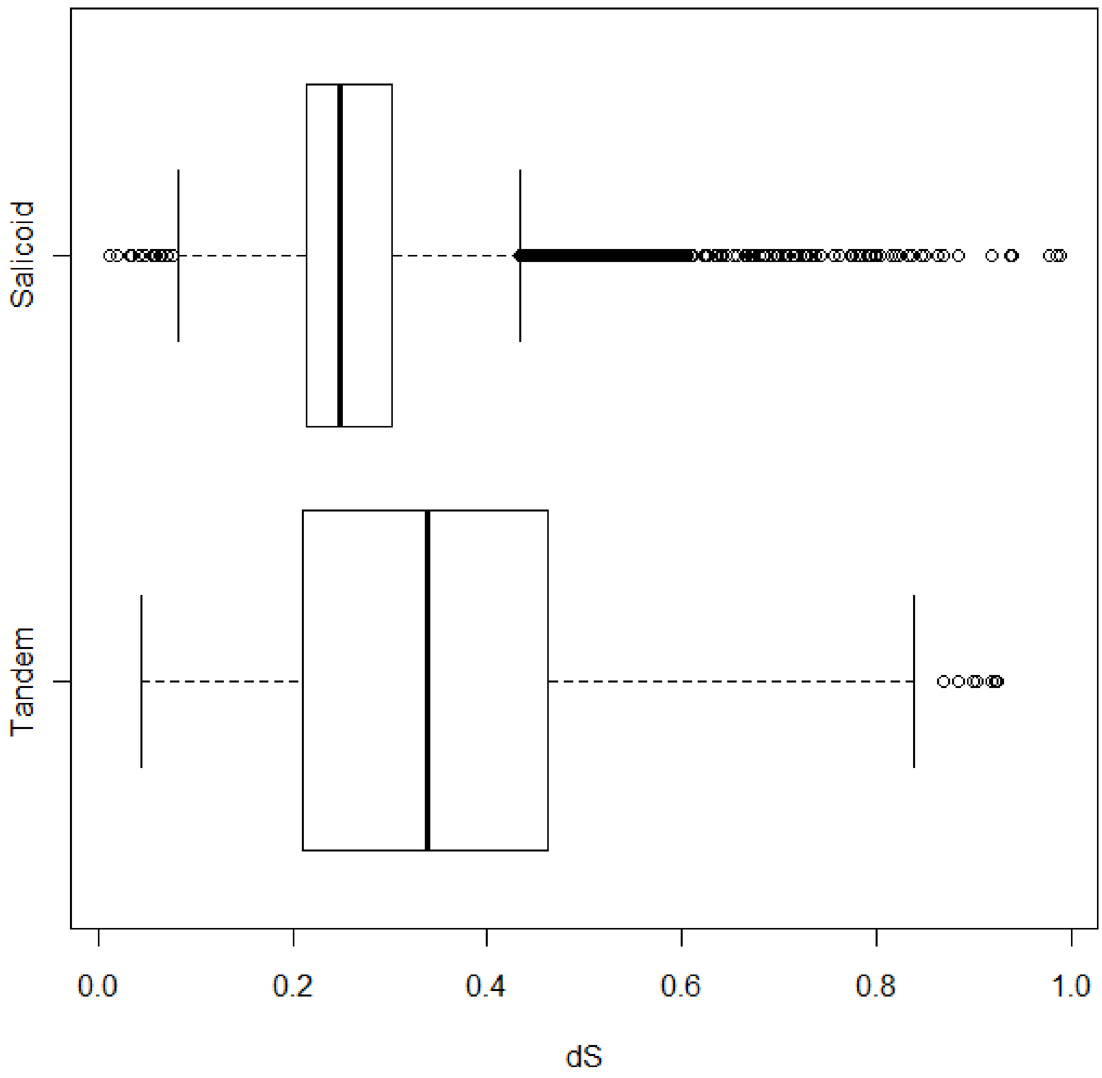
Supplemental Figure 1. Boxplots for the d_S ranges in Salicoid and tandem duplicate pairs.

