



Figure S1. Morphology and root sprouting regeneration process of *T. fargesii*. (A) Large-diameter timber morphology in Jiulianshan nature reserve natural forest. The growth period of new leaves in spring (March). (B) Formation of root buds on aboveground root. (C) Root sprouting seedling. (D) The ramets are connected by the mother root in root sprouts forest. The yellow circular dotted line shows the root buds; the red dotted line shows the seedlings or ramet; the black dotted line shows the mother root; The yellow dotted line shows the lateral roots with ramets.

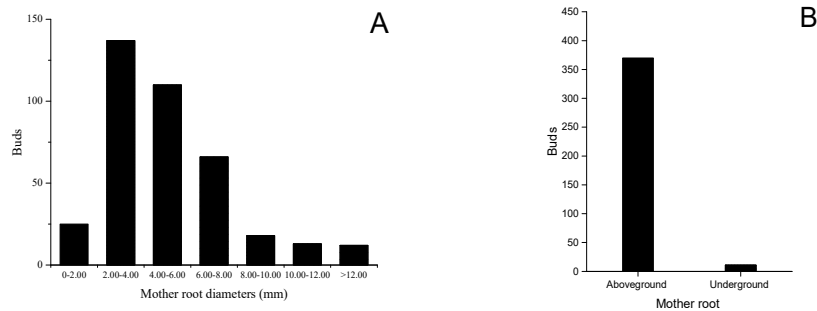


Figure S2. The mother roots (lateral roots) diameter and soil location of root bud formation was investigated in the natural secondary forest of *T. fargesii* to April. (A) Number of root buds with different mother root diameter; (B) Number of roots buds between aboveground roots and underground roots.

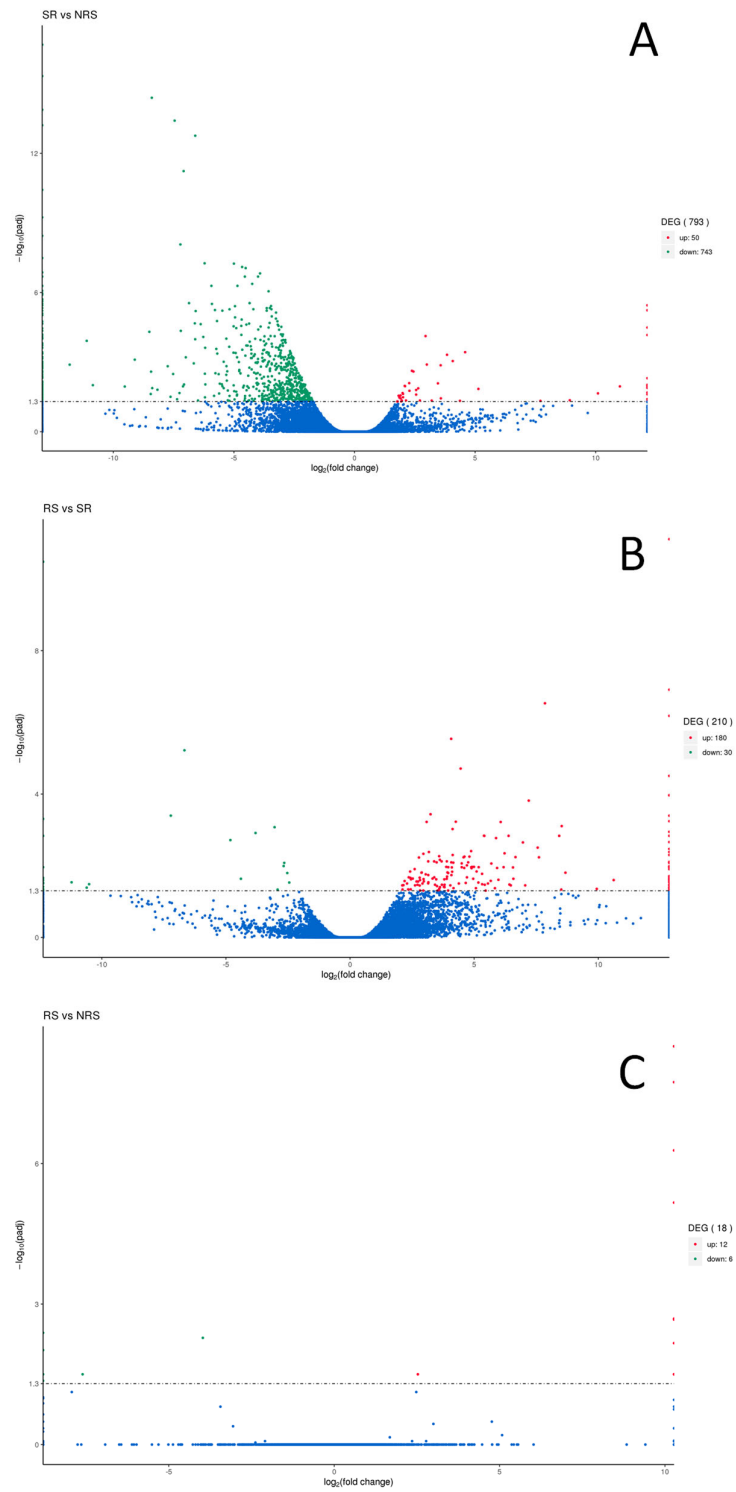


Figure S3. The venn diagram of DEGs between RS, NRS and SR.

