

Figure S1. Transcriptome profiling of CS and DM1

(A) Expressed TUs identified by RNA-seq analysis. (B) Venn diagram expressed Tus in DM1 and CS. (C) Go biological process annotation of specific 3,584 TUs in DM1

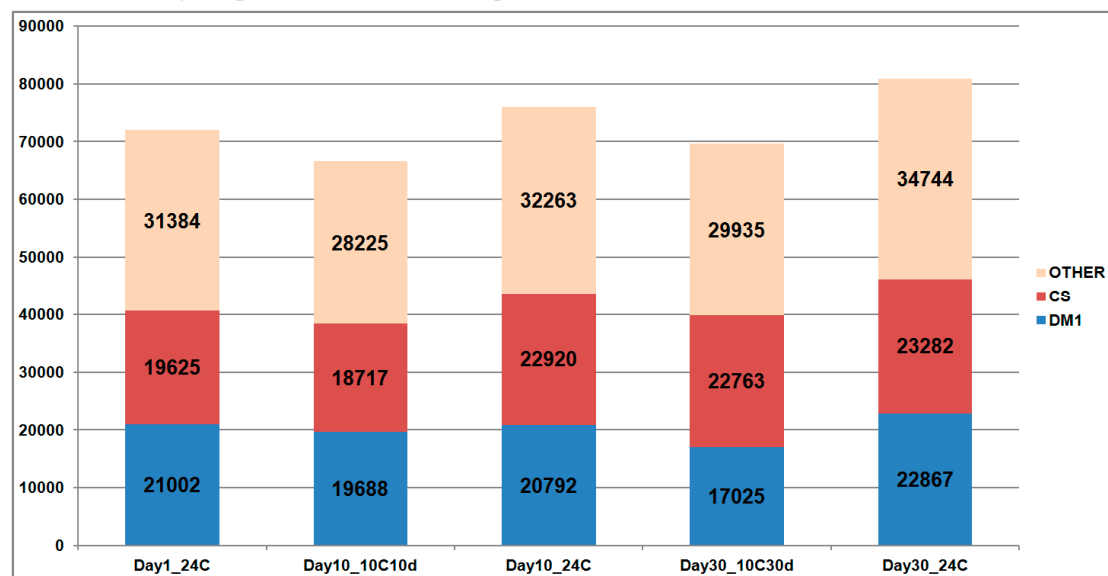


Figure S2 Histogram of CS and DM1 high expression gene stacking under different treatments, horizontal coordinates represent treatment time and temperature, vertical coordinates represent gene number

*Blue represents the number of genes with significantly higher expression of DM1 than CS, red represents the number of genes with significantly higher expression of CS than DM1, and yellow represents the number of genes with insignificant difference in expression of CS and DM1

