13	1.15	aldehyde dehydrogenase
Sugar catabolism	CcpA	SACOL0599	capD	capD	-1.69	-1.09	0.54	0.07	0.41	0.47	1.45	0.95	NAD dependent epimerase/dehydratase family protein
Sugar catabolism	CcpA	SACOL1786	capA	capA	2.82	1.94	-0.24	0.24	7.05	1.52	0.26	1.18	catabolite control protein A
Sugar catabolism	CcpA	SACOL0707	capM	capM	1.20	0.10	-0.52	0.14	0.67	0.74	1.07	0.71	phosphorylation kinase subunit DhaK
Sugar catabolism	CcpA	SACOL0708	dhxLM	dhxM	1.32	0.25	-0.42	0.61	2.50	1.19	0.75	1.13	DAK2 domain-containing protein DhaK
Sugar catabolism	CcpA	SACOL0709	dhxLM	dhxM	1.28	0.20	-0.39	0.62	2.43	1.15	0.76	1.54	PTS-dependent dihydroxyacetone kinase phosphotransferase subunit DhaM
Sugar catabolism	CcpA	SACOL0313	fadEX	fadX	0.65	-1.41	-0.22	0.34	0.36	0.34	1.27	1.44	acyl-CoA dehydrogenase
Sugar catabolism	CcpA	SACOL0214	fadDEX	fadEX	-0.92	-1.16	-0.44	-0.12	0.53	0.45	0.74	0.92	long-chain fatty-acyl-CoA ligase
Sugar catabolism	CcpA	SACOL0215	fadDEX	fadX	-2.20	-1.74	-0.52	0.91	0.22	0.30	0.70	0.53	propionate CoA-transferase
Sugar catabolism	CcpA	SACOL2319	fadEX	fadX	0.65	-0.42	0.52	0.27	0.52	0.56	1.26	1.03	PTS system, IIIC component
Sugar catabolism	CcpA	SACOL0173	ipdC	ipdC	1.64	0.89	-0.78	0.03	3.13	1.85	0.58	0.98	thiamine pyrophosphate TPP binding domain-containing protein
Sugar catabolism	CcpA	SACOL0960	ipdC	ipdC	1.15	-0.43	-1.26	0.30	2.22	0.74	0.42	1.23	ornithine-oxo acid transaminase
Sugar catabolism	CcpA	SACOL0961	ipdC	ipdC	0.21	-0.05	0.85	0.29	1.16	0.57	0.85	1.22	aldehyde dehydrogenase
Sugar catabolism	CcpA	SACOL0376	SACOL0376 murJ murP SACOL0179	SACOL0376	-1.90	-1.37	0.11	0.15	0.39	0.27	0.39	1.11	hyphoprotein
Sugar catabolism	CcpA	SACOL0177	SACOL0176 murJ murP SACOL0179	murJ	-1.35	-1.53	0.11	0.25	0.39	0.35	1.08	1.19	N-acetylmuramic acid-6-phosphate esterase
Sugar catabolism	CcpA	SACOL0178	SACOL0176 murJ murP SACOL0179	murP	0.29	0.10	-0.77	0.79	0.78	0.79	1.74	0.97	N-acetylmuramic acid phosphotransferase
Sugar catabolism	CcpA	SACOL0179	SACOL0176 murJ murP SACOL0179	SACOL0179	-0.90	-1.03	0.81	0.85	0.54	0.49	1.75	1.80	RifR family phosphotransferase-binding transcriptional regulator
Sugar catabolism	CcpA	SACOL0938	SACOL0938 ppsG nucP	SACOL0938	0.59	0.06	-0.45	0.04	1.51	1.04	0.73	1.03	carbohydrate kinase
Sugar catabolism	CcpA	SACOL0939	SACOL0938 ppsG nucP	ppsG	0.52	-0.26	-0.85	-0.22	1.25	0.84	0.55	0.86	Hypothetical protein
Sugar catabolism	CcpA	SACOL0940	SACOL0938 ppsG nucP	nucP	1.07	0.80	-0.37	0.60	0.90	0.90	1.28	1.02	glucosyltransferase
Sugar catabolism	CcpA	SACOL1158	sdhC sdhA sdhB	sdhC	-0.65	-0.38	0.64	0.38	0.64	0.77	1.56	1.27	succinate dehydrogenase, cytochrome b558 subunit
