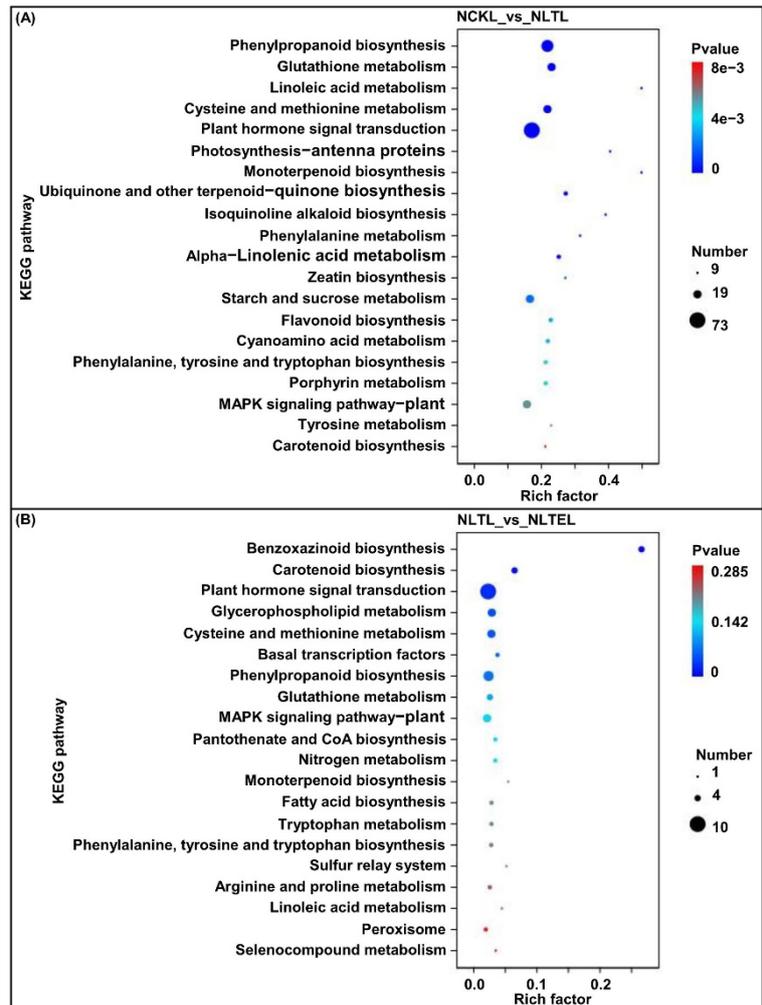


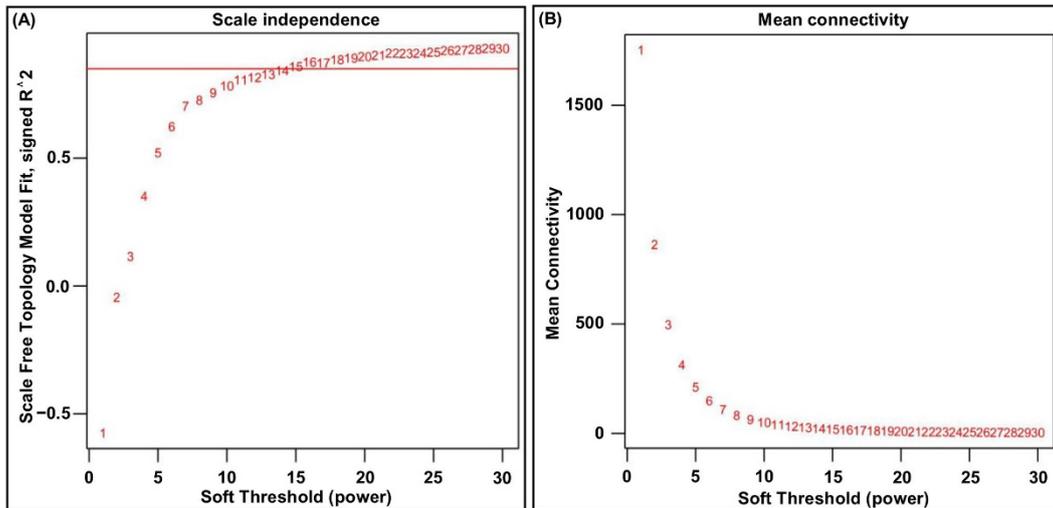
1

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).



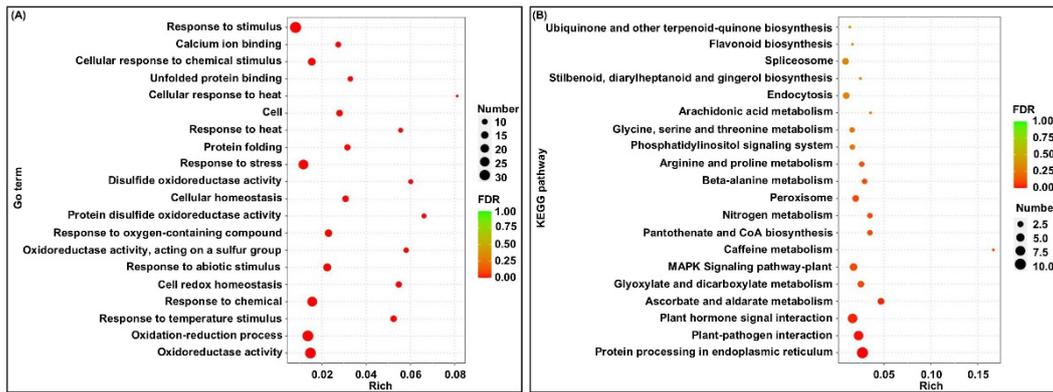
8

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).



15

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



19

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