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Electronic supplementary material

Supplementary Figure

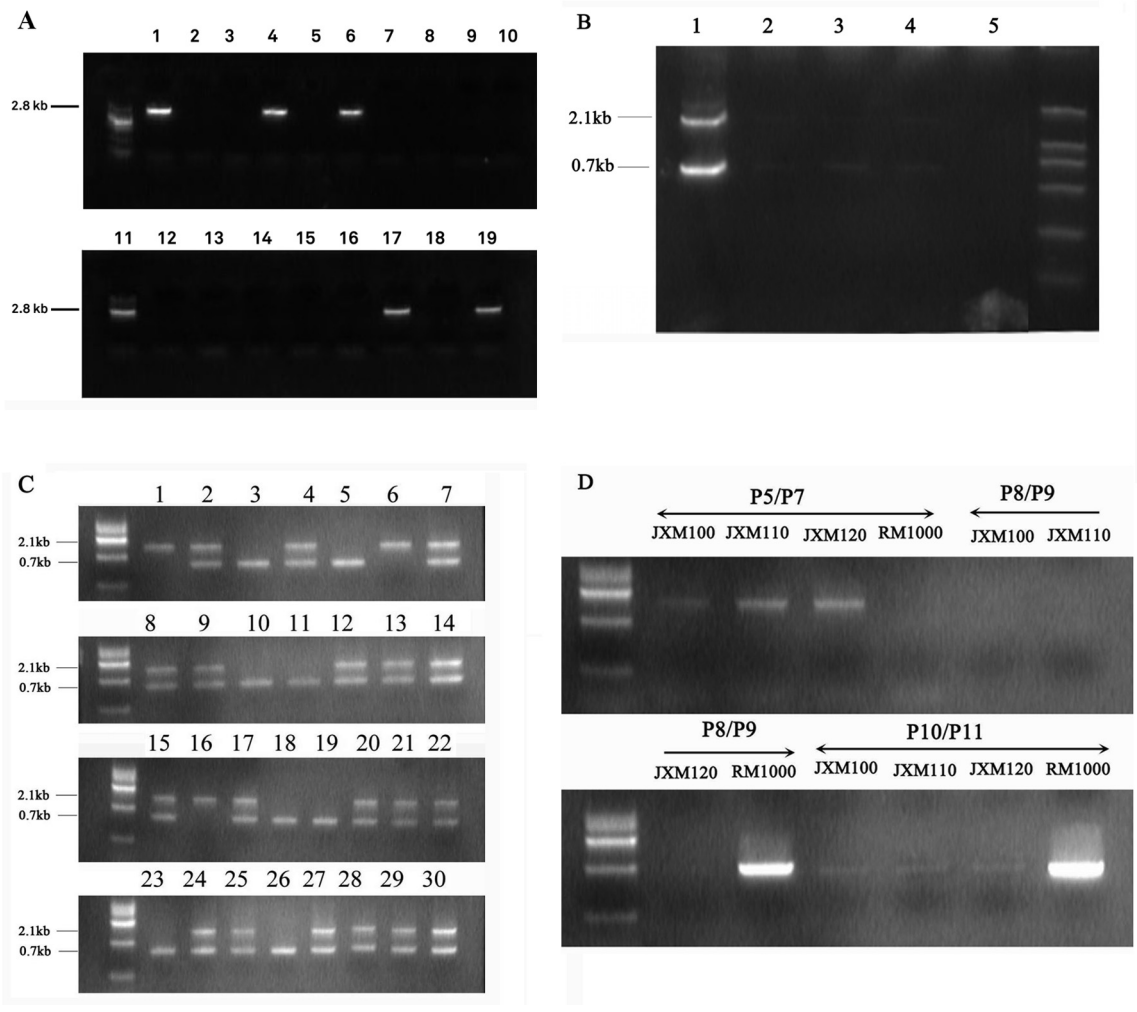

Figure 1. (*A*) Strains, with the first allele of *RTA2* deleted, yielded 2.8 kb product by PCR analysis with primers P5 (specific to *RTA2*) and P7 (specific to *URA3*). (*B*) After selection on 5-FOA, one positive transformant (JXM10) yielded 2.1 and 0.7 kb products by PCR analysis with primers P5 and P6 (specific for the RTA2 gene); the two products were correspond to the sizes expected from the *Δrta2::hisG* disrupted allele and the wild-type allele, respectively. (*C*) Strains, with both alleles of *RTA2* deleted, yielded only one 2.1kb PCR product, corresponding to that of the *Δrta2::hisG* disrupted allele. (*D*) The absence of a product using primers inside and outside the disruption fragment of the gene (primer pairs 8 and 9 and 10 and 11) also confirmed that the *RTA2* sequence had not relocated to another position in the genome.