| Tree scale: 0.0001 ⊢ | ATCC 19606(A) | | |
|----------------------|-------------------|-----------------|-----------------|
| | | ATCC 10606(H) | |
| | | - AICC 19606(H) | |
| | | | - ATCC 19606(M) |

Figure S1. Phylogenetic tree based on the concatenated alignment of 22 genes showing SNPs and INDELs in pairwise comparisons between *A. baumannii* ATCC 19606(A), ATCC 19606(M), and ATCC 19606(H) genomes. The tree was generated by the NJ method and rooted on ATCC 19606(A).



^aTM-score is a measure of global structural similarity between query and template protein; the value is comprised between 0 (lowest similarity) and 1 (highest similarity);

^b The global and per-residue model quality has been assessed using the QMEAN scoring function [5].

Figure S2. Homology modelling of p1ATCC19606 replicase. Superimposition of the p1ATCC19606 replicase and *E. coli* Pi initiator protein crystal structure (grey; 2NRA) interacting with 22-mer iteron of DNA. The query structure is shown in grey, while the p1ATCC19606 structural analog is displayed in orange or cyan for I-TASSER and SWISS-MODEL models, respectively. Only the first-ranked model predicted by I-TASSER and SWISS-MODEL for each query is shown, and the relative scores are indicated in the table. The image was generated using UCSF Chimera software (available at http://www.cgl.ucsf.edu/chimera).



Figure S3. Modulation of *higB2*-like and *higA2*-like expression and its effect on bacterial growth. *E. coli* DH5 α carrying both the pVRL2*higA2* and pME6032*higB2* plasmids were spread onto LA plates supplemented with Tc 10 µg/ml and the indicated arabinose concentrations, then challenged with disks containing different IPTG concentrations. IPTG concentrations are shown in the intermediate black ring in clockwise direction from 5 mM to 0 mM. The outermost grey ring displays the ZOI expressed in mm (values are the mean ± SD of three independent experiments).