

Supplementary materials

Luz *et al.*, Impact of environmental conditions on the protein content of *Staphylococcus aureus* and its derived extracellular vesicles

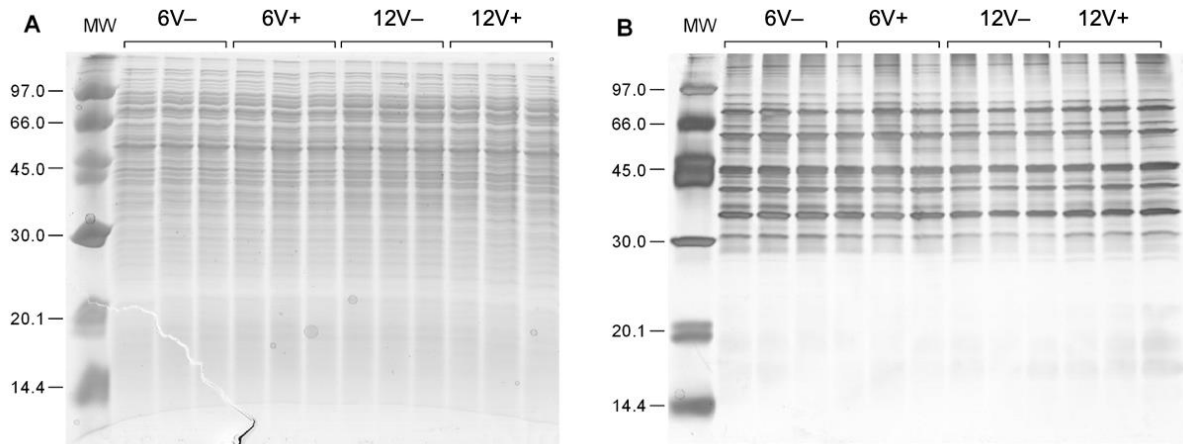


Figure S1. Protein profile of *S. aureus* HG003 WC and EVs. SDS-PAGE (12% gel) showing the protein profile of triplicates of WC (A) and EVs (B) in each condition. Molecular weight (MW) standards are indicated in kDa. Early- and late-stationary growth phases (6 and 12 h, respectively) in the absence (V-) or presence (V+) of vancomycin.

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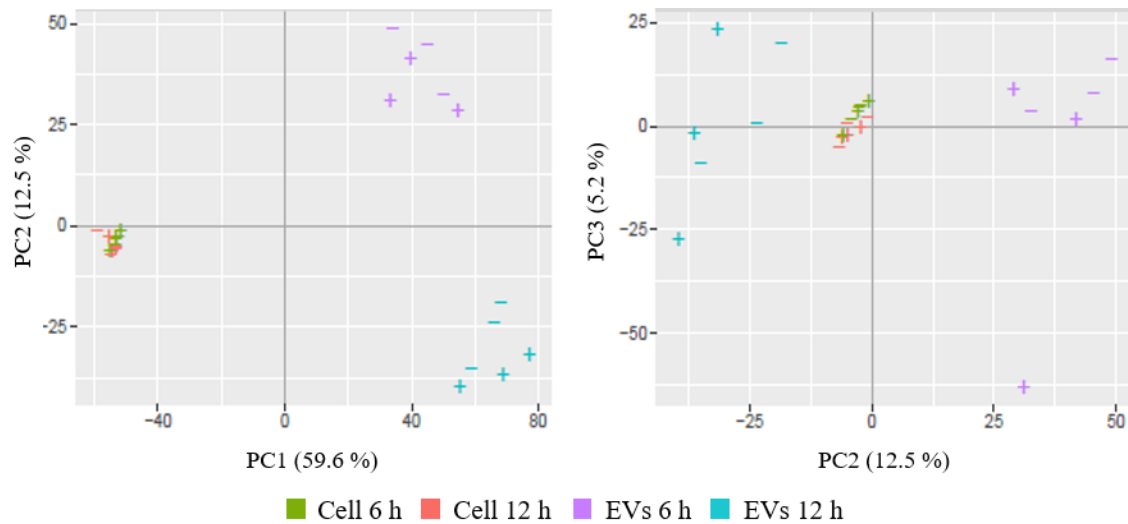


Figure S2. Principal component analysis (PCA) of peptide abundance in samples under each condition and across biological replicates. The percentages of variance that is associated with each axis are displayed. – and + corresponds to conditions in the absence and presence of vancomycin, respectively.

