

Supplementary Material

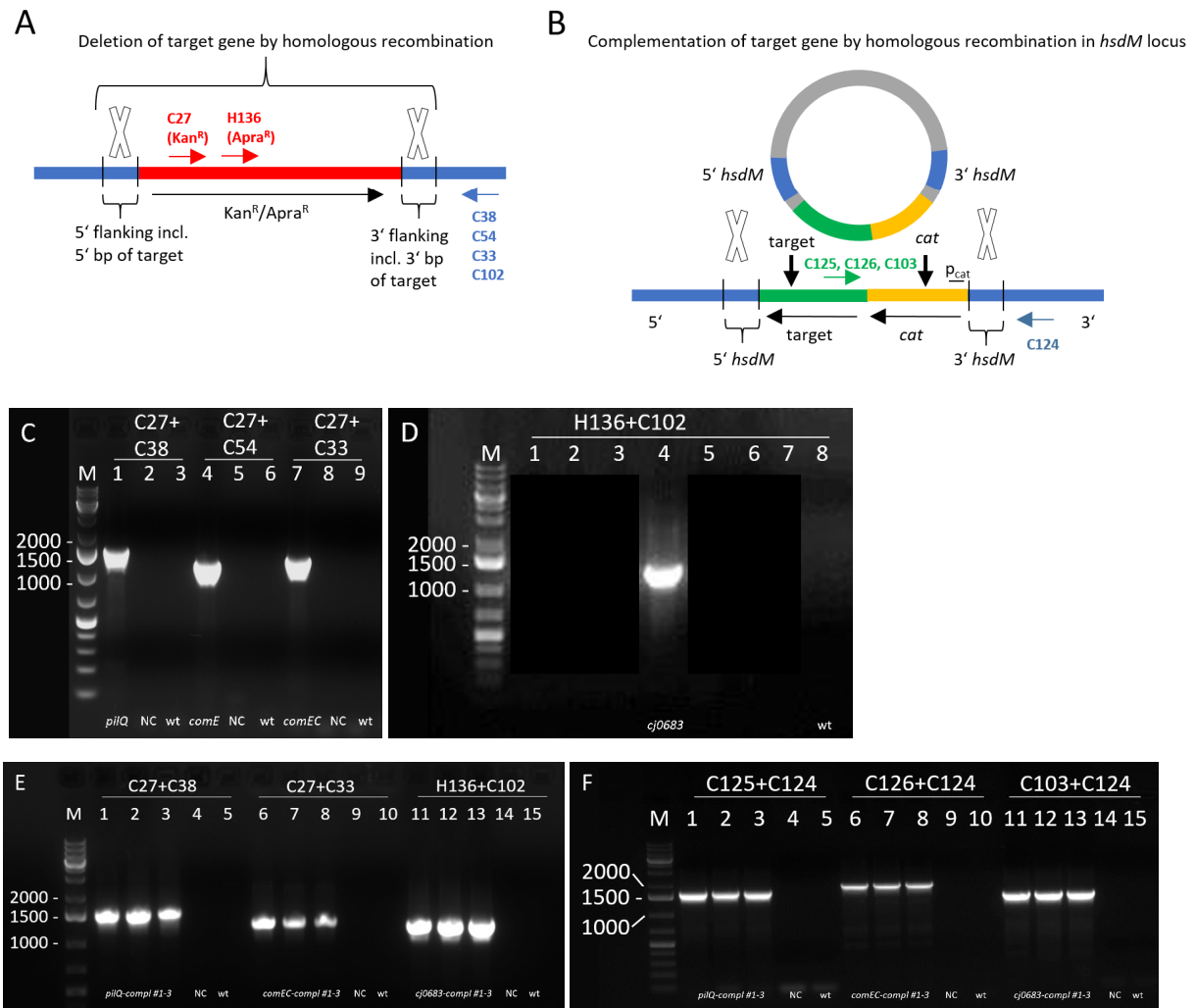


Figure S1. PCR results of successful allelic exchange of mutant strains used in the study. **A**, Cloning strategy for construction of deletion mutants and **B**, their complemented strains. Kan^R, kanamycin resistance cassette; Apra^R, apramycin resistance cassette; cat, chloramphenicol resistance cassette including the promoter (p_{cat}). Flanking regions include 6 to 123 bp of the respective target gene. PCR fragments were separated on a 1 % agarose gel (**C-E**). Lanes are numbered above and annotated below with the respective mutant name, wt (wild type), NC (negative control) or M (1 kb DNA ladder). Other non-relevant lanes are covered by black boxes. **C**, PCR results for verification of successful deletion of *pilQ* (C27+C38), *comE* (C27+C54), and *comEC* (C27+C33). **D**, PCR results for verification of successful deletion of *cj0683* (H136+C102). **E**, PCR results for verification of successful deletion of the target gene at its native location in the complemented strains *pilQ-compl* (C27+C38), *comEC-compl* (C27+C33), and *cj0683-compl* (H136+C102); three clones each are depicted (#). **F**, PCR results for verification of successful integration of the target genes in the complemented strains *pilQ-compl* (C125+C124), *comEC-compl* (C126+C124), and *cj0683-compl* (C103+C124) in *hsdM*; three clones each are depicted (#).

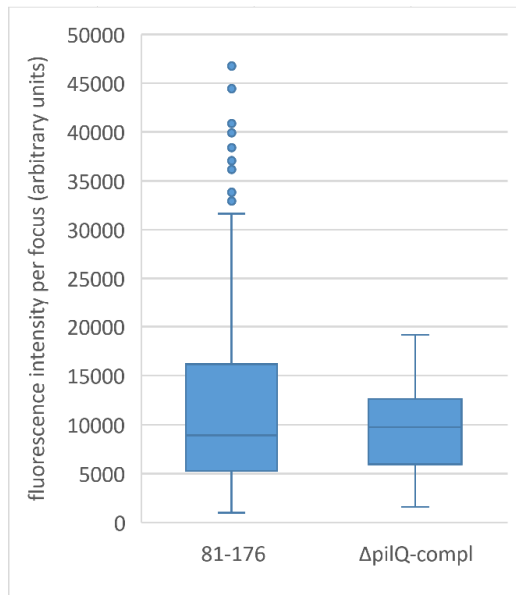


Figure S2. Median DNA amounts imported by $\Delta pilQ$ -compl (n=27) were comparable to the wild type (n=568). The boxplot length corresponds to the interquartile range (IQR; 50 %) of data, the horizontal bar indicates the median value; whiskers represent $1.5 \times$ IQR or the maximum/minimum value of the dataset; dots, outliers.

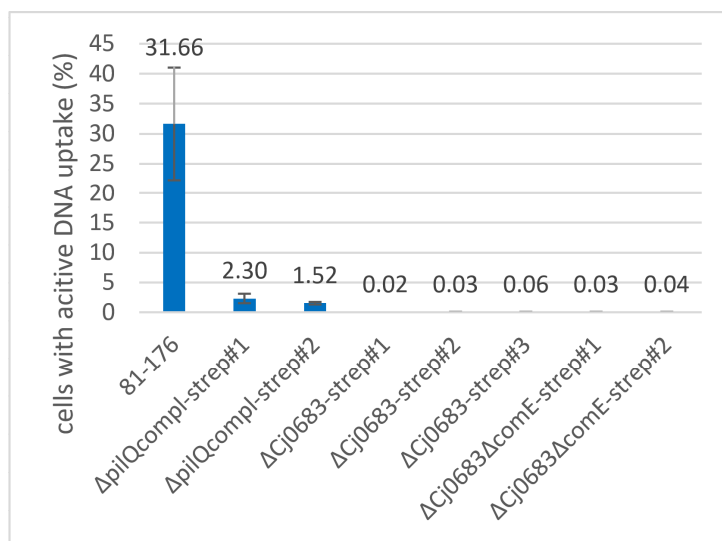


Figure S3. Successfully transformed mutant strains $\Delta pilQ$ -compl, $\Delta Cj0683$, and $\Delta Cj0683\Delta comE$ (name extension “-strep”) displayed similar fractions of competent cells as their respective parental strains. Fraction of cells with functional DNA uptake after incubation with Cy3-labelled *C. jejuni* DNA is depicted. #, clone number. Results of three independent experiments are shown.

