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Integration of transcriptome and metabolome reveals key regulatory defense pathways involved in high temperature stress in cucumber (*Cucumis sativus* L.)

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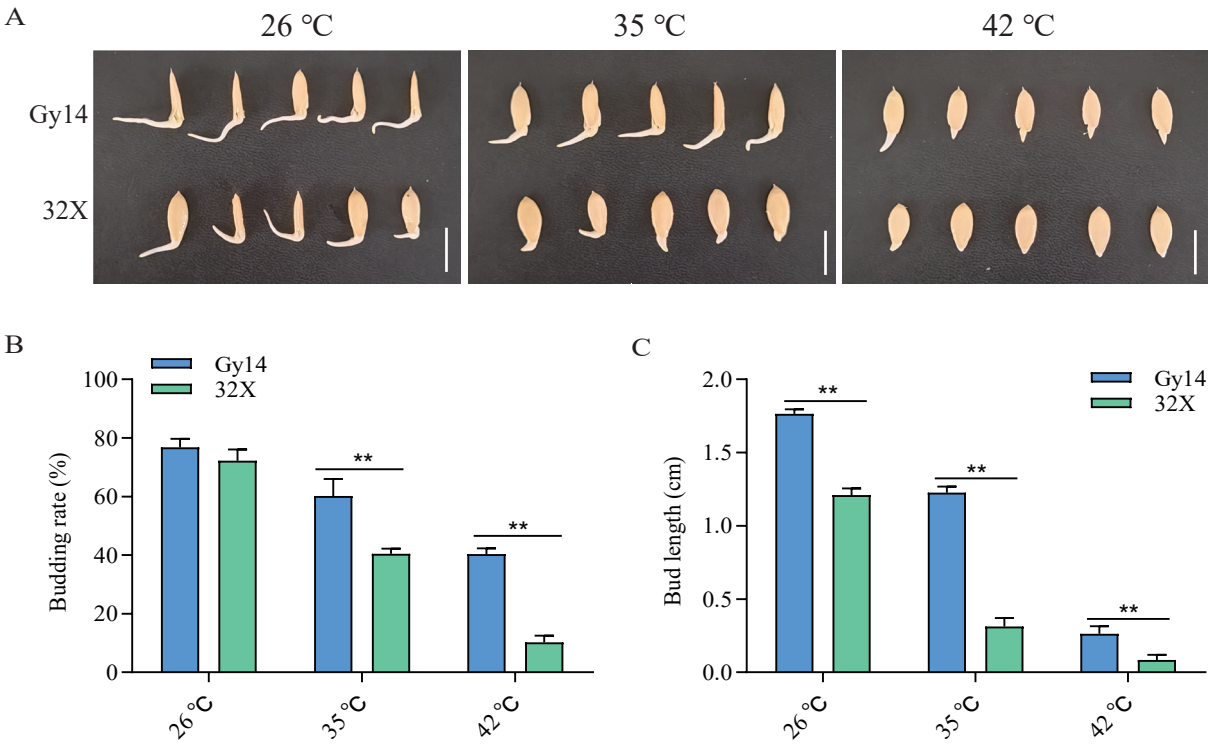


Fig S1. Seeds germination of Gy14 and 32X cucumbers under high temperature stress. (A) The seeds germination of Gy14 and 32X under 35℃ and 42℃ for 3 days. (B) Germination rate and the length of roots (C) after 3 days of high-temperature stress. Bar, 1 cm.