Supplemental Figure 2. Mean d_N/d_S for Salicoid and tandem duplicates grouped into bins of 0.2 d_S. Error bars indicate standard error of the mean.

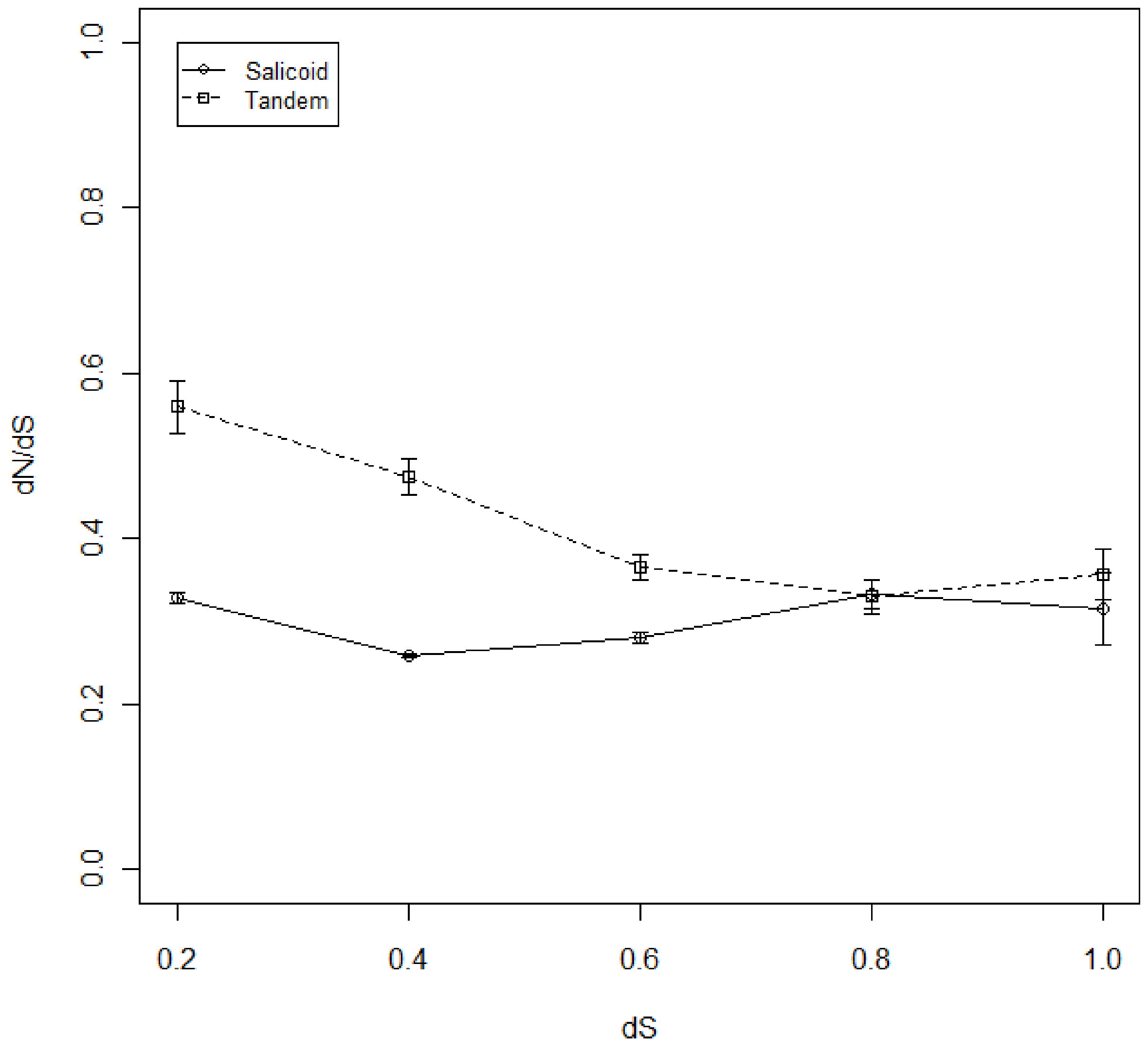
Supplemental Figure 3. Scatter plots of the replicates for the slides used in this analysis. Each plot contains a line of best fit based on least squares regression, along with the R-squared value.