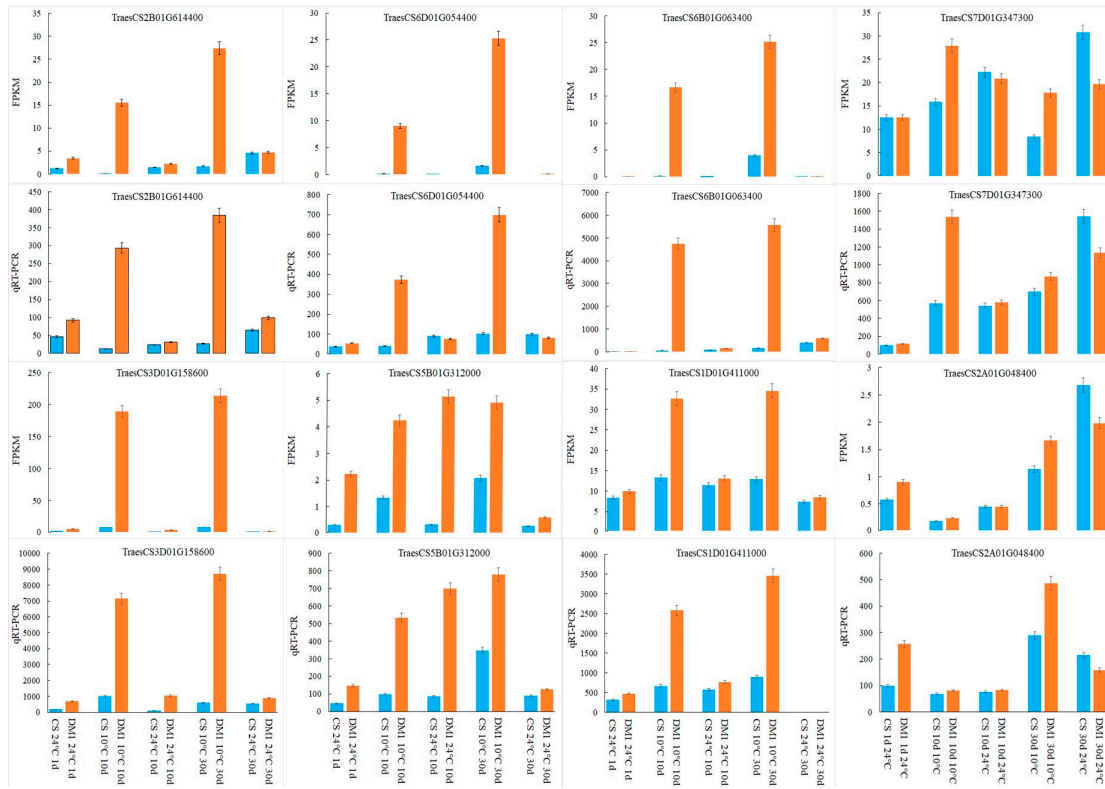


Figure S3. Comparison of RNA-seq results and qRT-PCR analysis of gene expression
*orange represents DM1, blue represents CS

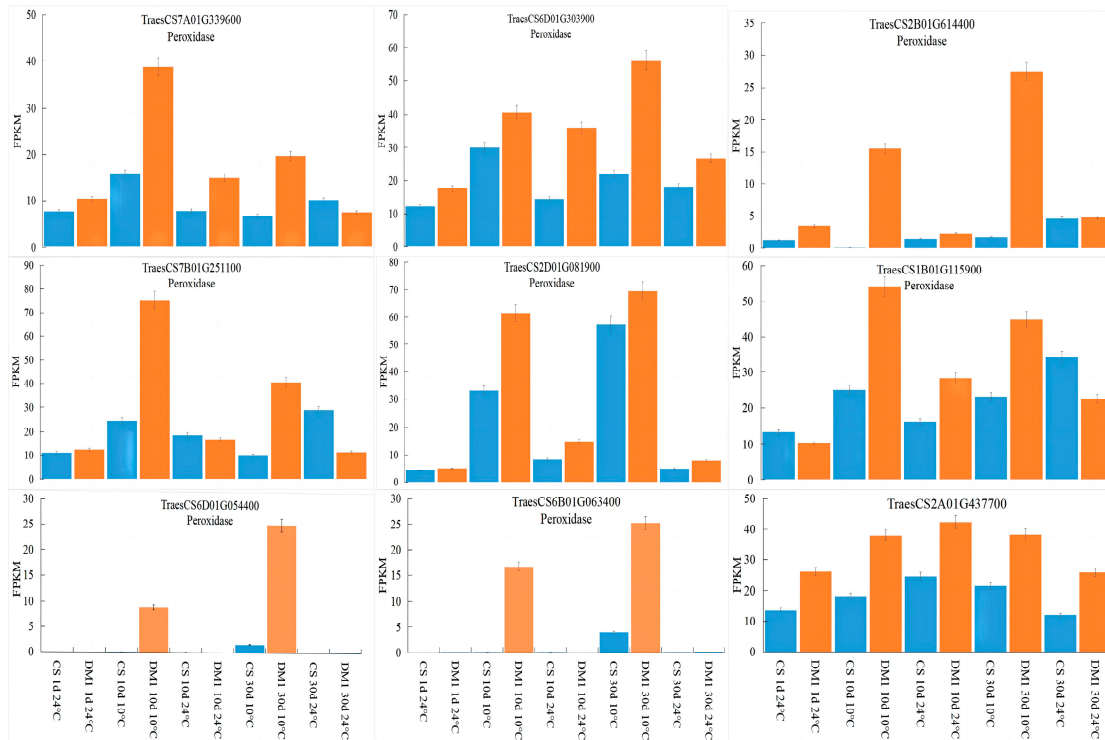


Figure S4. FPKM values of differentially expressed *POD* among wheat varieties under different temperature treatments
*orange represents DM1, blue represents CS