Sugar catabolism	CcpA	SACOL1159	sdhC sdhA sdhB	sdhA	-0.90	-0.58	0.86	0.51	0.54	0.67	1.82	1.42	succinate dehydrogenase flavoprotein subunit
Sugar catabolism	CcpA	SACOL1160	sdhC sdhA sdhB	sdhB	0.65	0.69	1.05	0.91	0.95	1.07	1.71	1.64	succinate dehydrogenase iron-sulfur subunit
Translocation	TrpA	SACOL0590	rplI3 rpsL rpsE fuaX tuf	rplI3	0.87	-0.11	0.51	0.51	0.51	0.61	1.16	0.69	possible RNA-binding ribosomal protein
Translocation	TrpA	SACOL0591	rplI3 rpsL rpsE fuaX tuf	rpsL	-0.89	-1.09	0.60	-0.09	0.54	0.88	1.52	0.94	ribosomal protein S12
Translocation	TrpA	SACOL0592	rplI3 rpsL rpsE fuaX tuf	rpsE	0.86	-0.61	0.35	0.89	0.59	0.71	1.02	1.06	ribosomal protein S16
Translocation	TrpA	SACOL0594	rplI3 rpsL rpsE fuaX tuf	tuf	0.27	-0.03	0.35	0.11	0.83	0.98	1.27	1.08	elongation factor EF1A
Transport	TrpB	SACOL2376	zrfA	zrfA	-1.54	-1.09	1.36	0.89	0.34	0.47	2.57	1.85	PTS family sucrose/isomer/transporter IIBC
Transport	TrpB	SACOL2368	zrfA	zrfA	0.46	0.56	0.67	0.67	1.48	1.48	1.48	1.48	PTS family cell wall surface anchor protein
Transport	TrpA	SACOL0608	zrfA	zrfA	-2.50	-1.20	-0.15	1.18	1.08	0.44	1.11	0.47	Ser-Asp rich fibronectin/bone sialoprotein-binding protein SdcC
Transport	TrpA	SACOL2023	zrfA	zrfA	-1.53	-0.58	-0.27	-1.15	0.35	0.67	0.83	0.45	accessory gene regulator protein B
Transport	TrpA	SACOL2024	zrfA	zrfA	1.29	0.25	-0.42	0.13	0.67	0.67	1.16	0.71	accessory gene regulator protein D
Transport	TrpA	SACOL2025	zrfA	zrfA	-0.47	0.07	-0.17	0.70	0.72	1.05	0.89	0.62	accessory gene regulator protein C
Transport	TrpA	SACOL2026	zrfA	zrfA	-0.08	0.22	-0.13	0.42	0.94	1.16	0.91	0.75	accessory gene regulator protein A
Transport	TrpA	SACOL0162	zrfA	zrfA	-1.71	-1.18	1.50	0.22	0.63	0.88	1.81	0.89	clumping factor B
Transport	TrpA	SACOL0162	zrfA	zrfA	1.41	0.63	-0.22	0.53	2.66	1.55	0.86	1.44	formate dehydrogenase
Transport	TrpA	SACOL0317	zrfA	zrfA	-1.90	-0.53	-0.17	1.48	0.27	0.69	0.89	0.36	tricarboxylate lyase
Transport	TrpA	SACOL2366	zrfA	zrfA	0.83	-0.30	-0.55	0.26	1.26	0.65	0.52	0.42	ESS family glutamate/sodium (Na+) symporter
Transport	TrpA	SACOL2364	zrfA	zrfA	-0.90	-0.81	-0.18	-0.26	0.54	0.57	0.88	0.84	hyaluronate lyase
Transport	TrpA	SACOL2688	zrfA	zrfA	1.24	0.25	-1.86	0.86	2.36	1.19	0.28	0.55	ico operon transcriptional regulator I
Transport	TrpA	SACOL0487	zrfA SACOL0487 SACOL0488 SACOL0489	zrfA	0.67	-0.62	-0.52	0.67	0.65	0.67	0.65	0.72	immunosuppressive lipoprotein
Transport	TrpA	SACOL0487	zrfA SACOL0487 SACOL0488 SACOL0489	SACOL0487	-0.30	-0.53	-0.52	-0.28	0.81	0.69	0.70	0.82	Hypothetical protein
Transport	TrpA	SACOL0488	zrfA SACOL0487 SACOL0488 SACOL0489	SACOL0488	-0.23	-0.11	-0.38	-0.29	0.85	0.81	0.77	0.62	Hypothetical protein
