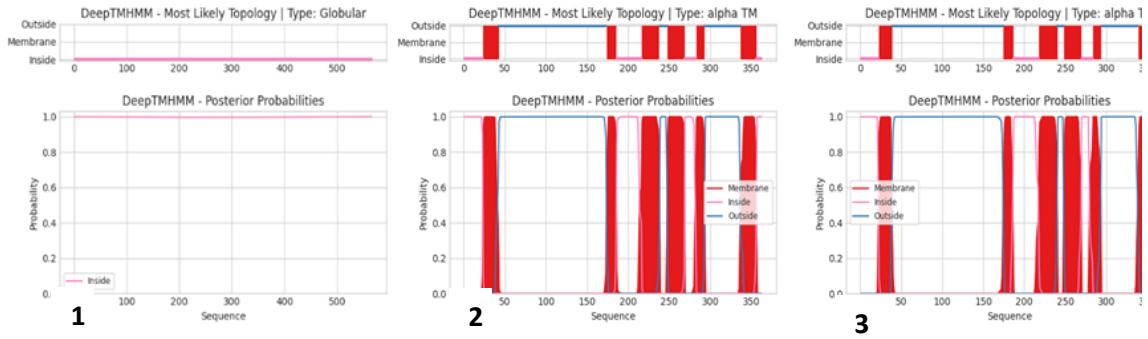


(a)



(b)

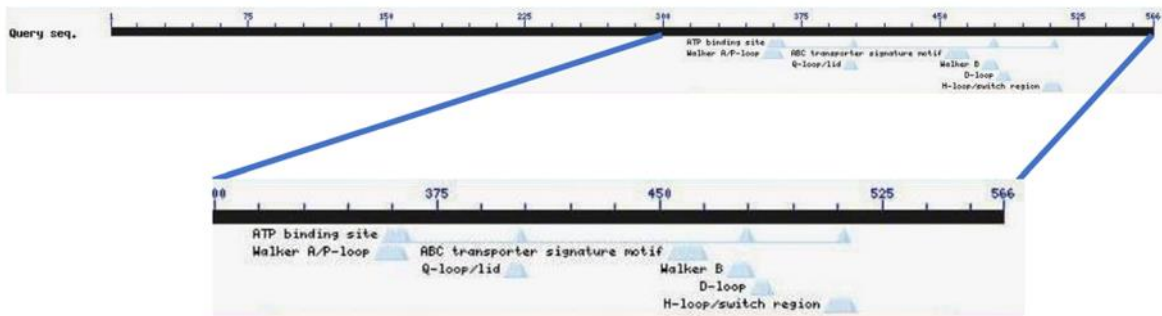


Figure S1. Bioinformatics Analysis of the YbhFSR Efflux System. (a) Prediction of YbhF (1), YbhS (2) and YbhR (3) transmembrane domains using DeepTMHMM software. (b) Representation of the YbhF conserved domains analysis, through the software Conserved Domains, NCBI.

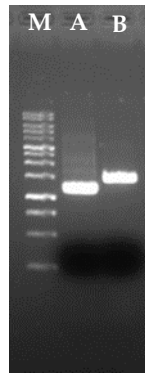


Figure S2. Confirmation of the mutant constructed by PCR technique. Lane A: PCR product using specific primers for *ybhF* for the parental strain Ab_2811; Lane B: PCR product using specific primers for *ybhF* for the mutant Ab_2811 Δ *ybhF* strain; M: Molecular weight.

