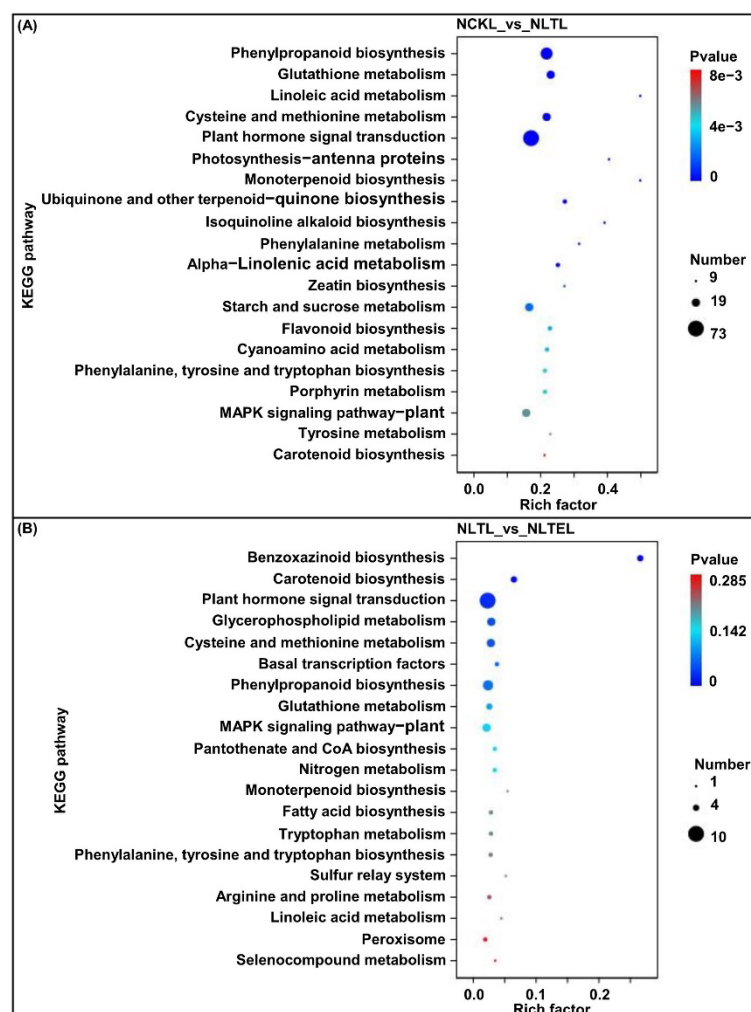


1
2 **Figure S1** GO enrichment analysis of the differentially expressed genes (DEGs) detected in
3 NCKL_vs_NLTL and NLTL_vs_NLTEL comparisons. The topmost enriched GO terms under the
4 three main GO categories are shown. NCKL: leaves of N192 seedlings treated with 0 μ M 2,4-
5 epibrassinolide (EBR) application at 25°C normal temperature (CK); NLTL: leaves of N192
6 seedlings treated with 0 μ M EBR application at 15°C low-temperature (LT); NLTEL: leaves of N192
7 seedlings treated with 2 μ M EBR application at 15°C normal temperature (LTE).



8

9 **Figure S2** The top20 KEGG pathway enrichment analysis of the differentially expressed genes
10 (DEGs) detected in NCKL_vs_NLTL and NLTL_vs_NLTEL comparisons. Rich factor is the ratio
11 of DEGs to the total number of genes in each pathway. NCKL: leaves of N192 seedlings treated
12 with 0 μ M 2,4-epibrassinolide (EBR) application at 25°C normal temperature (CK); NLTL: leaves
13 of N192 seedlings treated with 0 μ M EBR application at 15°C low-temperature (LT); NLTEL: leaves
14 of N192 seedlings treated with 2 μ M EBR application at 15°C normal temperature (LTE).

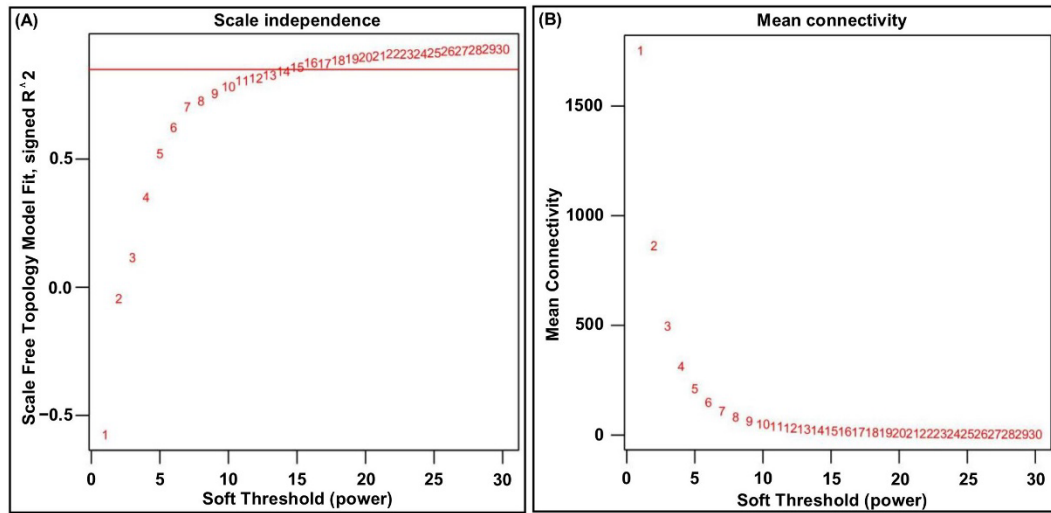


Figure S3 Soft threshold determination of gene co-expression network. **(A)** The abscissae is the soft threshold (β) and the ordinate is the scale-free network model index. **(B)** The abscissae is the soft threshold (β) and the ordinate is the mean connectivity.

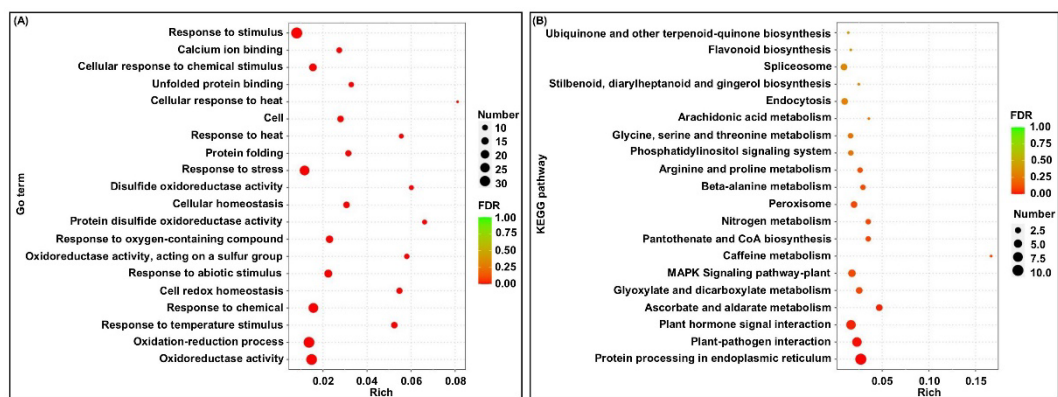


Figure S4 The function enrichment annotations of identified hub genes in four modules (blue, brown, salmon, and red). **(A)** GO enrichment analysis of these hub genes. **(B)** The top20 KEGG pathway enrichment analysis of these hub genes.