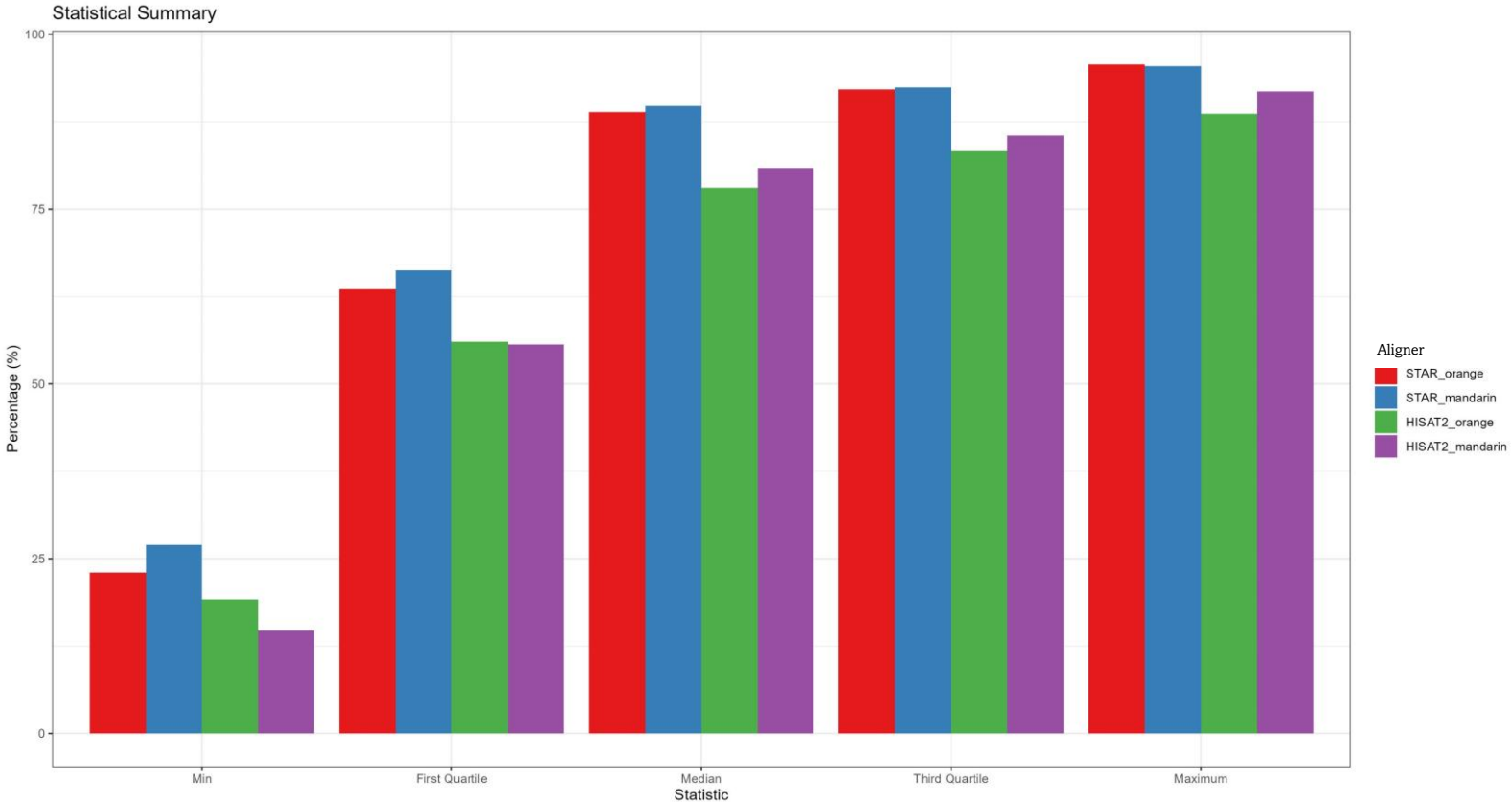


**Figure S1:** Statistical summary of mapping performance (STAR vs. HISAT2)

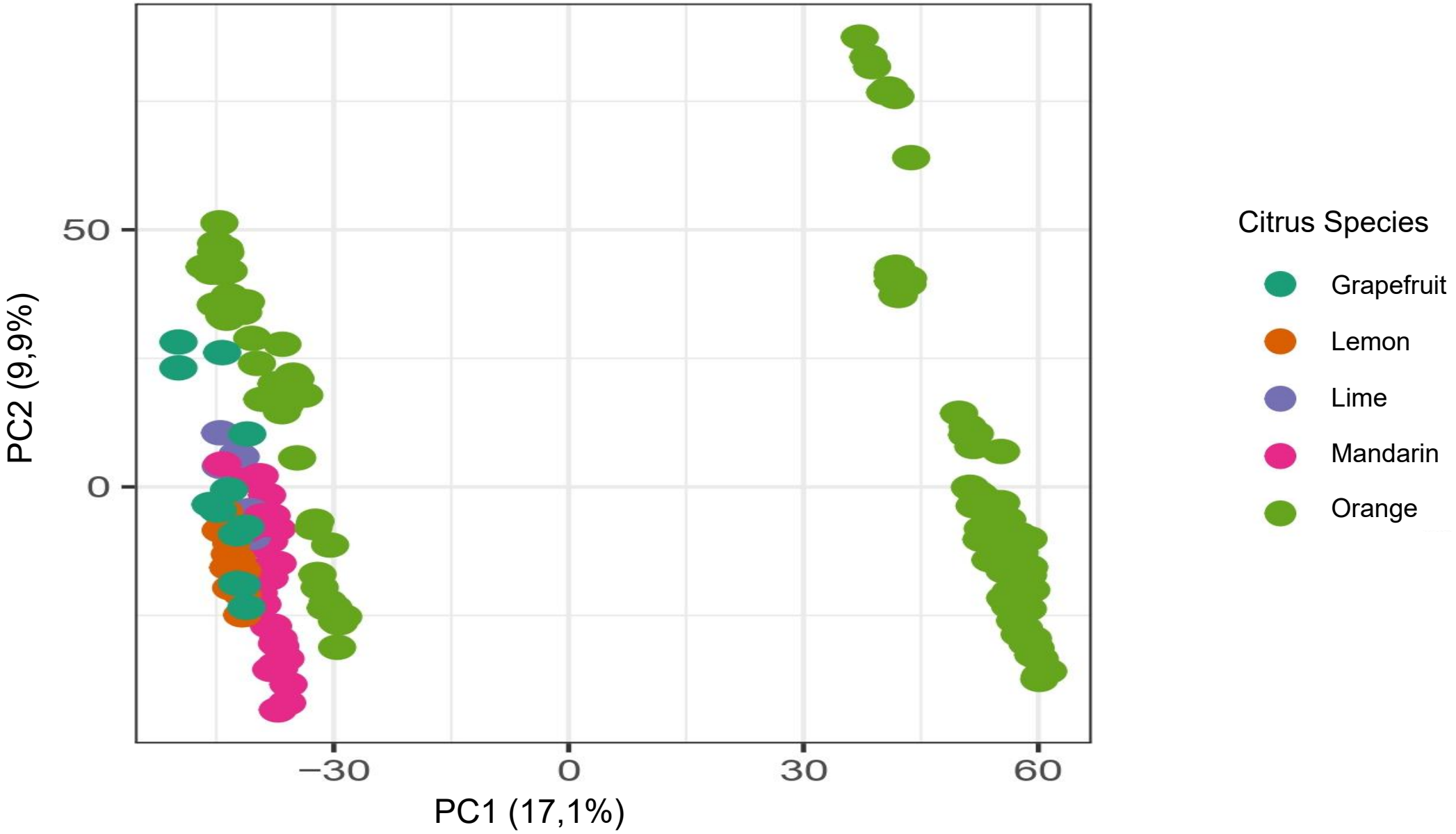


