

**Figure S4.** Phylogenetic relationships of wheat *F5H* and *CAD* genes with the homologs from other species. Phylogenetic trees of *F5H* (A, B) and *CAD* (B) were generated based on nucleic acid sequence similarity of wheat genes with 7 *F5H* and 22 *CAD* 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. Two separate phylogenetic trees were generated for wheat *F5H1* (A) and *F5H2* (B) genes as MEGA could not find common sites between *F5H1* and *F5H2*.