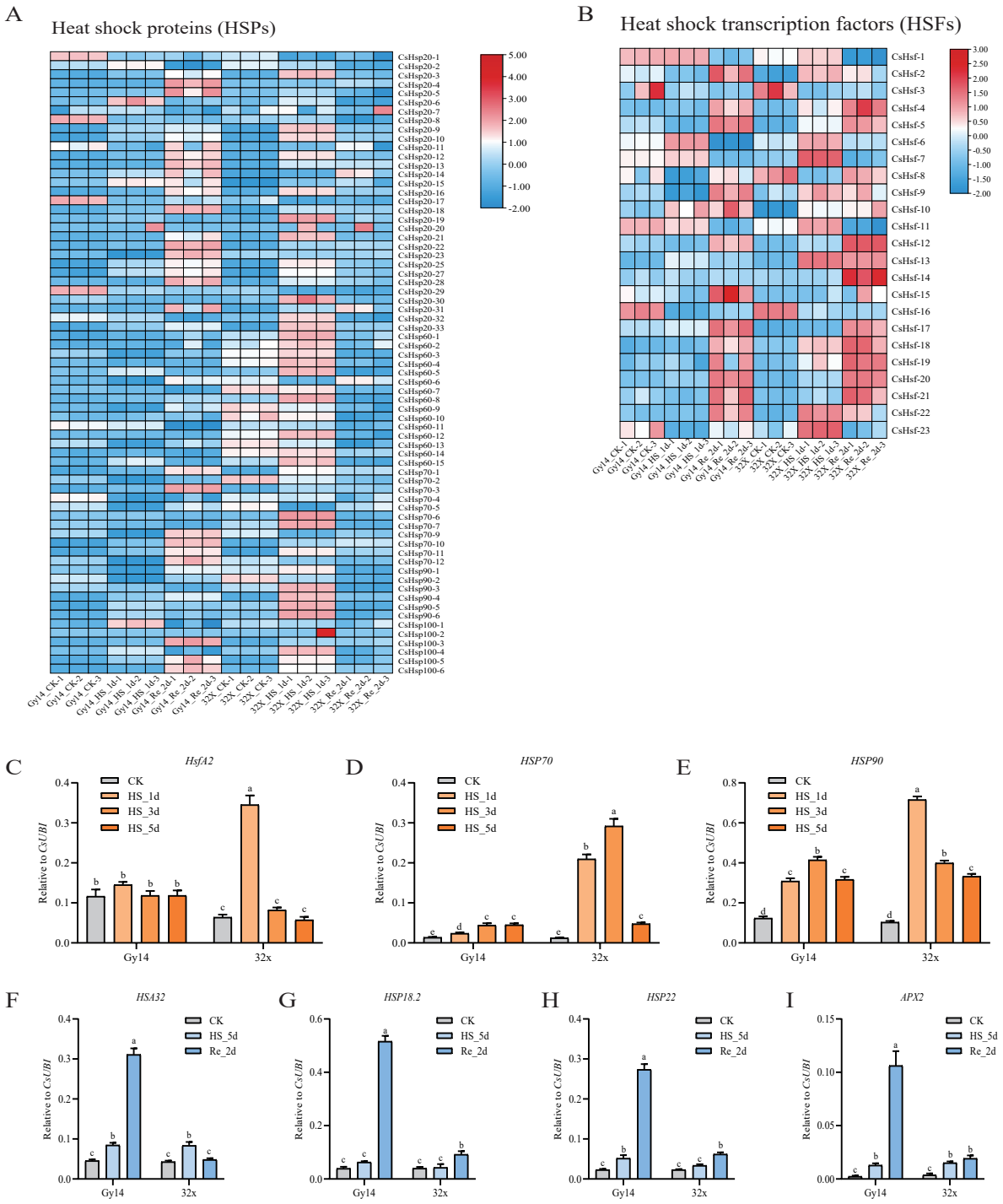


Fig S2. Expression analysis of heat stress induced genes in Gy14 and 32X. (A-B) Heatmap of heat shock transcription factors (A) and heat shock transcription factors (HSFs) (B) in Gy14 and 32X after high temperature stress. (C-E) RT-qPCR analysis of heat stress response genes in Gy14 and 32X at short heat stress conditions. (F-I) RT-qPCR analysis of heat stress memory genes in Gy14 and 32X at long-term of heat stress and after 2 days of recovery conditions. Different letters indicate significant differences relative to the CK at $P < 0.05$.

