Supplementary Figure 1. Draft phylogenetic tree for NtLEA7-3 and Arabidopsis LEA groups. The individual LEA from Arabidopsis was aligned and a phylogenetic relationship was derived by using the Neighbor-Joining method. The numbers on the branches represent bootstrap values based on 1000 replications. The set of LEA protein sequences used in this analysis was the same as the sets used in the analyses reported in (33), and the genes were classified according to the same report.
Supplementary Figure 1