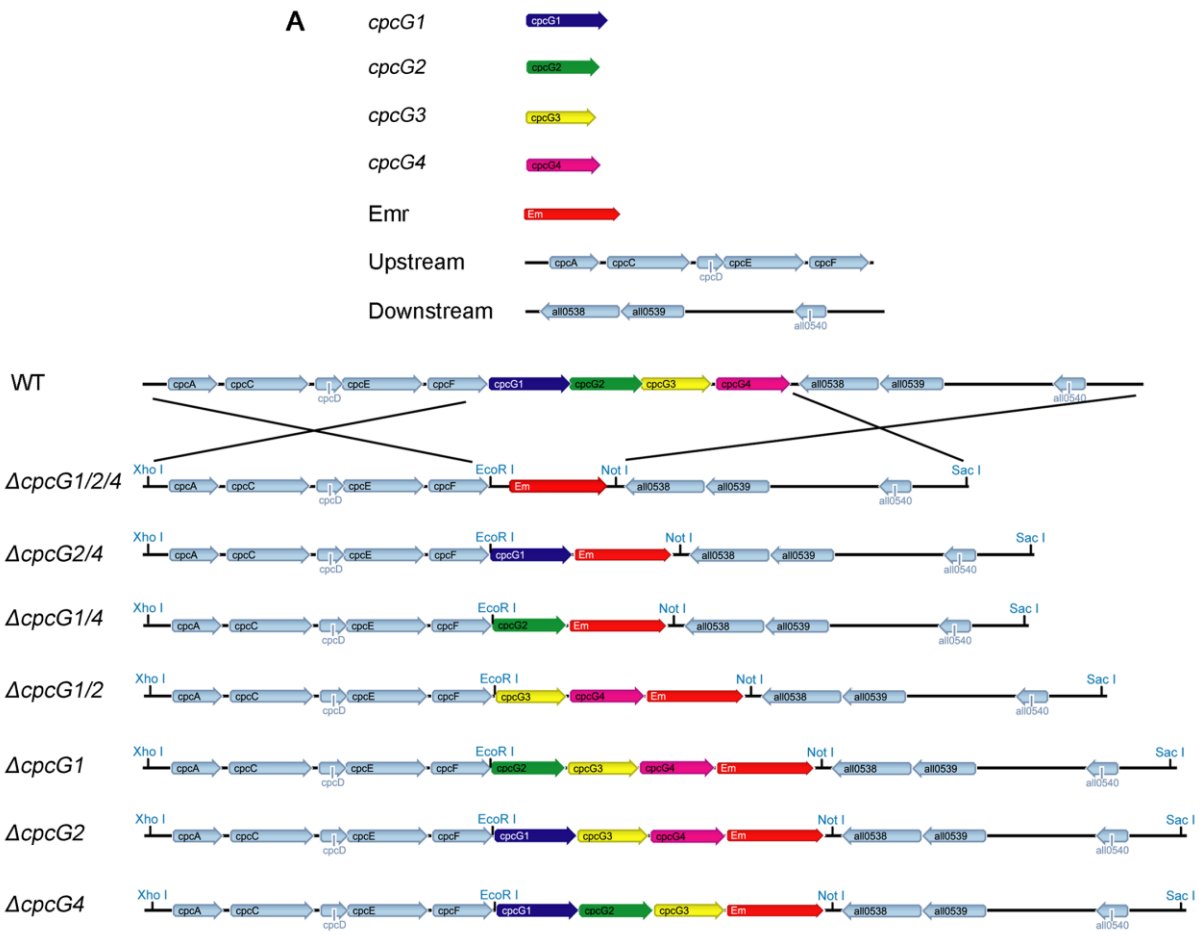
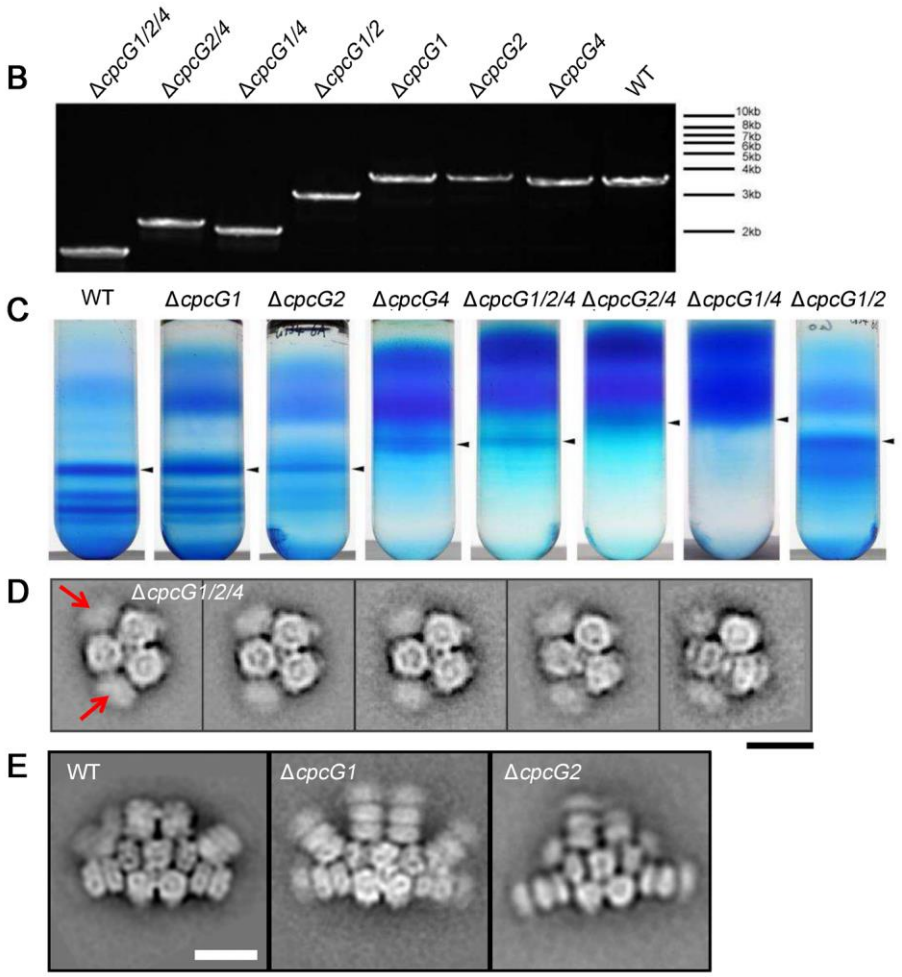