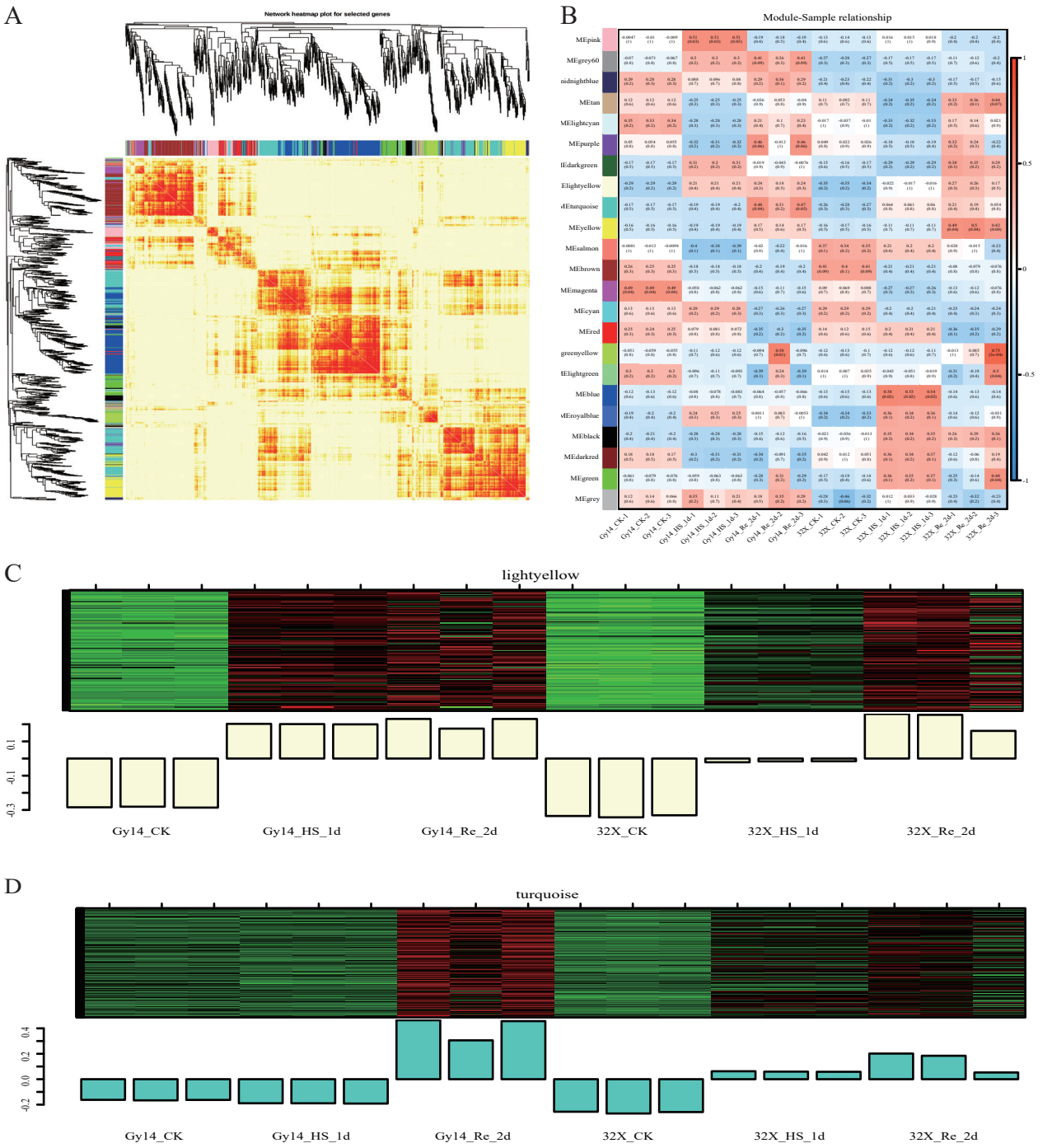


Fig S3. Co-expression network of cucumber response to high temperature stress. (A) Clustering tree based on the correlation between gene expression levels. (B) Heatmap showing the module sample relationship. Each row represents a gene module. The red color indicates a positive correlation between the cluster and the tissue. The blue color indicates a negative correlation. (C-D) Heatmap of modular gene expression patterns which are deeply associated with high temperature stress.

