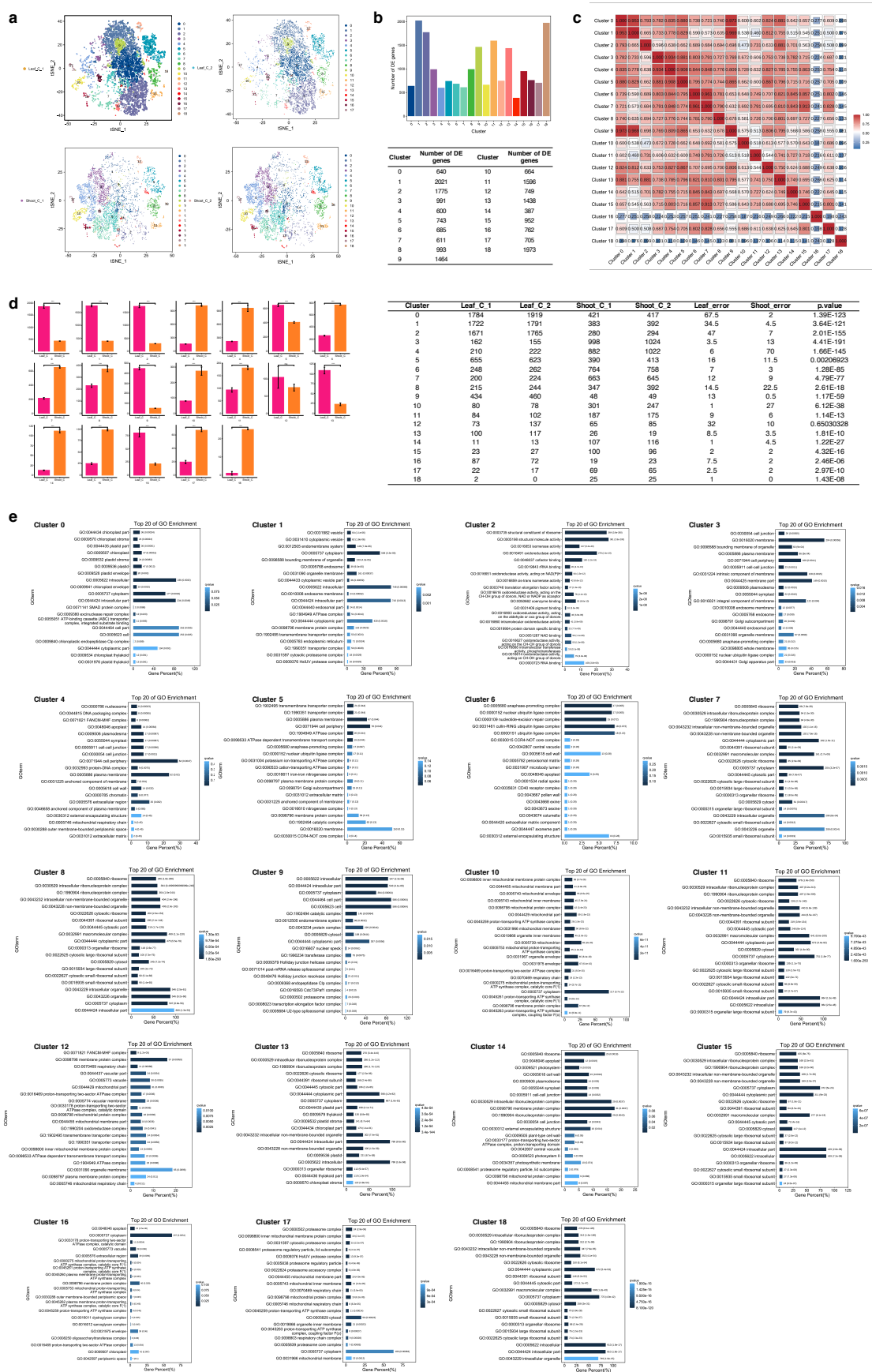




Differentially expressed gene numbers in 19 cell clusters. (c) Correlations between 19 cell clusters. (d) Statistical analysis of cell enrichment between shoot and leaf samples in each cluster. Symbols indicate statistical significance from vehicle with p value thresholds of ≤ 0.05 (*), ≤ 0.01 (**) and ≤ 0.001 (***). (e) GO enrichment annotation of cellular components for genes in 19 cell clusters.

