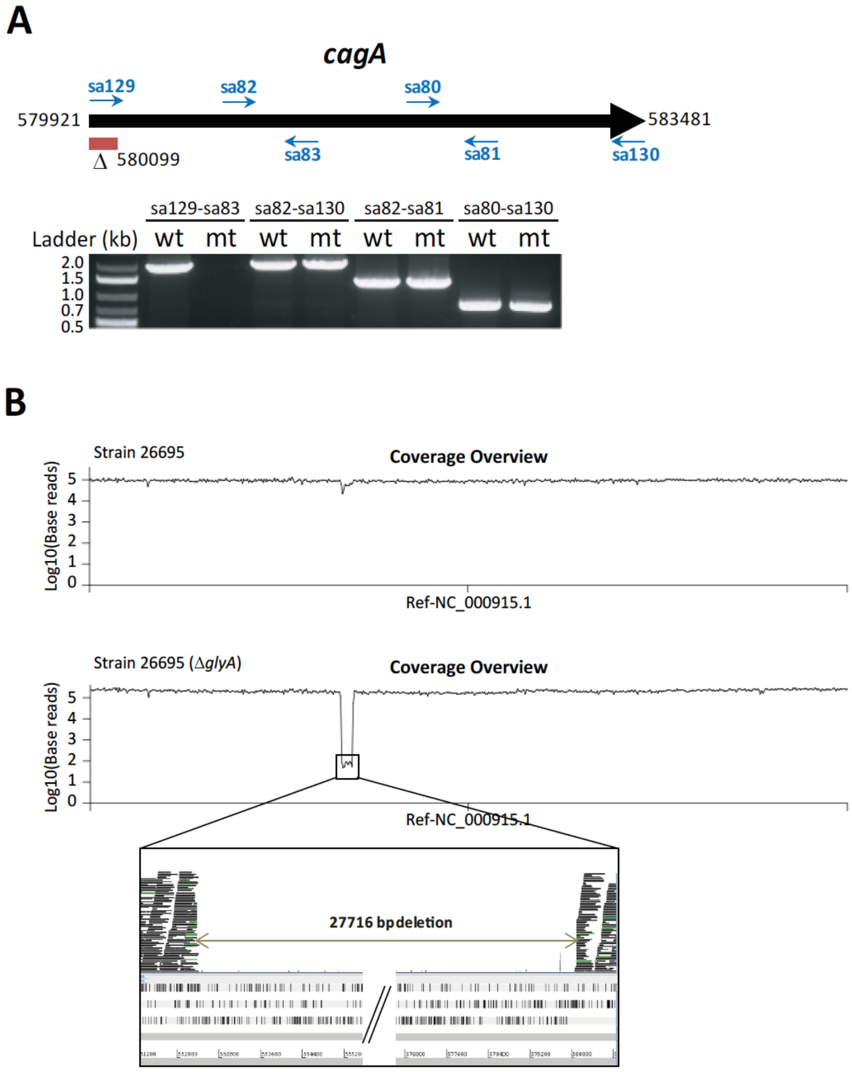
S2 Fig



S2 Fig. Loss of 77% of *cagPAI* in *H. pylori* Δ*glyA*. (A) PCR amplification of *cagA* internal regions with different sets of primers. Oligonucleotides are represented by blue arrows. The red box corresponds to the 178 bp sequence deleted at the 5' extremity of the *cagA* coding sequence in the *Hp*Δ*glyA* mutant. The numbers, flanking the black arrow representing the *cagA* gene and the red box, correspond to the genomic coordinates in *H. pylori* 26695 (NC_000915.1). Wt: wild type and mt: Δ*glyA* mutant. **(B)** Artemis genome browser screenshots illustrating the coverage overview of the 26995 wild type and Δ*glyA* mutant genomes sequenced on an Ion Torrent PGM. The inset shows the 27,716 bp deletion into the *cag*-PAI in the Δ*glyA* mutant (coordinates: 552,383 - 580,099). The extremities of the gap are located at 80 bp from the 5' extremity of the *cag5* gene (HP0524) (left end) and at 178 bp from the 5' extremity of the *cagA* gene (HP0547) (right end).