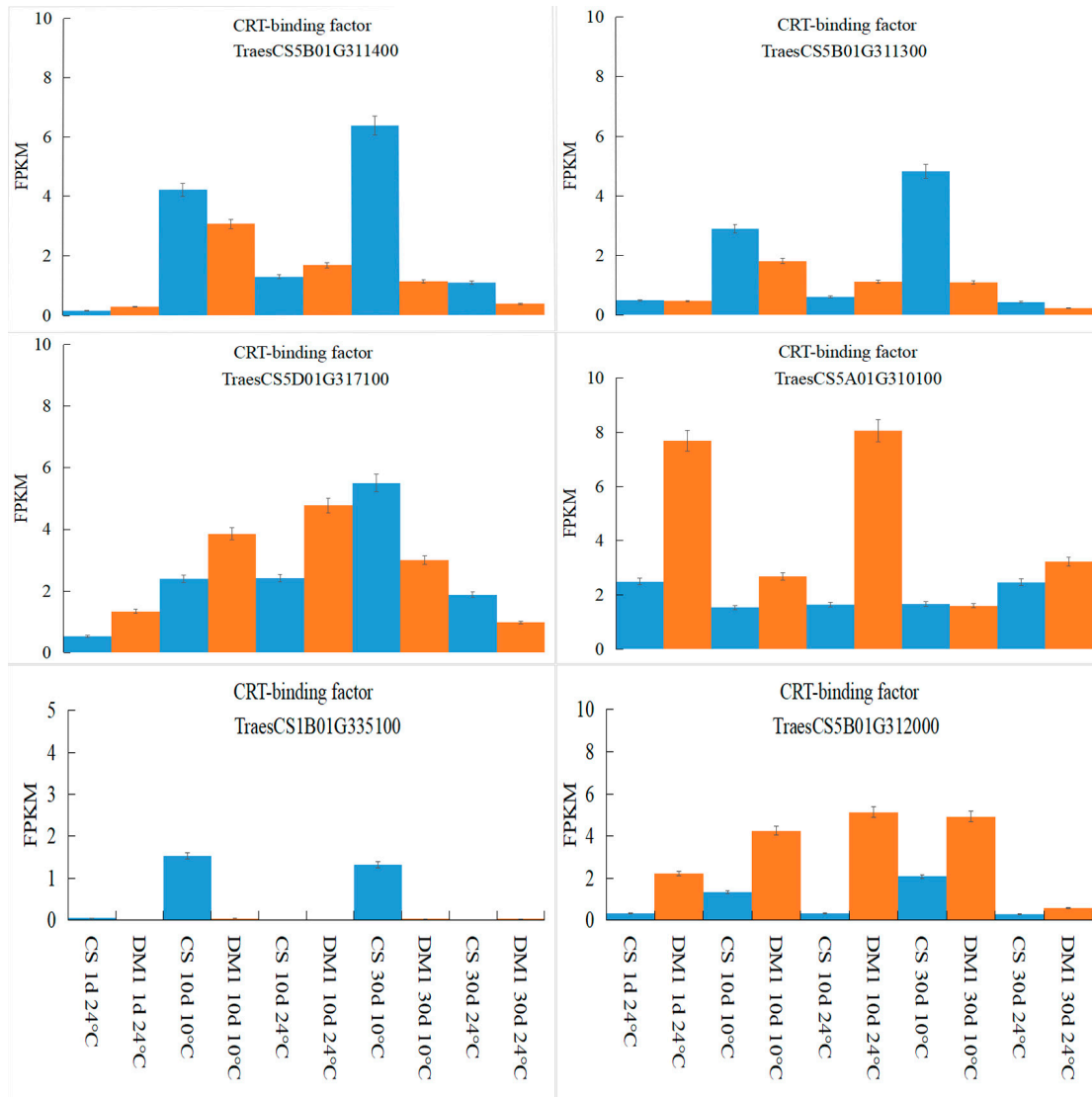


Figure S5. FPKM values of differentially expressed CBF among wheat varieties under different temperature treatments

