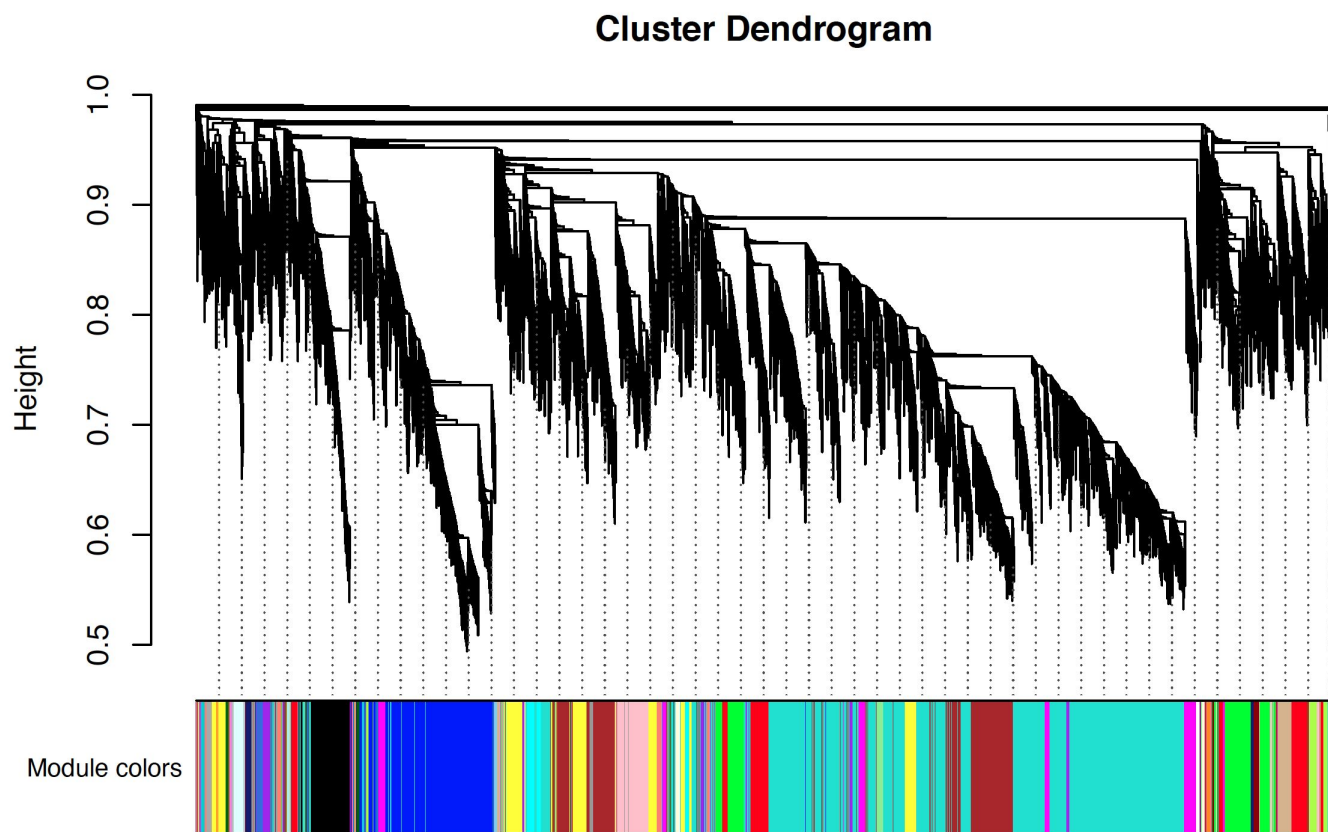
