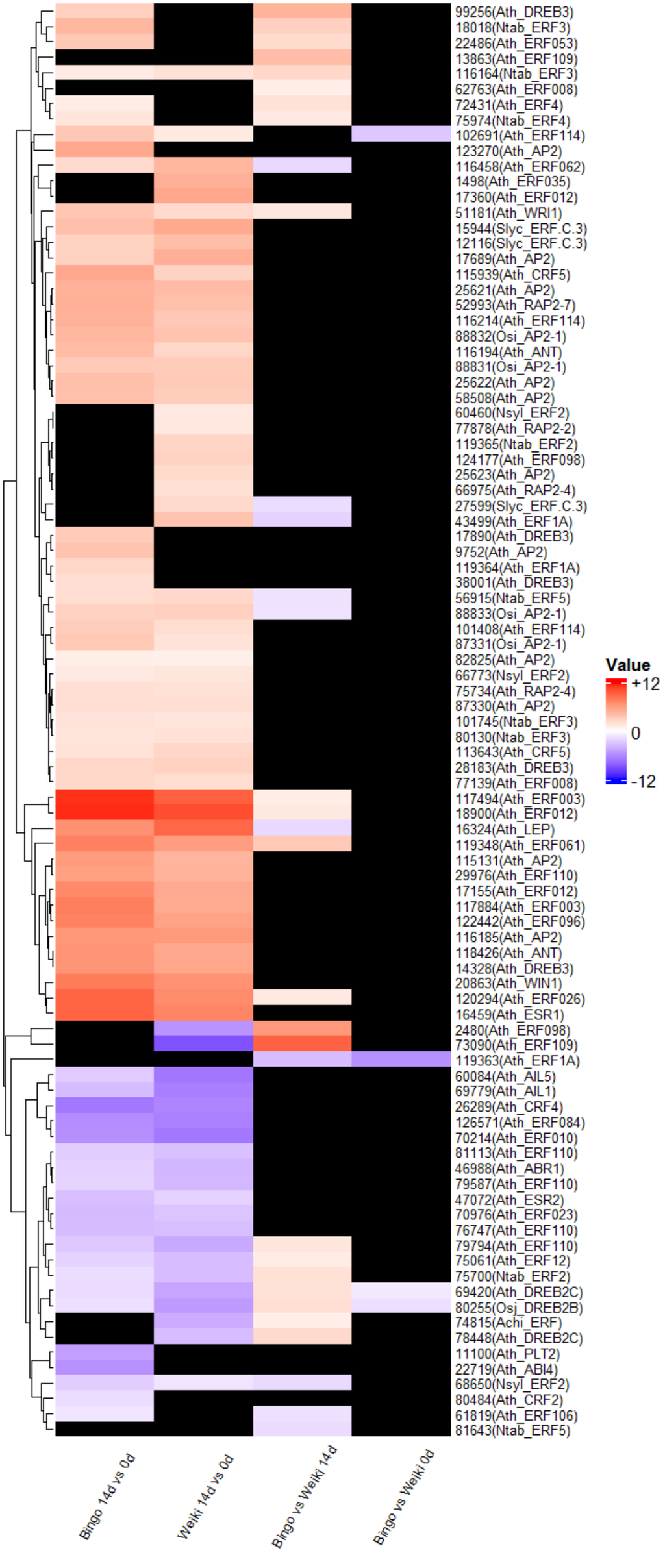


Figure S1 Heatmap of log2 fold change values for AP2-EREBP transcripts across four experimental comparisons. Hierarchical clustering was performed using average linkage. Colors indicate down-regulation (blue), no change (white), and up-regulation (red); black indicates missing data.