*orange represents DM1, blue represents CS

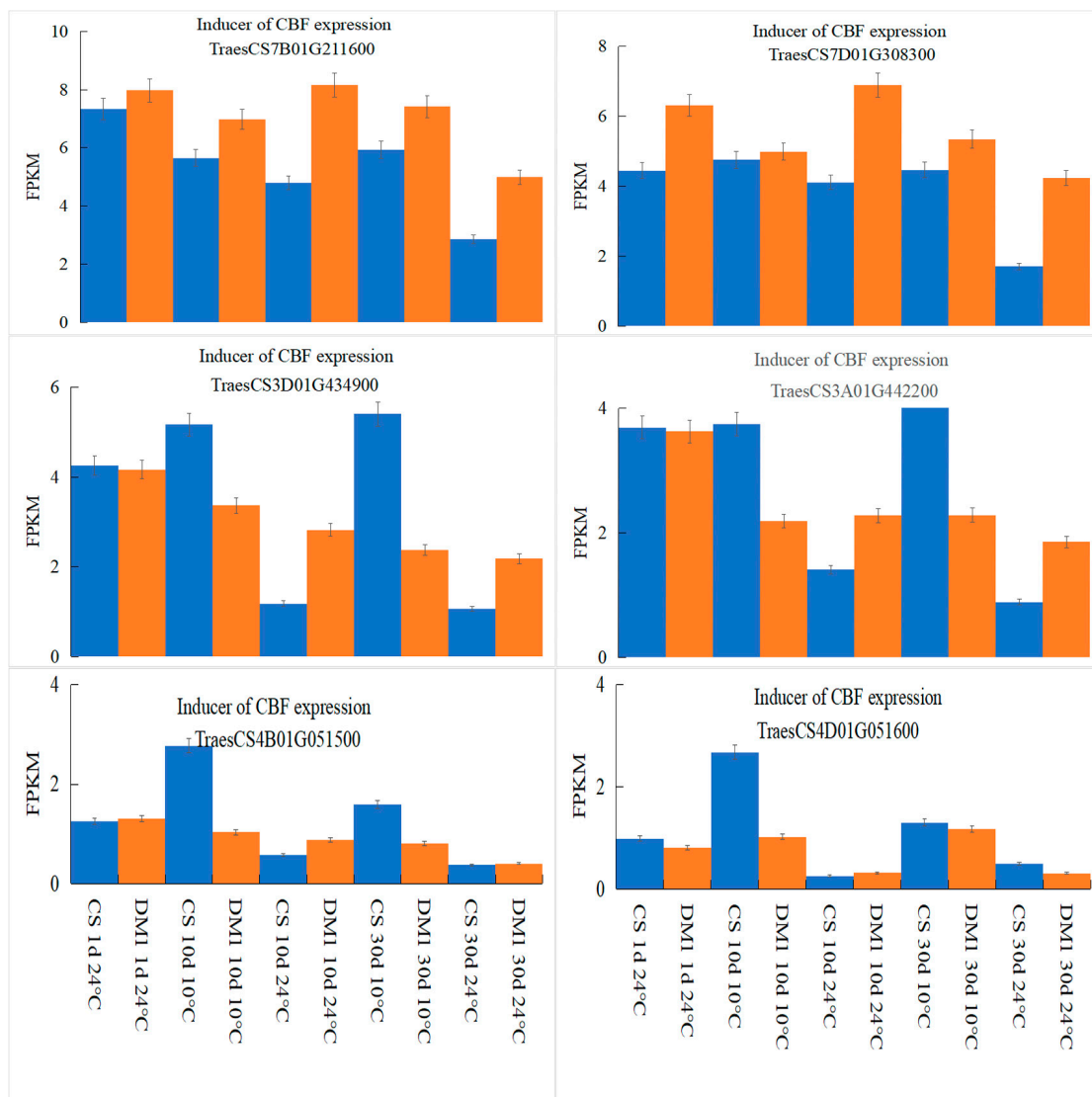


Figure S6. FPKM values of differentially expressed ICE among wheat varieties under different temperature treatments