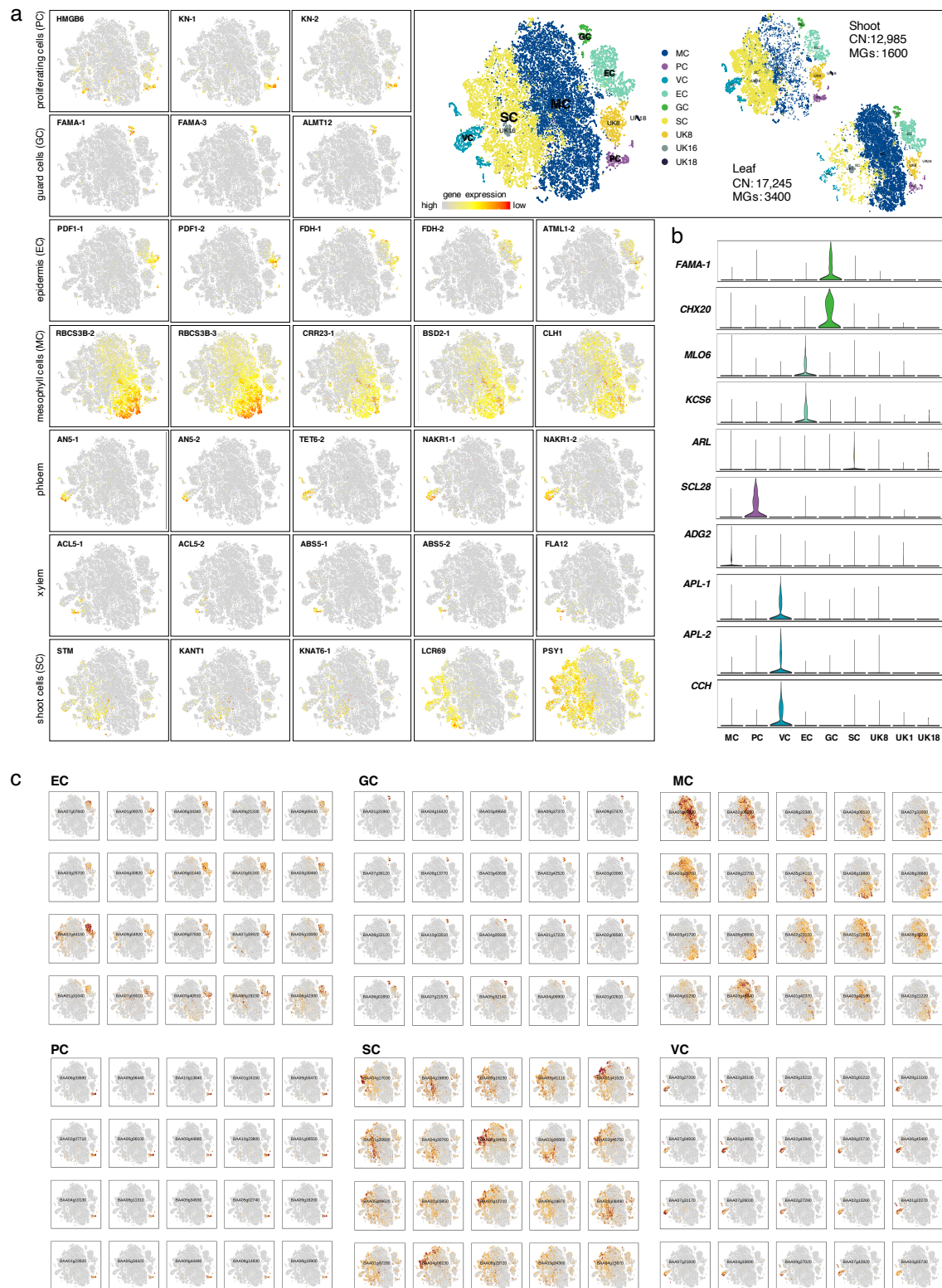


Figure S2. Marker genes for different cell types. (a) t-SNE plot showing the cell distribution of shoot and leaf samples and the expression distribution of selected marker genes. (b) Examples of novel cell-type marker genes for six major cell populations. (c) t-SNE plots

show the top 20 marker genes with the highest expression in each cell type in shoot and leaf samples.