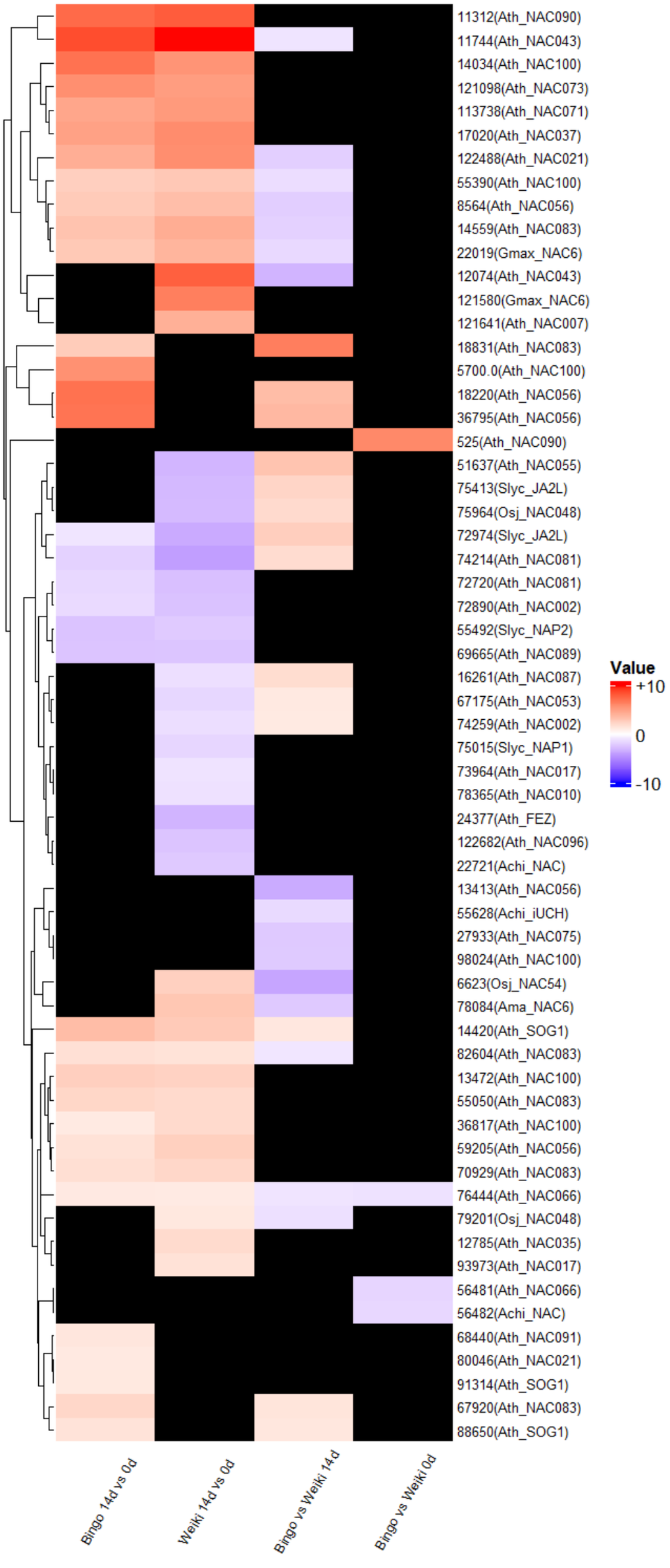


Figure S2 Heatmap of log2 fold change values for NAC transcripts across four experimental comparisons. Hierarchical clustering was performed using average linkage. Colors indicate down-regulation (blue), no change (white), and up-regulation (red); black indicates missing data.

