

Integration of transcriptomic and metabolomic data reveals key regulatory defense pathways involved in high temperature stress in cucumber (*Cucumis sativus*)

Author:

Yong Yuan, Chuang Li, Xiao Ma, Xitong Zhong, Yuyan Li, Jianyu Zhao, Xiaolan Zhang, Zhaoyang Zhou*.

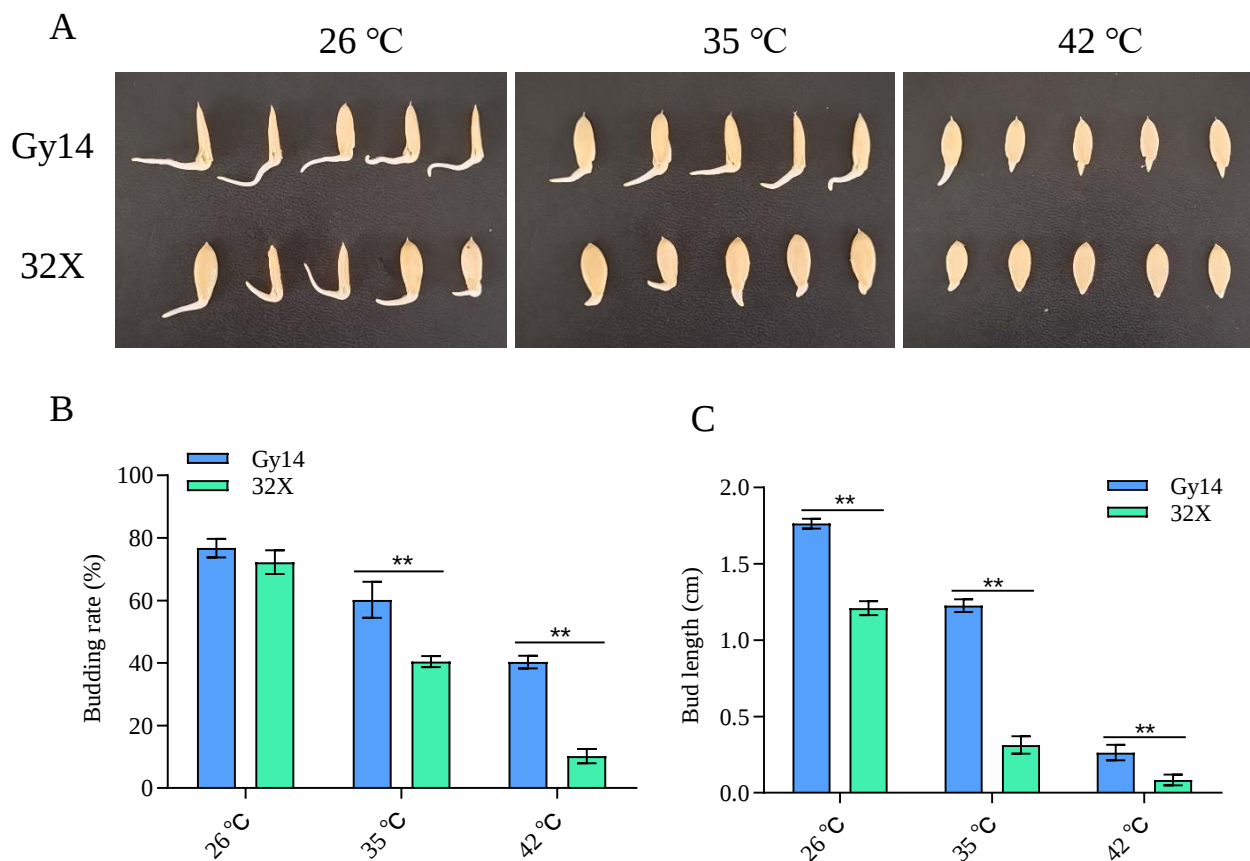


Fig S1. Seeds germination of Gy14 and 32X cucumbers under high-temperature stress. (A) The seeds germination of Gy14 and 32X under 35°C and 42°C for 3 days. (B) Germination rate and the length of roots (C) after 3 days of high-temperature stress.

