

Supplemental Figure 1. Hierarchical clustering among the 618 genes responsive in the process of cold acclimation and cold deacclimation identified by 7K RAFL cDNA microarray analyses. The fold-change values for each sample, relative to control samples, were \log_2 transformed and subjected to the hierarchical clustering using standard correlation. The numbers on the left side represents relative expression ratio (cold acclimation/untreatment, or deacclimation from cold acclimation/cold acclimation). Expressions values higher and lower in the treated samples than those of the control are shown in red and blue, respectively. Expression values approximately equal levels between the treated samples and the control are shown in yellow.