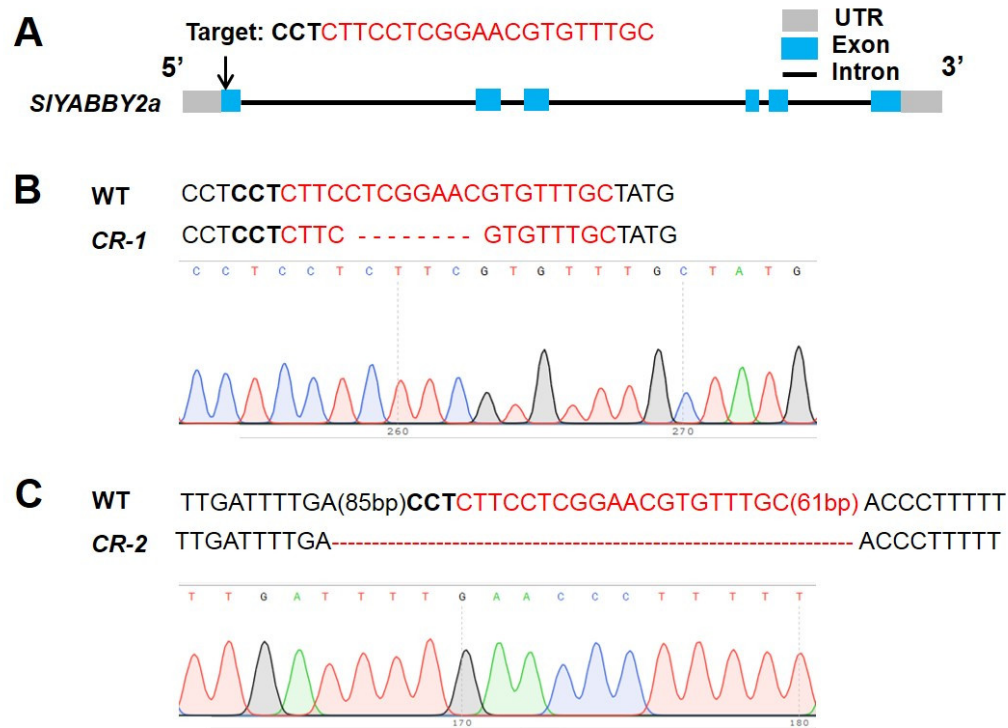
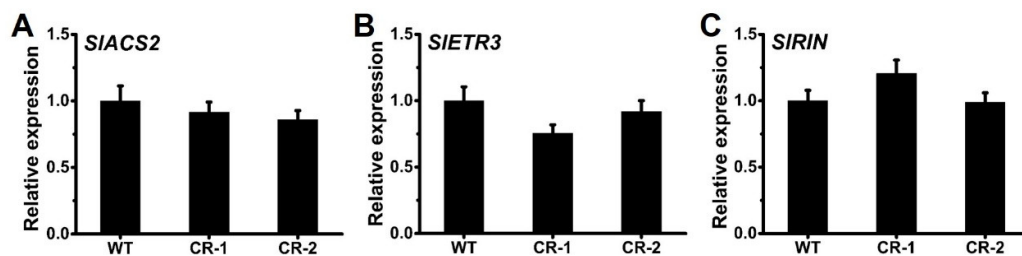


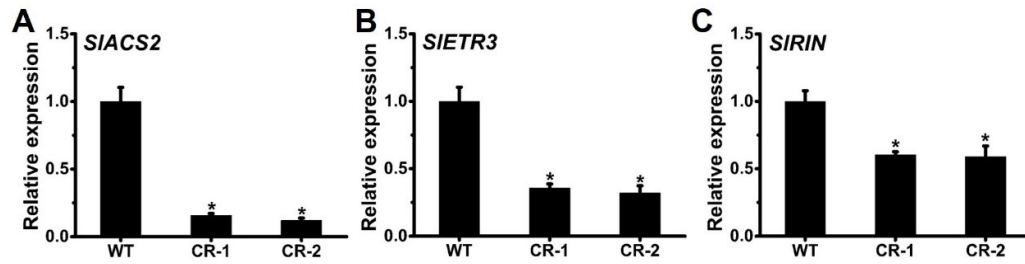
**Figure S1. Expression analysis of *SIYABBY2a*.** RNA-seq data and visualization were produced by Shinozaki et al., 2018 [45].



**Figure S2. Knockout site and sequence alignment.** (A) The gene knockout site was located in the first exon of *SIYABBY2a* and near the ATG start codon. (B) Genomic sequences flanking the knockout site of wild-type (WT) and CR-1 mutant. (C) Genomic sequences flanking the knockout site of WT and CR-2 mutant.



**Figure S3. Transcripts quantification of fruit pericarp at the B stage from WT and *Slyabby2a* lines.** (A-C) The relative expression of the ethylene biosynthesis gene *SIACS2* (A), the ethylene receptor gene *SIETR3* (B), and the master ripening regulator gene *SIRIN* (C). Each value represents the mean  $\pm$  SE of three biological replicates.



**Figure S4. Transcripts quantification of fruit septum at the B+2 stage from WT and *Slyabby2a* lines.** (A-C) The relative expression of the ethylene biosynthesis gene *SIACS2* (A), the ethylene receptor gene *SIETR3* (B), and the master ripening regulator gene *SIRIN* (C). Each value represents the mean  $\pm$  SE of three biological replicates. Asterisks indicate significant differences between WT and each *Slyabby2a* mutant lines, CR-1 and CR-2 (\*  $p < 0.05$ ; Student's  $t$  test).