**Supplemental Table 1.** Comparison of FlaA and FlaB sequence within strains of *C. jejuni*

| Strain | Length (AA)[a] | % Identity[b] |
|---|---|---|
| NCTC 11168 | 572 | 93.9 |
| 81116 | 576 | 94.6 |
| 81-176 | 576 | 94.8 |
| Rm1221 | 573 | 95.3 |
| F38011 | 580 | 90.0 |
| CF93-6 | 572 | 93.7 |
| 260.94 | 577 | 93.6 |
| 84-25 | 572 | 93.9 |

a. AA, amino acids.

b. Percent identity calculated from amino acid sequence.

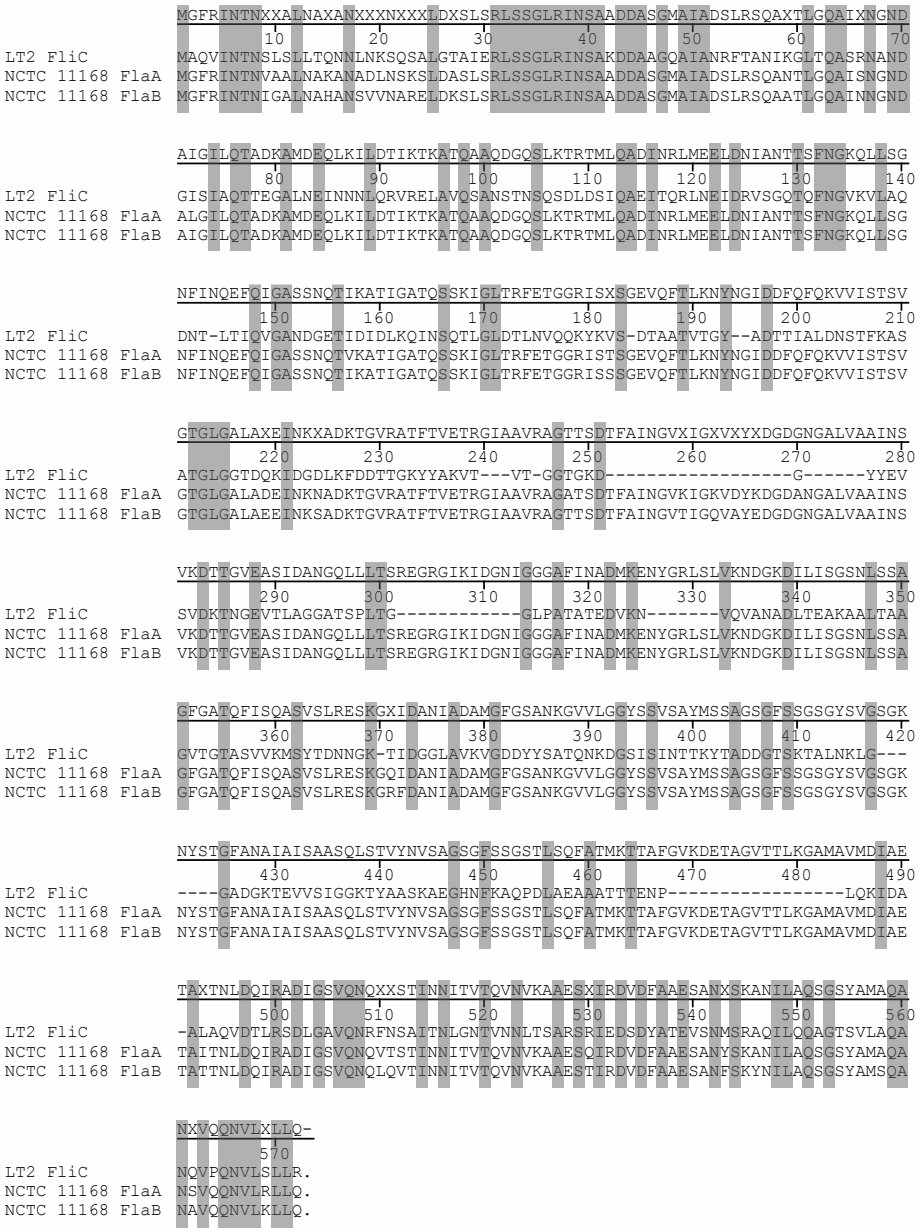
**Supplemental Table 2.** Primers used in this study