Table S1. Strains used in this study.

| Strain | Reference | Species | Description |
|--------------------------------------|-----------------|---------|---|
| 81-176 | [31] | Cj | wild type strain |
| NCTC 11168 | [35] | Cj | wild type strain |
| 81-176 Δ <i>pilQ</i> | This study | Cj | Mutant strain lacking of the outer membrane pore PilQ (=CtsD=Cj1474c), <i>pilQ</i> ::Kan ^R |
| 81-176 Δ <i>comE</i> | This study | Cj | Mutant strain lacking ComE (=Cj0011c), <i>comE</i> ::Kan ^R |
| 81-176 Δ <i>comEC</i> | This study | Cj | Mutant strain lacking the inner membrane channel ComEC (=Cj1211), <i>comEC</i> ::Kan ^R |
| 81-176 Δ <i>cj0683</i> | This study | Cj | Mutant strain lacking the periplasmic protein Cj0683, Δ <i>cj0683</i> ::Apra ^R |
| 81-176 Δ <i>pilQ</i> -compl | This study | Cj | Complemented strain of <i>pilQ</i> |
| 81-176 Δ <i>comEC</i> -compl | This study | Cj | Complemented strain of <i>comEC</i> |
| 81-176 Δ <i>cj0683</i> -compl | This study | Cj | Complemented strain of <i>cj0683</i> |
| DH5 α -pSB3021 | [37]/this study | Ec | Suicide vector for integration of target gene in <i>hsdM</i> for complementation |
| J99 | [32] | Hp | wild type strain |

Cj *Campylobacter jejuni*; Ec *Escherichia coli*; Hp *Helicobacter pylori*

Table S2. Oligonucleotides used in this study.

| Name | Sequence (5'-3') |
|------|--|
| C27 | GGACATGATGCTATGGCTG |
| C29 | TTGGATCCGGTTGGAATTTAGCTGCAG |
| C30 | CACCCGGGTACCGAGGAGAAAAATAAATAATGAAATCTTTAAAG |
| C31 | TTTGTACCTGGAGGGAATAATGGAATAATATCCATATCCATTTTG |
| C32 | TTTGTGACCCAAACAACTTTAGATGATTATAAAATAG |
| C33 | GCAACAAGATGTTGTTGCTAC |
| C34 | TTGGATCCGCAATAAAAAAGACGCTCAAC |
| C35 | CACCCGGGTACCGAGCGTTAATACTGATATCAAAAAGACG |
| C36 | TTTGTACCTGGAGGGAATAATGGATAGCGTAAATGCTCCAAGTC |
| C37 | TTTGTGACCTTAAATTCCTTGAGAAATTTTGTG |
| C38 | GCACCGCTTAACTTCTCTAG |
| C44 | TTGGATCCCATGCAAGAGCAGAATTTAAAG |
| C45 | CACCCGGGTACCGAGAAAATAGTAATTTTTTCATTTCTTATCC |
| C46 | TTTGTACCTGGAGGGAATAATGGATATCACAATAGAATAAAAGGGC |
| C47 | TTTGTGACTTTTGTGCCATAGGCTTTG |
| C54 | TTGAATTCCTTTGTGCCATAGGCTTTG |
| C98 | GTTGCGAATTCATGGCTTCTGTTGATCAGG |
| C99 | CGTATTGCATGACATTGCACTCCACCGCTTCAGTTTCATTTGTCTGGGAGTTC |
| C100 | CGGAGAACGAGATGCAAGATCTGATATAAGATATTATGAACCTG |
| C101 | GGTCTGAATTCTAAAGCTTGCTTACCCTGTTC |
| C102 | TAAAGATGGGGTTGCAGAAC |
| C103 | AGATAATGCGCAAAACAATC |
| C113 | GTACAGCCATGGGAATTCAAAGAGCATAAAGGCTTAAATGATAAGATTAATATTAATTAATTAACATTCTTTTTTG |
| C114 | ATGATCCTCGAGGAATTCCTTACTCATAATGCTTAAATCCTAGATCTTTAAG |
| C115 | GTACAGCCATGGGAATTCAAAGAGCATAAAGGCTTAAATGTCTCTATGGAATTCCTTTTCTTACTC |
| C116 | ATGATCCTCGAGGAATTCCTAAATCACAATCATAATGAAGGG |
| C117 | GTACAGCCATGGGAATTCAAAGAGCATAAAGGCTTAAATGAACAAAGCTTTTACTCTGCTTG |
| C118 | ATGATCCTCGAGGAATTCCTATATCAGATCTTTCATCTAGAACTTCC |
| C124 | ATTGACGCTTTTGGAGAATG |
| C125 | TAGGCATTTTACTCAATATCTTGCC |
| C126 | GCAATTAGCGGTTATCACATAG |
| H11 | GCAGCTCCATCAGCAAAAGGG |
| H12 | TCCAACGTCATCTCGTTCTCCG |
| H13 | GCTCGGTACCCGGGTGACTAAC |
| H14 | TCCCCGGGTCATTATCCCTC |
| H136 | GAGCAGATCATCTCTGATCC |