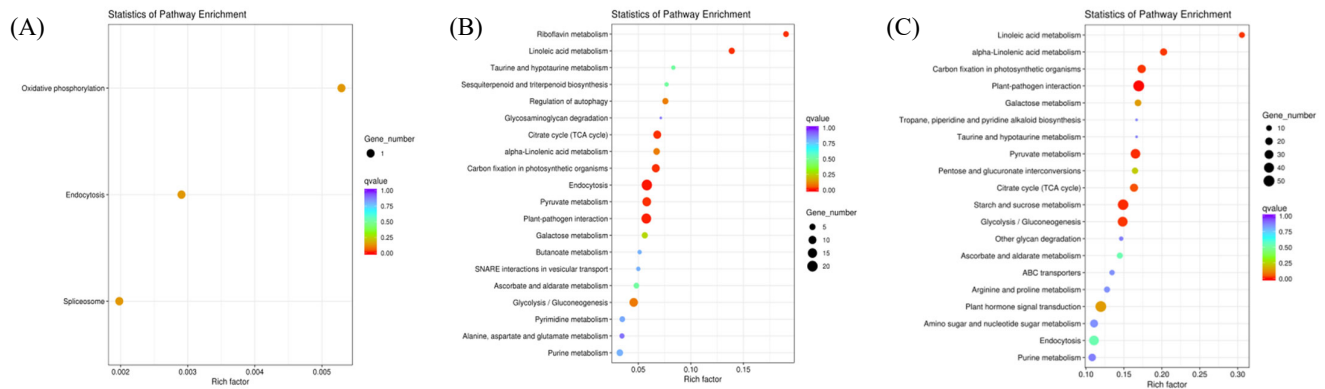


Figure S4. KEGG pathway enrichment of the annotated DEGs. (A) RSs vs NRSs. (B) NRSs vs SRs. (C) RSs vs SRs. The Y-axis indicates the KEGG pathway, the X-axis indicates the rich factor. The dot size indicates the number of DEGs of the pathway, and the dot color indicates the q-value.

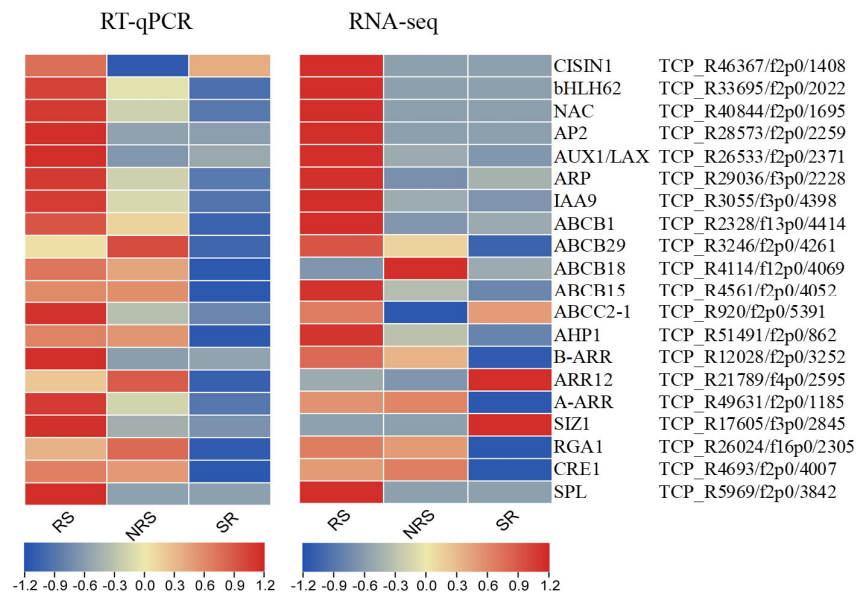


Figure S5. Heat map diagram showing changes in gene expression obtained by RNA-seq versus RT-qPCR analysis. Each column represents a root status (RS, NRS, and SR). The FPKM value of RNA-seq and gene relative normalized expression value of RT-qPCR is designated as log2 which is the average of three biological replicates. Red color indicated up-regulated genes and blue color indicates down-regulated genes as compared to control.