

Figure S1. All DEGs in the transcriptome sequencing data in LW and MS pigs at 25°C and 4°C. **(A)** Cluster map of DEGs between LW-25 and MS-25 groups at 25°C. **(B)** Cluster map of DEGs between LW-4 and MS-4 groups at 4°C. **(C)** Cluster map of DEGs between LW-25 and LW-4 groups at 25°C and 4°C. **(D)** Volcanic map of DEGs between LW-25 and MS-25 groups at 25°C. **(E)** Volcanic map of DEGs between LW-4 and MS-4 groups at 4°C. **(F)** Volcanic map of DEGs between LW-25 and LW-4 groups at 25°C and 4°C. **(G)** Venn diagram of 4 groups. **(H)** The number of up-regulated and down-regulated in the LW pig group at 25°C and 4°C. **(I)** The number of up-regulated and down-regulated in MS pig group at 25°C and 4°C. **(J)** GO enrichment analysis of specific DEGs in LW pigs at 25°C and 4°C. **(K)** KEGG pathway classification of specific DEGs in MS pigs at 25°C and 4°C.

Figure S2. Weighted co-expression network analysis. **(A)** The results of soft threshold β calculation indicated a scale-free network linear model, with network connectivity corresponding to different soft thresholds. The blue line represents a correlation coefficient of 0.8, and the red line represents a correlation coefficient of 0.9. **(B)** Clustering of module eigengenes.

Figure S3. qRT-PCR verification on thermogenesis and energy metabolism of longissimus dorsi in LW and MS pigs at 25°C and 4°C.

Figure S4. Protein statistical results. **(A)** Western blot statistical results of candidate genes in longissimus dorsi muscle tissues of LW and MS pigs at 25 ° C and 4 ° C. **(B)** Statistical results of heat production and energy metabolism related proteins in porcine skeletal muscle satellite cells interfered with PRSS8.