*orange represents DM1, blue represents CS

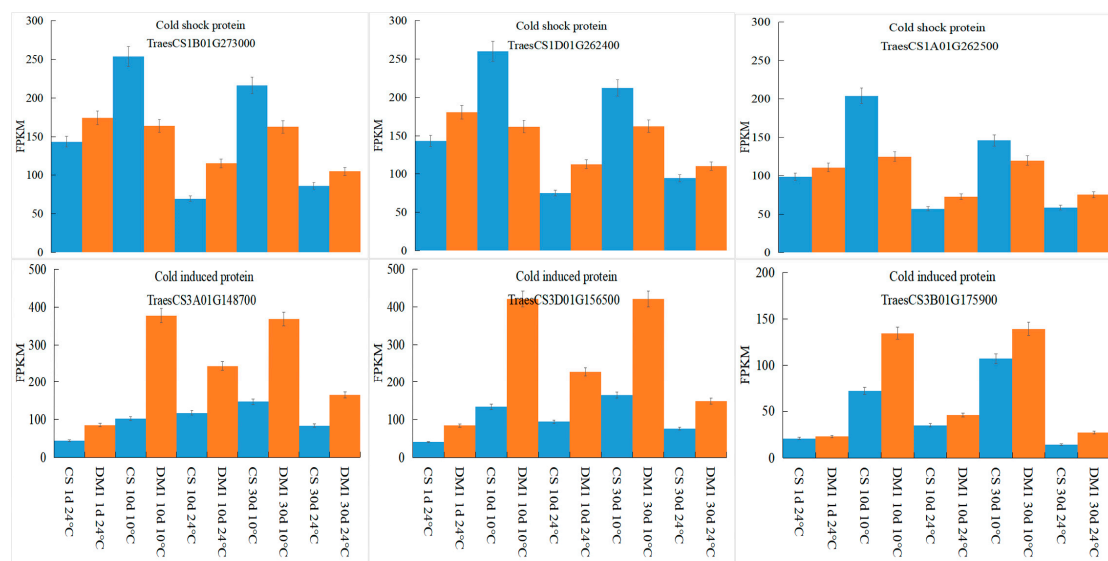


Figure S7. FPKM values of differentially expressed cold shock protein among wheat varieties under different temperature treatments
*orange represents DM1, blue represents CS

