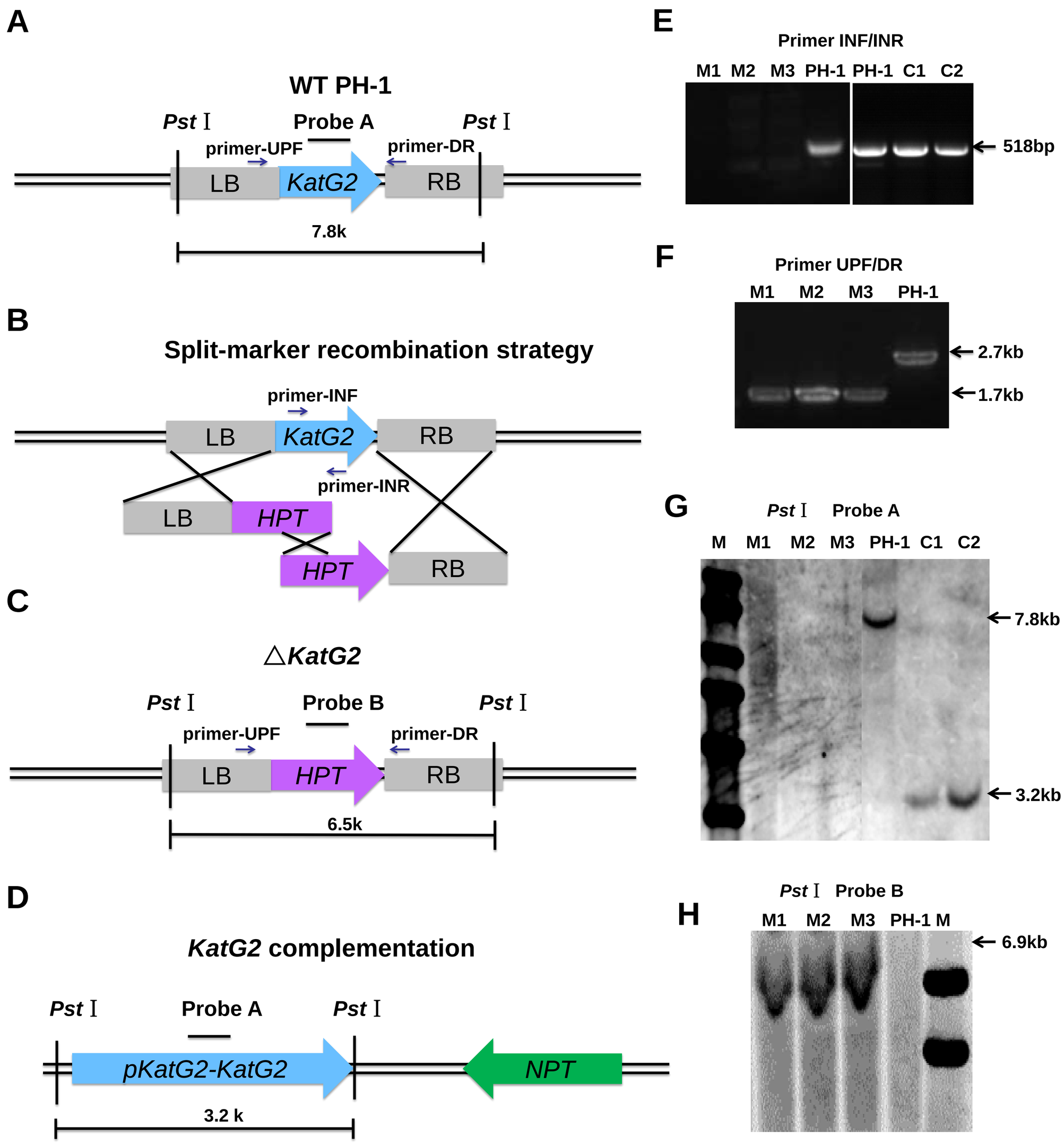

Fig. S2 Construction of Δ*KatG2* mutants and complemented strains. (A) Restriction maps of genomic fragments containing *KatG2* in PH-1. (B) Schematic presentation of the split-marker recombination strategy used to generate the *KatG2* gene knockout mutants. (C) and (D) Restriction maps of genomic fragments containing the Δ*KatG2* allele and the *KatG2* complementation fragment. (E) and (F) Verification of *KatG2* gene deletion mutants and complemented lines by PCR. A specific product was amplified in the wild-type PH-1, and no product was amplified in the Δ *KatG2* mutants M1, M2 and M3 using *KatG2* gene-specific primers in (B); PCR products of different sizes were amplified by primers in the left border (LB) and right border (RB) regions in (A) and (C). (G) and (H) Southern hybridization of PH-1, Δ *KatG2* mutants and complemented strains. Genomic DNA of each strain was digested with *Pst* I and hybridized with probe A or probe B. Whereas probe A hybridized to the *KatG2* gene to produce a 7.8-kb band in PH-1 and a 3.2-kb band in complemented strains but did not produce these bands in Δ *KatG2* mutants, probe B reported the *HPH* gene with a 6.9-kb band in Δ *KatG2* mutants. LB: 5’ flanking sequences of *KatG2*; RB: 3’ flanking sequences of *KatG2*; *HPT*: Hygromycin B phosphotransferase gene; *NPT*: Neomycin phosphotransferase gene; M: DNA marker.