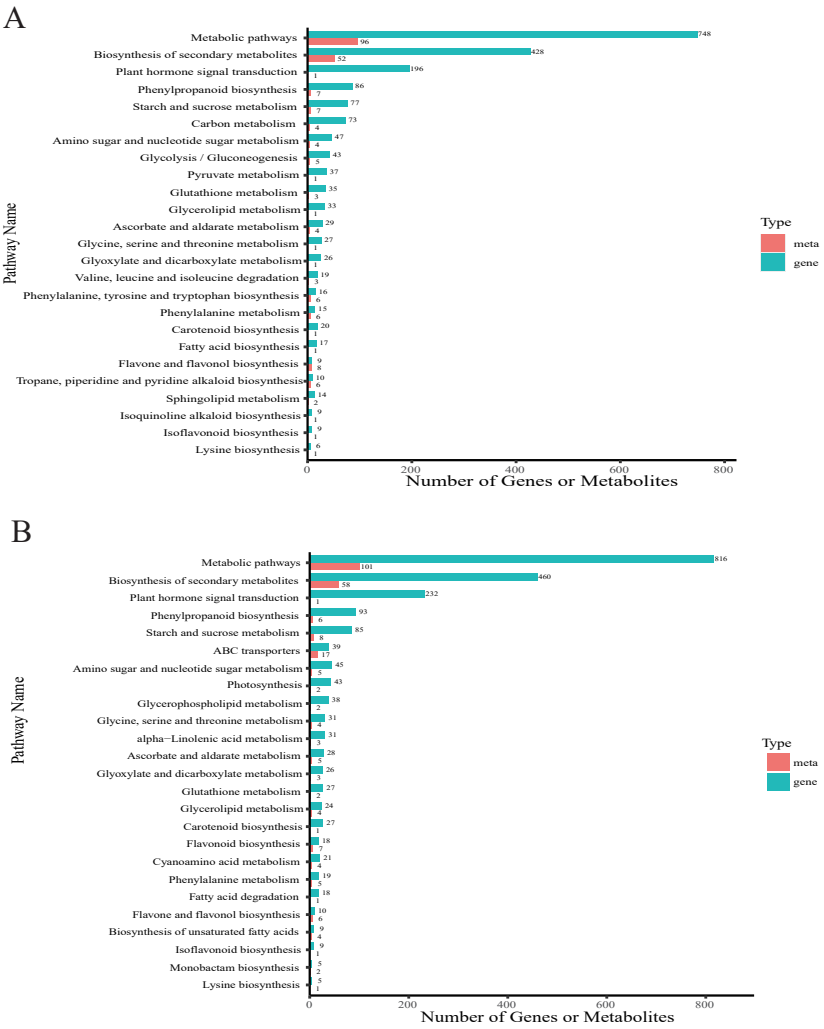


Fig S4. GO classification of DEGs and DAMs in cucumber seedling after high temperature stress. (A) GO classification showing the DEGs and DAMs in Gy14. (B) GO classification showing the DEGs and DAMs in 32X. Data are filtered out from transcriptome and metabolome.

