S2 Figure: Multidimensional analyses of the transcriptomes of *S. ambofaciens* ATCC 23877 grown under various conditions

A. **Main characteristics of the various growth conditions** analyzed in this study.

B. **Ascending hierarchical classification** (Euclidean distance, Ward criterion) of the whole data set (37 samples). Transcriptomes form clusters based on biological conditions specified in blue near each node. The acronyms and colors indicate the condition (see panel A) with a distinct letter (a, b, c or d) for each replicate.

C. **Principal component analysis** (PCA) of the whole data set, with percentages of variance associated with each axis. The acronyms and colors indicate the condition (see panel A) with a distinct letter (a, b, c or d) for each replicate.

The data and scripts underlying these panels can be found in **S1 Data** and **S2 Data**, respectively. The analyses were performed on raw counts using the SARTools DESeq2-based R pipeline (1). The statistical report generated by this pipeline is presented in **S3 Data**.
Reference: