



Supplementary Figure 1. Homological analysis of TaCYP20-2.

(A) Phylogenetic tree of cyclophilin proteins from different organisms. The tree was

constructed by use of Clustal software.

(B) Alignment of the amino acid sequence for TaCYP20-2 and sequences encoded by related genes of wheat, rice, Arabidopsis, maize, tomato, fava bean and human. Multiple sequence alignment was constructed by Clustal software. Conserved residues in all sequences are highlighted in gray. Amino acids marked by * represent those required for PPIase catalysis and that marked by + for CsA binding.