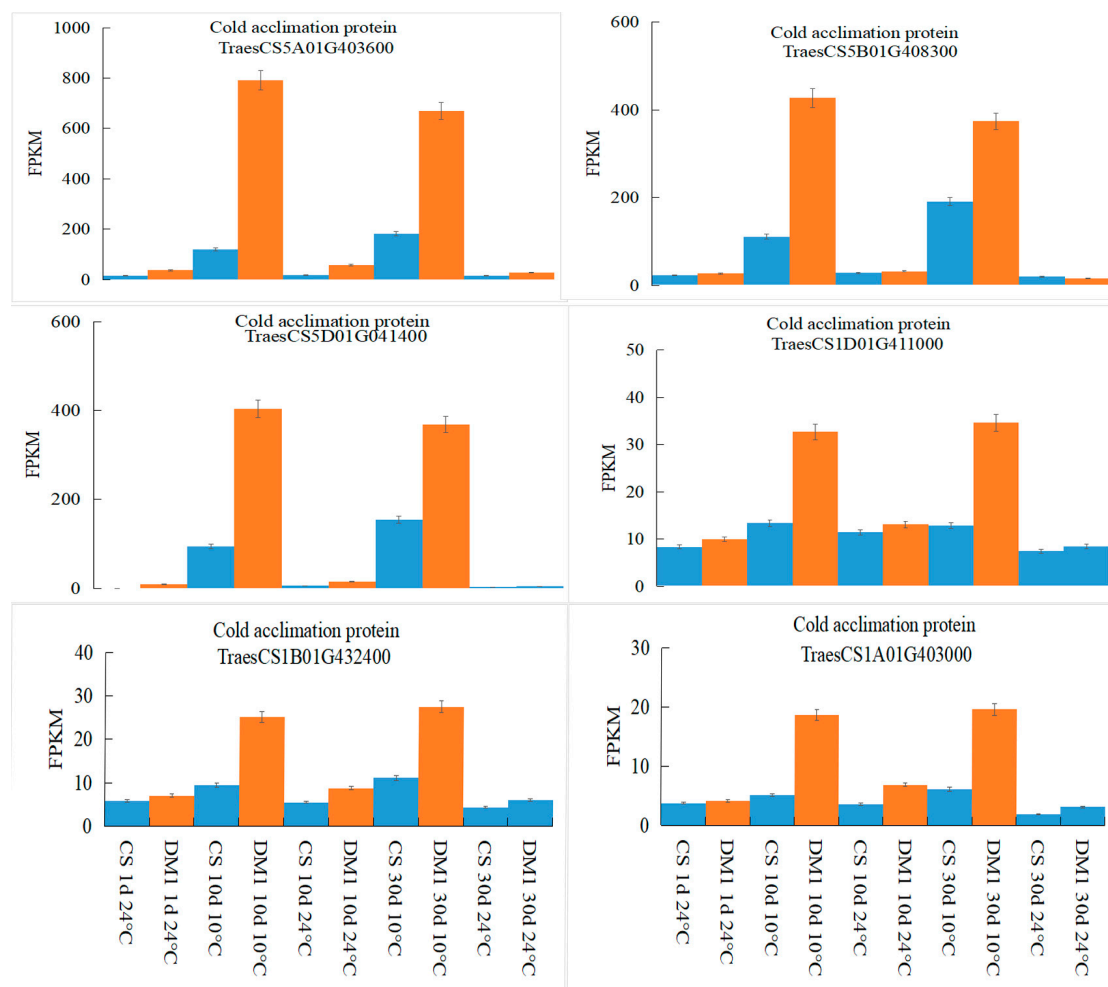


Figure S8. FPKM values of differentially expressed Cold acclimation protein genes among wheat varieties under different temperature treatments

*orange represents DM1, blue represents CS

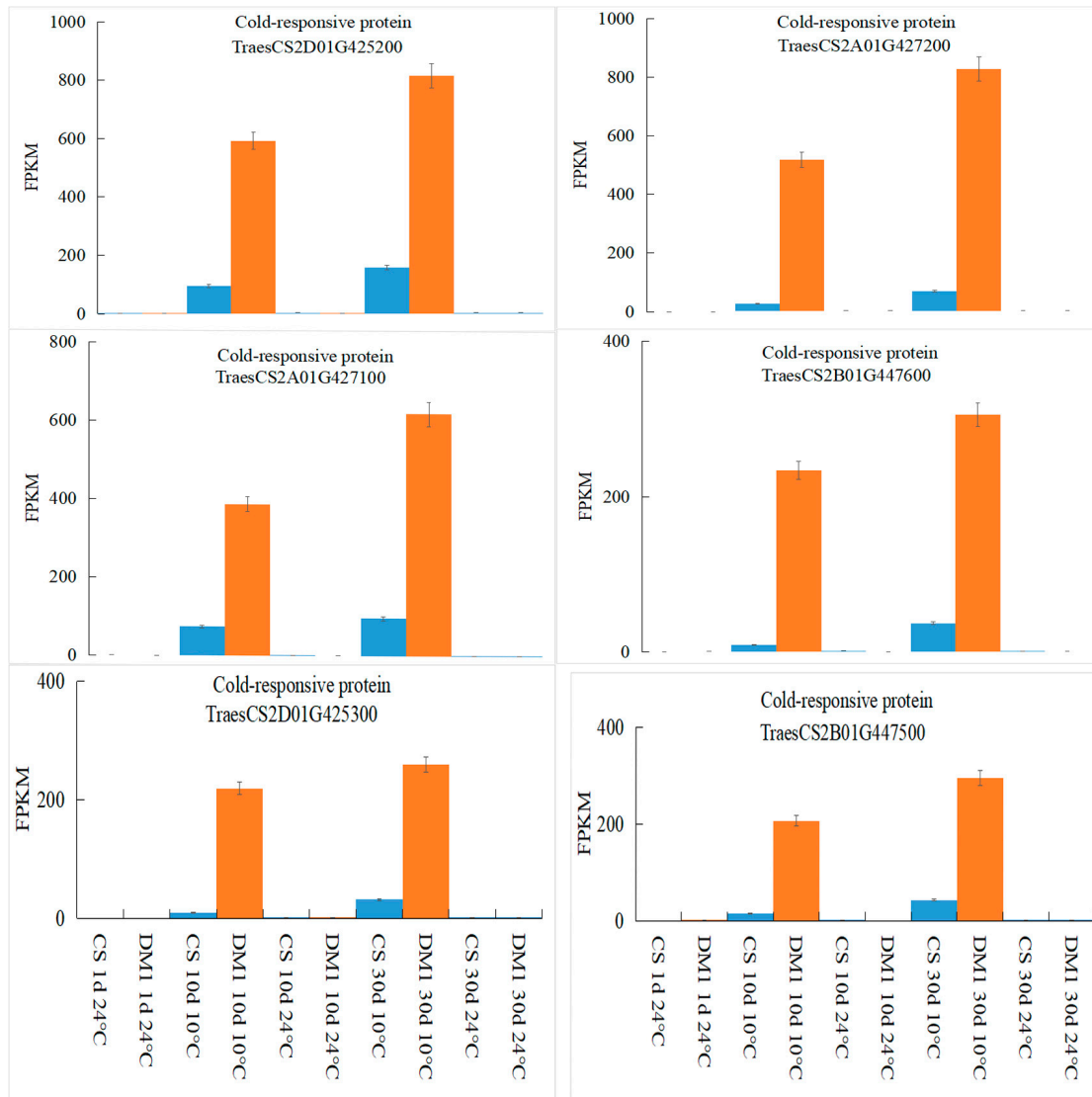


Figure S9. FPKM values of differentially expressed Cold responsive protein gene among wheat varieties under different temperature treatments