**Figure S2-A**. PCA plot shows distinct clustering of 230 RNA-seq samples by *Citrus species*.

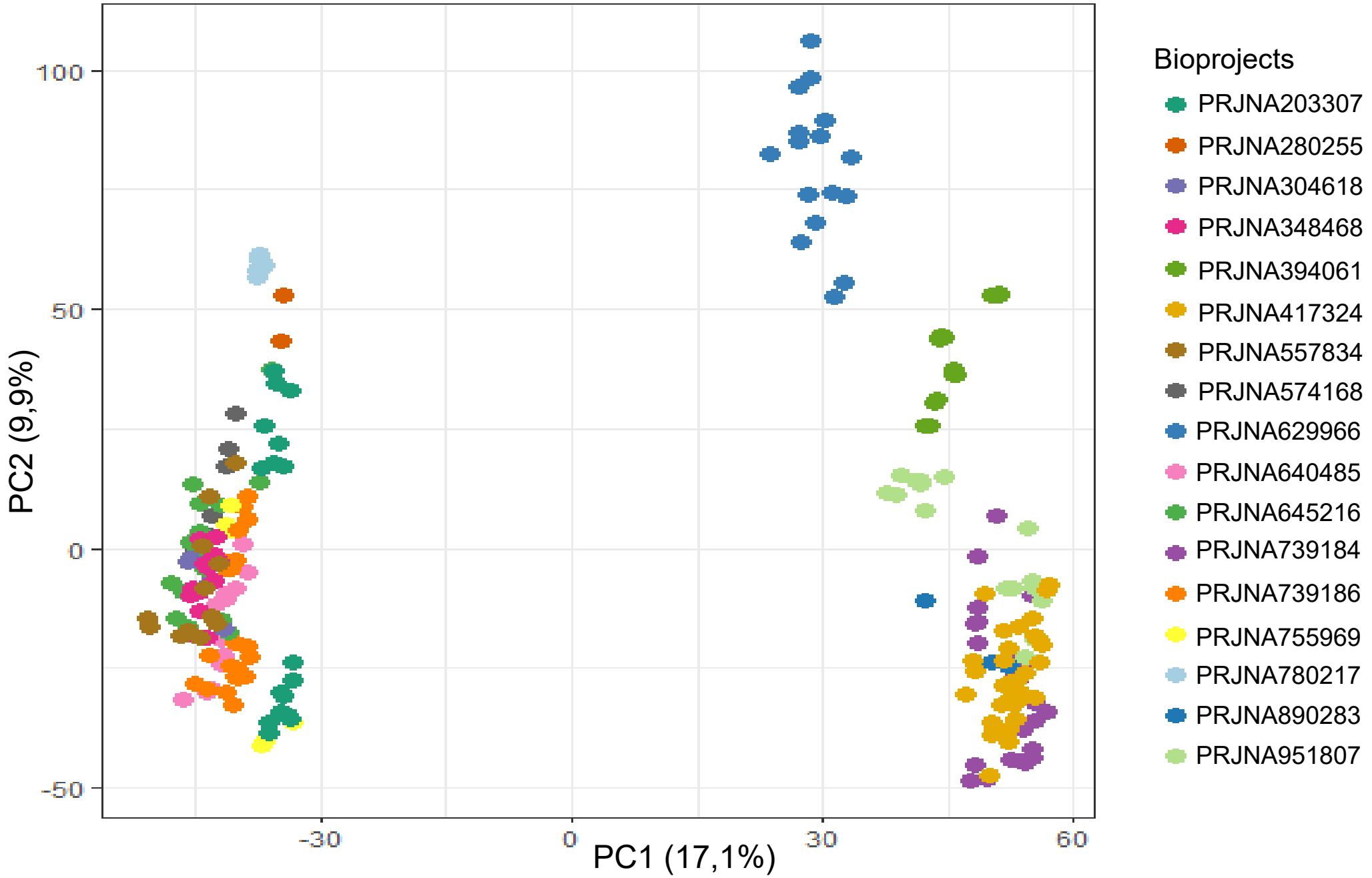