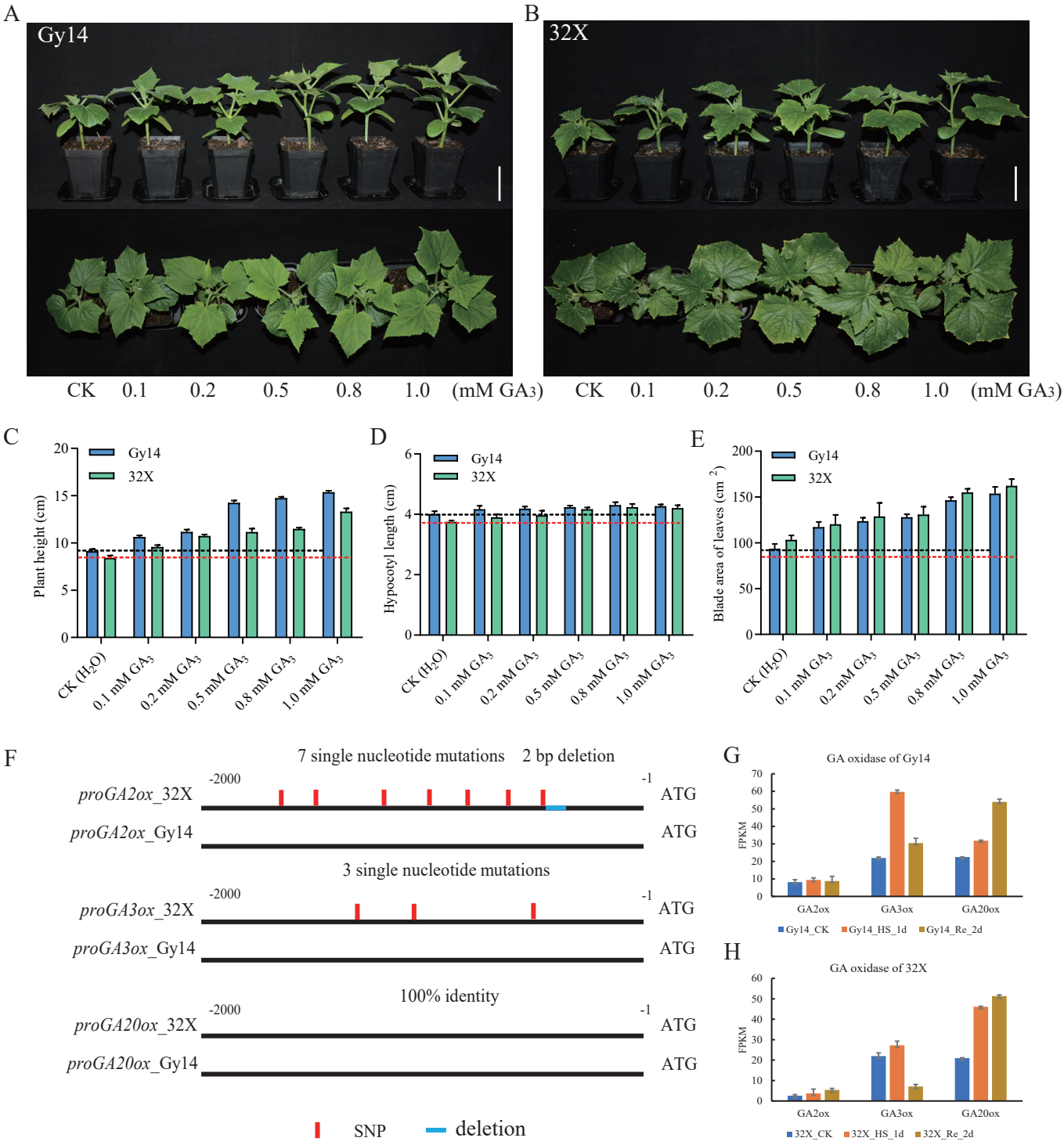


Fig. S5 Gibberellins improve cucumber seedling growth. (A-B) The representative phenotype of Gy14 (A) and 32X (B) seedlings treated with different concentrations of GA_3. Bar, 5 cm. (C-E) Calculated the cucumber seedling of plant height (C), hypocotyl length (D), and blade area of leaves (E) after GA_3 application. (F-H) Promoter sequence (F) and expression analysis of GA-oxide genes in Gy14 (G) and 32X (H).