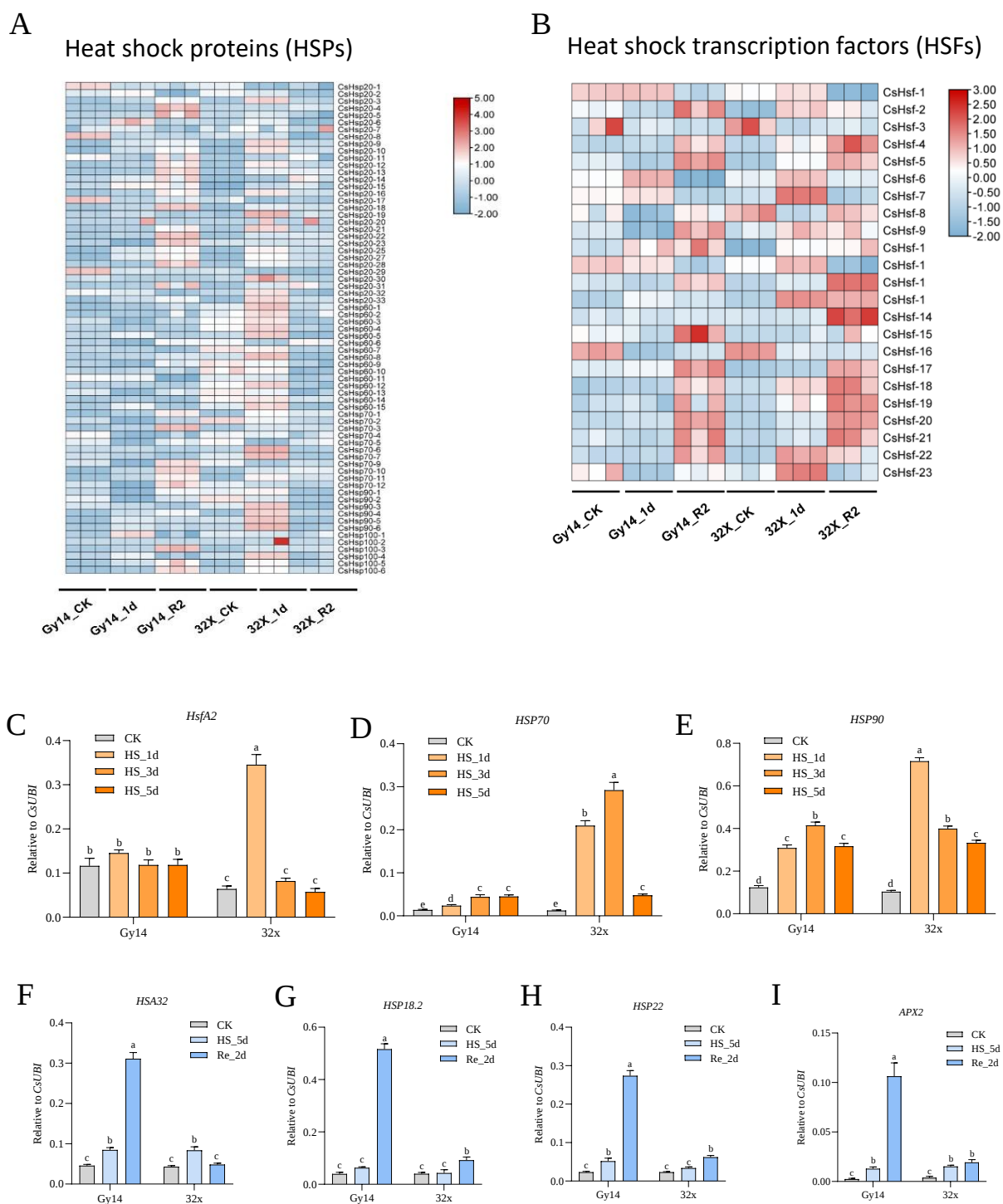


Fig S2. Expression analysis of heat stress induced genes in Gy14 and 32X. (A-B) Heatmap of heat shock transcription factors (A) and co-expressed transcription factors with heat stress memory genes (B) in Gy14 and 32X after high temperature stress. (C-E) RT-qPCR analysis of heat stress response genes. (F-I) RT-qPCR analysis of heat stress memory genes.

