

Content of supplemental material

S1_Supporting information Refiner MS_HG001 wild type and mutant internalized in S9 epithelial cells.pdf Detailed information about the Genedata Refiner settings for the identification of proteins from label-free proteome approach analyzing internalized *S. aureus* HG001 wild type and $\Delta sigB$ mutant. (Section 2.2.9)

S2_Quantified proteins from SILAC labeled internalized *S. aureus* HG001 wild type and *sigB* mutant BR1-3.xlsx Presented is the ratio of the heavy (^{13}C) versus the light (^{12}C) protein intensities from internalized *S. aureus* HG001 wild type and $\Delta sigB$ mutant. For reliable quantification the proteins had to be identified with two peptides per protein, and the proteins had to be present in two out of three biological replicates. Furthermore, the heavy and light protein version had to be identified. Proteins in the first column highlighted in gray are part of the SigB core regulon. (Section 3.1)

S3_ *S. aureus* SigB core regulon.xlsx Proteins defining the SigB core regulon. The genes of these proteins were commonly identified as SigB-dependent in microarray studies of Bischoff *et al*, 2004, Pané-Farré *et al*, 2006 and Schulthess *et al*, 2011. (Section 3.1)

S4_Identified proteins from internalized *S. aureus* HG001 wild type and *sigB* mutant.xlsx Listed are the normalized protein intensities and the numbers of identified peptides per protein of the identified proteins from internalized *S. aureus* HG001 wild type and $\Delta sigB$ mutant. Proteins in the first column highlighted in gray are part of the SigB core regulon. (Section 3.2)

S5_Voronoi-like treemaps of the adaption patterns of *S. aureus* HG001 wild type and *sigB* mutant to internalization by S9 epithelial cells.pdf Presented are the Voronoi-like treemaps from Section 3.2 to allow enlargement of the figures.

S6_Absolute numbers of internalized *S. aureus* HG001 wild type and *asp23* mutant in A549 cells BR1&BR2.xlsx Shown are the numbers of internalized *S. aureus* HG001 wild type and $\Delta asp23$ mutant in A549 cells from biological replicates one and two and the average of both experiments. (Section 3.2)

S7_Cytoplasmic proteins quantified from culture supernatants of *S. aureus* LS1 and its isogenic mutants.xlsx Listed are proteins identified from culture supernatants of *S. aureus* LS1 and its isogenic mutants, which are predicted to be localized in the cytoplasm. The ratio of the wild type versus the mutants is presented. A ratio of a two-fold higher protein intensity in the wild type compared to the mutant is highlighted in green. A ratio of a two-fold higher protein intensity in the mutant compared to the wild type is highlighted in red. (Section 3.4)

S8_Extracellular proteins quantified from culture supernatants of *S. aureus* LS1 and its isogenic mutants.xlsx Listed are proteins identified from culture supernatants of *S. aureus* LS1 and its isogenic mutants, which are predicted to be localized in the cytoplasmic membrane, cell wall, or extracellular. Presented is the ratio of the wild type versus the mutants. A ratio of a twofold higher protein intensity in the wild type compared to the mutant is highlighted in green. A ratio of a twofold higher protein intensity in the mutant compared to the wild type is highlighted in red. (Section 3.4)

S9_Comparison of proteins identified with the *S. aureus* 6850 strain specific database and the pan proteome database.xlsx Presented are the proteins identified with two peptides per protein with the *S. aureus* 6850 strain specific database and with the pan proteome database. Yes indicates that the protein was identified and No refers to proteins not identified. (Section 3.5)

S10_Comparison of proteins identified with the *S. aureus* HG001 strain specific database and the pan proteome database.xlsx Presented are the proteins identified with two peptides per protein with the *S. aureus* HG001 strain specific database and with the pan proteome database. Yes indicates that protein was identified and No refers to proteins not identified. (Section 3.5)

S11_Comparison of proteins identified with the *S. aureus* SH1000 strain specific database and the pan proteome database.xlsx Presented are the proteins identified with two peptides per protein with the *S. aureus* SH1000 strain specific database and with the pan proteome database. Yes indicates that the protein was identified and No refers to proteins not identified. (Section 3.5)

S12_Comparison of proteins identified with the *S. aureus* USA300 strain specific database and the pan proteome database.xlsx Presented are the proteins identified with two peptides per protein with the *S. aureus* USA300 strain specific database and with the pan proteome database. Yes indicates that the protein was identified and No refers to proteins not identified. (Section 3.5)

S13_Cytoplasmic proteins quantified from culture supernatants of *S. aureus* 6850, CowanI, HG001, LS1, SH1000, and USA300.xlsx Listed are the proteins quantified from culture supernatants of *S. aureus* 6850, CowanI, HG001, LS1, SH1000, and USA300, which are predicted to be localized in the cytoplasm. Presented are the average quantified protein intensities from three biological replicates and the numbers of identified peptides per protein. (Section 3.5)

S14_Extracellular proteins quantified from culture supernatants of all six *S. aureus* wild type strains (core extracellular proteome).xlsx Listed are the proteins quantified from culture supernatants of all six *S. aureus* wild type strains analyzed, which are predicted to be localized in the cytoplasmic membrane, cell wall, or extracellular. The proteins are defined as the core extracellular proteome. Presented are the average and quantified protein intensities from three biological replicates and the numbers of identified peptides per protein. (Section 3.5)

S15_Extracellular proteins quantified from culture supernatants of at least one of the six *S. aureus* wild type strains (variable extracellular proteome).xlsx Listed are the proteins quantified from culture supernatants of at least one of the six *S. aureus* wild type strains analyzed, which are predicted to be localized in the cytoplasmic membrane, cell wall, or extracellular. The proteins are defined as the variable extracellular proteome. Presented are the average and quantified protein intensities from three biological replicates and the numbers of identified peptides per protein. (Section 3.5)