

## Content of supplemental material

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**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 ( $^{13}\text{C}$ ) versus the light ( $^{12}\text{C}$ ) 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)