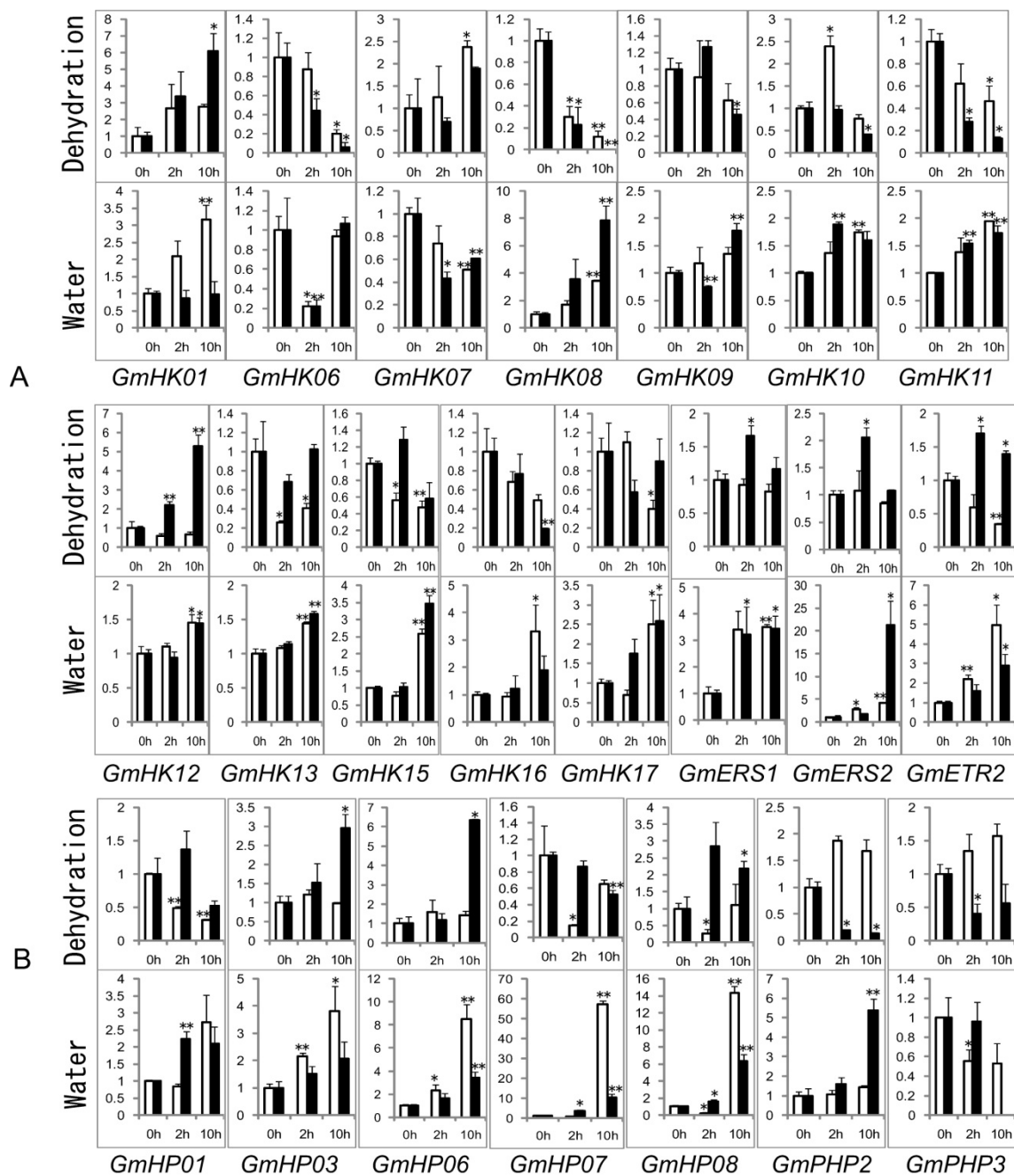
