Table S2

Transcripts decreased in abundance in ΔhrtA grown in heme [a]

Carbohydrate transport and metabolism[b]

Locus[c]	Decrease in heme	Gene Name[d]	Description
SACOL0312	2.9	*nanA*	N-acetylneuraminate lyase
SACOL0200	15.0		phosphoglycerate transporter family protein
SACOL0407	2.9	*glpT*	glycerol-3-phosphate transporter

Cell wall/membrane biogenesis

Locus	Decrease in heme	Gene Name	Description
SACOL1659	3.9		conserved hypothetical protein
SACOL2578	16.1		glycosyl transferase, group 2 family protein

Inorganic ion transport and metabolism

Locus	Decrease in heme	Gene Name	Description
SACOL2176	8.0	*opuD*	osmoprotectant transporter, BCCT family

N.D.

Locus	Decrease in heme	Gene Name	Description
SACOL0085	3.7		peptidase, M20/M25/M40 family
SACOL0178	15.6		PTS system, IIBC components
SACOL2197	47.3		surface protein, putative
SACOL2621	16.6		hypothetical protein

Resistance

Locus	Decrease in heme	Gene Name	Description
SACOL0050	2.8	*pls*	homology to methicillin-resistant surface protein

Transcription

Locus	Decrease in heme	Gene Name	Description
SACOL0403	21.5		transcriptional antiterminator, BglG family

Virulence

Locus	Decrease in heme	Gene Name	Description
SACOL0137	11.5	*cap5B*	capsular polysaccharide biosynthesis protein
SACOL0138	11.2	*cap5C*	capsular polysaccharide biosynthesis protein
SACOL0143	8.3	*cap5H*	capsular polysaccharide biosynthesis protein
SACOL1637	42.1	*lukD*	leukotoxin *lukD*
SACOL1865	***20.8***	*splE*	serine protease *splE*
SACOL1866	***22.2***	*splD*	serine protease *splD*
SACOL1867	***9.1***	*splC*	serine protease *splC*
SACOL1872	12.3	*epiE*	epidermin immunity protein F
SACOL1873	17.3	*epiF*	epidermin immunity protein F
SACOL2007	8.7		peptidase, M20/M25/M40 family
SACOL2419	52.8	*hlgA*	gamma-hemolysin, component A
SACOL2421	80.9	*hlgC*	gamma hemolysin, component C
SACOL2422	42.4	*hlgB*	gamma hemolysin, component B

[a] All transcripts with at least 2-fold changes in ΔhrtA + heme compared to ΔhrtA alone which are statistically significant are shown. Grey boxes indicate that in ΔhrtA alone, transcript abundance approaches the lower limit of sensitivity and thus values may not be accurate. Bold, italicized values indicate that in ΔhrtA alone, no transcript was detected and thus values may not be accurate.

[b] Predicted functions are assigned according to COG annotation and/or gene name

[c] All genes with SACOL designation are from *S. aureus* strain COL (SACOL)

[d] Transcripts with no gene name have no designated name in the *S. aureus* COL genone annotation