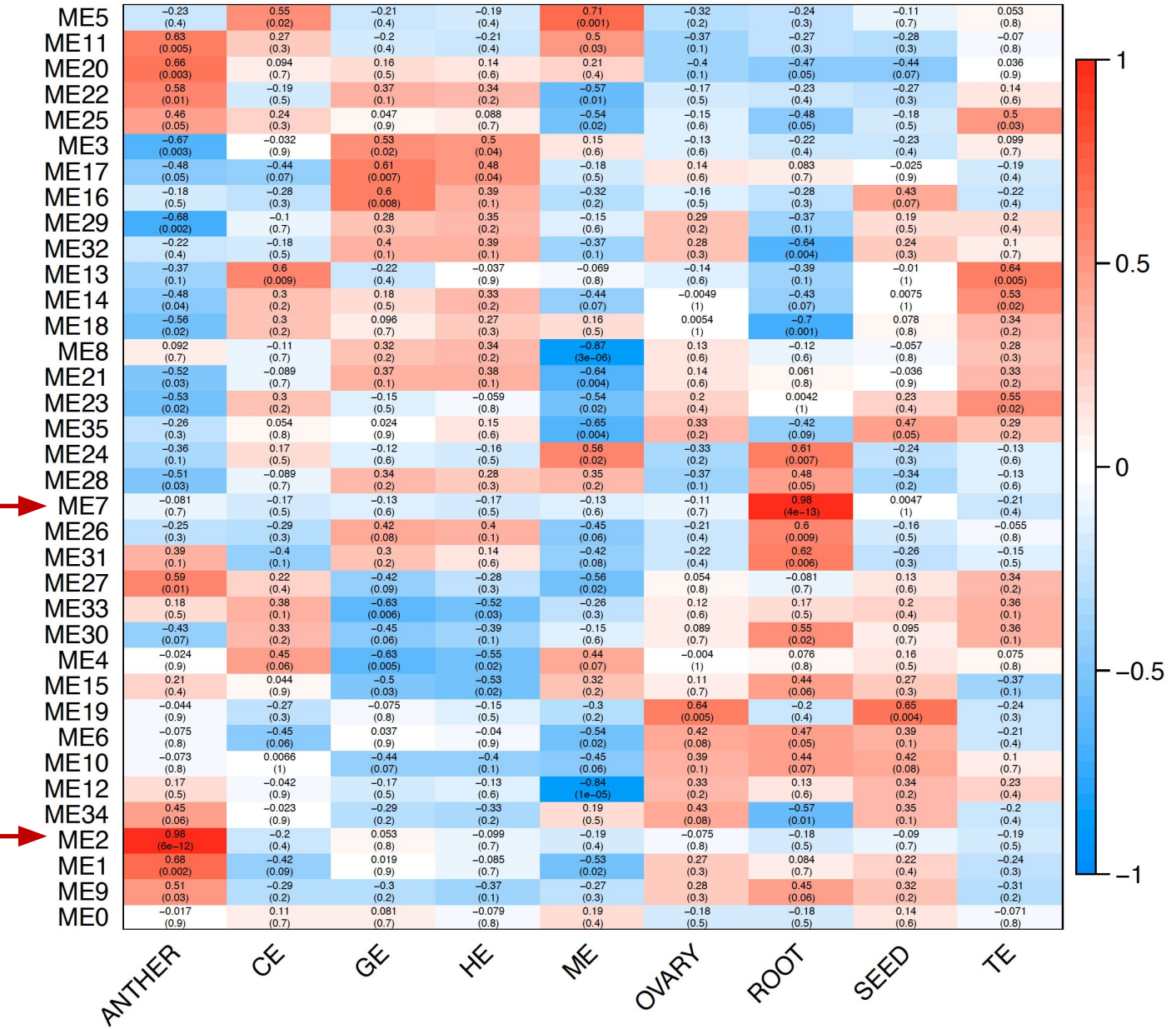