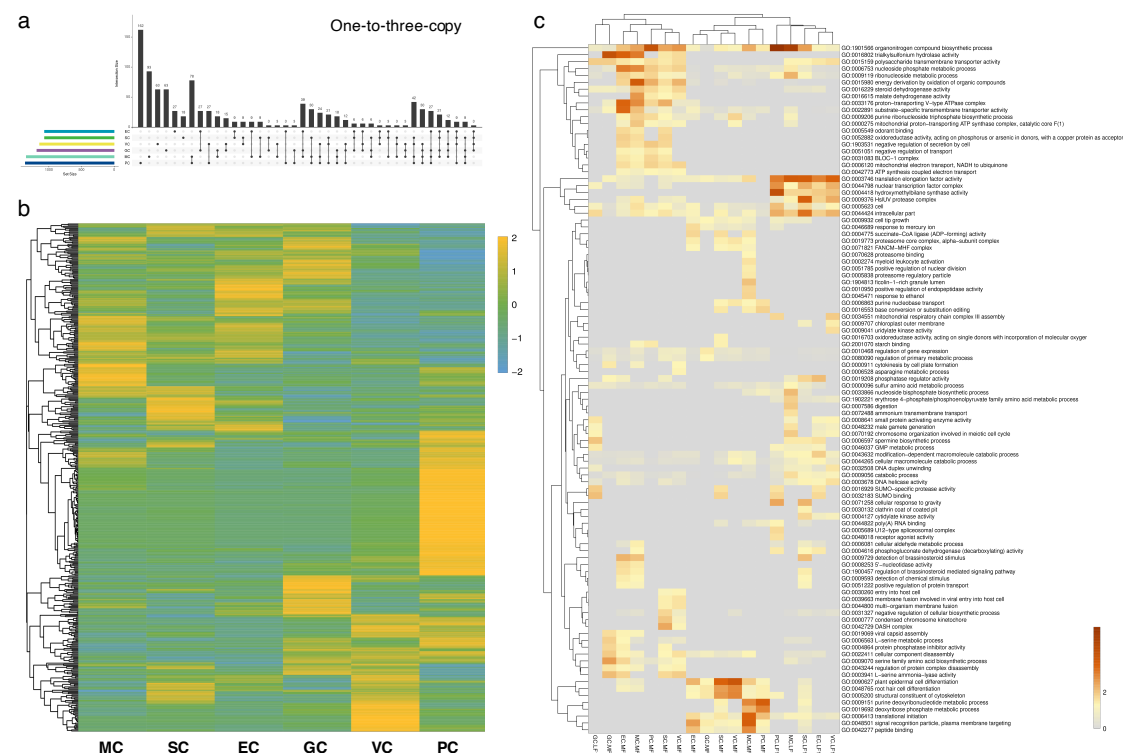