Supplemental Figure 4. Plots of the replicates for two of the slides used in this analysis that had relatively poor correspondence between replicates. These were used for further analysis because they clustered with other floral tissues (Supplemental Figure 5).

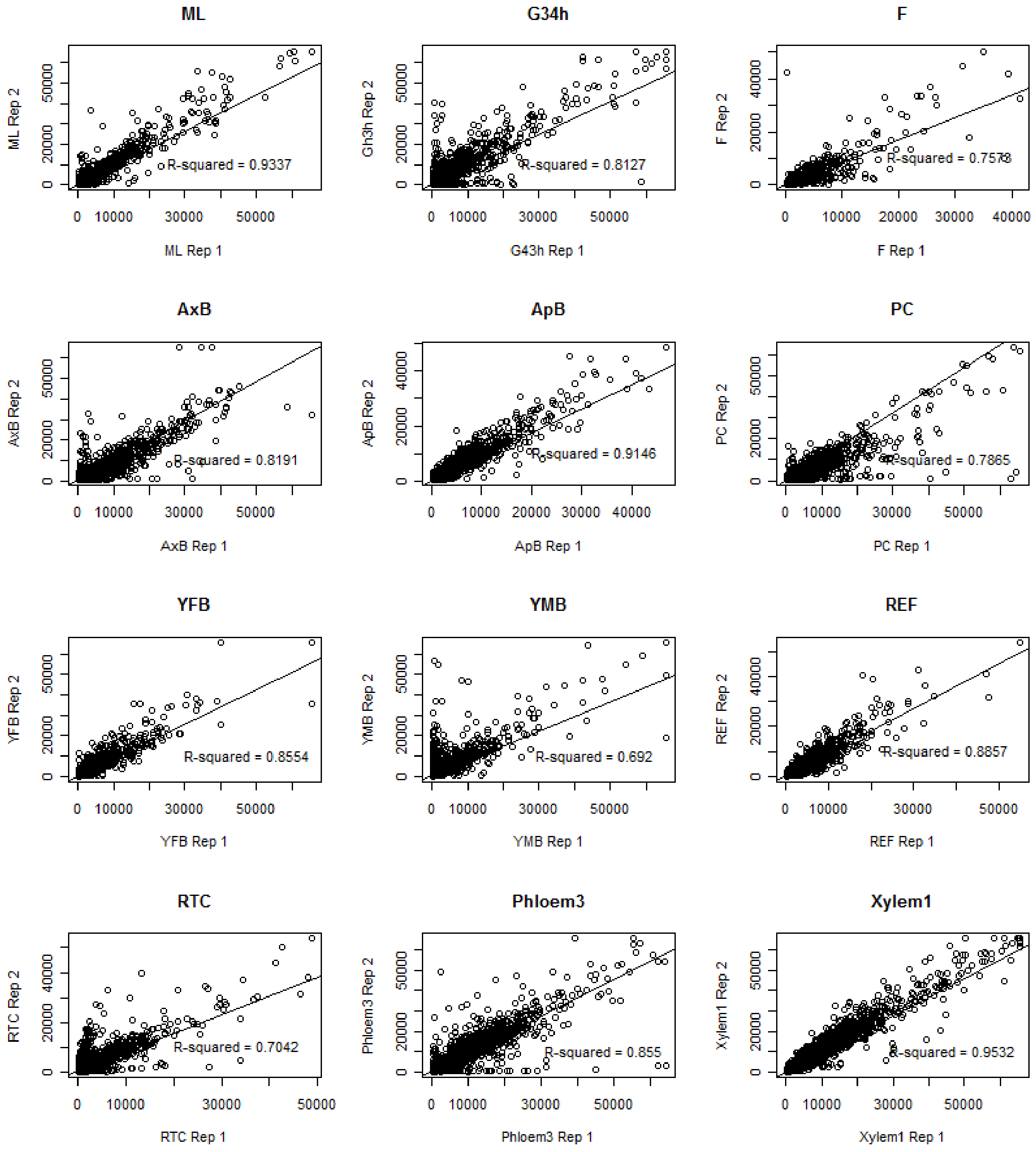
Supplemental Figure 5. Hierarchical clustering based on the Euclidean distance for all replicates in the original microarray. VYL, SE, ApL, and Xpi slides were dropped for subsequent analyses.



