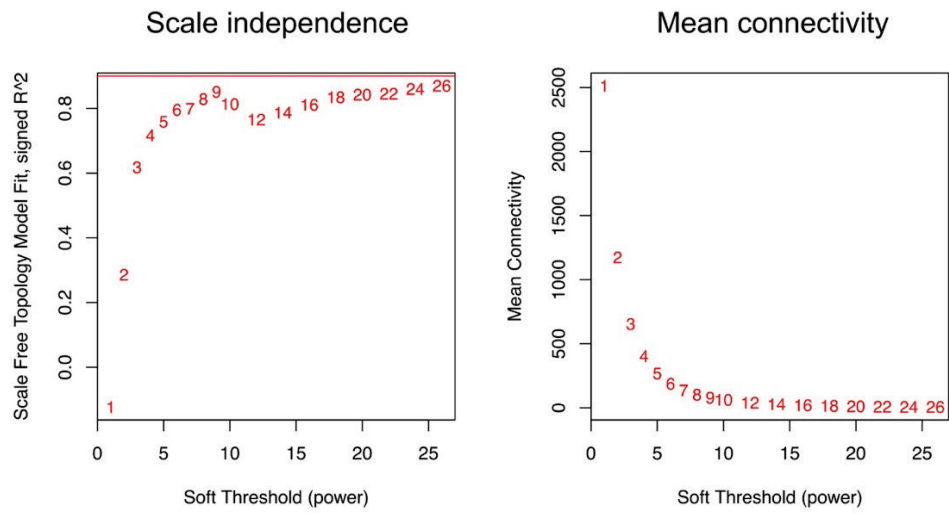
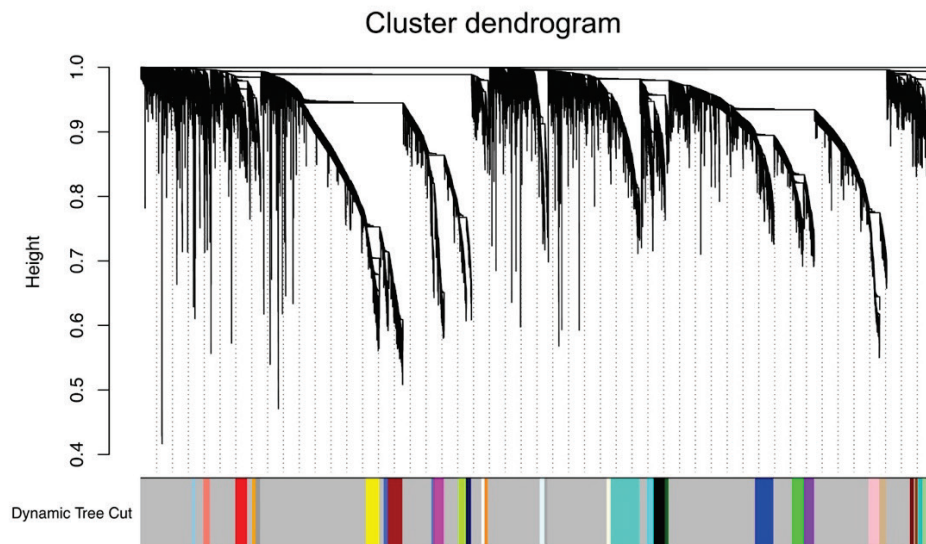


A**B**

Supplementary Fig. 2. Weighted gene co-expression network construction and module detection. **(A)** Selection of the soft-thresholding powers. The left figure shows the scale-free fit index versus soft-thresholding power. The right figure displays the mean connectivity versus soft-thresholding power. **(B)** Cluster dendrogram and module assignment from weighted gene co-expression network analysis. Genes were clustered based on a dissimilarity measure (1-TOM). The branches correspond to modules of highly interconnected groups of genes. Colors in the horizontal bar represent the modules.