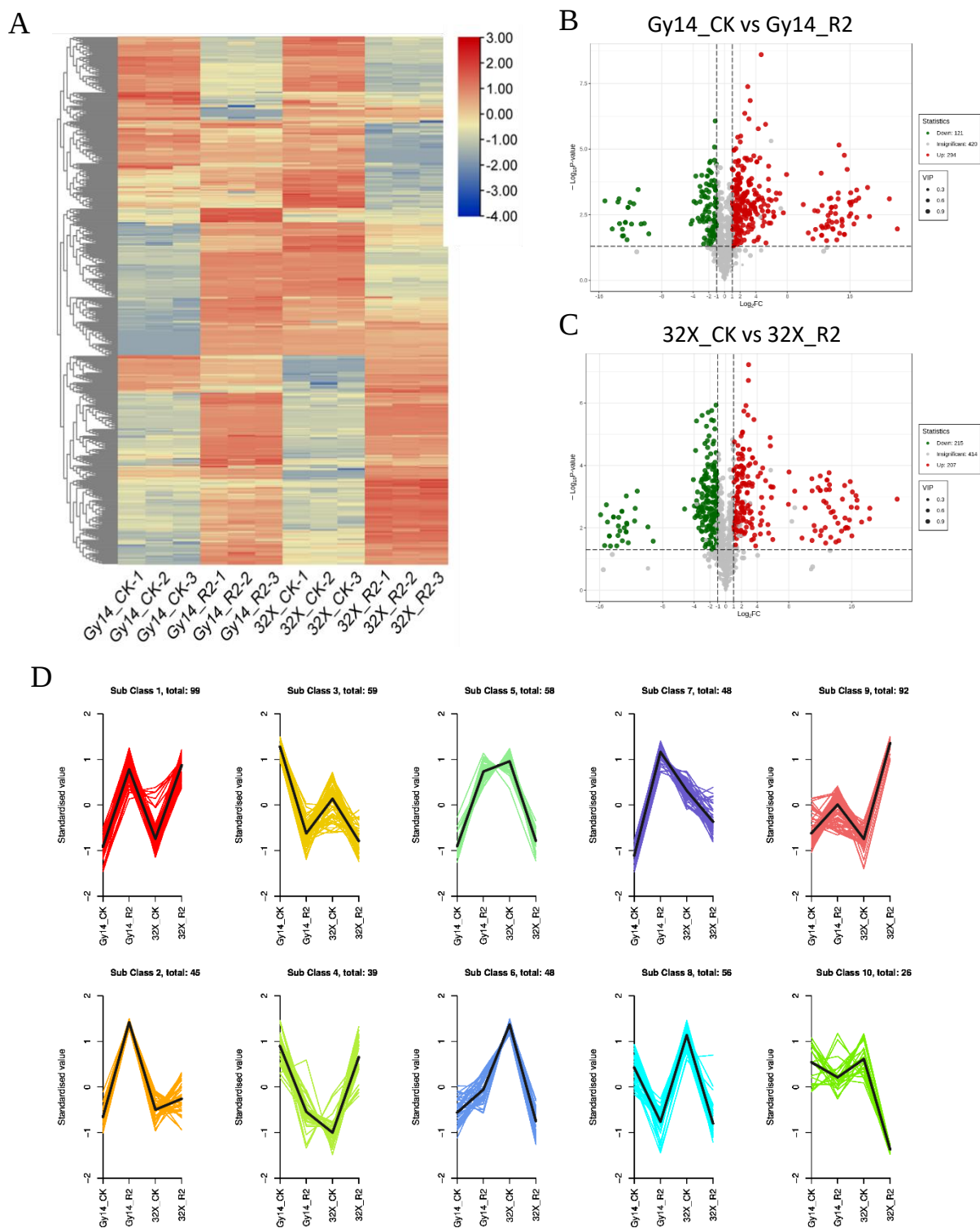


Fig S3. Secondary and primary metabolism of Gy14 and 32X cucumber leaves under high temperature stress. (A) Heatmap of metabolites in Gy14 and 32X. (B-C) Differentially accumulated metabolites in Gy14 (B) and 32X (C). (D) Clustering grouped the expression profiles of the metabolites in the Gy14 and 32X.

