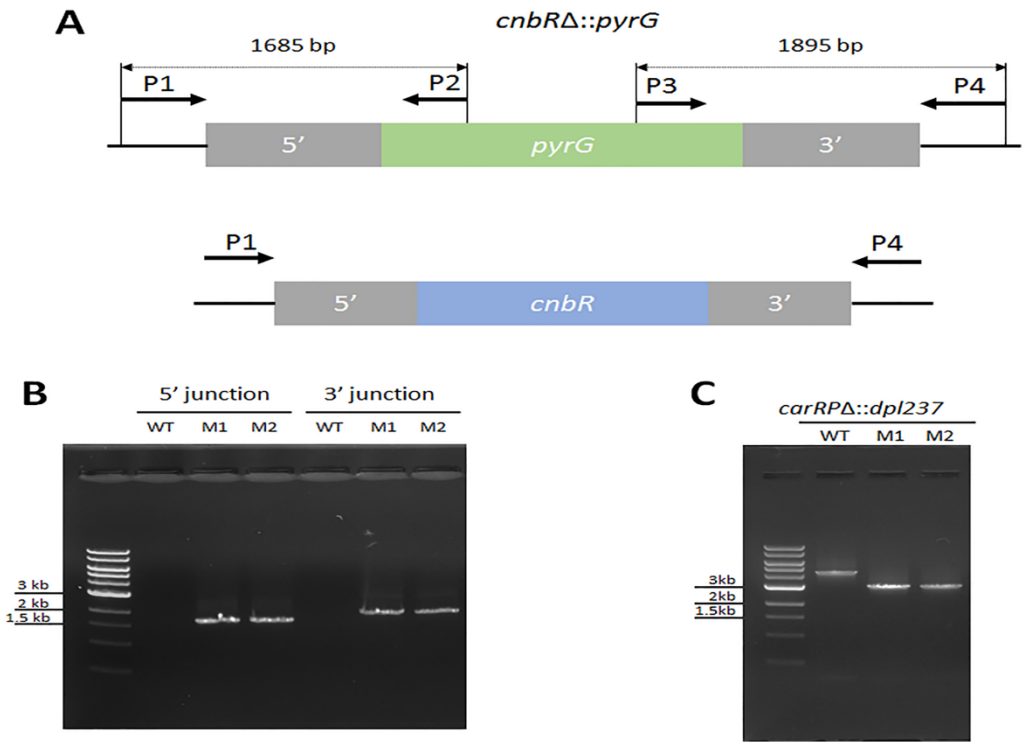

Supplemental Figure 1. Confirmation of *cnbR* and *carRP* gene deletion in the double mutants, MAG1 and MAG2. (A) The *cnbR*Δ::*pyrG* allele was confirmed by junction PCR. P1 and P4 primers recognize the sequences outside of the disruption construct. P2 and P3 primers only recognize the *pyrG* gene marker. P1: JOHE22226; P2, SCL566; P3, SCL567; P4, JOHE22231 (Table 2). Gene size is not to scale. (B) 5' and 3' junction PCR verify the deletion of the *cnbR* gene, where primers P1 and P2 amplify 1,685-bp fragment in the mutant strains MAG1 (M1) and MAG2 (M2) while in the WT the same primers do not amplify the fragment. This result confirms the *cnbR* gene was replaced with the *pyrG* gene in the mutants. (C) Confirmation of the *carRP*Δ::*dpl237* allele via PCR analysis. By using the primers SCL649 and SCL650, both double mutants MAG1(M1) and MAG2 (M2) harbor the leftover *dpl237* allele after excision as shown in Fig 2, confirming the *carRP*::*dpl237* allele has not been modified during transformation.