**Figure S2-B**. PCA plot shows distinct clustering of 230 RNA-seq samples by *Bioprojects*

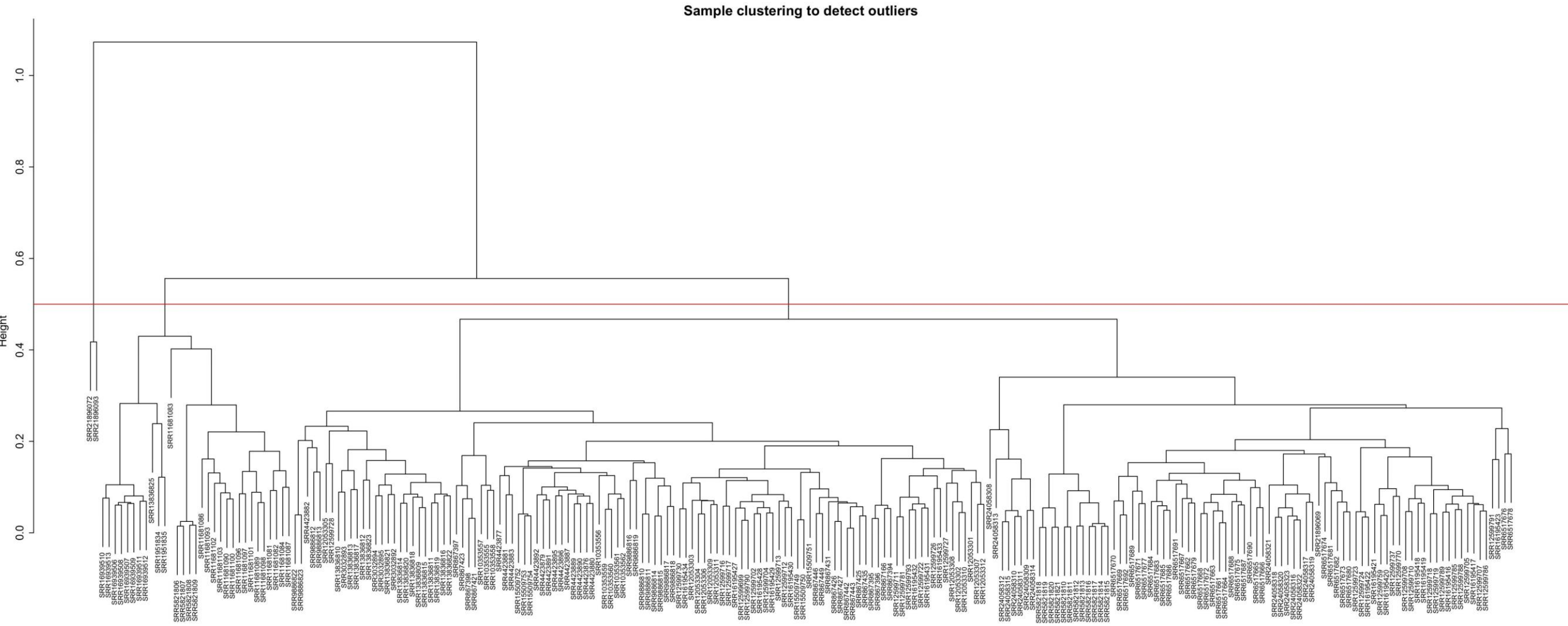


**Figure S3.** Hierarchical clustering dendrogram of gene expression samples based on Pearson correlation. A height cutoff of 0.5 identified 197 retained samples (Cluster 1) and excluded 33 outliers.