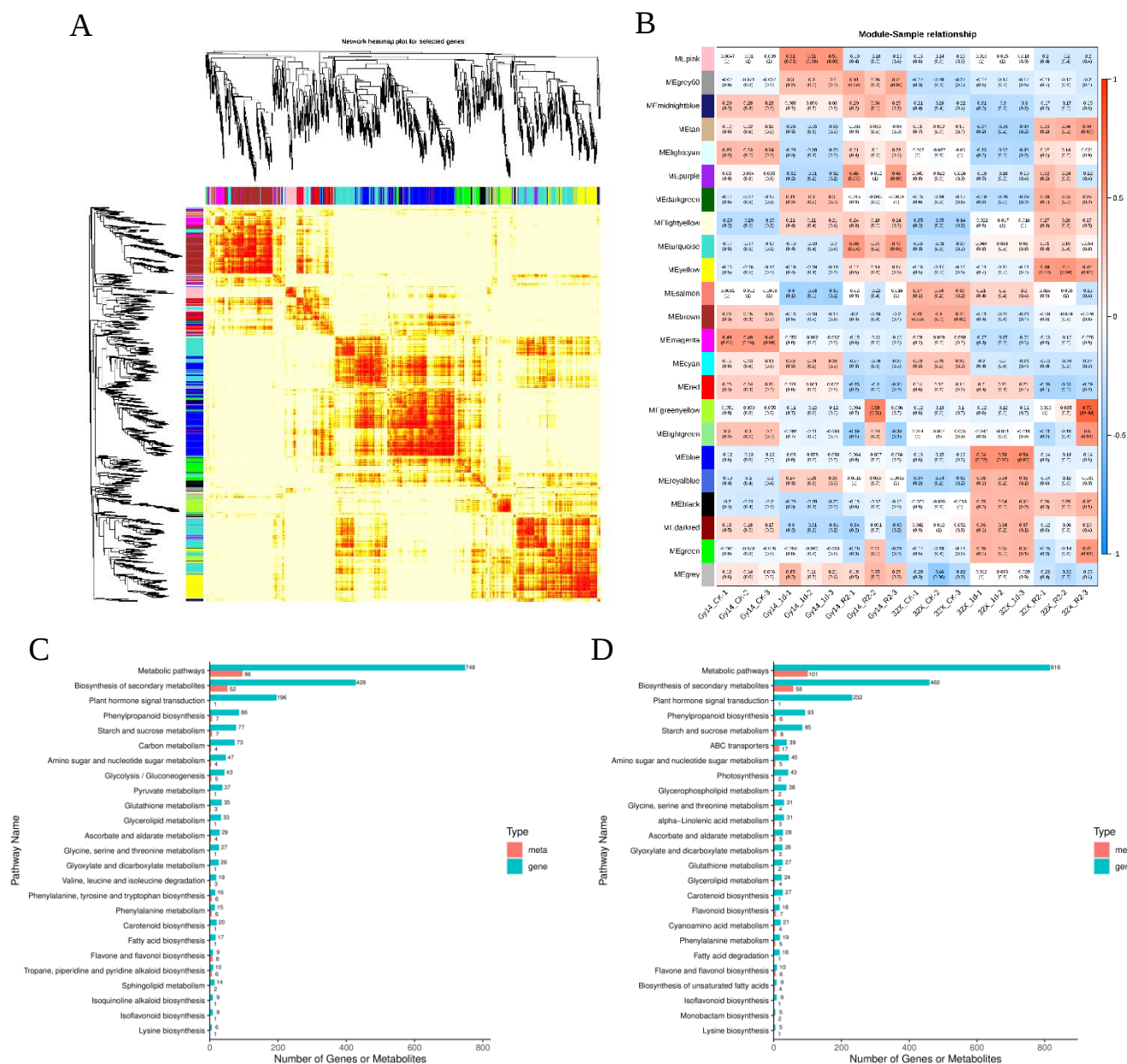


Fig S4. Co-expression network of cucumber response to high temperature stress. (A) Clustering tree based on the correlation between gene expression levels. (B) Heat map showing the module sample relationship. Each row represents a gene module. The red color indicates a positive correlation between the cluster and the tissue. The blue color indicates a negative correlation. (C-D) GO classification of DEGs and DAMs in Gy14 (C) and 32X (D).