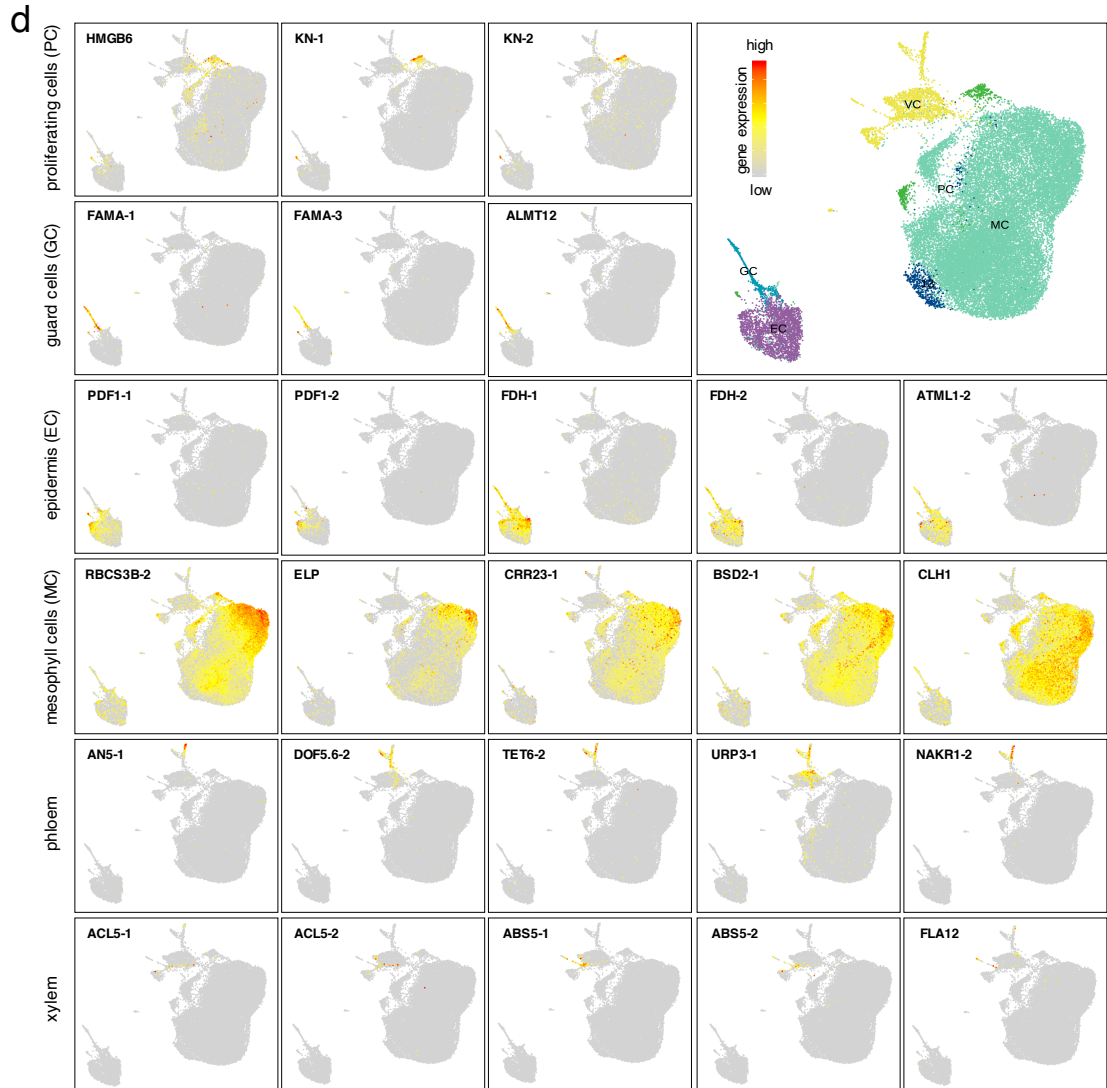
