Figure S10.

```
PrstA               -------TAAAATAAATATAAGTTATAATTATATTA------
                                                   -10
PtcdA               ----ACATTAAAAAAATATAAGATATGTTTACAAATT-----
                                                  -35
PtcdB               AATTTTTATATTTTATATATAGAACAAAGTTTACATATT-----
                                                  -35
PtcdR(σA)                    --TGATTTAATTCCAATGTTGTCAAAATTTTCAAATAAATCA
                                                  -35
PtcdR(σD)           -----------ATTAATGTATTCATAATGCATATTTTCAT--

PflgB               --ATATTTAAAAAATTTGTTATTTAT----------------
                            -35
```

Figure S10. Alignment of inverted repeats within the promoters of direct RstA targets. The inverted repeats identified by EMBOSS Palindrome Finder (Rice, *et al.* 2000) within each promoter that RstA directly binds are shown. The conserved -10 or -35 elements within each promoter are underlined. The predicted -35 element for PtcdR(σ^D) begins immediately following the sequence shown here. The two nucleotides that are important for RstA binding to P*rstA* DNA are marked in red.

Rice P, Longden I, Bleasby A. 2000. EMBOSS: the European molecular biology open software suite. *Trends Genet* 16: 276–277.