Supporting Information

Label-free Proteomic Approach to Characterize Protease-dependent and Independent Effects of *sarA* Inactivation on the *Staphylococcus aureus* Exoproteome

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Figure S1. Unsupervised hierarchical clustering of exoproteins from *S. aureus* wild-type (LAC), *sarA,* and *sarA/protease* mutants shows distinct profiles. Exoproteins identified by the total proteoform (A) and full-length protein (B) methods were clustered according to relative abundance. Unsupervised hierarchical clustering of the total spectral counts for significantly differentiating proteins and for each strain was performed using the Euclidean distance metric with Hierarchical Clustering Explorer (HCE, version 3.5). The count values were normalized protein by protein by the standardization method where the mean is zero and the standard deviation is 1 (Z-score).

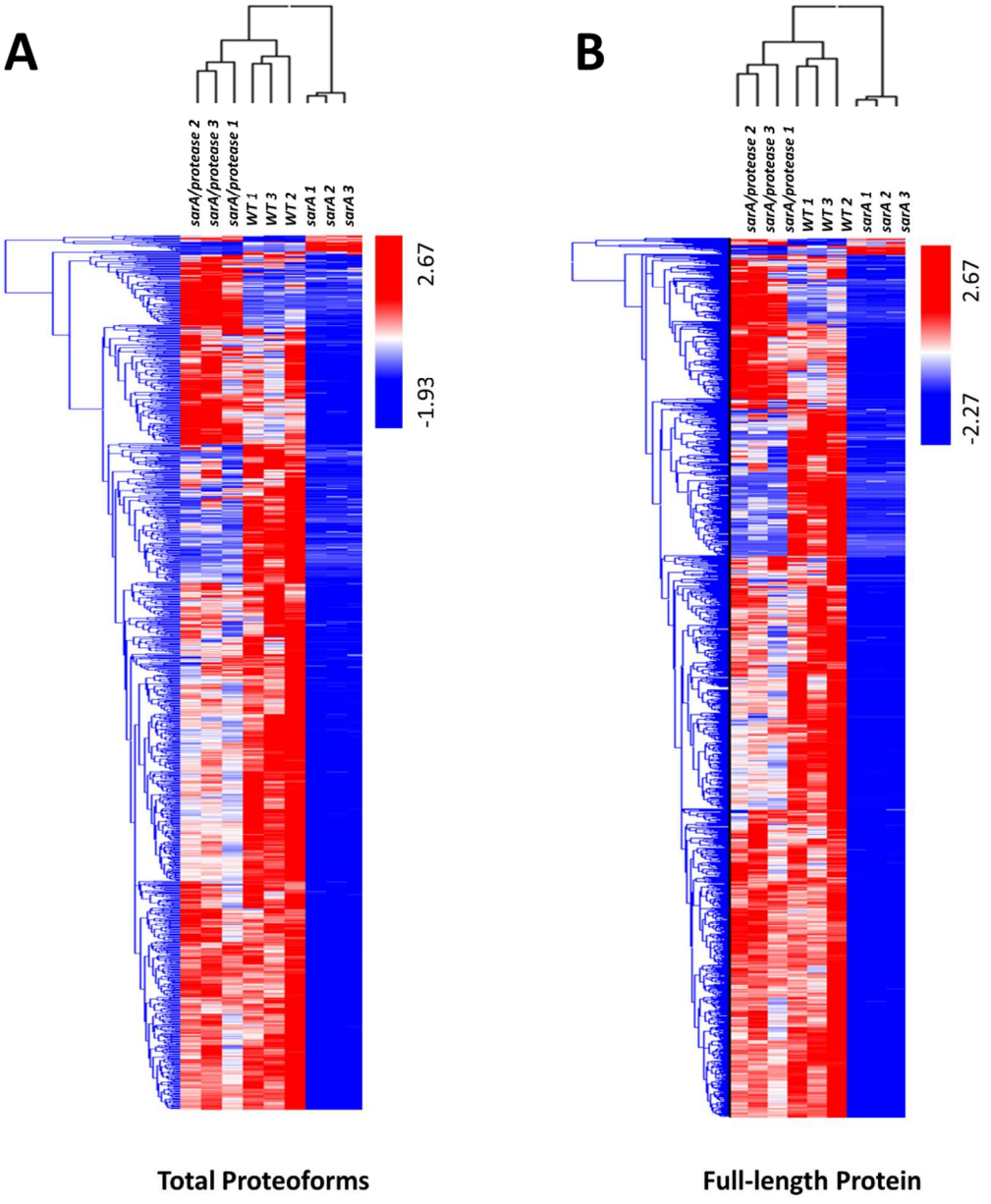

Figure S2. **Total proteoform and full-length protein methods provide complementary and unique information on the presence of exoproteins.** Venn diagrams of the number of exoproteins identified as significantly down-regulated in the *sarA* mutant compared to wild-type (A), *sarA* mutant compared to *sarA/protease* mutant (B), and wild-type compared to *sarA/protease* (C). These proteins are shown in Figure 2A-F as the red dots in the upper right quadrants of each plot.