| Primer Name | Sequence 5' > 3'[a] |
|---|---|
| MEK 1001 | ATACCGCGGGAACTTGTTAAATGCTATATCGTTAC |
| MEK 1011 | ATAGAGCTCCTTTAAGCACGATAGATTTGAGTG |
| MEK 1332 | ATATACCGCGGATGGGATTTCGTATTAACACC |
| MEK 1334 | ATATACCGCGGATGGGTTTTAGGATAAACACC |
| MEK 1611 | ATATAGAGCTCTAAAACTTGAATATCTTTTTGCTTGC |
| MEK 1612 | ATATACCGCGGTCCTTTTAAAAAAATTCAAGCTCATCC |
| MEK 1613 | ATATAGAGCTCTGAGTAGCGCAGGAAGTGG |
| MEK 1614 | ATATACCGCGGTCCTTTCAAAATATTGCATCGAAAAG |
| MEK 1655[b] | GATATTGGTGTTAATACGAAATCC |
| MEK 1656[b] | GCAGCTTTAAATGCAAAAGCAAAC |
| MEK 1657[b] | ACCAACATTGGTGTTAATACG |
| MEK 1658[b] | GCTTTAAATGCAAAAGCAAACG |
| MEK 1659[b] | ATGTGCATTTAAAGCTGCAACATTG |
| MEK 1660[b] | GCAAACGCTGATTTAAATAGTAAAAG |
| MEK 1661[b] | AACAGCGTTTGCTTTTGCATTTAAAG |
| MEK 1662[b] | TTAAATAGTAAAAGTTTAGATGCTTCTTTAAG |
| MEK 1663[b] | AACATCAGCGTTTGCTTTTGC |
| MEK 1664[b] | AATAGTAAAAGTTTAGATGCTTC |
| MEK 1665[b] | TTCTTTACTATTTAAATCAGCGTTTG |
| MEK 1666[b] | TTAGATGCTTCTTTAAGCAGAC |
| MEK 1667[b] | CTTATCTAAACTTTTACTATTTAAATCAG |
| MEK 1668[b] | TCTTTAAGCAGACTTAGTTCAGG |
| MEK 1844 | ATATACTCGAGTATGCAAATAAAGCTATTATATTTTGTGC |
| MEK 1851 | ATATAGGATCCAAACTTTTACAATAATCTTTCTAAAGAGC |
| MEK 1858[b] | ATATATCTAGATCAAATCAGAGCCGACATTGG |
| MEK 1859[b] | ATATATCTAGATTTGTTATAGCTGTTTCAGC |
| MEK 1860[b] | ATATATCTAGATCAAATCAGAGCAGACATTGG |
| MEK 1861[b] | ATATATCTAGATTTGTTGTGGCTGTTTCAGC |
| MEK 2015 | ATTAGAATTCTATTGCATCGAAAAGATTAAAGC |
| MEK 2025 | ATTAGAATTCCATAGAACTTTTAGAAGTTCAAG |
| MEK 2255[b] | CAGCATTAAATGCACATGCAAATTC |
| MEK 2256[b] | CGATGTTGGTGTTTATCCTAAAAC |
| MEK 2257[b] | ATGTTAATGCTAGAGAACTGGATAAG |
| MEK 2258[b] | CTGAATTTGCATGTGCATTTAATGC |
| MEK 2259[b] | TTAAATGCTAGAGAACTGGATAAGTC |
| MEK 2260[b] | AACTGAATTTGCATGTGCATTTAATG |
| MEK 2391[b] | AAGATCAGCGTTTGCTTTTGC |
| MEK 2392[b] | CAAATCAGCGTTTGCTTTTGC |
| MEK 2393[b] | TAGATCAGCGTTTGCTTTTGC |
| MEK 2394[b] | GAGATCAGCGTTTGCTTTTGC |
| MEK 2395[b] | CAGATCAGCGTTTGCTTTTGC |

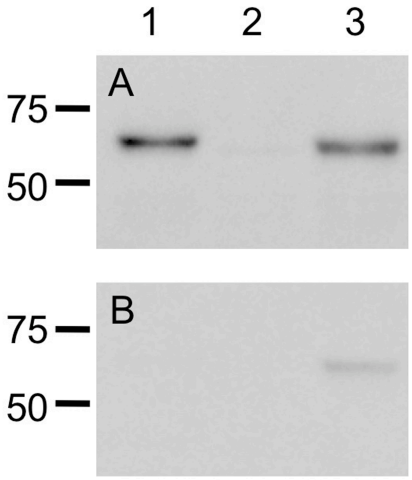
a. Restriction endonuclease cleavage sites are underlined.

b. Primers with 5' phosphorylation.

**Supplemental Figure 1.** Alignment of *C. jejuni* NCTC 11168 FlaA and FlaB with *S. typhimurium* LT2 FliC. *C. jejuni* NCTC 11168 FlaA and FlaB were aligned with *S. typhimurium* LT2 FliC at the peptide level using the ClustalW algorithm. A consensus sequence is displayed above the three peptide sequences. Residues that are identical among the three sequences are highlighted in gray.



**Supplemental Figure 2.** Immunoblots of wild-type, *flaAB* mutant, and promoter swap strains. Analysis of FlaA and FlaB protein synthesis in the *C. jejuni* F38011 wild-type strain, F38011 *flaAB* mutant, and F38011 *flaAB* mutant transformed with *PflaA-flaA*. Whole cell lysates were prepared from broth cultures of *C. jejuni* in mid-exponential growth phase, and separated in 12% SDS-polyacrylamide gels. Panels: A)Whole cell lysates; and B) Supernatants probed with a polyclonal serum that recognizes both FlaA and FlaB. The samples in each lane are the: 1) *C. jejuni* F38011 wild-type strain; 2) *C. jejuni* F38011 *flaAB* mutant; and 3) *C. jejuni* F38011 *flaAB* mutant harboring *PflaA-flaA*. The protein loads in the immunoblots (Panels A and B) are normalized according to culture density, so the levels of flagellin can be directly compared.



**Supplemental Figure 3.** Phase variation motility plates.

*C. jejuni* F38011 wild-type and the *flaAB* mutant harboring *flaA* expressed from the *flaA* promoter were grown for 48 h on MHB agar plates and diluted in MH soft agar (0.4% agar) to a density that would yield ~30 CFUs when plated. After 48 h incubation, the motility of 500 CFU were observed to determine the percentage of the population that were non-motile. A representative plate of the *flaAB* mutant harboring *flaA* expressed from the *flaA* promoter is shown, which contains only motile colonies. The percentage of non-motile colonies observed for the *C. jejuni* F38011 wild-type strain and the *C. jejuni flaAB* mutant harboring pRY111 containing *flaA* expressed from the *flaA* promoter were 2% and 1.4%, respectively.