

630	AAGTTACTATTTTACAAAAA-	GAGCAACTTTTCGAAGAAATATTTAAATAC	CATATTTAAAATTTT	64		
BI9	AAGTTACTATTTTACAAAAAA	GAGCAACTTTTCGAAGAAATATTTAAATAC	CATATTTAAAATTTT	65		
M68	AAGTTACTATTTTACAAAAAA	GAGCAACTTTTTGAAGAAATATTTAAATAC	CATATTTAAAATTTT	65		
CF5 Inverse	AAGTTACTATTTTACAAAAAA	GAGCAACTTTTTGAAGAAATATTTAAATAC	CATATTTAAAATTTT	65		
R20291	AAGTTACTATTTTACAAAAAA	AGGCAACTTTTATAAAGAAATATTTAAATTT	TATATTTAAAATATTT	65		
CD196	AAGTTACTATTTTACAAAAAA	AGGCAACTTTTATAAAGAAATATTTAAATTT	TATATTTAAAATATTT	65		
BI1 Inverse	AAGTTACTATTTTACAAAAAA	AGGCAACTTTTATAAAGAAATATTTAAATTT	TATATTTAAAATATTT	65		
2007855	AAGTTACTATTTTACAAAAAA	AGGCAACTTTTATAAAGAAATATTTAAATTT	TATATTTAAAATATTT	65		
630	TTATATTTTCATGGGACTTCATTAAAAA	AAATATTAGTTTTCTTACTAAAAT	TGATACATTATTGTATT	131		
BI9	TTATATTTTCATGGGACTTCATTGAAAA	AAATATTAGTTTTCTTACTAAAAT	TGATACATTATTGTATT	132		
M68	TTATATTTTCATGGGACTTCATTGAAAA	AAATATTAGTTTTCTTACTAAAAT	TGATACATTATTGTATT	132		
CF5 Inverse	TTATATTTTCATGGGACTTCATTGAAAA	AAATATTAGTTTTCTTACTAAAAT	TGATACATTATTGTATT	132		
R20291	TTATATTTTATTAGGATTTACGAAAAT	TAATATTAGTTTTCTTACC	CAAAGTGATACATTATTATATT	132		
CD196	TTATATTTTATTAGGATTTACGAAAAT	TAATATTAGTTTTCTTACC	CAAAGTGATACATTATTATATT	132		
BI1 Inverse	TTATATTTTATTAGGATTTACGAAAAT	TAATATTAGTTTTCTTACC	CAAAGTGATACATTATTATATT	132		
2007855	TTATATTTTATTAGGATTTACGAAAAT	TAATATTAGTTTTCTTACC	CAAAGTGATACATTATTATATT	132		
630	AATGTAATG	GAAATGCC	GATTAATTTAAAT	AAATAAAGAAGTCA	TT-TTTTGTAATATAGCAACTT	195
BI9	AATGTAATG	GAAATGCC	GATTAATTTAAAT	GAATAAAGAAGTCA	TTTTTTGTAATATAGCAACTT	196
M68	AATGTAATG	GAAATGCC	GATTAATTTAAAT	GAATAAAGAAGTCA	TTTTTTGTAATATAGCAACTT	196
CF5 Inverse	AATGTAATG	GAAATGCC	GATTAATTTAAAT	GAATAAAGAAGTCA	TTTTTTGTAATATAGCAACTT	196
R20291	AATGTAATG	GAAATGTAATTAATTT	GGATGAATAAAGAAGTCA		TTTTTTGTAATATAGCAACTT	196
CD196	AATGTAATG	GAAATGTAATTAATTT	GGATGAATAAAGAAGTCA		TTTTTTGTAATATAGCAACTT	196
BI1 Inverse	AATGTAATG	GAAATGTAATTAATTT	GGATGAATAAAGAAGTCA		TTTTTTGTAATATAGCAACTT	196
2007855	AATGTAATG	GAAATGTAATTAATTT	GGATGAATAAAGAAGTCA		TTTTTTGTAATATAGCAACTT	196

**S11 Fig. Sequence alignment of the flagellar switch and inverted repeat sequences from NCBI accessible genomes of *C. difficile*.** The following *C. difficile* genomes were used in a sequence alignment with Clustal Omega for the flagellar switch: 630, BI9, M68, CF5, R20291, CD196, BI1, and 2007855.