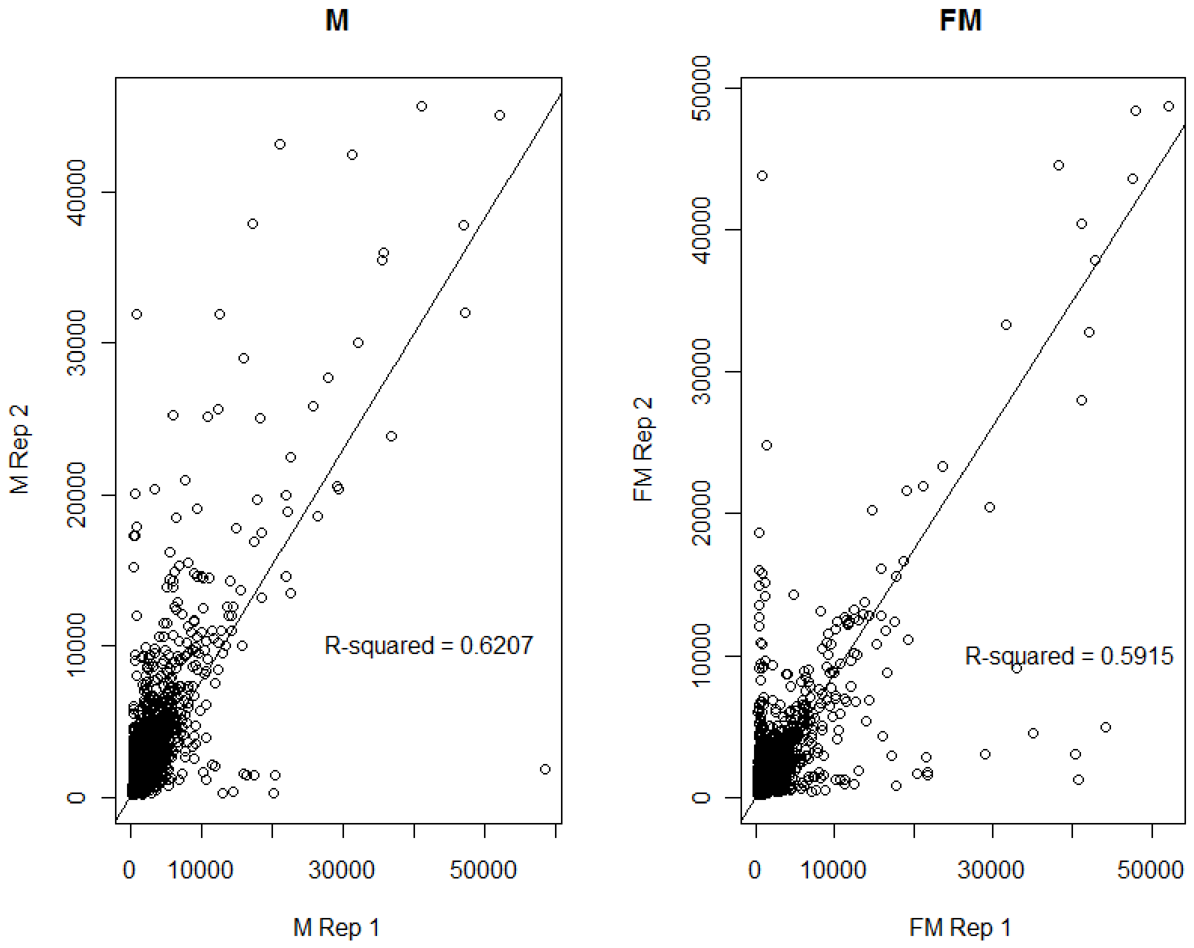
Supplemental Figure 1.



