

## Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: **Proteins differentially regulated by pAB5 on STc.** Quantitative proteomic analysis of *A. baumannii* UPAB1 whole cell proteome with and without pAB5 under static growth. A list of the selected proteins and accession numbers shown in figure 6C is provided.

File Name: Supplementary Data 2

Description: **Genes differently regulated by pAB5 in SHc.** Transcriptomic analysis of *A. baumannii* UPAB1 whole cell proteome with and without pAB5 under shaking growth. A list of the selected genes and accession numbers shown in figure 7A is provided.

File Name: Supplementary Data 3

Description: LFQ based analysis of *A. baumannii* UPAB1 Whole cell proteome with and without pAB5 under shaking growth. A total of the 1638 protein groups were observed across eight biological replicates, four with pAB5 and four without pAB5. LFQ experiment 1 to 4 correspond to UPAB1 without plasmid biological replicate 1 to 4 and LFQ experiment 5 to 8 correspond to UPAB1 with pAB5 biological replicate 1 to 4. For each protein group the LFQ values, t-test significance, number of peptides, score, number of MS/MS events, intensity values, identification type and protein name gene identified using Maxquant are provided. The fold change difference in the mean log<sub>2</sub>(LFQ) value of biological conditions is provided as the difference between condition while the t-test p-value is presented as the -log<sub>10</sub> value.

File Name: Supplementary Data 4

Description: LFQ based analysis of *A. baumannii* UPAB1 Secretome with and without pAB5. A total of the 908 protein groups were observed across eight biological replicates, four with pAB5 and four without pAB5. LFQ experiment 1 to 4 correspond to the secretome of UPAB1 without plasmid biological replicate 1 to 4 and LFQ experiment 5 to 8 correspond to secretome of UPAB1 with pAB5 biological replicate 1 to 4. For each protein group the LFQ values, t-test significance, number of peptides, score, number of MS/MS events, intensity values, identification type and protein name gene identified using Maxquant are provided. The fold change difference in the mean log<sub>2</sub>(LFQ) value of biological conditions is provided as the difference between condition while the t-test p-value is presented as the -log<sub>10</sub> value.

File Name: Supplementary Data 5

Description: LFQ based analysis of *A. baumannii* UPAB1 Whole cell proteome with and without pAB5 under static growth. A total of the 1903 protein groups were observed across eight biological replicates, four with pAB5 and four without pAB5. LFQ experiment 1 to 4 correspond to UPAB1 without plasmid biological replicate 1 to 4 and LFQ experiment 5 to 8 correspond to UPAB1 with pAB5 biological replicate 1 to 4. For each protein group the LFQ values, t-test significance, number of peptides, score, number of MS/MS events, intensity values, identification type and protein name gene identified using Maxquant are provided. The fold change difference in the mean log<sub>2</sub>(LFQ) value of biological conditions is provided as the difference between condition while the t-test p-value is presented as the -log<sub>10</sub> value.