



Appendix S1. Three transcription factors encoding *CBF* genes in tandem array in the SW and IT ecotypes, and two lines with CRISPR-induced mutations in the *CBF2* gene. Open boxes indicate *CBF1*-, *CBF2*-, and *CBF3*-coding regions (shaded portion indicates DNA binding domain) in the order they are arranged in the genome. The green lines indicate the transcription activation domains. The filled triangle indicates the site of the naturally occurring 13-bp deletion in the IT *CBF2* gene. Open triangles indicate the two independent CRISPR-induced deletions. SW:cbf2 a is the same line as used by Park et al. (2018).