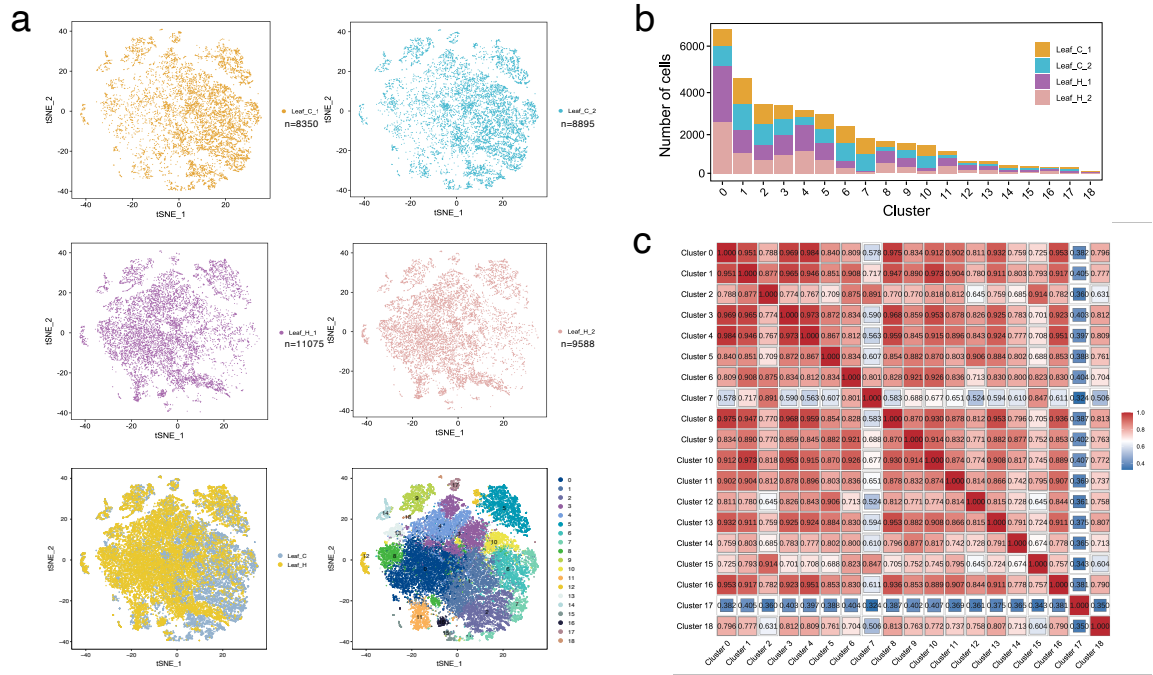