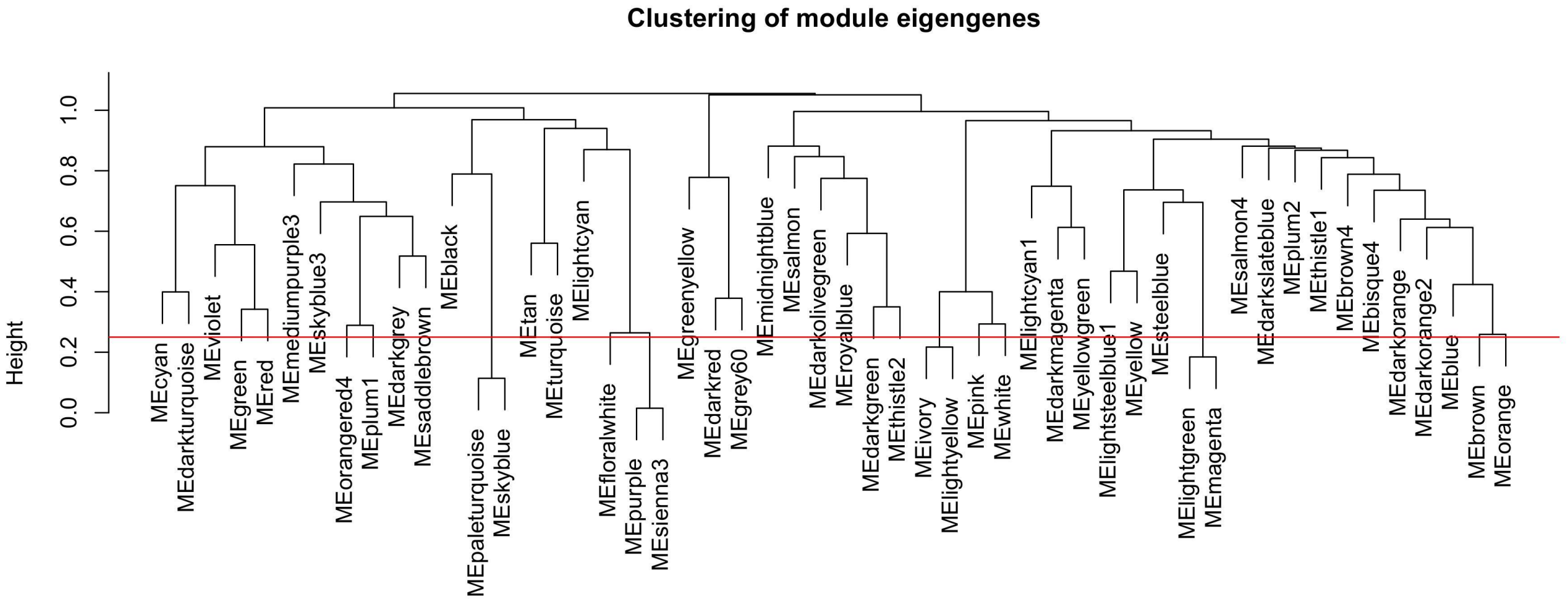


**Figure S4**. Hierarchical clustering of module eigengenes based on their correlation, where a red horizontal line signifies the chosen cut-off height (dissimilarity of 0.25) for merging modules with eigengene correlations exceeding 0.75.

