Figure S15 - Phylogenetic tree resulting from the alignment of the $\sigma^{70}$-family and unannotated sigma factors from 10 bacterial species

$\sigma^{70}$-family and unannotated sigma factors from *C. acetobutylicum* (CAC and CAP), *E. coli* (EC), *B. subtilis* (Bs), *C. crecentus* (Cc), *M. tuberculosis* (Mt), *C. thermocellum* (Cthe), *C. tetani* E88 (CTC and pE88), *C. perfringens* strain 13 (CPE), *C. difficile* (CD), and *C. novyi* NT (NT01CX) were filtered for a Region 2, because Region 2 of $\sigma^{70}$ is the most conserved region of the entire protein, and were then aligned based on the entire sequence. It should be noted that although CAC1766, CAP0157, and CAC0550 do not contain a Region 2, they were also included in the alignment for completeness. These three sigma factors are indicated by a red dot before their names, while the remaining *C. acetobutylicum* sigma factors and the *B. subtilis* sigma factors are indicated by a green dot and a blue dot, respectively. The branches can be classified as: extracytoplasmic function (ECF) (A), unknown (possible ECF family) (B), unknown (possible
ECF family) (C), unknown (D), $\text{sig}H$ (E), unknown (possible ECF family) (F), $\text{sig}A$ annotated (G), $\text{sig}D$ (H), $\text{sig}A$ (I), $\text{sig}B$ (J), and sporulation ($\text{sig}F$, $\text{sig}E$, and $\text{sig}G$) (K).