



**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; *TtrpC*, *trpC* Terminator.