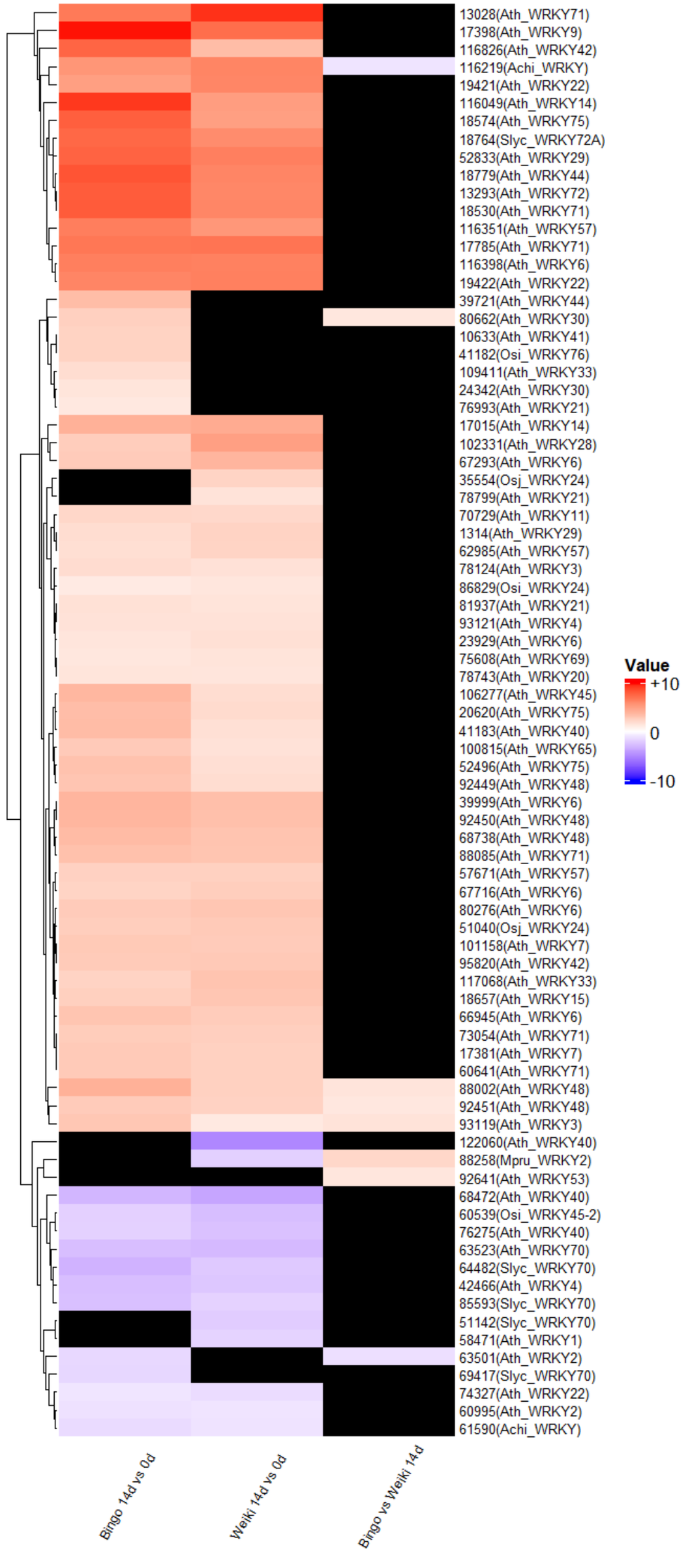


Figure S3 Heatmap of log2 fold change values for WRKY transcripts across three experimental comparisons. Hierarchical clustering was performed using average linkage. Colors indicate down-regulation (blue), no change (white), and up-regulation (red); black indicates missing data.

