

Figure S2. Phylogenetic relationships of wheat *4CL* and *HCT* genes with the homologs from other species. Phylogenetic trees of *4CL* (A) and *HCT* (B) were generated based on nucleic acid sequence similarity of wheat genes with 20 *4CL* and 9 *HCT* genes, respectively, of other monocot and dicot species collected from the NCBI nucleotide database [39] using MEGA program [41], and the trees were inferred using Maximum Likelihood method based on the Tamura-nei model. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test of 500 replicates is shown next to the branches. ●, wheat candidate gene; ▲, genes from dicot species other than Arabidopsis; *, wheat sequence used for the analysis.