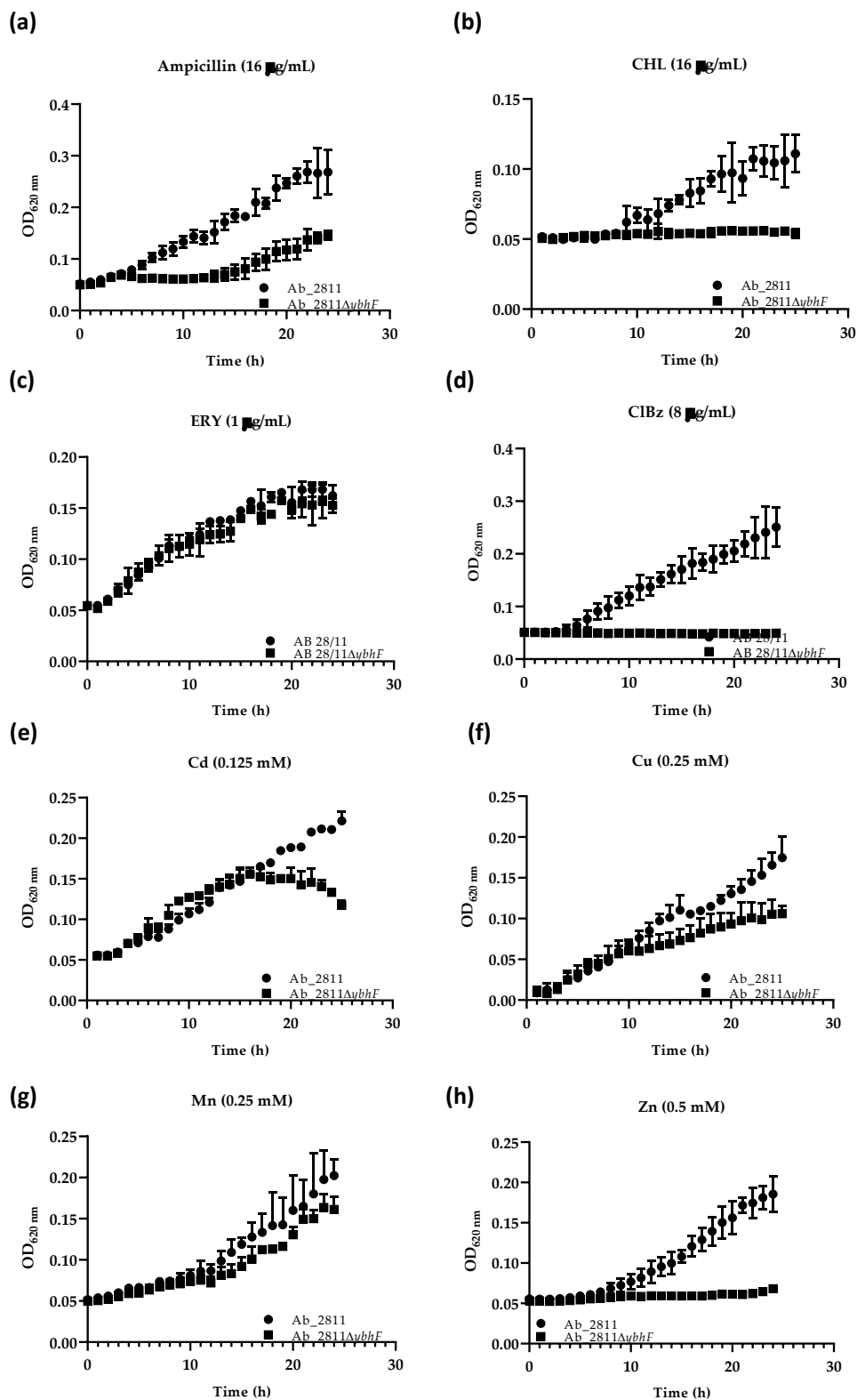


Figure S3. Growth tests for parental strain *Aliarcobacter buzleri* Ab_2811 and respective mutant strain Ab_2811ΔybhF. (a) 16 μg/mL Ampicillin; (b) 16 μg/mL Chloramphenicol; (c) 1 μg/mL Erythromycin; (d) 8 μg/mL Benzalkonium chloride; (e) 0.125 mM CdCl₂; (f) 0.25 mM CuCl₂·2H₂O; (g) 0.25 mM Cl₂Mn·4H₂O; (h) 0.5 mM O₄SZn·7H₂O.

Table S1. Identification of the primers used for amplification of the upstream and downstream regions of *ybhF*.

Identification of primers	Sequence
ybhF_A1	5'-AGC CCC TAC TTT TGG TGA ATT-3'
ybhF_A2	5'- <i>TTA TTC CTC CTA GTT AGT CAT CAC</i> AAT TTT GAG CCT CAT CCA-3'
ybhF_B1	5'- <i>TAC CTG GAG GGA ATA ATG AAC TCT</i> ATT GGT TAT ATG GCG CA-3'
ybhF_B2	5'-ACA GAA CAT GCA AGT GAG AGT C-3'

Note: Adapter sequences for binding to the *aphA-3* resistance cassette were used and identified in italics.