Supplemental Figure S1. Principal component analysis (PCA) of the transcriptomes for nine different tissues and stages in Flax. Biological replicates from the same tissue/stage are represented by the same color as defined in the right inset.

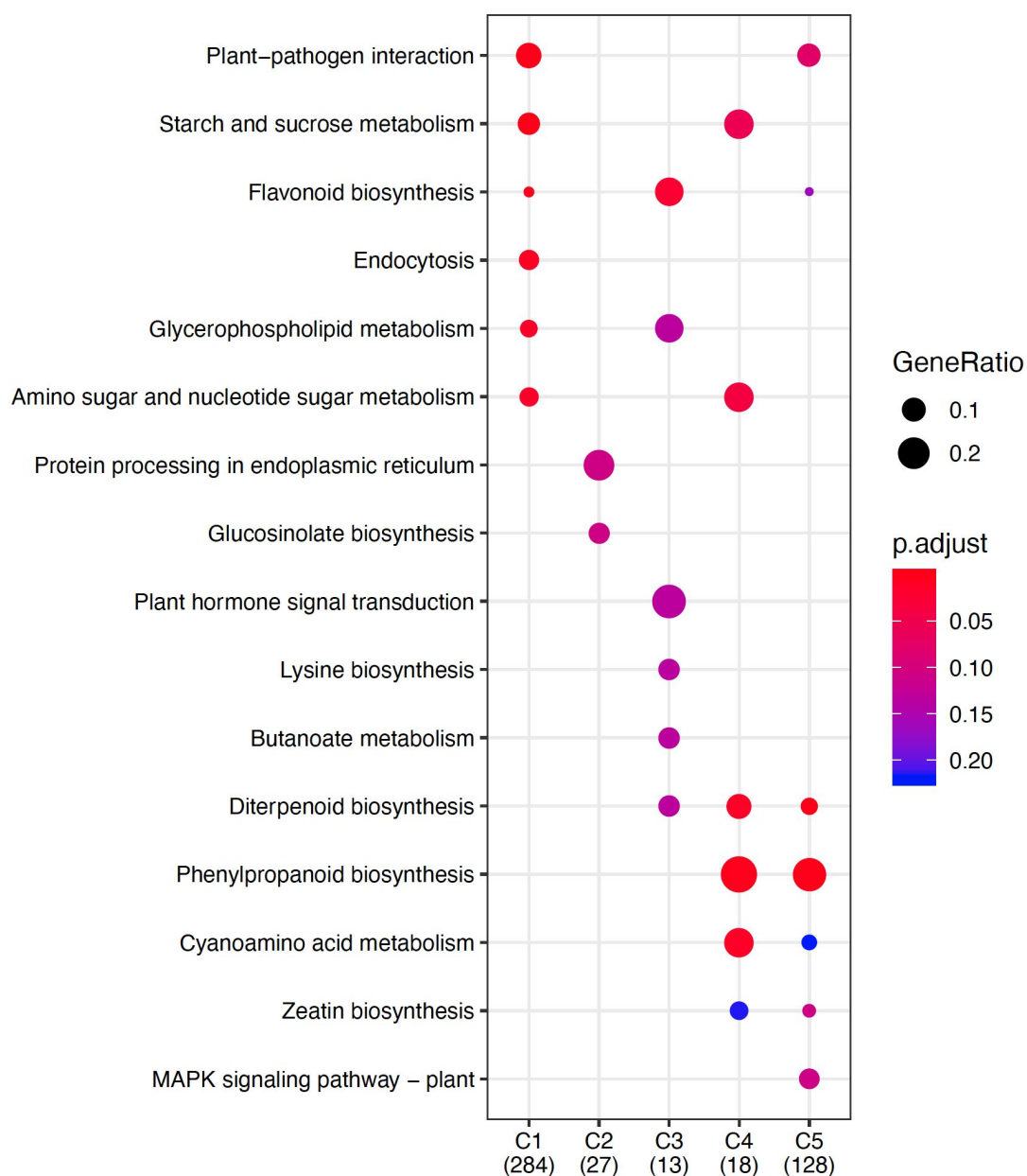


Supplemental Figure S2. WGCNA modules (Clusters) dendrogram. Hierarchical cluster tree showing modules of co-expressed genes, was identified with a total of 36 co-expressed gene modules identified. The height (y-axis) indicates level of correlation. Colors represent the 36 different modules, with gray indicating genes that could not be assigned to any module.

Module-tissue relationships



Supplemental Figure S3. Correlation relationship between modules and tissues. Heatmap of correlations between co-expressed gene modules and nine tissues and stages of embryo development, with numerical Pearson's correlation coefficient (top) and corresponding p-values (bottom). The color scheme, from red through white to blue, indicates the level of correlation, from high to low. Anther-specific (ME2) and root-specific (ME7) modules are identified by $r > 0.8$, $p < 0.001$ with red arrows.



Supplemental Figure S4. KEGG enrichment for each dominant genes cluster. A visual representation of KEGG enrichment for the genes in five tissue-specific clusters was plotted against each cluster (x-axis). The KEGG terms with a significant p (< 0.20) are shown and p -values are associated with dot colors as defined in the right inset. Dot size represents related gene ratio in total genes of each cluster.