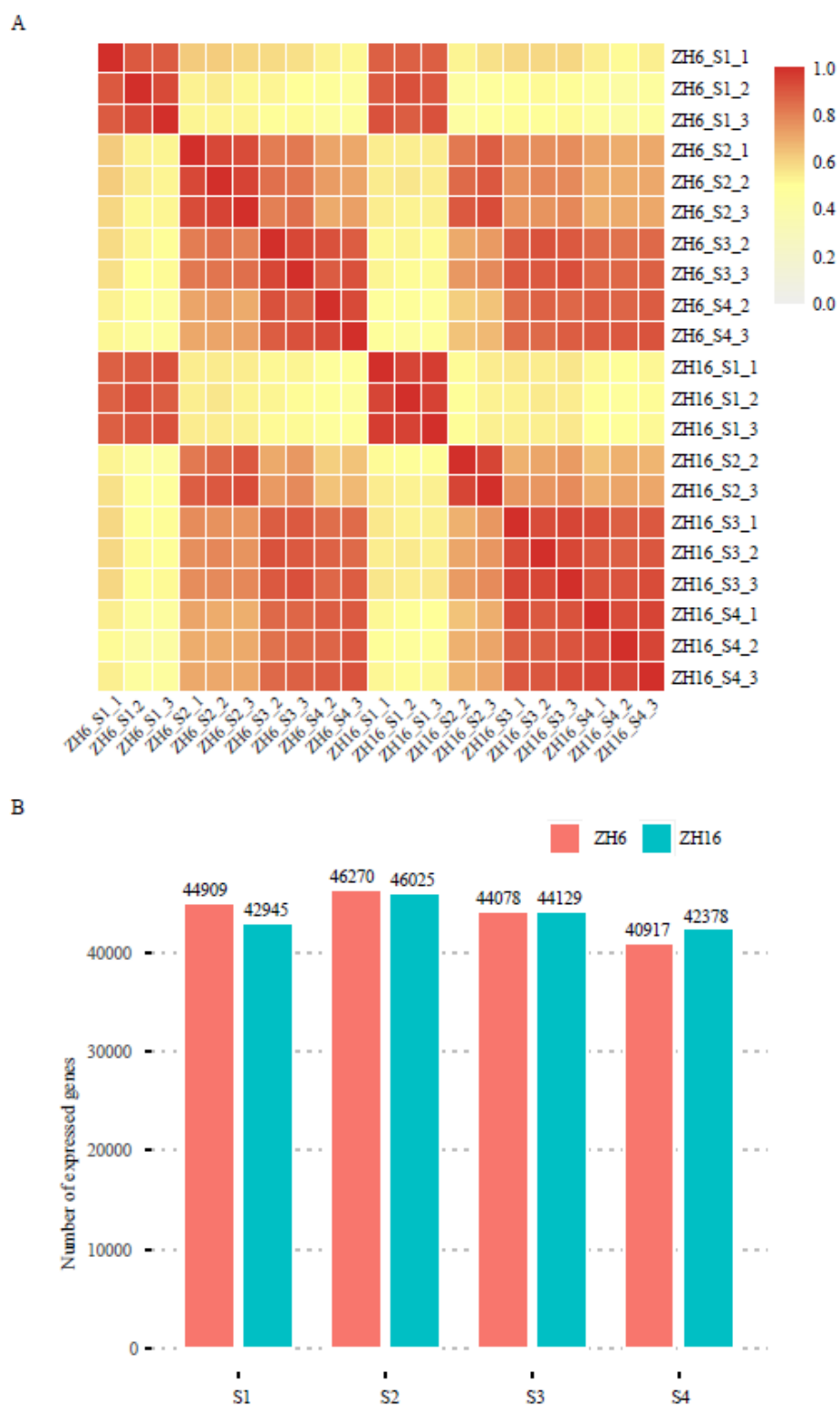
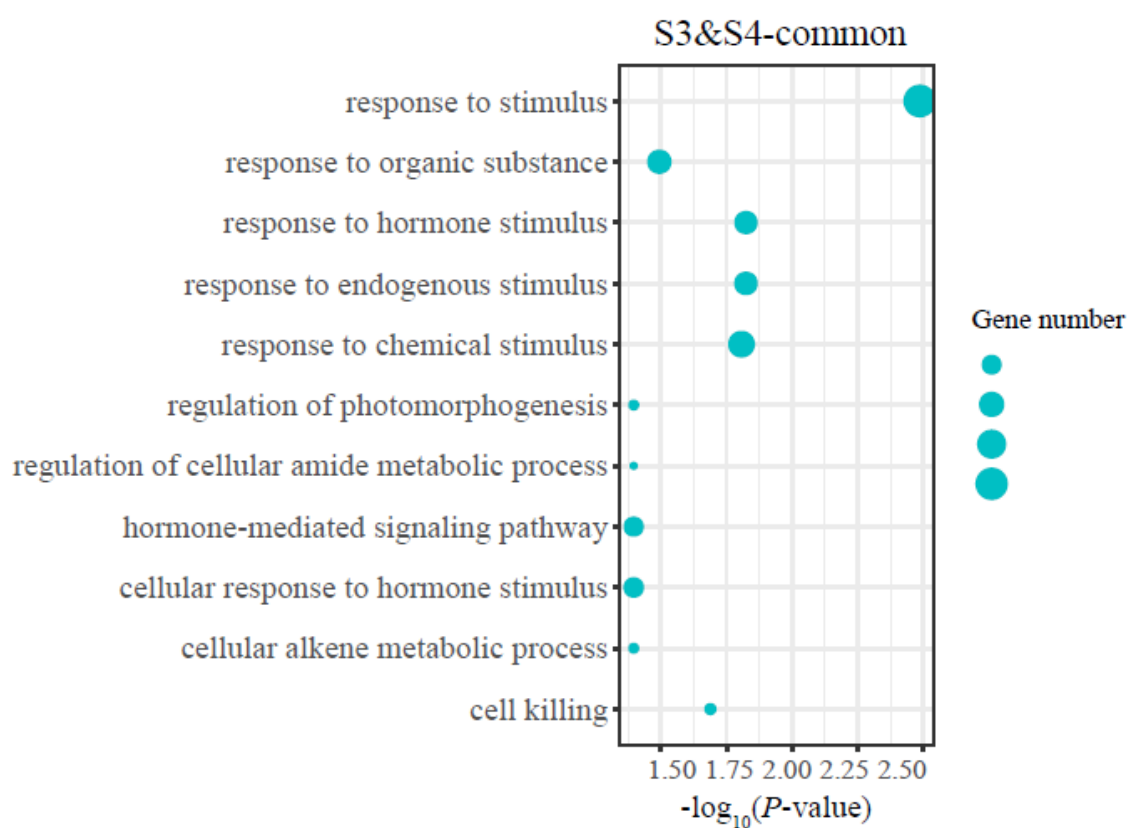


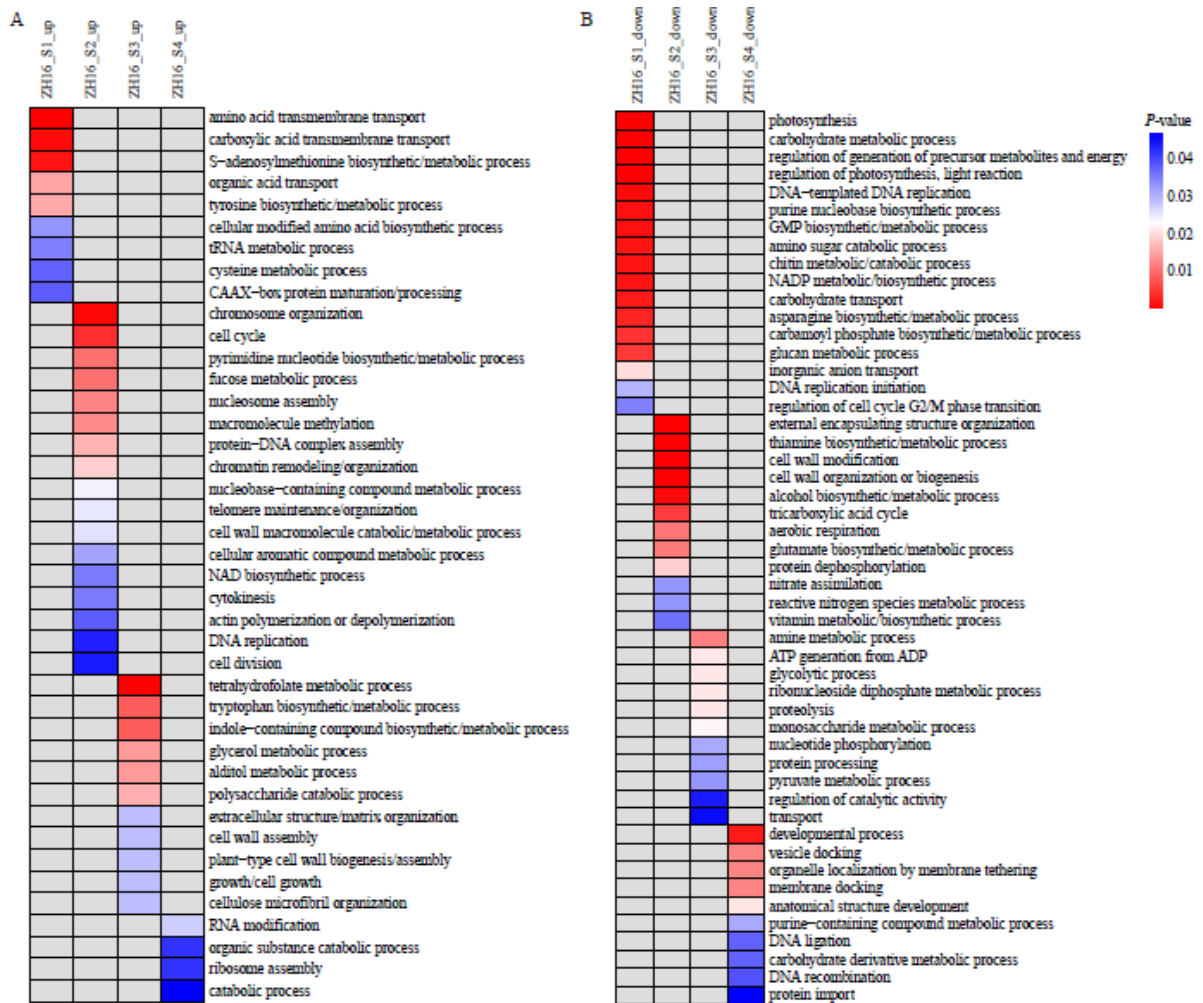
Supplementary Materials



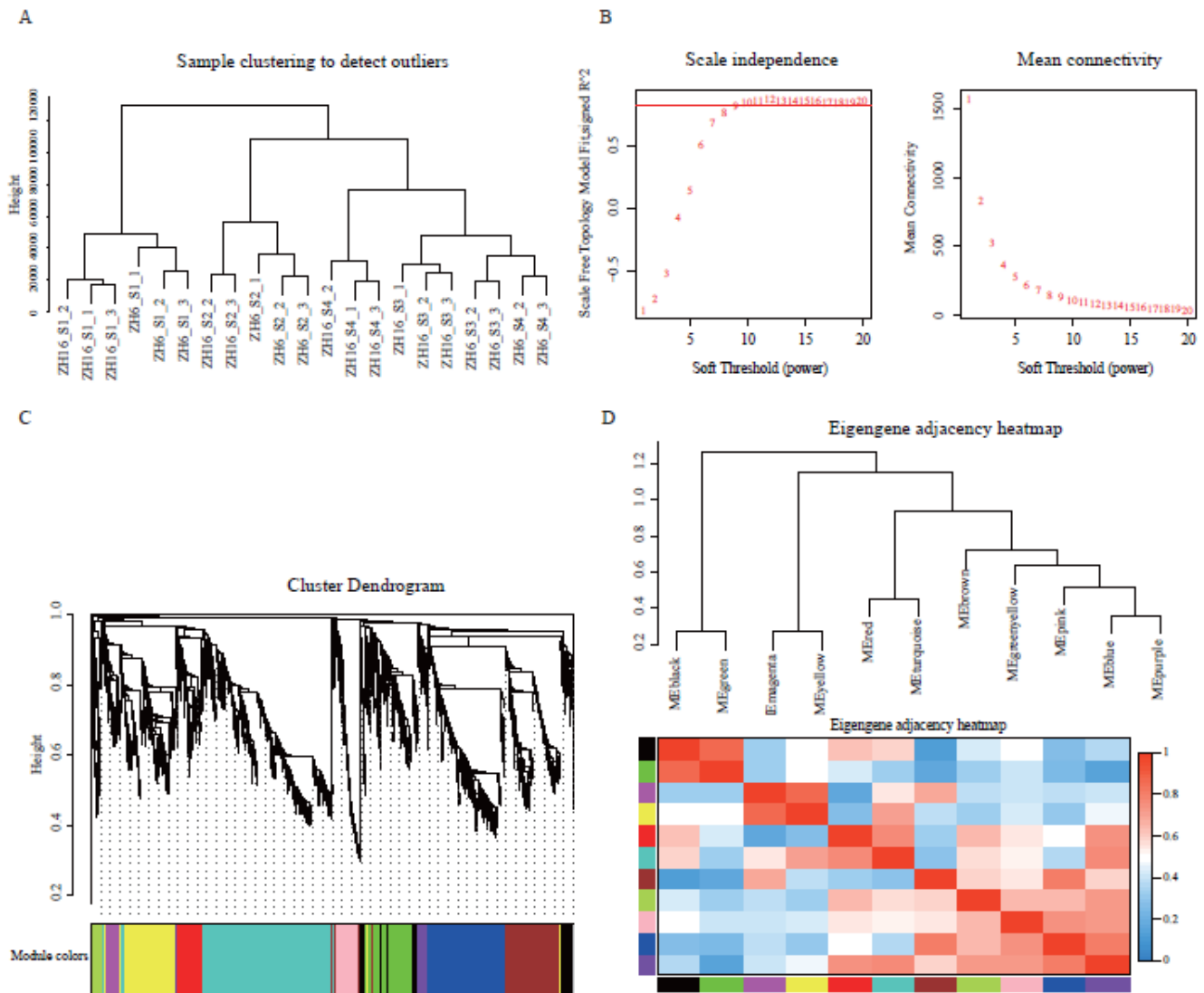
**Figure S1.** Correlation statistics and number of expressed genes at different stages of seed development between ZH16 and ZH6. (A) Spearman correlation coefficient (SCC) of RNA-seq data. (B) Bar plot showing number of expressed genes.



**Figure S2.** Enriched GO terms (biological process) of common stage-specific expressed genes in two cultivars at the S3 and S4 stages. The x-axis represents  $-\log_{10}(p\text{-value})$ . Bubble size represents the number of enriched genes.



**Figure S3.** Specifically enriched GO terms of up-regulated (A) or down-regulated (B) genes at each stage of seed development.



**Figure S4.** Network topology analysis. (A) Sample clustering. (B) Topology and connectivity based on soft thresholding powers. (C) Hierarchical clustering of co-expression modules. Each leaf on the tree represents a gene. The major branches form 11 color-coded modules. (D) Correlation heatmap across different modules.