Transport	TrpA	SACOL0489	zrfA SACOL0487 SACOL0488 SACOL0489	SACOL0489	-0.28	-0.10	-0.43	-0.49	0.88	0.79	0.88	0.71	Hypothetical protein
Transport	TrpA	SACOL2389	zrfA	zrfA	-4.94	-2.40	0.58	0.67	0.03	0.19	1.49	0.19	transcriptional regulator NtrR
Transport	TrpA	SACOL0078	zrfA	zrfA	0.90	0.33	0.74	0.42	0.54	1.26	1.67	0.75	phosphatidylinositol diacylglycerol lyase
Transport	TrpA	SACOL0253	zrfA	zrfA	-1.04	-0.45	0.63	0.02	0.49	0.73	1.55	1.05	Fibronectin
Transport	TrpA	SACOL0254	zrfA	zrfA	1.24	0.47	0.65	0.40	0.92	1.42	1.46	1.07	ribonucleoside triphosphate: membrane protein
Transport	TrpA	SACOL0255	zrfA	zrfA	-1.50	-0.62	0.45	0.43	0.35	0.65	1.37	1.04	DMT superfamily drug/metabolite transporter
Transport	TrpA	SACOL0462	zrfA	zrfA	2.26	1.12	-0.65	0.43	4.90	2.17	0.66	3.25	possible bacteriophage integrase
Transport	TrpA	SACOL0678	zrfA	zrfA	2.89	2.89	0.09	0.12	0.99	0.91	0.82	1.00	possible bacteriophage integrase
Transport	TrpA	SACOL0679	zrfA	zrfA	1.48	1.1							

GeneSet	Regulon	Gene	Organ	Gene symbol	log ₂ -fold change (M-value)				Fold changes				Function
					WT MMR/ WT co	ΔmmhQ MMR/ ΔmmhQ co	ΔmmhQ MMR/ WT MMR	ΔmmhQ co/ WT co	WT MMR/ WT co	ΔmmhQ MMR/ ΔmmhQ co	ΔmmhQ MMR/ WT MMR	ΔmmhQ co/ WT co	
Violence	Agfa	SACOL2544	sdAA	sdAA	0.84	-0.61	-0.47	0.94	1.79	0.66	0.72	1.92	L-serine dehydratase, iron-sulfur-dependent subunit alpha
Violence	Agfa	SACOL2545	sdAA	sdAA	0.70	-0.61	-0.31	0.95	1.62	0.64	0.81	1.93	L-serine dehydratase, iron-sulfur-dependent subunit beta
Violence	Agfa	SACOL2546	sdAA	sdAA	0.66	-0.72	-0.33	0.98	1.58	0.61	0.80	1.97	hypothetical protein
Violence	Agfa	SACOL1864	spfl	spfl	2.47	0.97	0.86	0.97	0.85	1.93	0.91	1.80	serine protease Spfl
Violence	Agfa	SACOL1865	spfl	spfl	1.87	1.21	0.43	0.87	1.67	2.31	0.74	1.05	serine protease Spfl
Violence	Agfa	SACOL1866	spfl	spfl	2.45	0.23	-0.45	1.04	5.48	1.17	0.73	2.06	serine protease Spfl
Violence	Agfa	SACOL1867	spfl	spfl	1.79	0.76	0.51	0.91	3.41	1.37	1.46	1.33	serine protease Spfl
Violence	Agfa	SACOL1868	spfl	spfl	1.32	0.76	0.04	0.81	2.49	1.69	0.97	1.24	serine protease Spfl
Violence	Agfa	SACOL1869	spfl	spfl	0.94	0.64	-0.34	0.66	1.92	1.56	0.79	0.96	serine protease Spfl
Violence	Agfa	SACOL1448	tucA	tucA	0.79	-1.36	-0.31	0.54	0.66	0.75	0.91	1.45	glyoxylate decarboxylase
Violence	Agfa	SACOL1449	tucA	tucA	-0.81	-1.50	-0.45	0.21	0.57	0.35	0.73	1.16	2-oxoglutarate dehydrogenase II component
Violence	Agfa	SACOL0626	tdhD1	tdhD1	2.10	0.74	-1.43	-0.09	4.30	1.67	0.37	0.94	phosphomethylpyrimidine kinase
Violence	Agfa	SACOL1676	trmU	trmU	2.09	0.81	1.01	0.26	0.56	1.75	0.50	1.20	RNA-specific 2-thiouridine kinase