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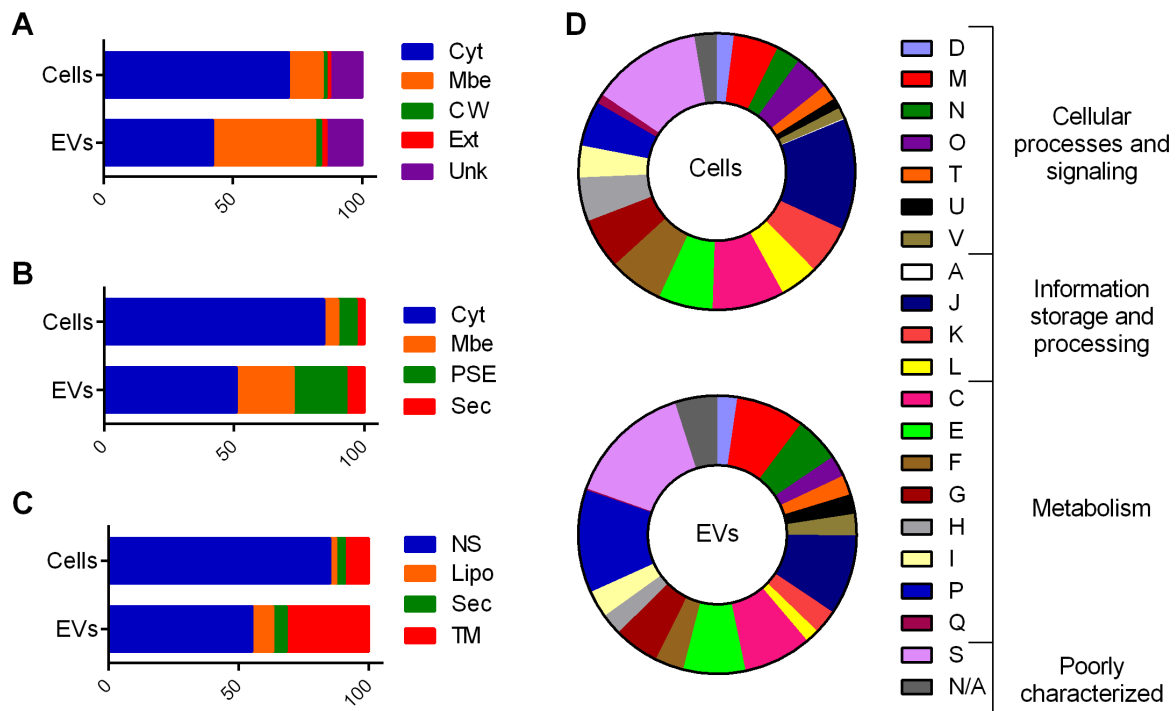


Figure S3. Comparative proteome analysis of *S. aureus* HG003 WC and EVs at 6 h without vancomycin (6V-). Prediction of sub-cellular locations of proteins with PSORTb (A), SurfG+ (B), and PRED-LIPO (C), and the prediction of COG functional categories of proteins with eggNOG-mapper (D). Cyt, cytoplasmatic; Mbe, membrane; CW, cell wall; Ext, extracellular; Unk, unknown; PSE, surface-exposed; Sec, secreted; NS, no signals found; Lipo, lipoprotein; TM, transmembrane; COG functional categories: D, Cell cycle control, cell division, chromosome partitioning; M, cell wall/membrane/envelope biogenesis; N, cell motility; O, Post-translational modification, protein turnover and chaperones; T, signal transduction mechanisms; U, Intracellular trafficking, secretion and vesicular transport; V, defense mechanisms; A, RNA processing and modification; J, translation, ribosomal structure and biogenesis; K, transcription; L, replication, recombination, and repair; C, energy production and conversion; E, amino acid transport and metabolism; F, nucleotide transport and metabolism; G, carbohydrate transport and metabolism; H, coenzyme transport and metabolism; I, lipid transport and metabolism; P, inorganic ion transport and metabolism; Q, secondary metabolites biosynthesis, transport, and catabolism; S, function unknown; NA, not available