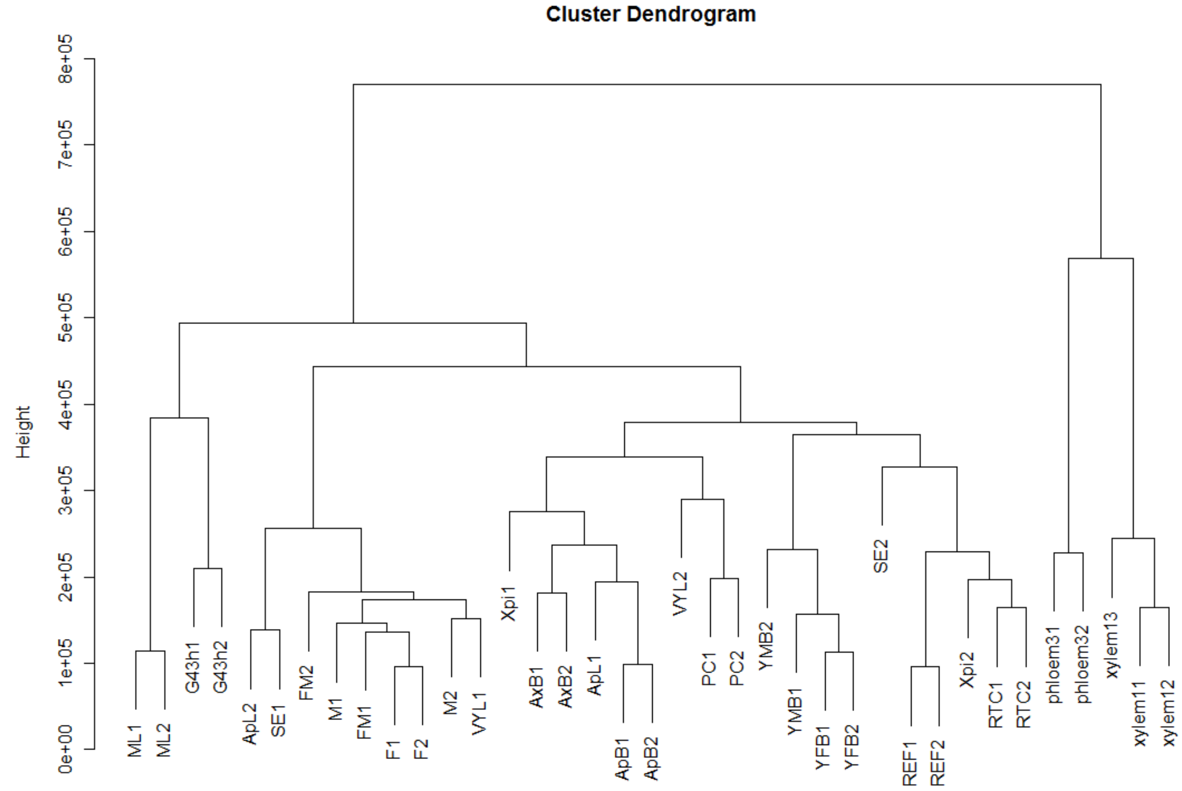
Supplemental Figure 2.



Supplemental Figure 3.



Supplemental Figure 4.



Supplemental Figure 5.