Violence	Agfa	SACOL1677	trmU	trmU	1.90	0.79	-1.01	0.08	3.72	1.73	0.50	1.06	class V aminotransferase
Violence	Agfa	SACOL0003	yaac	yaac	1.31	0.87	-0.23	0.19	2.48	1.83	0.85	1.14	hypothetical protein
Violence	Agfa	SACOL0004	yaac	yaac	0.95	0.66	-0.20	0.02	1.93	1.58	0.81	1.09	recombination protein F
Violence	Agfa	SACOL0005	yaac	yaac	0.69	0.33	-0.11	0.24	1.62	1.26	0.93	1.18	DNA gyrase, B subunit
Violence	Agfa	SACOL0006	yaac	yaac	0.92	0.30	-0.18	0.08	1.48	1.23	0.88	1.06	DNA gyrase, A subunit
Violence	Agfa	SACOL0115	capB	capB	-1.58	-1.16	-0.46	-0.89	0.33	1.12	1.38	0.54	glycosyltransferase
Violence	Agfa	SACOL0116	capB	capB	-0.81	-0.07	0.73	-0.12	0.57	1.05	1.66	0.92	hypothetical protein
Violence	Agfa	SACOL0117	capB	capB	-1.47	-0.63	-0.84	-0.22	0.57	1.03	1.07	0.57	polysaccharide biosynthesis protein
Violence	Agfa	SACOL0856	dtd	dtd	1.90	0.48	0.51	0.87	3.74	1.39	0.70	1.83	Fibronectin-binding protein
Violence	Agfa	SACOL2355	ddh	ddh	1.62	0.60	0.80	0.19	3.08	1.52	0.57	1.14	D-lactate dehydrogenase
Violence	Agfa	SACOL0858	pbpT	pbpT	-1.15	-0.24	-0.22	0.66	0.45	0.85	1.16	0.63	secretory extracellular matrix and plasma binding protein
Violence	Agfa	SACOL2620	pbpT	pbpT	-1.15	-0.24	-0.22	0.66	0.45	0.85	1.16	0.63	4-aminobutyrate transaminase
Violence	Agfa	SACOL0113	pafl	pafl	-2.52	-1.09	-1.12	-1.14	0.17	0.47	1.09	0.45	UDP-glucose 4-epimerase
Violence	Agfa	SACOL0114	pafl	pafl	-1.39	-0.97	-0.79	-0.81	0.38	0.51	0.88	0.57	capsular polysaccharide biosynthesis protein
Violence	Agfa	SACOL1349	prf1	prf1	1.03	0.84	0.13	0.01	0.51	0.41	0.51	0.41	aromatic amino acid beta-eliminating lysyl/threonine aldolase
Violence	Agfa	SACOL0526	hoIB	hoIB	0.83	0.68	-0.09	0.09	1.78	1.60	0.97	1.00	DNA-directed DNA polymerase III delta' subunit
Violence	Agfa	SACOL0527	hoIB	hoIB	0.83	0.68	-0.09	0.09	1.78	1.60	0.97	1.00	hypothetical protein
Violence	Agfa	SACOL0528	hoIB	hoIB	0.83	0.68	-0.09	0.09	1.78	1.60	0.97	1.00	DNA replication initiation control protein YabA
Violence	Agfa	SACOL1777	htrA1	htrA1	1.00	0.49	-1.18	0.66	2.00	1.40	0.44	0.63	Trypsin-like serine endoprotease
Violence	Agfa	SACOL2680	htrB	htrB	1.09	-0.49	-1.74	-0.20	2.13	0.71	0.30	0.87	immunoglobulin antiporter
Violence	Agfa	SACOL0864	htrB	htrB	0.97	0.07	-0.92	0.07	1.92	1.59	0.92	1.35	peptidylarginine hydrolase related protein
Violence	Agfa	SACOL1051	menF	menF	0.34	-0.24	-0.40	0.17	1.27	0.85	0.76	1.13	isochorismate synthase
Violence	Agfa	SACOL1052	menF	menF	0.35	-0.08	-0.01	0.41	1.28	0.95	0.99	1.33	2-oxoglutarate decarboxylase
Violence	Agfa	SACOL1053	menF	menF	0.29	-0.10	-0.41	0.00	1.48	1.16	0.88	1.15	S33 family peptidase