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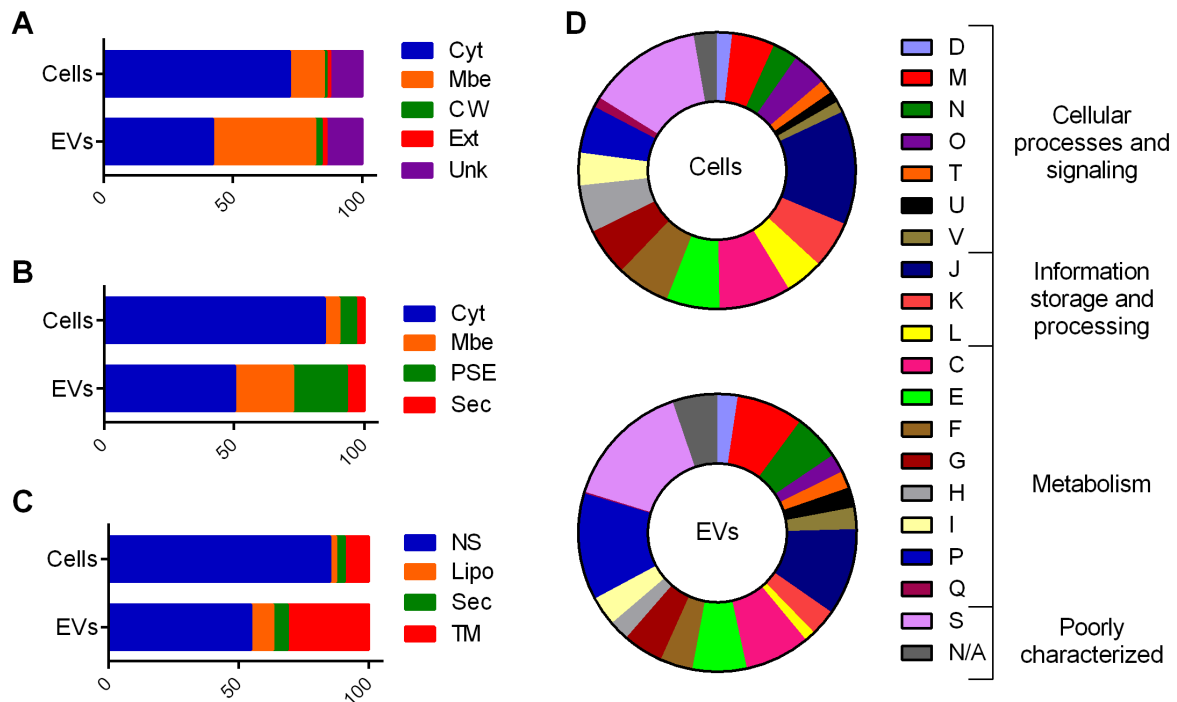


Figure S4. Comparative proteome analysis of *S. aureus* HG003 WC and EVs at 6 h with vancomycin (6V+). Prediction of subcellular locations of proteins with PSORTb (A), SurfG+ (B), and PRED-LIPO (C), and prediction of COG functional categories of proteins with eggNOG-mapper (D). For legend, please refer to Figure S3.

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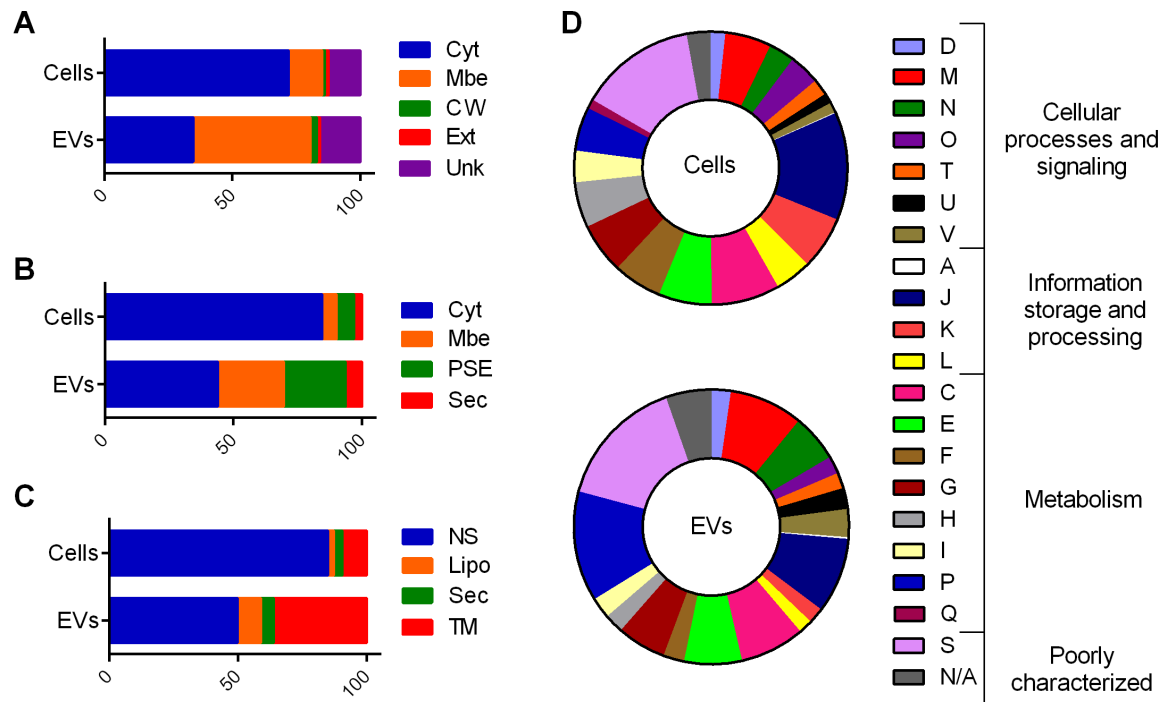


