



**Supplementary Fig. S1. Multiple alignment of the deduced protein sequences of CBF/DREB1-homologous genes in cucumber, wild cucumber, melon, watermelon and bitter melon, with Arabidopsis CBF/DREB1 protein sequences. The NLS, AP2/EREBP domain, and CBF/DREB1-conserved amino acid residues (D1 and D2) are indicated by red, blue and pink boxes, respectively. Shaded vertical boxes indicate conserved residues among compared protein sequences. The alignment was made using MUSCLE in MEGA 7 program and visualized using GeneDoc software.**