Figure S3. Predominantly expressed genes in three subgenomes. (a) Distribution of expressed one-to-three-copy genes in different cell types. (b) Heatmap for predominantly expressed genes in different cell types. (c) GO analysis of predominantly expressed genes in LF, MF1 and MF2 in different cell types.



response marker genes showing changed expression patterns after heat treatment only in one cell type.

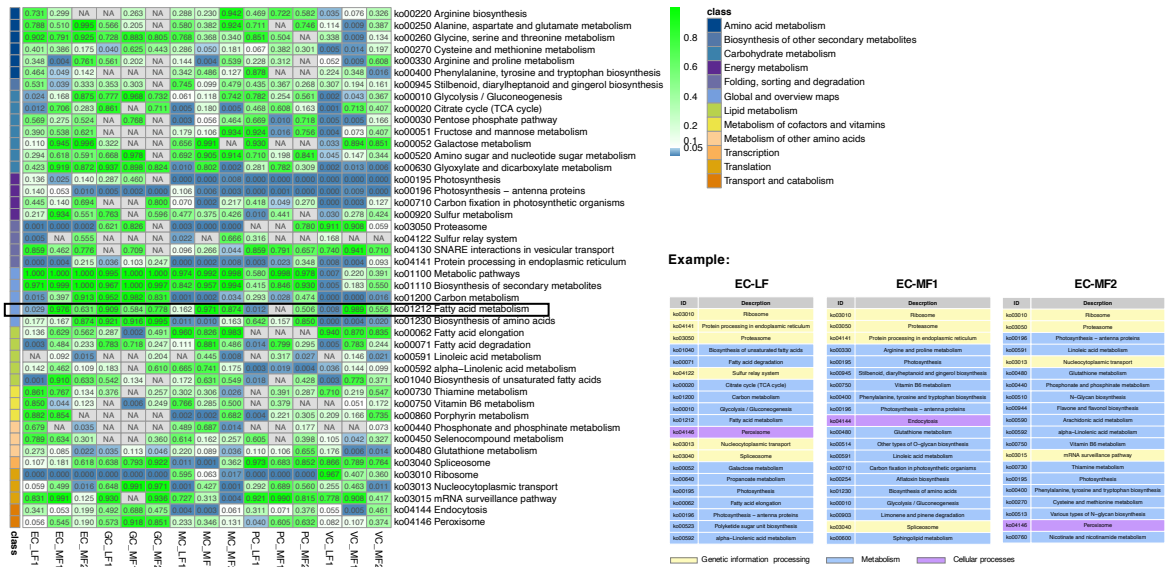


Figure S6. KEGG enrichment of differentially expressed genes across subgenomes in each cell type.

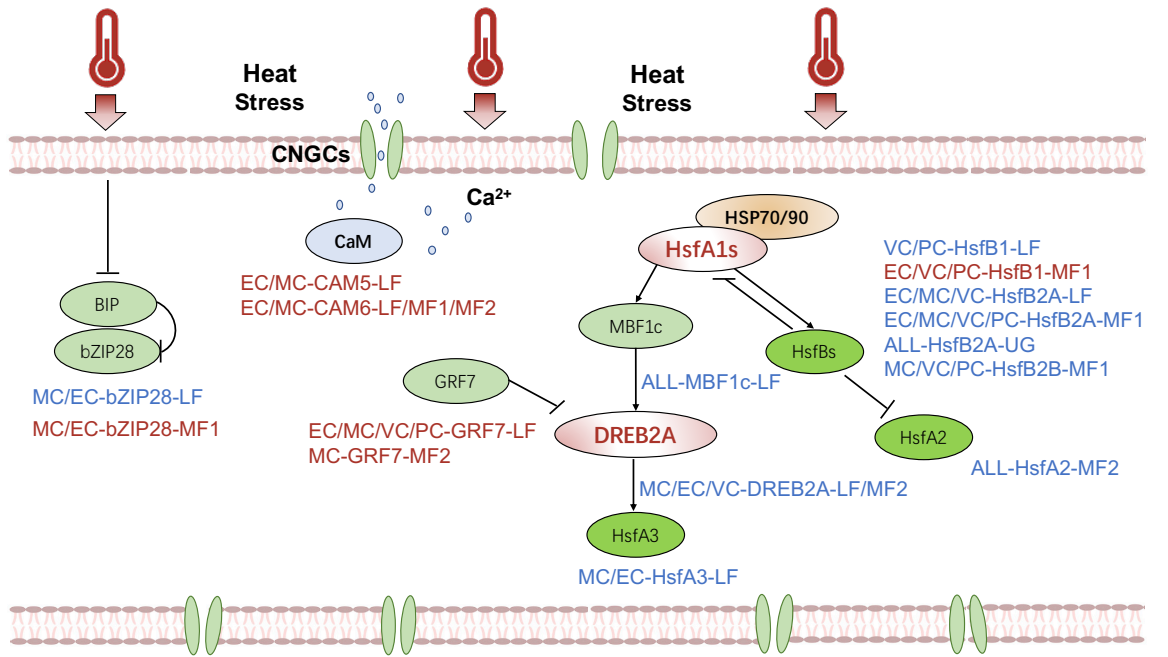


Figure S7. Expression overview of regulators involved in the heat stress response. Red indicates upregulation under HS, and blue indicates downregulation under HS.