Figure S5. Comparative proteome analysis of *S. aureus* HG003 WC and EVs at 12 h without vancomycin (12V-). Prediction of subcellular locations of proteins with PSORTb (A), SurfG+ (B), and PRED-LIPO (C), and prediction of COG functional categories of proteins with eggNOG-mapper (D). For legend, please refer to Figure S3.

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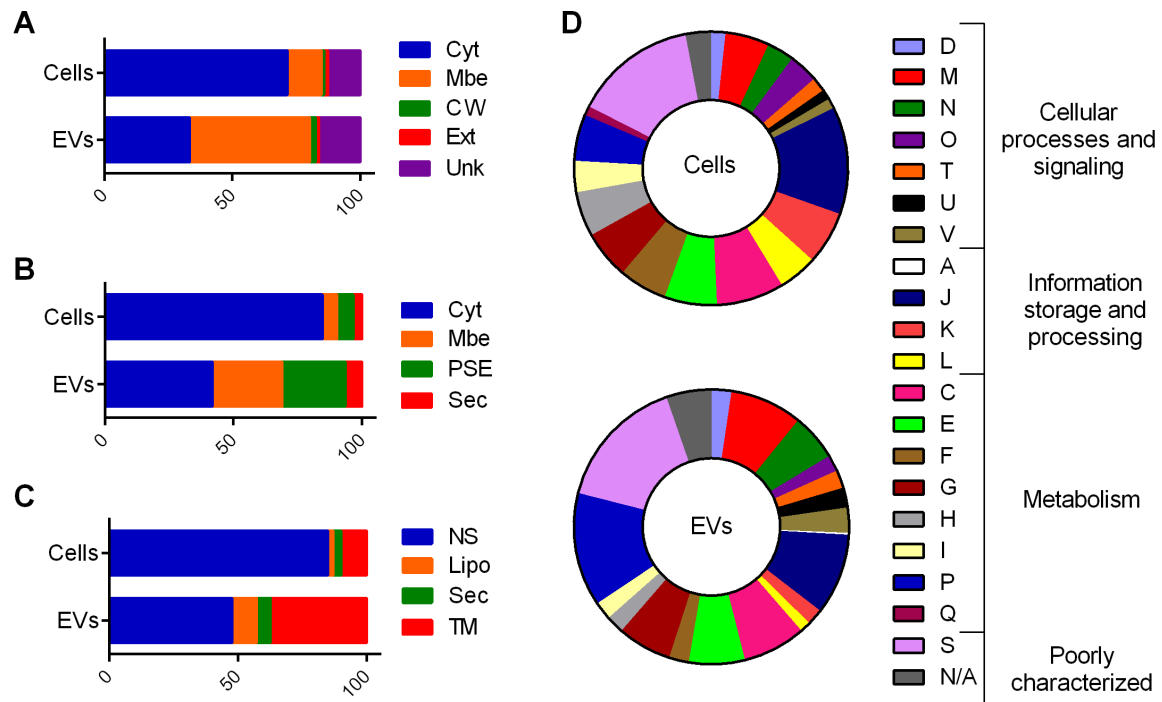


Figure S6. Comparative proteome analysis of *S. aureus* HG003 WC and EVs at 12 h with vancomycin (12V+). Prediction of subcellular locations of proteins with PSORTb (A), SurfG+ (B), and PRED-LIPO (C), and prediction of COG functional categories of proteins with eggNOG-mapper (D). For legend, please refer to Figure S3.