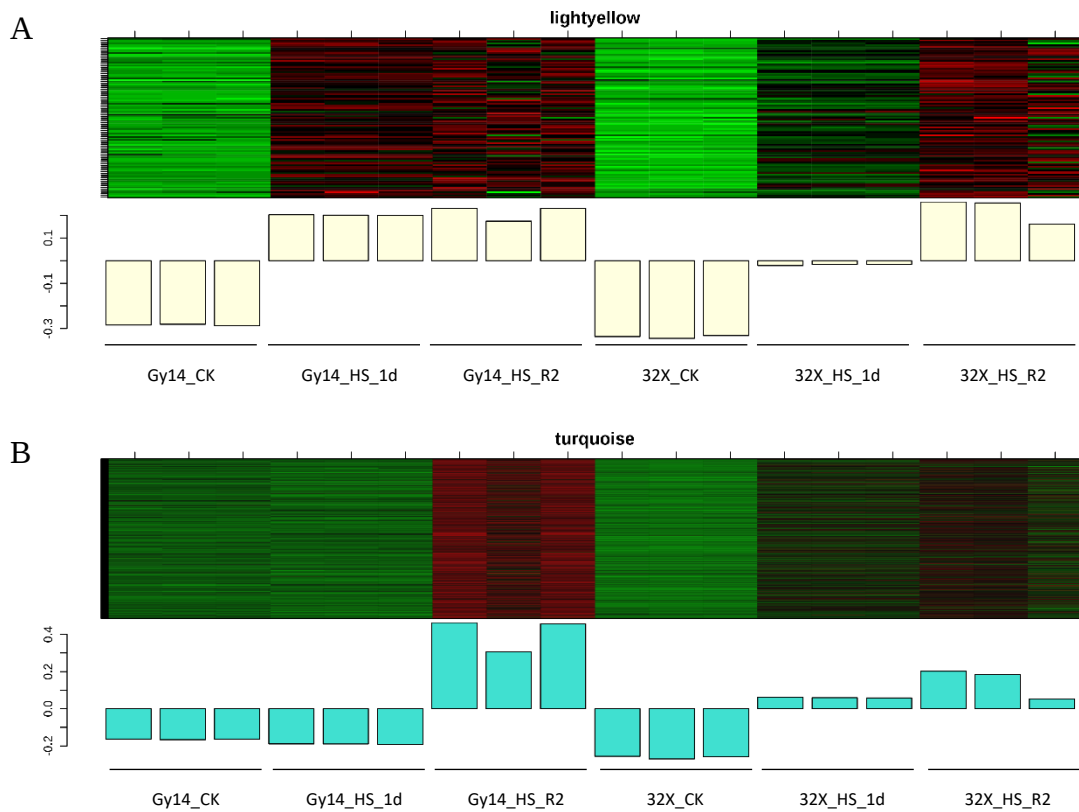


Fig. S5 The interaction of gene and metabolite in response to high temperature stress. (A-B) Heatmap of modular gene expression patterns which are deeply associated with high temperature stress.