Figure S1

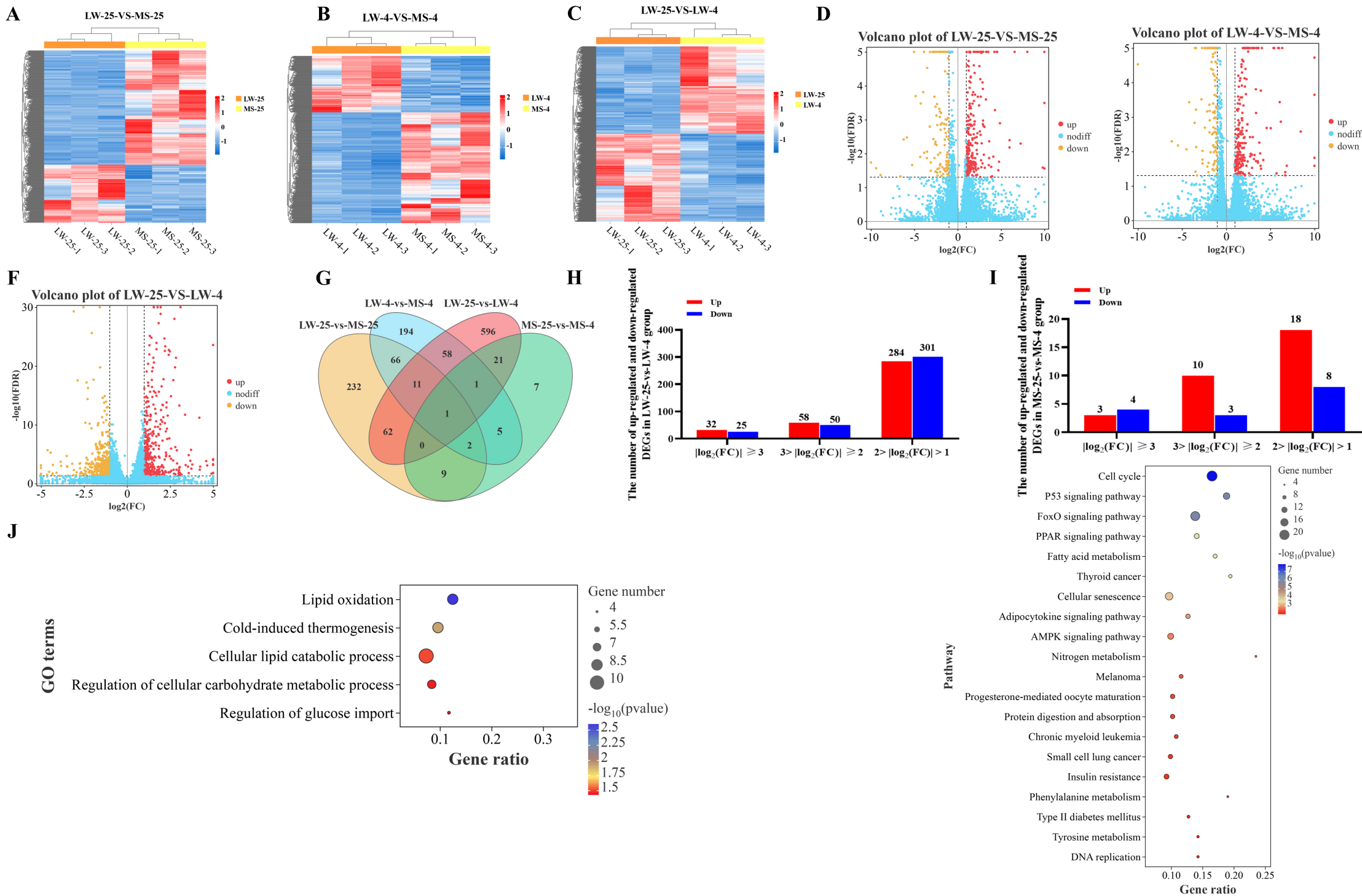


Figure S2

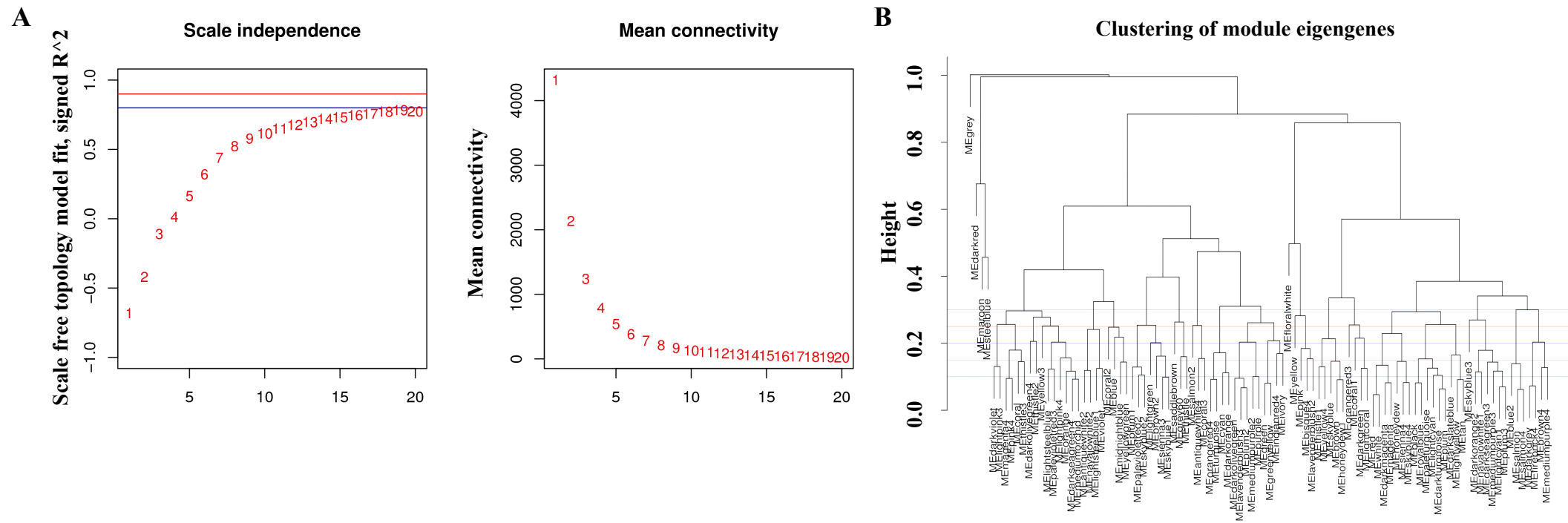