Violence	Agfa	SACOL1054	menF	menF	1.34	0.61	-0.47	0.24	2.52	1.53	0.72	1.18	naphthate synthase
Violence	Agfa	SACOL0428	metE	metE	-0.67	0.15	-0.17	-0.95	0.63	1.11	0.89	0.52	5-methyltetrahydropteroylglutamate - homocysteine S-methyltransferase
Violence	Agfa	SACOL0429	metE	metE	-0.74	0.26	-0.96	-0.40	0.66	1.06	0.68	0.51	methylenetetrahydrofolate reductase/Phenocysteine S-methyltransferase
Violence	Agfa	SACOL0430	metE	metE	-1.70	-0.23	-0.40	-0.91	0.31	0.85	1.32	0.53	ubiquinol:cytochrome gamma-lyase/gamma-synthase
Violence	Agfa	SACOL0431	metE	metE	-2.05	-1.15	-0.51	-0.31	0.24	0.45	1.42	0.81	ubiquinol:cytochrome gamma-lyase/gamma-synthase
Violence	Agfa	SACOL2261	mobA	mobA	1.37	0.45	-1.08	-0.59	0.14	0.25	1.38	0.81	difunctional cytochrome gamma-lyase/gamma-synthase
Violence	Agfa	SACOL2262	mobA	mobA	1.31	0.30	-1.03	-0.04	2.48	1.23	0.49	0.97	molibdenum (MoCo) cofactor biosynthesis protein A
Violence	Agfa	SACOL2263	mobA	mobA	1.13	0.21	-1.01	-0.10	2.19	1.16	0.50	0.93	molibdenum (MoCo) cofactor biosynthesis protein A
Violence	Agfa	SACOL2264	mobA	mobA	1.24	0.17	-1.04	-0.08	2.20	1.15	0.50	0.93	molibdenum (MoCo) cofactor biosynthesis protein A
Violence	Agfa	SACOL2265	mobA	mobA	1.26	0.21	-0.96	-0.15	1.77	1.01	0.51	0.90	molibdenum (MoCo) cofactor biosynthesis protein B
Violence	Agfa	SACOL2266	mobA	mobA	1.41	-0.07	-0.68	-0.22	1.52	0.95	0.62	0.99	molibdenum (MoCo) cofactor biosynthesis protein B
Violence	Agfa	SACOL1196	murD	murD	-1.48	-0.26	-0.84	-0.25	1.38	1.02	0.64	0.85	phospho-N-acetylmuramoyl-pentapeptide transferase
Violence	Agfa	SACOL1197	murD	murD	-0.99	-0.51	-0.52	-0.04	0.50	0.70	1.43	1.03	UDP-N-acetylmuramoyl-D-glutamate lyase
Violence	Agfa	SACOL0791	dwib	dwib	0.77	-0.51	-0.20	0.05	0.59	0.70	1.15	0.97	cell division protein PsaQ
Violence	Agfa	SACOL2659	pbpB	pbpB	1.13	0.01	-1.10	0.00	2.18	1.01	0.47	1.00	M56 family major facilitator transporter
Violence	Agfa	SACOL2109	hemK	hemK	-1.79	-0.80	-1.16	-0.16	0.29	0.57	2.23	1.12	HemK family methyltransferase
Violence	Agfa	SACOL2110	hemK	hemK	-1.87	-0.81	-1.23	-0.31	0.25	0.55	0.49	0.91	peptide chain release factor RF3
Violence	Agfa	SACOL2111	hemK	hemK	-1.93	-0.91	-1.12	-0.09	0.26	0.53	2.17	1.06	thymidine kinase
Violence	Agfa	SACOL2119	pyrG	pyrG	-1.82	-0.94	-1.17	0.29	0.28	0.52	2.25	1.22	CTP synthase
Violence	Agfa	SACOL0217	SACOL0217	SACOL0217	1.14	0.13	-0.82	0.26	2.36	1.09	0.57	1.20	ABC transporter, binding protein
Violence	Agfa	SACOL0529	SACOL0529	SACOL0529	0.90	0.82	0.08	0.80	0.71	1.06	1.77	1.07	hypothetical protein
Violence	Agfa	SACOL0530	SACOL0530	SACOL0530	0.60	0.09	1.05	0.35	0.66	1.06	2.07	1.27	hypothetical protein
Violence	Agfa	SACOL0531	SACOL0531	SACOL0531	-0.62	0.04	1.02	0.36	0.65	1.03	2.03	1.28	tetraylamine methylase
