Additional file 3. Phylogenetic trees for individual genes and/or regions, without significant signal for recombination, located in the genomic islets SPI-18, CdtB-islet and the GICT18/1 (artAB) islet. Recombination/breakpoint analyses for SPI-18, CdtB-islet and GICT18/1 were performed using GARD (Kosakovsky Pond SL et al. 2006, Bioinformatics 22(24):3096-3098). Maximum likelihood phylogenies for the individual fragments between breakpoints were inferred with PAUP* 4.010b. Bootstrap values are based on 100 ML bootstrap replicates. Bootstrap values <50% are not shown in the trees.
A. SPI-18: TaiA

B. SPI-18: hlyE

C. SPI-18 without first 494 bp: TaiA and hlyE plus intergenic region.
D. CdtB-islet position 1-543: IS related transposase (first 165 bp of fragment)

E. CdtB-islet position 544-2692: CdtB, prophage derived protein, hypothetical protein

F. SPI-22 position 2693-3766 (mainly pltA part of pltB)
G: CdtB-islet position 3767-4495 pltB, small part of pltA

H: GICT18/1 insert: position 1-488 (integrase plus intergenic region)

I: GICT18/1 insert, position 489-4139.