*orange represents DM1, blue represents CS

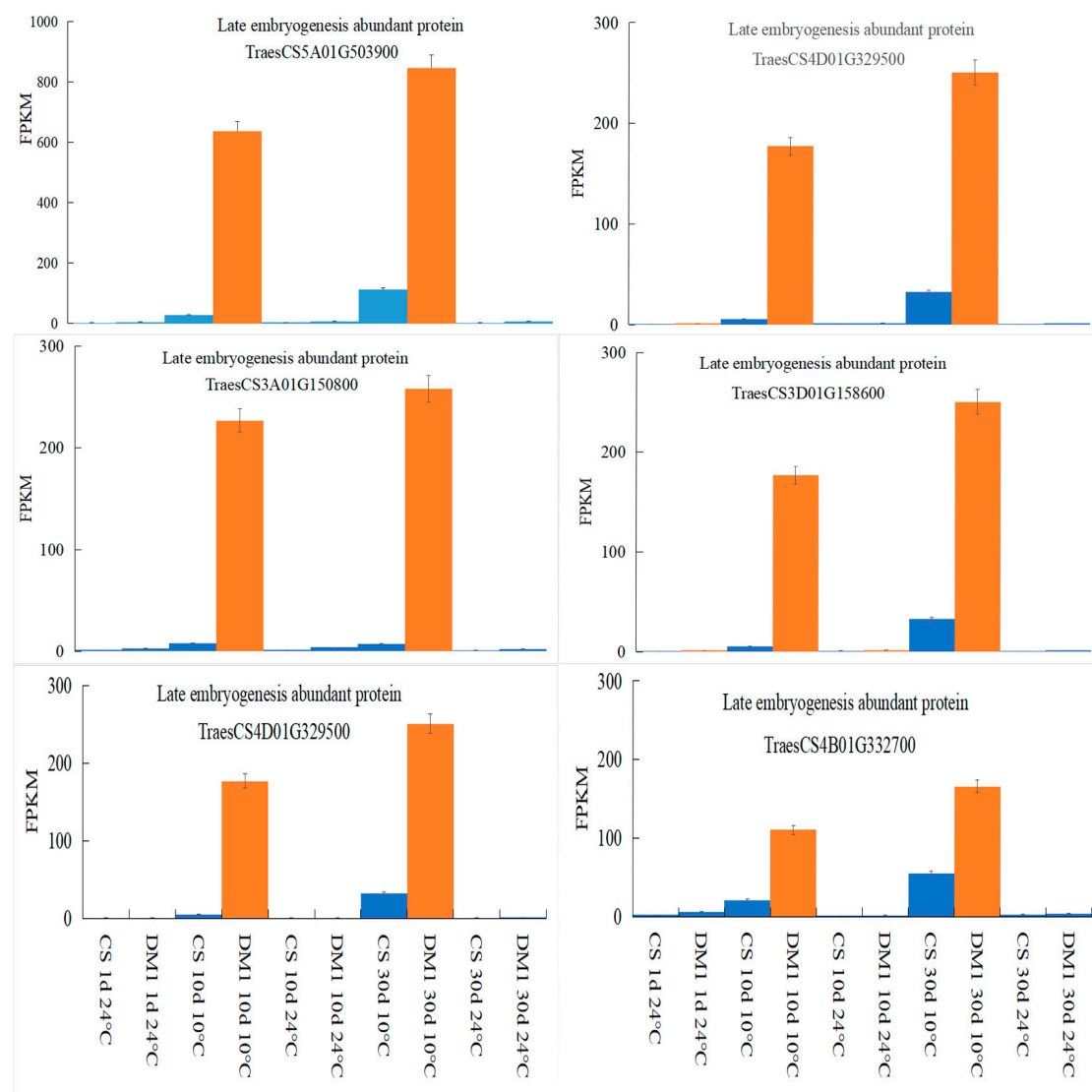


Figure S10. FPKM values of differentially expressed Late embryogenesis abundant protein among wheat varieties under different temperature treatments