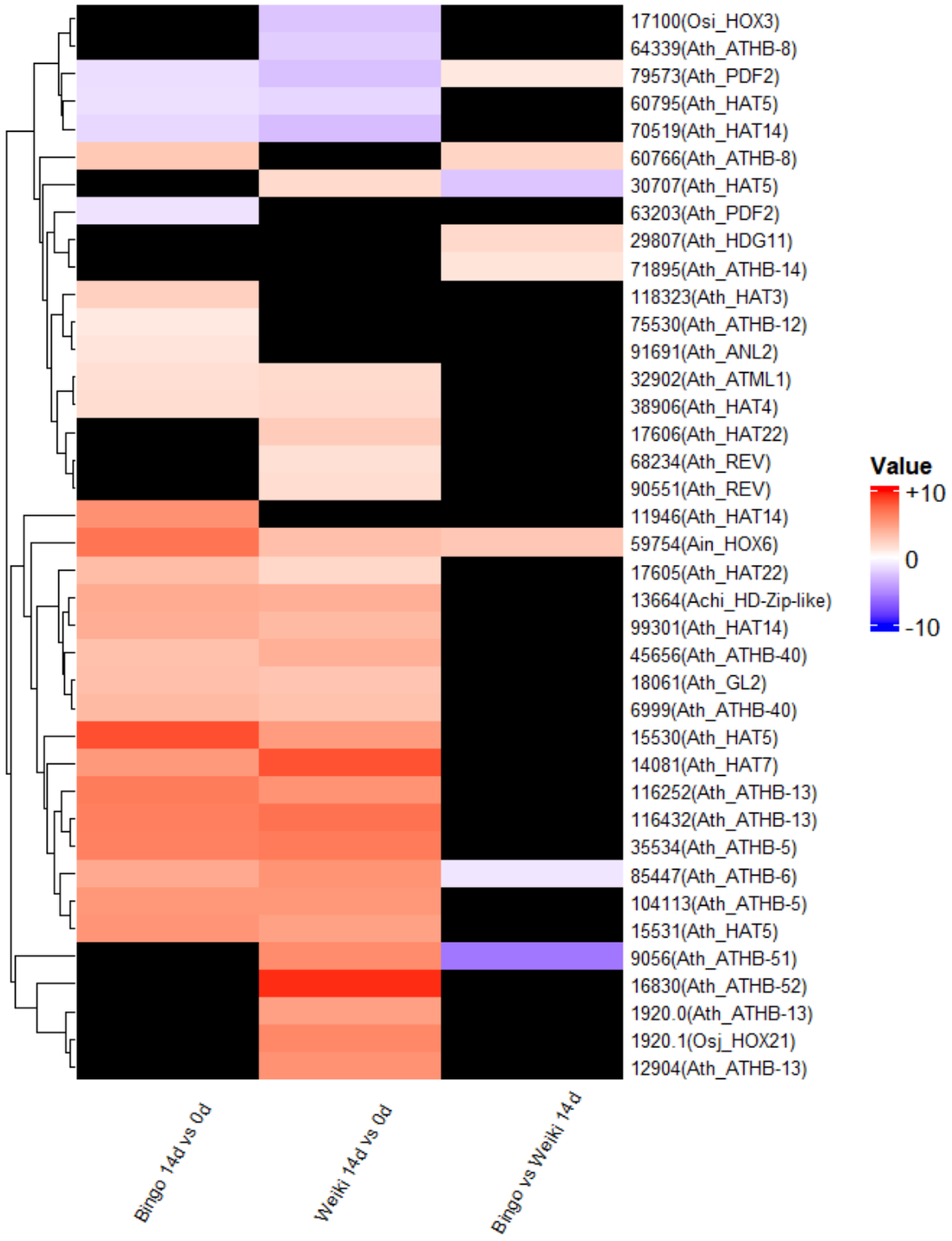


Figure S4 Heatmap of log2 fold change values for HD-ZIP transcripts across three experimental comparisons. Hierarchical clustering was performed using average linkage. Colors indicate down-regulation (blue), no change (white), and up-regulation (red); black indicates missing data.

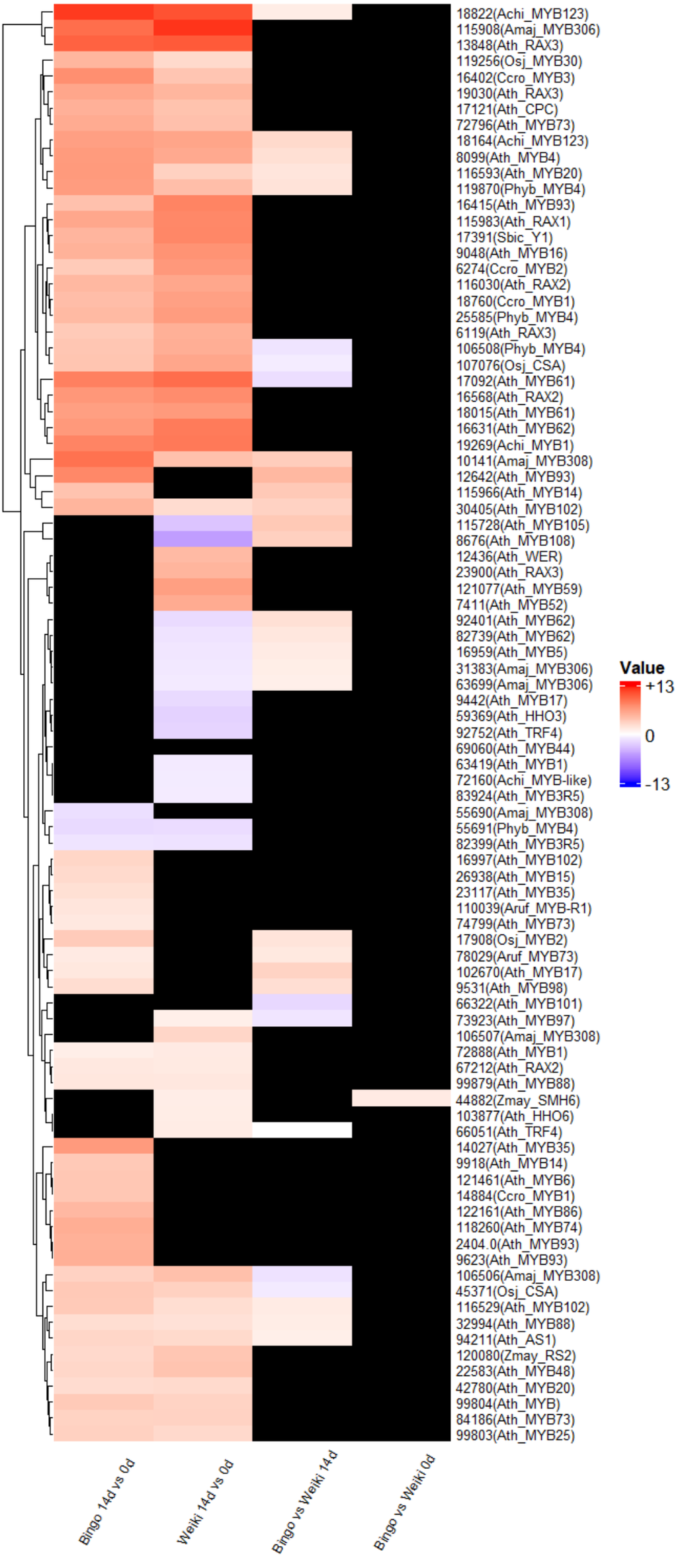


Figure S5 Heatmap of log2 fold change values for MYB transcripts across four experimental comparisons. Hierarchical clustering was performed using average linkage. Colors indicate down-regulation (blue), no change (white), and up-regulation (red); black indicates missing data.