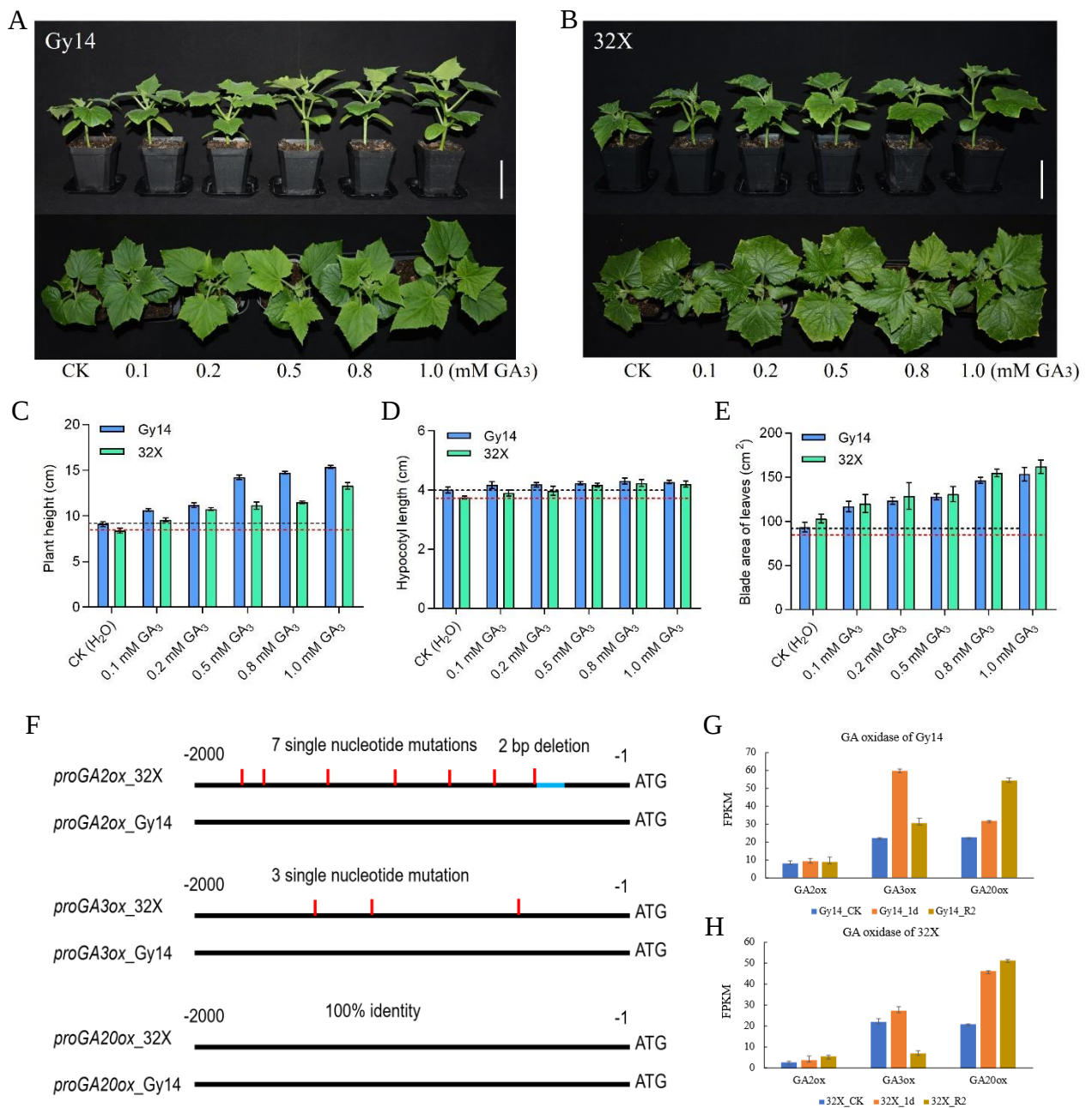


Fig. S6 Gibberellins promote cucumber seedling growth. (A-B) The representative phenotype of Gy14 (A) and 32X (B) seedlings treated with different concentrations of GA₃. (C-E) Calculated the plant height (C), hypocotyl length (D), and blade area of leaves (E) after GA₃ application. (F-H) Promoter sequence (F) and expression analysis of *GA-oxide* genes in Gy14 (G) and 32X (H).

