

## **Description of Additional Supplementary Files**

### **Supplementary Data 1**

*S. aureus* proteins identified as having a significant (adjusted p value  $\leq 0.05$ , z-score of  $\log_2$  fold change  $\geq 1$  or  $\leq -1$ ) difference in abundance in the presence of one or more antibiotics during biofilm growth.

Adjusted p values determined by a two-sided Welch's t-test with adjustment for multiple comparisons using a Permutation-based False Discovery Rate (FDR) method with a FDR cutoff of 0.05.

### **Supplementary Data 2**

*S. aureus* genes identified via TnSeq as having a significant (adjusted p value  $\leq 0.05$ , z-score of  $\log_2$  fold change  $\geq 1$  or  $\leq -1$ ) effect on fitness in the presence of one or more antibiotics during biofilm growth.

Adjusted p values determined by a two-sided permutation test with correction for multiple comparisons using the Benjaminin-Hochberg procedure.

### **Supplementary Data 3**

*S. aureus* genes identified via TnSeq as having a significant (adjusted p value  $\leq 0.05$ , z-score of  $\log_2$  fold change  $\geq 1$  or  $\leq -1$ ) effect on fitness during biofilm growth. Adjusted p values determined by a two-sided permutation test with correction for multiple comparisons using the Benjaminin-Hochberg procedure.