Figure S3

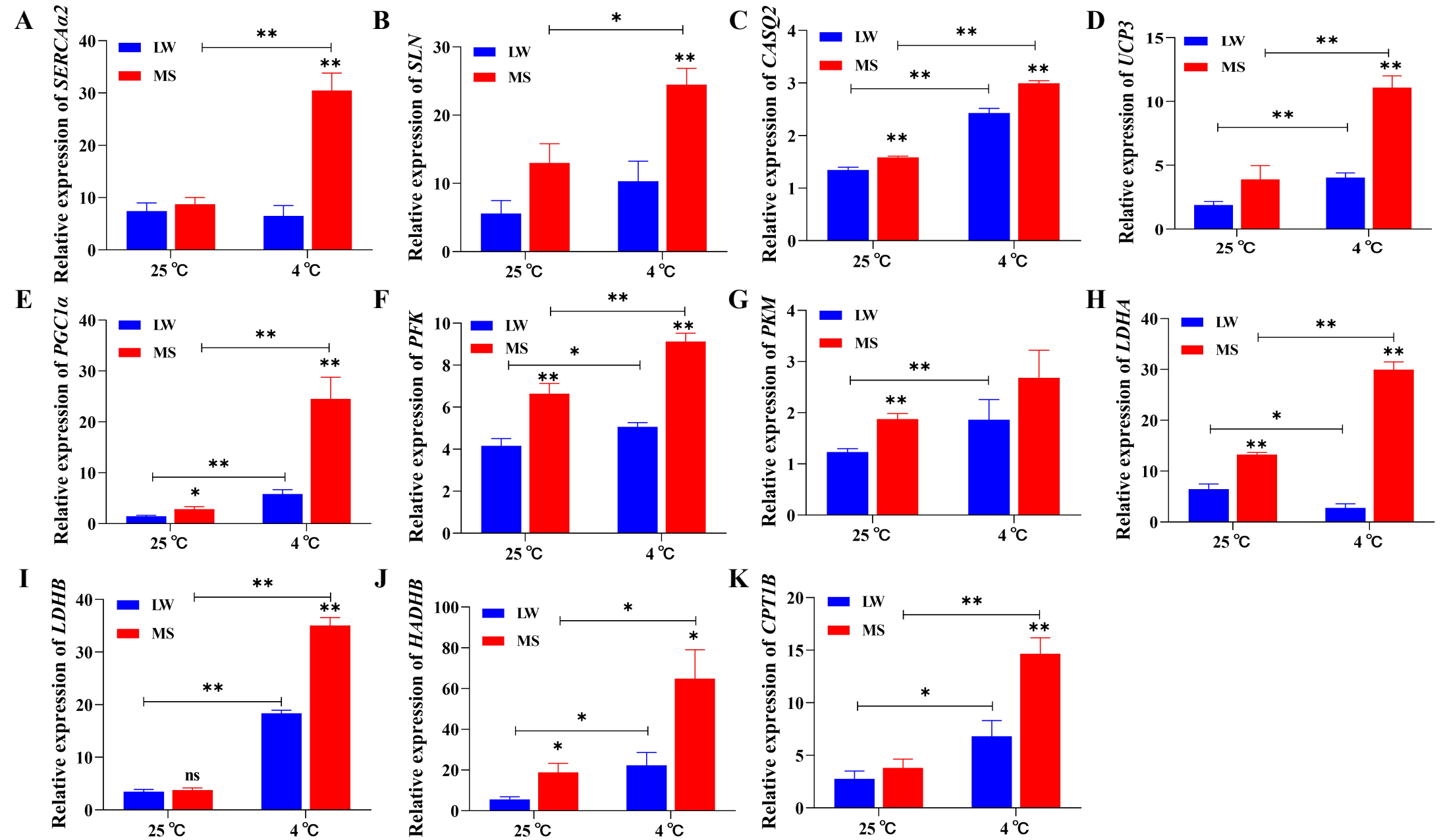
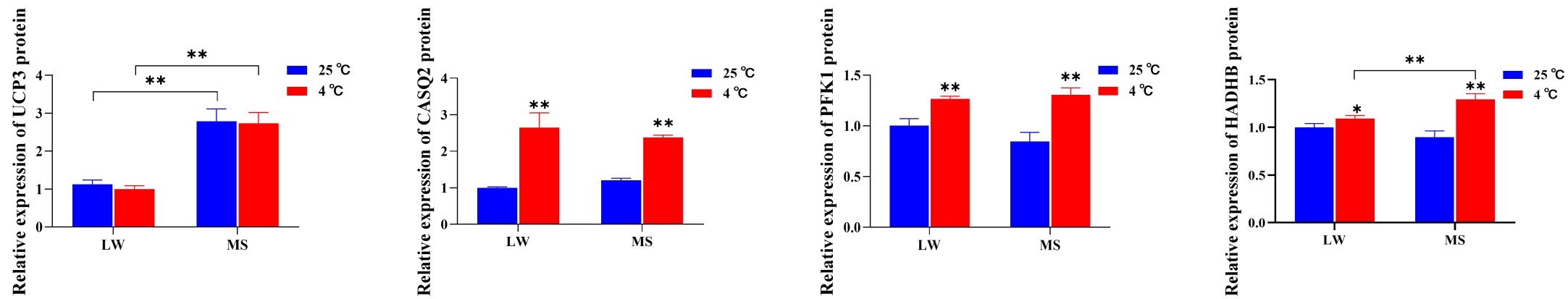


Figure S4

A



B

