Figure S1: *S. aureus* biofilms exhibit differential expression compared to planktonic cell populations. Genomic maps were created for each strain depicting changes in the planktonic (inner histograms, light colors) and biofilm (outer histograms, dark colors) transcriptomes at 10 h (top) and 24 h (bottom) reported as TPM expression values. The outermost circle is a heat map demonstrating fold change in expression, where red or blue indicates higher expression in the biofilm or planktonic cell population, respectively.
Figure S2: RT-qPCR validation of RNA-seq findings. RT-qPCR was performed using gene specific primers for four randomly selected genes (left), each timepoint (top), and each strain (USA100, red; USA200, orange; USA300, green; USA400, blue; USA500, purple). Expression levels were normalized to 16s rRNA and calculated using the 2^{-\Delta\Delta C t} method. Data is reported as mean fold change of biofilm expression relative to planktonic expression ± standard error of the mean.
organized by KEGG ontological function hierarchies.

Genetic Information Processing

Human Diseases

Metabolism of terpenoids and polyketides

Metabolism of other amino acids

Membrane transport

Signal transduction

Chloroalkane and chloroalkene degradation

Phosphonate and phosphinate metabolism

Cysteine and methionine metabolism

Pantothenate and CoA biosynthesis

Phosphotransferase system (PTS)

alpha-Linolenic acid metabolism

Starch and sucrose metabolism

Inositol phosphate metabolism

Cyanoamino acid metabolism

Arachidonic acid metabolism

Ethylbenzene degradation

beta-Alanine metabolism

Two-component system

Thiamine metabolism

Lysine biosynthesis

Lysine degradation

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