

Figure S1. (A) Frequency distribution of plant height in the BC₈ population. (B) Frequency distribution of main inflorescence length in the BC₈ population. (C) Frequency distribution of average length of primary branches in the BC₈ population.



Figure S2. Plant architecture of offspring derived from crosses between 4942C-5 and 8008.

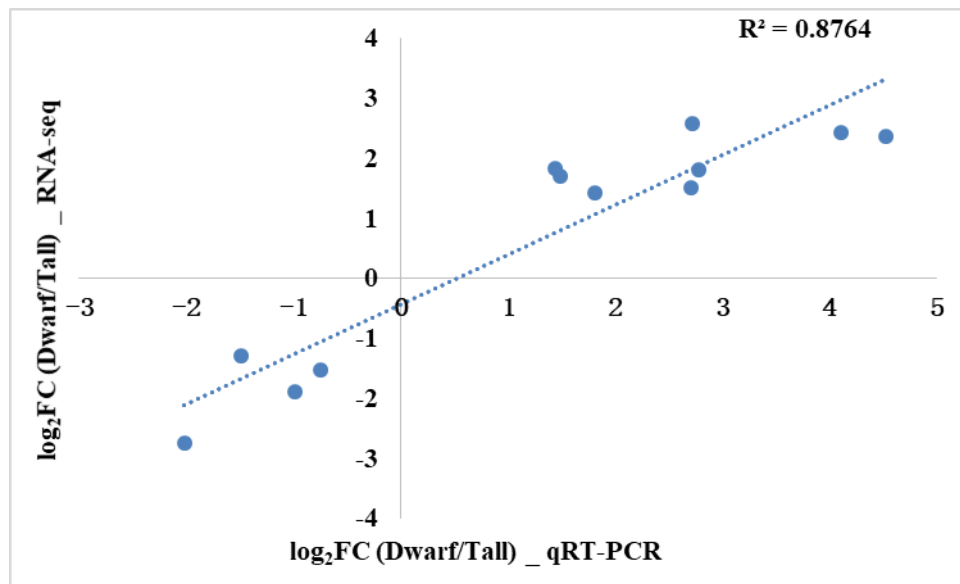


Figure S3. Correlation of the gene expression ratios between qRT-PCR and RNA-seq data. Expression abundance of 12 selected DEGs is presented as the ratio of Tall and Dwarf plants. Data represent mean values \pm SE of three biological replicates and three technical replicates of each sample.

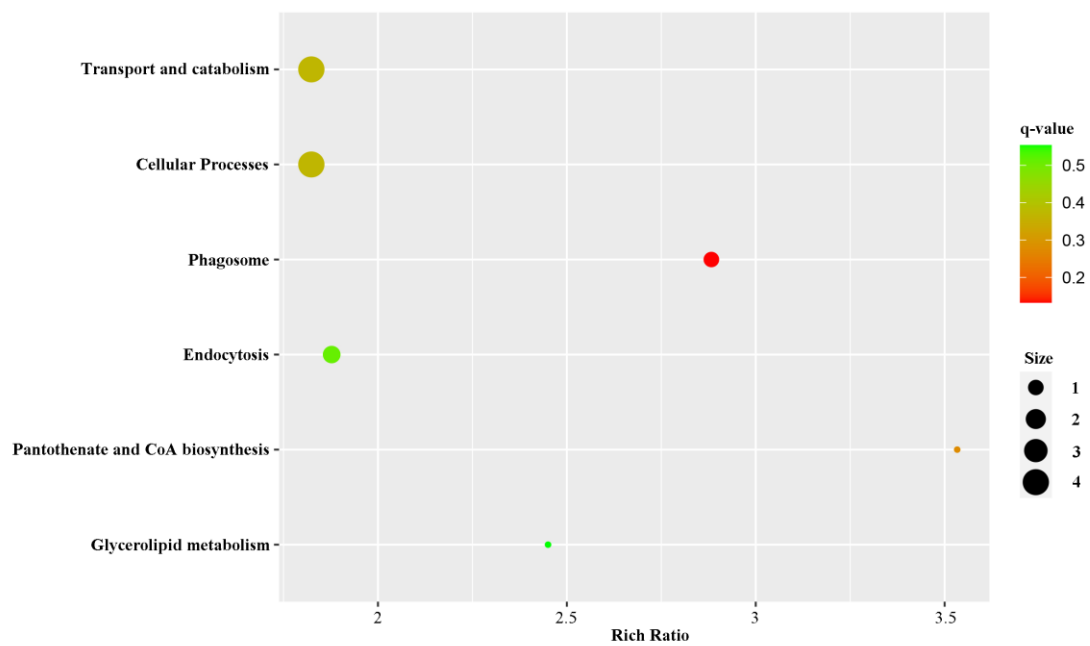


Figure S4. KEGG pathway enrichment of 542 DEGs in the candidate intervals.