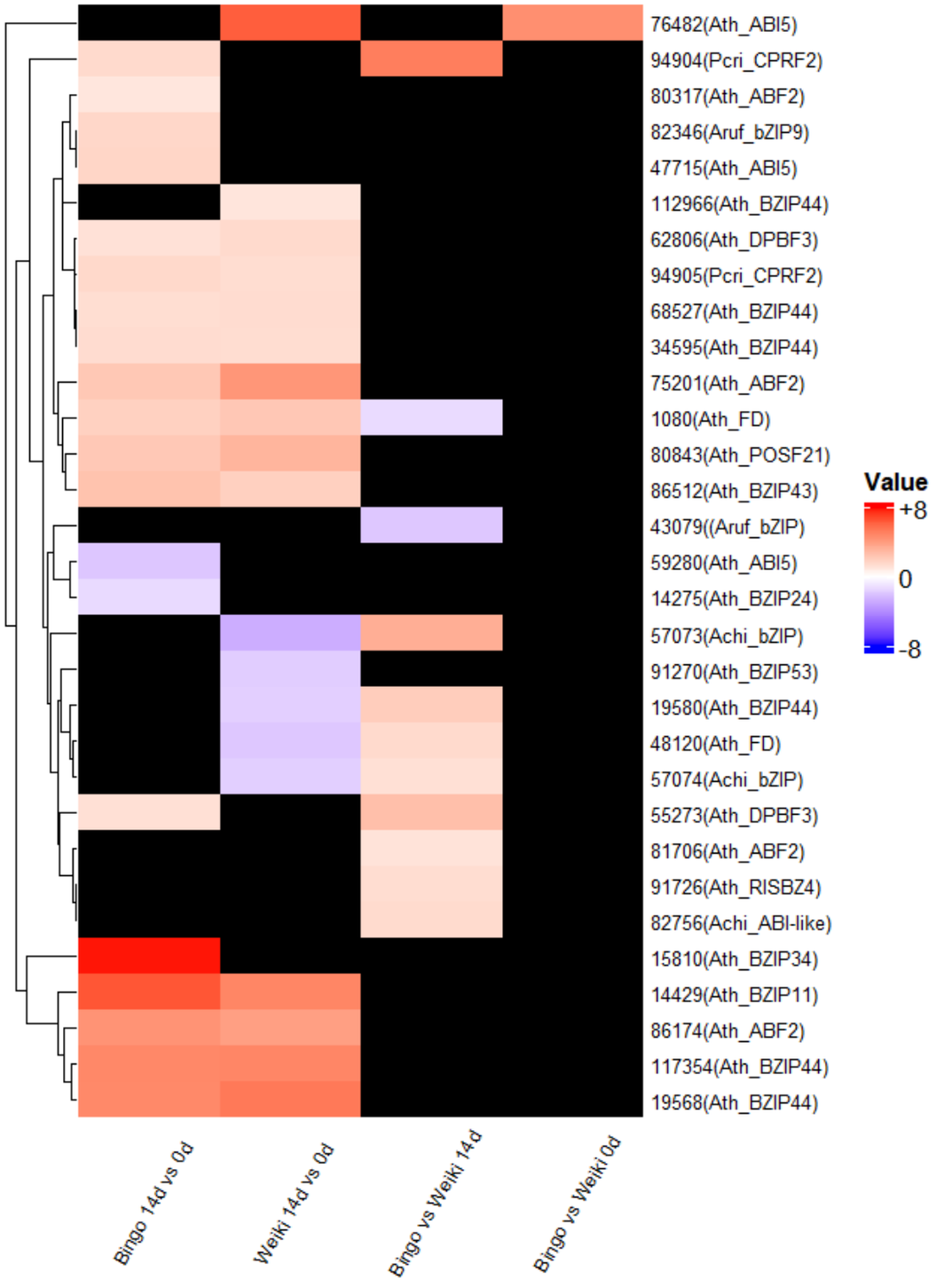


Figure S6 Heatmap of log2 fold change values for bZIP/ABF transcripts across four experimental comparisons. Hierarchical clustering was performed using average linkage. Colors indicate down-regulation (blue), no change (white), and up-regulation (red); black indicates missing data.