Figure S4.

```
630           ------TGCTTTTAATGAAATTATTGT-AAAAGACAAATTTAGAATAAATTTATTTTATA -176
R20291        GATATATTGTACAAATAAAATTGAAATATATGGAAGAATATAGAATAAAGATGAGATTTG -169
                    *  *   *** *****    *  *  **  *** *********  *    * *

630           TTGTAAATTTTTGTAAATTTTTAATATATATGTACATCATATAAATTAAATGTTATAAAT -116
R20291        TCTAATATTTTTATAAATTAAAAATATTTTCAAAGAG--TTTATTATAAAATTGTAGACT -111
              *   * ****** ******   ***** *    * *   * **   ****  *    * *

630           ATAAATATATTAAAAATATTATAAAATTTAATATTAGAAATTAAATTAAAAAATT---AC -59
R20291        ATA--------GTGTTTATAATCTTTGTAATTATTGGTAACTAAATTTAAAAAATAAAAT -59
              ***             *** **     * * **** * ** ****** ***** *   *
                                        -35                    -10
                                      ______                 ______
630           ATAAAAAAAATACTTAAAAAAATATTTAAAAAATTTGTTATTTATTGTATACTTAAGTT +1
R20291        ATTTAATTATACACAAAAAAGATATTTAAAAAATTTGTTATTTATTGTATACTTAAGTT
              **  **  *      ***** **************************************
```

Figure S4. **Sequence alignment of the *flgB* promoters from *C. difficile* 630 and R20291 (229 bp total)**. The P*flgB* sequence is identical between 630 and its derivative 630Δ*erm*. The asterisks below the sequence indicate identical nucleotides. The -35 and -10 consensus sequence of the σ^A-dependent promoter are marked, which are identical between both the 630 and the R20291 strains (Soutourina, *et al*. 2013).

Soutourina OA, Monot M, Boudry P, Saujet L, Pichon C, Sismeiro O, Semenova E, Severinov K, Le Bouguenec C, Coppee JY, Dupuy B, Martin-Verstraete I. 2013. Genome-wide identification of regulatory RNAs in the human pathogen *Clostridium difficile*. *PLoS Genet* 9:e1003493.