Fig. S7. Molecular reconstitution and purification of L_{RC} mutated PBSs.

(**A**) Construction of PBS mutants. Genes of *cpcG1-4* and erythromycin resistance (Emr), the upstream and downstream homologous fragments flanking the genes are shown at the top. Mutants were constructed by recombination between the homologous fragments of every mutant and wild-type locus. Mutant fragments digested by XhoI and SacI were cloned into plasmid pRL-277 for DNA transformation.



(B) PCR experiments verifying the mutant reconstructions. The lengths of these PCR products are as follows: Δ*cpcG1/2/4*-1163bp, Δ*cpcG2/4*-2169bp, Δ*cpcG1/4*-2033bp, Δ*cpcG1/2*-3020bp, Δ*cpcG1*-3800bp, Δ*cpcG2*-3889bp, Δ*cpcG4*-3656bp, WT-3559bp.

(C) Isolation of PBSs from *cpcG1-4* mutant strains by sucrose density gradient centrifugation. Arrows indicate the samples used for EM analysis.

(D) Reference free 2D classification of isolated cores from Δ*cpcG1/2/4* sample. The result indicates that without surrounding rods, the C1/C2 cylinders are flexible (indicated by arrows for the first image). Scale bar 20 nm.

(E) Comparison of 2D average of wild-type PBS (WT) and Δ*cpcG1* and Δ*cpcG2* mutants. Scale bar 20 nm.