

Description of Additional Supplementary Files:

Supplementary Data 1: Genome accession numbers and coordinates corresponding to dcw clusters shown in Figure 1.

Supplementary Data 2: Accession numbers of the sequences and summary data used to infer the information presented in Fig. 1, Supplementary Fig. 1-2, and Supplementary Data 3.

Supplementary Data 3: Jaccard similarity coefficients between sets of organisms grouped according to presence/absence of dcw SEDS (spoVE/ftsW) and sporulation (spo0A & spoIIIE) genes.

Supplementary Data 4: *C. difficile* strains used in this study.

Supplementary Data 5: *E. coli* strains used in this study.

Supplementary Data 6: RT-qPCR primers used for gene expression analyses shown in Supplementary Fig. 6.