



FIG S1. Alignment of some family 3 CBM sequences. His, Tyr and Trp residues proposed to interact with crystalline cellulose in CBM of *C. thermocellum* CipA are boxed. The other important amino acids are marked with #. Pc, *P. curdlanolyticus*; YK9, *P. curdlanolyticus* YK9; N115\_EG, *Paenibacillus* sp. KSM-N115 endoglucanase; Pl, *P. lautus*; Ccv, *C. cellulovorans*; Tok, *Caldicellulosiruptor* strain Tok7B.1; Cl, *C. lentocellum*; Cc, *C. cellulolyticum*; Ct, *C. thermocellum*; Tf, *T. fusca*.