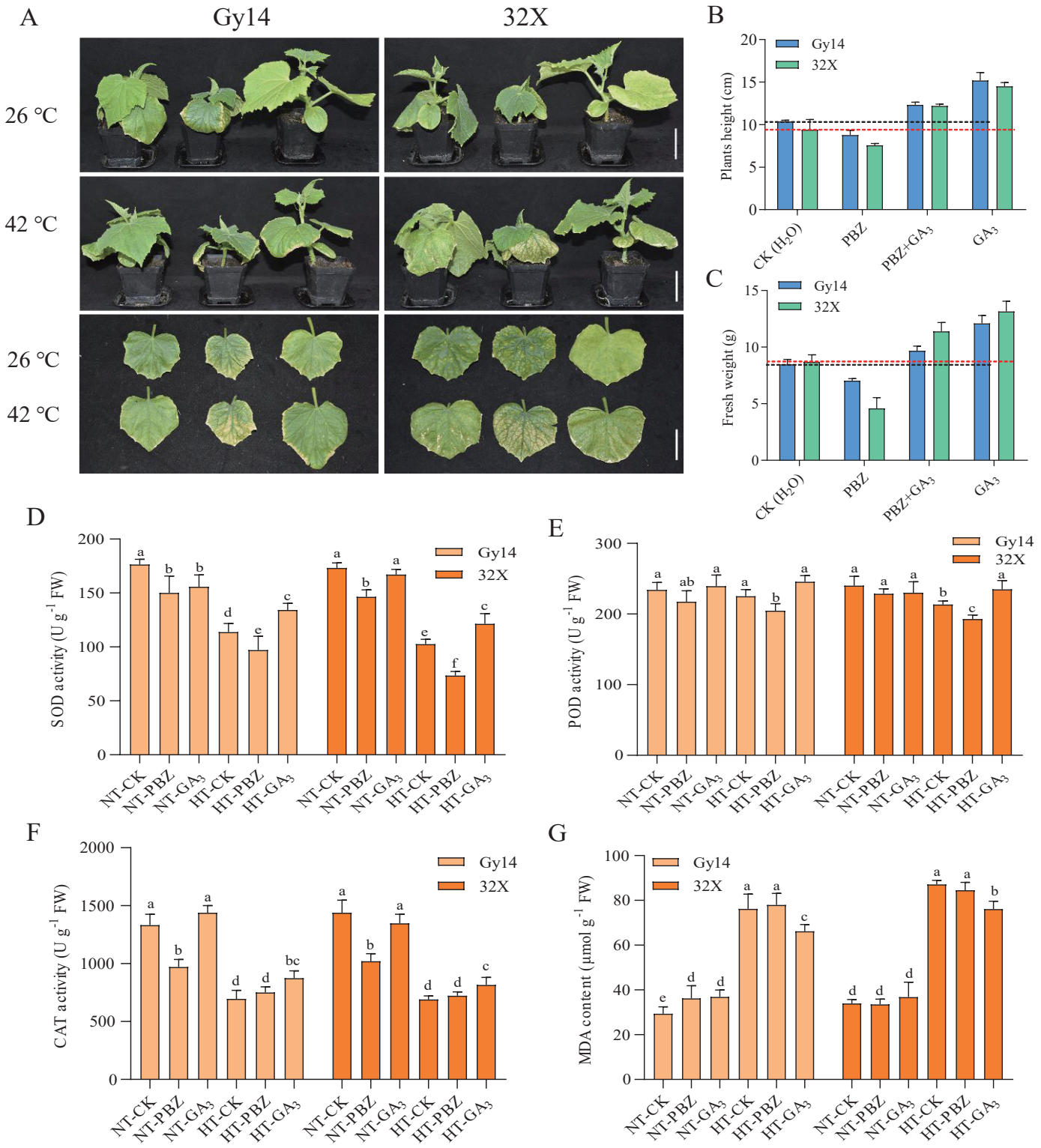


Fig. S6 Inhibition of endogenous gibberellin synthesis leading to plants being more sensitive to high temperature stress. (A) The representative phenotype of PBZ treatment cucumbers. (B-C) Calculated the plant height (B) and fresh weight (C) of Gy14 and 32X under high temperature stress after PBZ treatment. (D-G) In vitro antioxidant activities of Gy14 and 32X, (D) SOD activity, (E) POD activity, (F) CAT activity, and (G) MDA content. Different letters indicate significant differences relative to the CK at $P < 0.05$.