Global dynamic proteome study of a pellicle-forming *Acinetobacter baumannii* strain

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Supplemental figures

Figure SI-1: Principal coordinate analysis (PCoA) comparing the level of variance among biological and technical replicates in the 3 growth conditions for (A) all the 620 proteins and (B) the 69 proteins obtained after ANOVA one way. P: planktonic, P1: 1-day pellicle and P4: 4-days pellicle states.
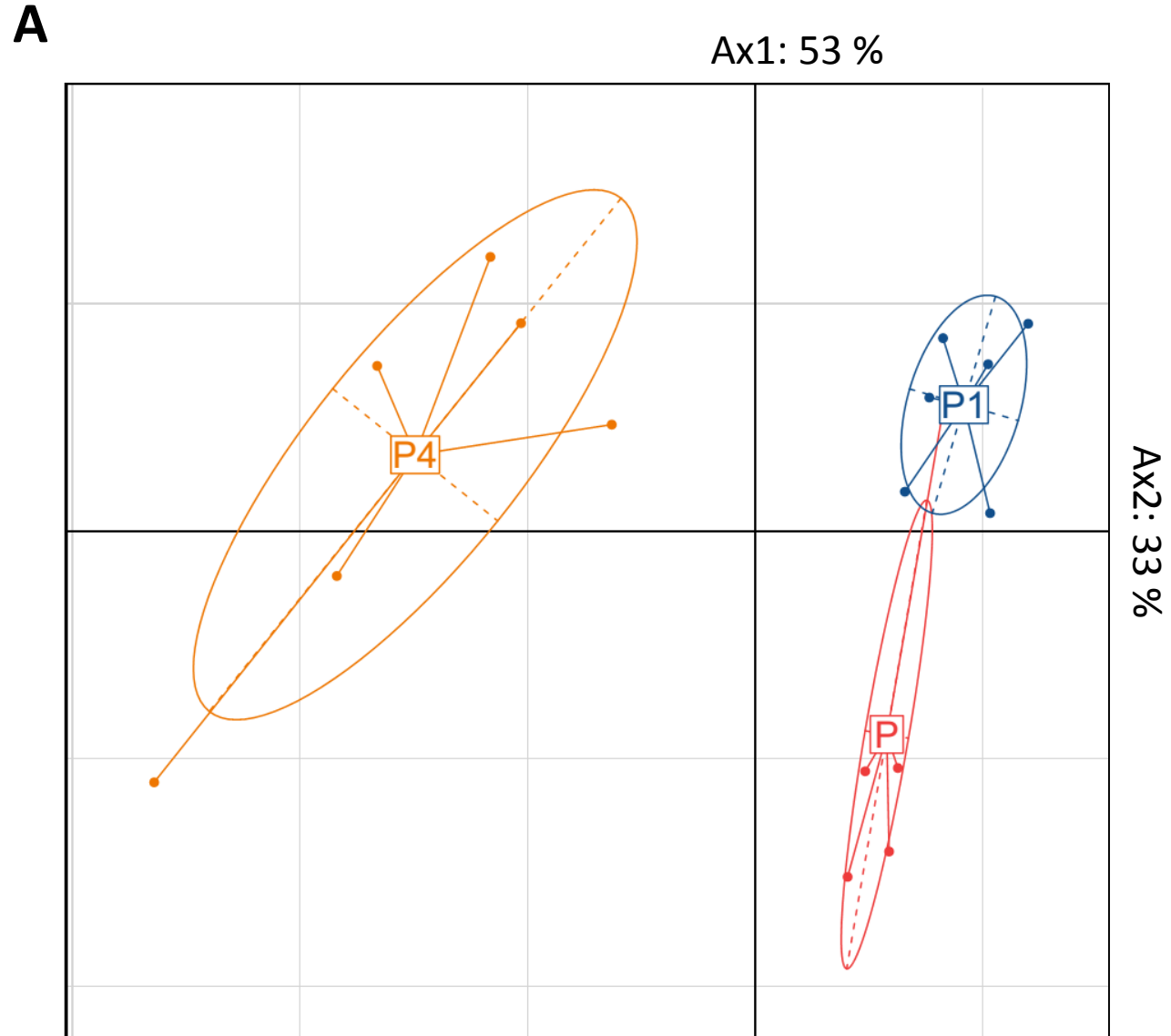
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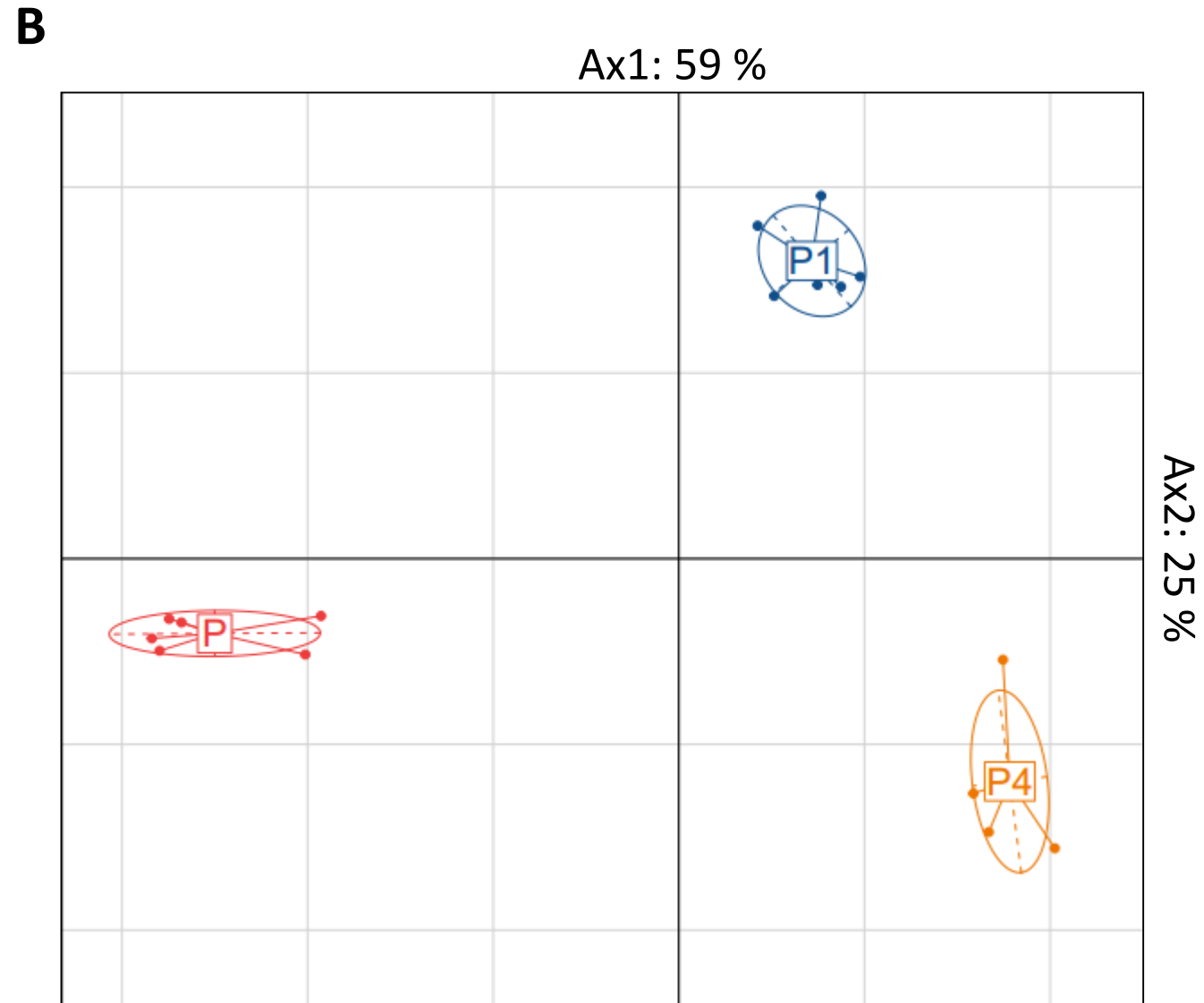
Figure SI-2: Protein-protein interaction map (highest confidence, score of 0.900) for the 620 differentially expressed proteins in *A. baumannii*. Interactions between HisC-AroA (A1S_0688-A1S_2276) and HisC-Hpd (A1S_0688-A1S_3418), indicated in yellow, present interaction scores of 0.973 and 0.904, respectively.
