



Figure S1. Structure, motif and transmembrane domain (TM) analysis of *CsSWEET2*. (A) The exon-intron structure of *CsSWEET2* was analysed using the web-based bioinformatics tool Gene Structure Display Server (GSDS, <http://gsds.gao-lab.org>). Exons and introns are shown as red boxes and black lines, respectively. Upstream and downstream untranslated regions are shown as blue boxes. The numbers above the boxes indicate the nucleotide numbers of the upstream and downstream untranslated regions, as well as each exon. Scales are shown at the bottom of the diagram. (B) Conserved motifs of *CsSWEET2* were analysed by MOTIF Search (<https://www.genome.jp/tools/motif>). (C) TMs of the *CsSWEET2* protein. The prediction website was TMHMM-2.0 (<https://services.healthtech.dtu.dk/service.php?TMHMM-2.0>).