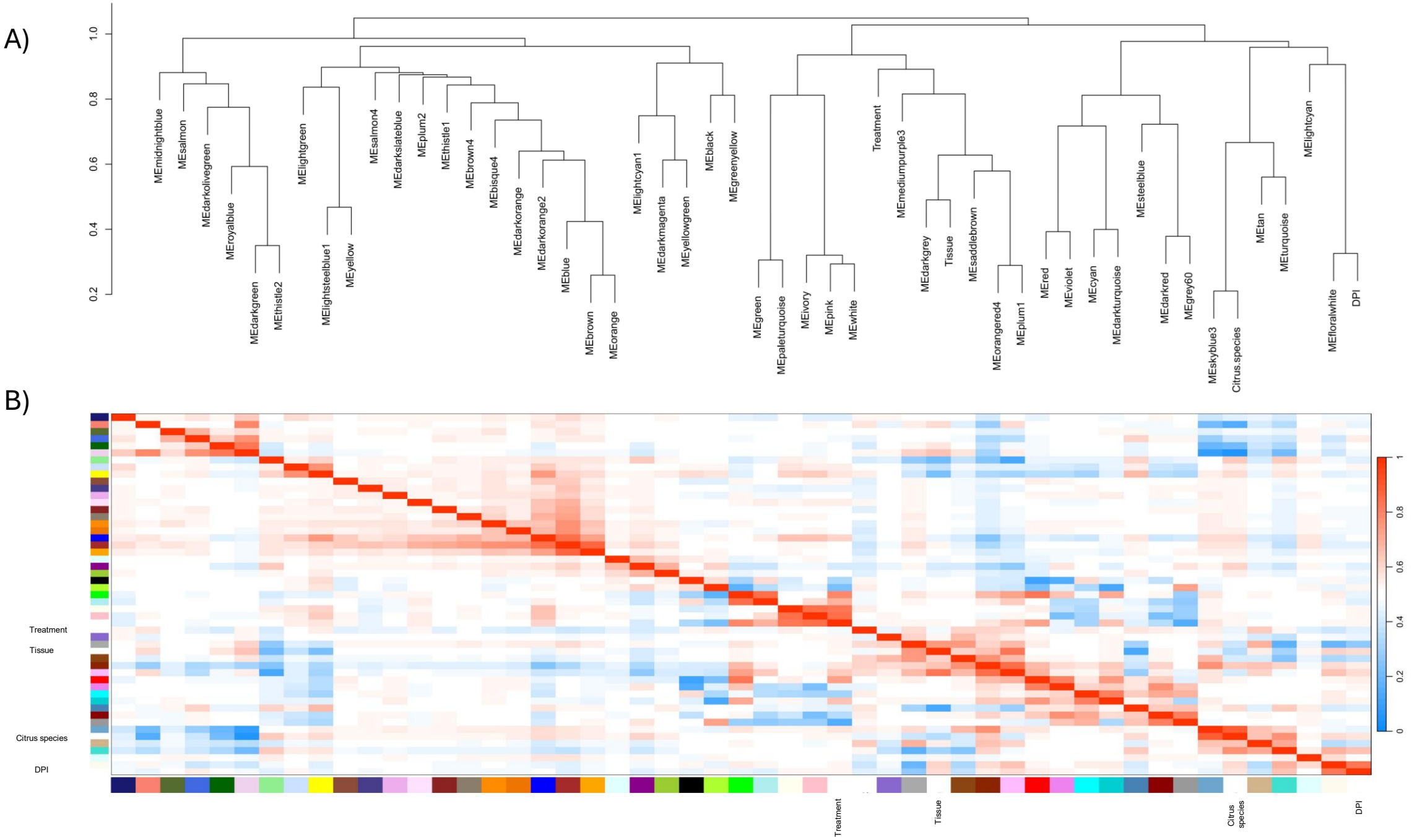


**Figure S5.** Eigengene Network and Module-Trait Relationships. (A) Dendrogram of module eigengene clustering. (B) Heatmap of module eigengene adjacency, with color-coded boxes indicating correlation strength. Traits (citrus species, DPI, tissue type and treatment) are integrated to visualize their relationships with the module eigengenes.