Violence	Agfa	SACOL0664	SACOL0664	SACOL0664	0.94	0.40	0.51	0.31	0.71	0.64	1.01	1.01	diquarylate cyclase GGDEF domain protein
Violence	Agfa	SACOL0809	SACOL0809	SACOL0809	-1.63	-1.35	-0.29	-0.01	0.32	0.39	1.22	1.01	diquarylate cyclase GGDEF domain protein
Violence	Agfa	SACOL0871	SACOL0871	SACOL0871	-1.02	-0.38	-0.01	-0.89	0.49	0.95	0.99	0.54	hypothetical protein
Violence	Agfa	SACOL0991	oppP	oppP	1.28	0.20	0.90	0.41	1.68	0.91	0.81	0.81	oligopeptide ABC transporter, membrane protein
Violence	Agfa	SACOL0992	oppP	oppP	-1.30	-0.36	0.11	-0.80	0.41	0.78	1.08	0.57	oligopeptide ABC transporter, membrane protein
Violence	Agfa	SACOL0993	oppP	oppP	-0.69	-0.21	-0.07	-0.53	0.62	0.86	0.95	0.69	oligopeptide ABC transporter, ATP-binding protein
Violence	Agfa	SACOL0994	oppP	oppP	-0.25	-0.17	-0.02	-0.18	0.67	0.70	1.17	0.61	oligopeptide ABC transporter, ATP-binding protein
Violence	Agfa	SACOL0995	oppP	oppP	-0.38	-0.04	-0.02	-0.34	0.77	0.97	0.99	0.79	oligopeptide ABC transporter, binding protein
Violence	Agfa	SACOL1009	ppkK	ppkK	0.34	-0.62	-0.82	0.12	1.27	0.65	0.57	1.09	hypothetical protein
Violence	Agfa	SACOL1010	ppkK	ppkK	0.21	-0.17	-0.14	0.22	1.34	1.27	1.16	1.16	CTP diphosphokinase
Violence	Agfa	SACOL1011	ppkK	ppkK	0.70	-0.39	-0.78	0.23	0.67	0.76	0.58	1.22	inosinic polyphosphate/ATP-NAD kinase
Violence	Agfa	SACOL1012	ppkK	ppkK	0.90	-0.04	-0.67	0.26	1.87	0.97	0.63	1.20	RubP subfamily ribosomal large subunit pseudouridine synthase
Violence	Agfa	SACOL1013	ppkK	ppkK	1.10	0.76	-0.16	-0.45	0.45	0.66	0.75	1.05	MstE family magnesium (MgCo)-hydrolyase (HcpA) transporter
Violence	Agfa	SACOL1014	ppkK	ppkK	0.68	0.04	-0.52	0.11	1.60	1.03	0.70	1.08	CPA2 family monovalent cation porters (H+) antiporter-2
Violence	Agfa	SACOL1101	SACOL1101	SACOL1101	2.02	1.04	-1.50	-0.52	4.05	2.06	0.35	0.70	hypothetical protein
Violence	Agfa	SACOL1175	SACOL1175	SACOL1175	1.16	0.76	-0.16	-0.45	0.45	0.66	0.75	0.97	hypothetical protein
Violence	Agfa	SACOL1176	SACOL1176	SACOL1176	-1.08	-0.74	-0.17	-0.48	0.47	0.60	0.89	0.72	hypothetical protein
Violence	Agfa	SACOL1345	SACOL1345	SACOL1345	-1.72	-0.51	-0.37	-0.80	0.30	0.70	1.29	0.57	hypothetical protein
Violence	Agfa	SACOL1346	SACOL1346	SACOL1346	-1.62	-0.39	-0.47	-0.47	0.33	0.37	0.72	0.72	hypothetical protein
Violence	Agfa	SACOL1347	SACOL1347	SACOL1347	-1.42	-0.43	-0.83	-0.15	0.37	0.74	1.78	0.90	hypothetical protein
Violence	Agfa	SACOL1348	SACOL1348	SACOL1348	-1.32	-0.27	-0.17	-0.79	0.40	0.83	1.13	0.58	hypothetical protein
Violence	Agfa	SACOL1660	SACOL1660	SACOL1660	1.59	0.41	2.10	0.47	1.33	0.23	0.43	0.85	hypothetical protein