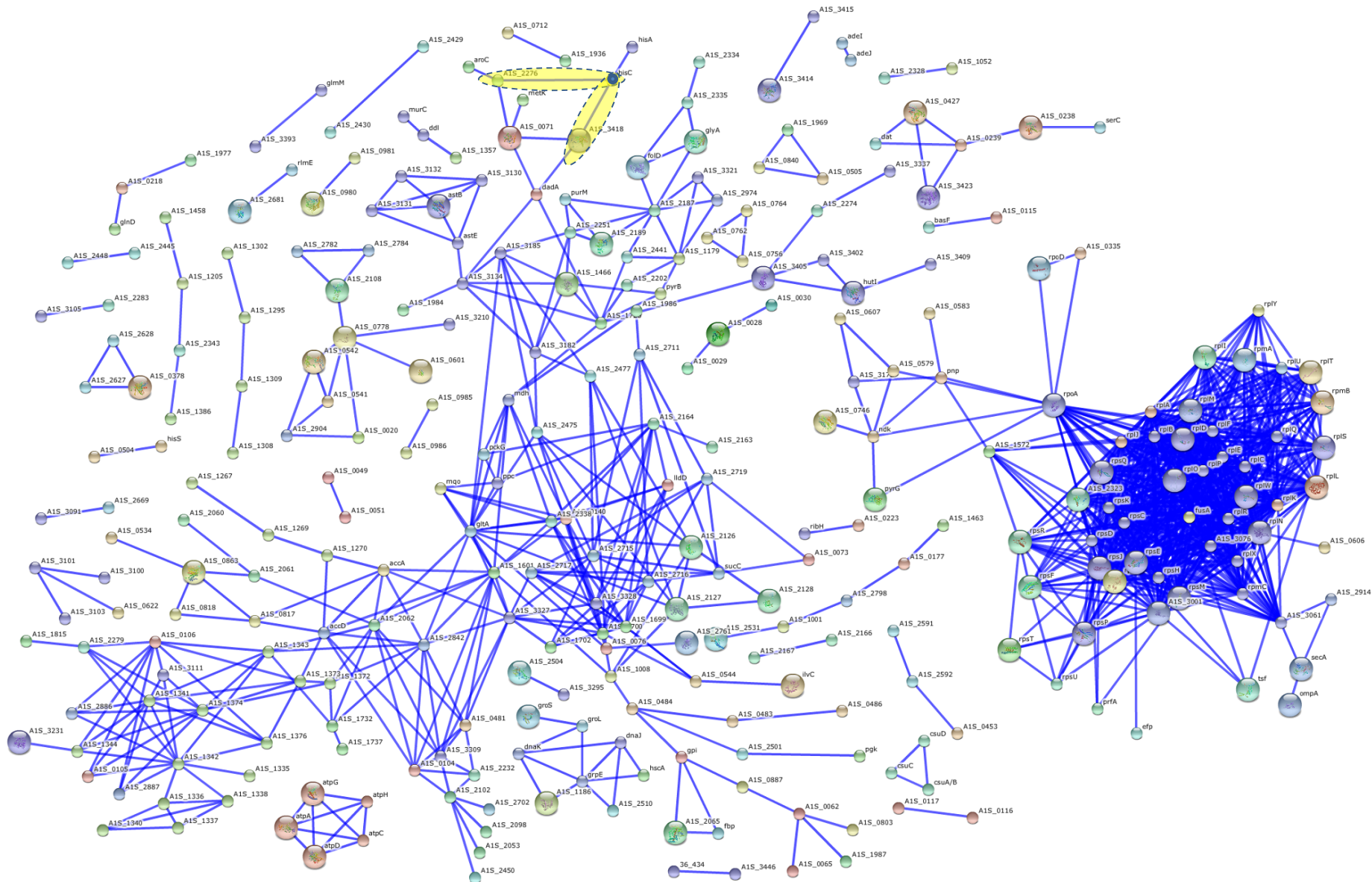
Figure SI-3: The genetic organization of the A1S_0103-0119 region harboring QS-related genes in the strain ATCC 17978. Genes shown with the arrows representing open reading frames and the transcription direction. Predicted gene function are colored in red for Acyl biosynthesis and activation; in blue for S-adenosyl methionine biosynthesis; in dark blue for ACP biosynthesis; in yellow for AHL externalization; in green for QS regulation; in grey for associated genes; and in white for unknown function. Black boxes shown the predicted aba-box location and their respective sequences that could be recognized by AbaR.