Figure S2. Verification of triple-gene deletions of cre-1, res-1 and gh1-1 in selected transformants by using Pooled single-crRNA-based CRISPR-Cas12a system (A) or crRNA Array-based CRISPR-Cas12a system (B). PCR analysis of triple-gene deletion of cre-1, res-1 and gh1-1 in selected transformants using one primer (cre1/res1/gh1-1-out-F) located upstream of the 5′ flanking region of genomic DNA and the other primer (cre1/res1/gh1-1-in-R) located in the 3′ flanking region of genomic DNA. The expected lengths of disrupted transformants of cre-1, res-1 and gh1-1 were 0.8, 0.7 and 1.9 kb, respectively, while those of WT strain (rightmost lane) was 1.2, 0.9 and 1.0 kb, respectively. Heterokaryotic transformants showed two PCR bands (both of wild-type and knockout). The symbol of star indicated deletion mutant. HDR, homology-directed repair; WT, wild type. U6p, U6 promoter; Ptef1, tef1 promoter; TrpC, trpC Terminator.