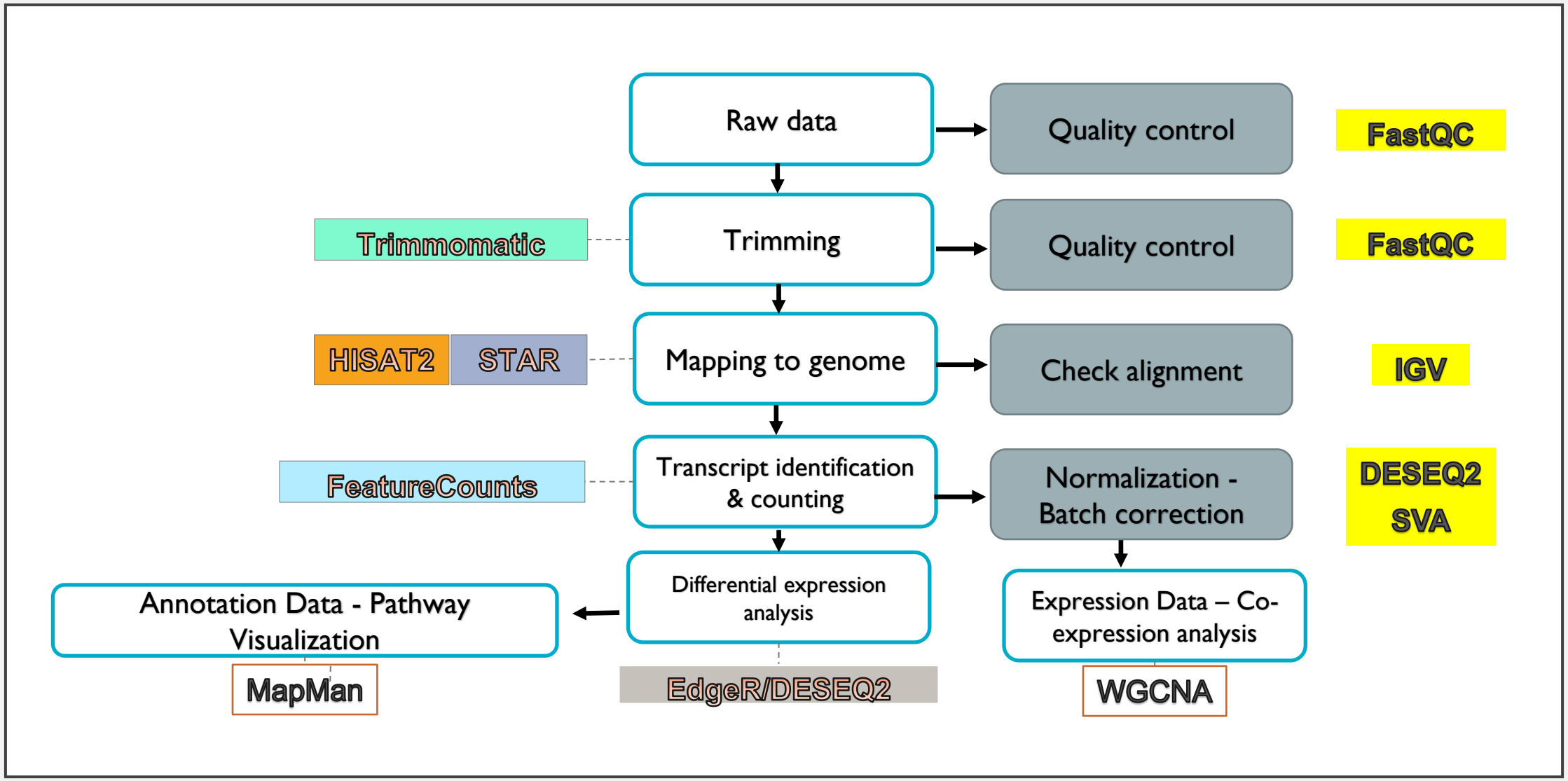


**Figure S6.** Bioinformatic workflow describing sample processing for co-expression network analysis and differential expression analysis (DEGs)