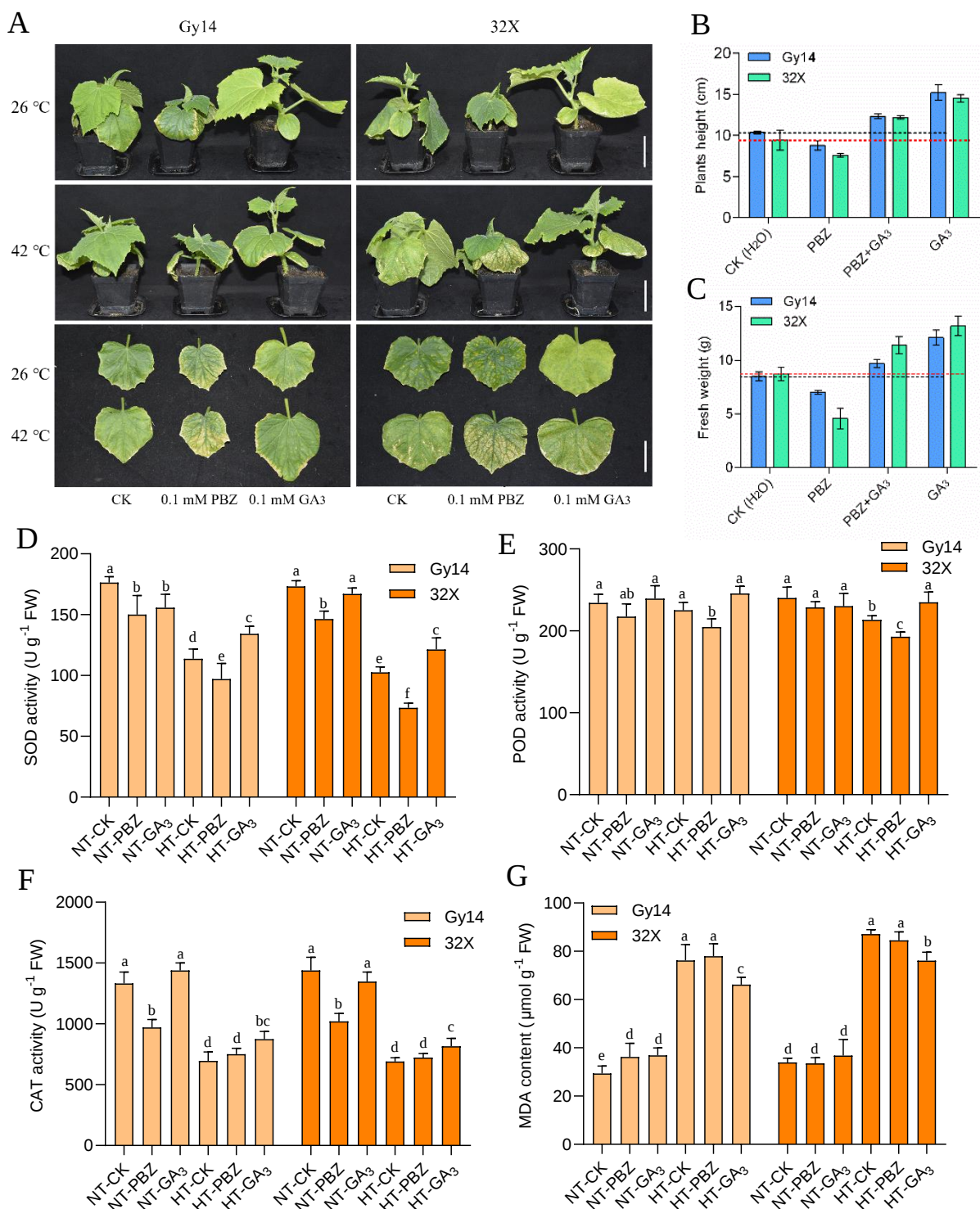


Fig. S7 Inhibition of endogenous gibberellin synthesis leading to plants being more sensitive to high temperature stress. (A) The representative phenotype of PBZ treatment cucumbers. (B-C) Calculated the plant height (B) and fresh weight (C) of Gy14 and 32X under high temperature stress after PBZ treatment. (D-G) In vitro antioxidant activities of Gy14 and 32X, (D) SOD activity, (E) POD activity, (F) CAT activity, and (G) MDA content.