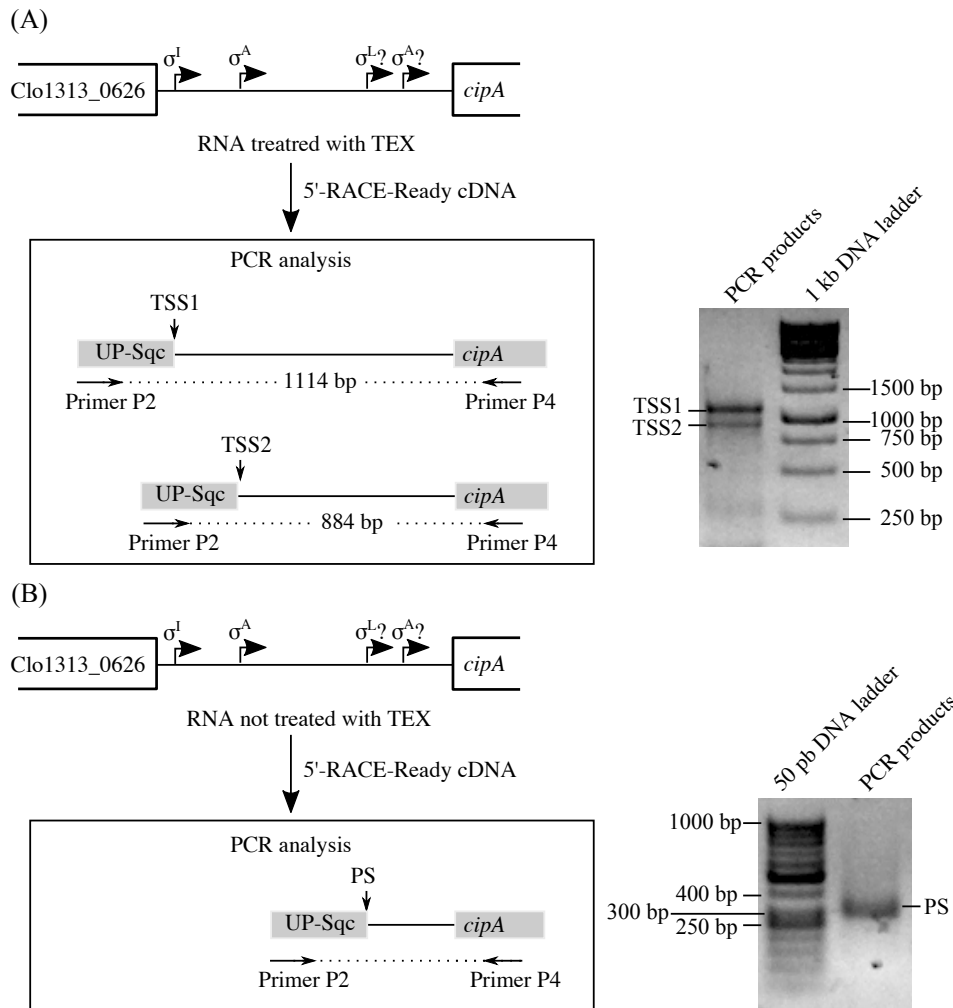
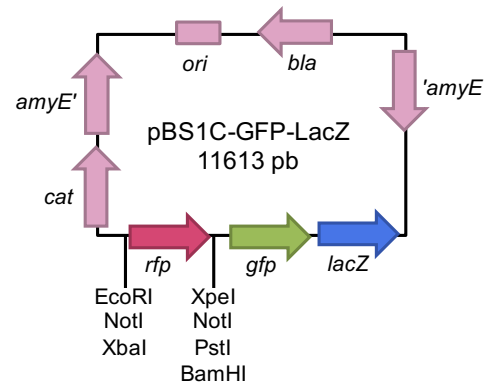
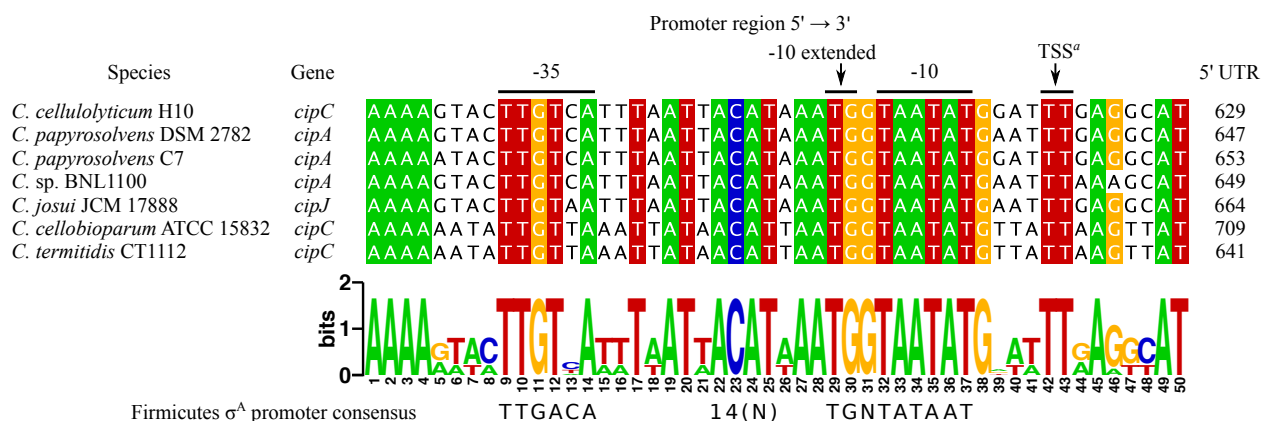


**Figure S1. Schematic depiction of plasmid pBS1C-GFP-LacZ.** The only difference between the pBS1C-GFP-LacZ plasmid constructed in the present work and the pBS1CLacZ plasmid constructed by Radeck and colleagues (1) is the *gfp* gene. The *rfp* gene allows cloning with selection of white colonies in *E. coli*, which if still present leads to formation of red colonies.



**Figure S2. Comparison of total RNA treated with Terminator™ 5'-Phosphate-Dependent Exonuclease (TEX) (A) and total RNA not treated with TEX (B) during the TSS analysis of *C. thermocellum* *cipA*.**

In (A) the length of both sequences were confirmed by Sanger sequencing. TSS, transcriptional start site; PS, post-transcriptional processed site; UP-Sqc, universal primer sequence that is attached to the RNA 5'-end by using the SMARTer technology (Clontech Laboratories, Takara). Primers P2 and P4 are described in Table S1. DNA ladders used were GeneRuler 1 kb DNA Ladder (A) and GeneRuler 50 pb DNA Ladder (B) (both ladders from Thermo Scientific).



**Figure S3. Identification of a highly conserved  $\sigma^A$ -dependent promoter upstream of the primary scaffoldin genes of cellulolytic clostridia producing simple cellulosome.**

<sup>a</sup> The transcriptional start site (TSS) has been experimentally validated in *C. cellulolyticum* (2,3).

## References

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2. Maamar H, Abdou L, Boileau C, Valette O, Tardif C. 2006. Transcriptional analysis of the *cip-cel* gene cluster from *Clostridium cellulolyticum*. *J Bacteriol* 188:2614–2624.
3. Abdou L, Boileau C, De Philip P, Pagès S, Fiérobe HP, Tardif C. 2008. Transcriptional regulation of the *Clostridium cellulolyticum cip-cel* operon: A complex mechanism involving a catabolite-responsive element. *J Bacteriol* 190:1499–1506.