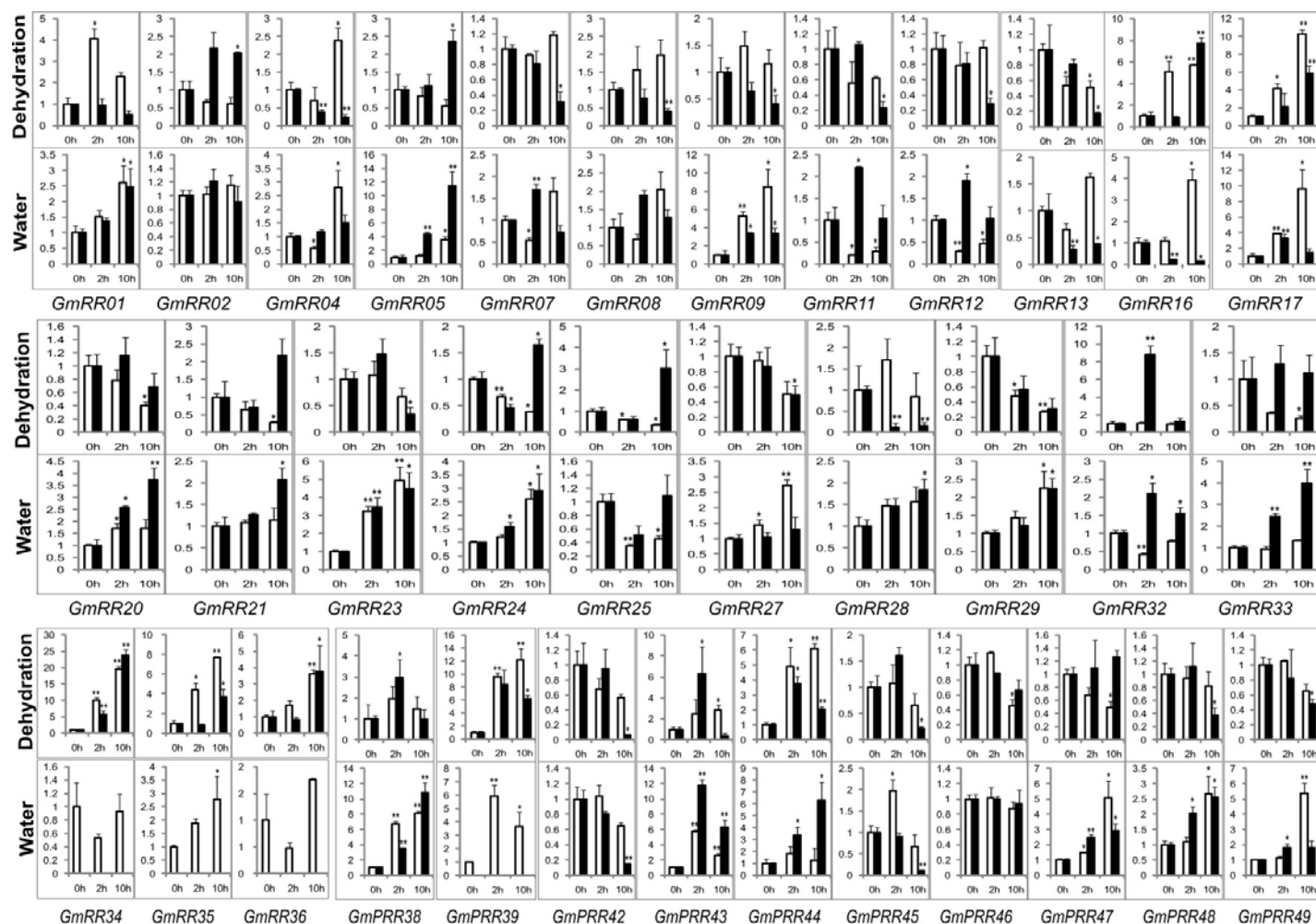


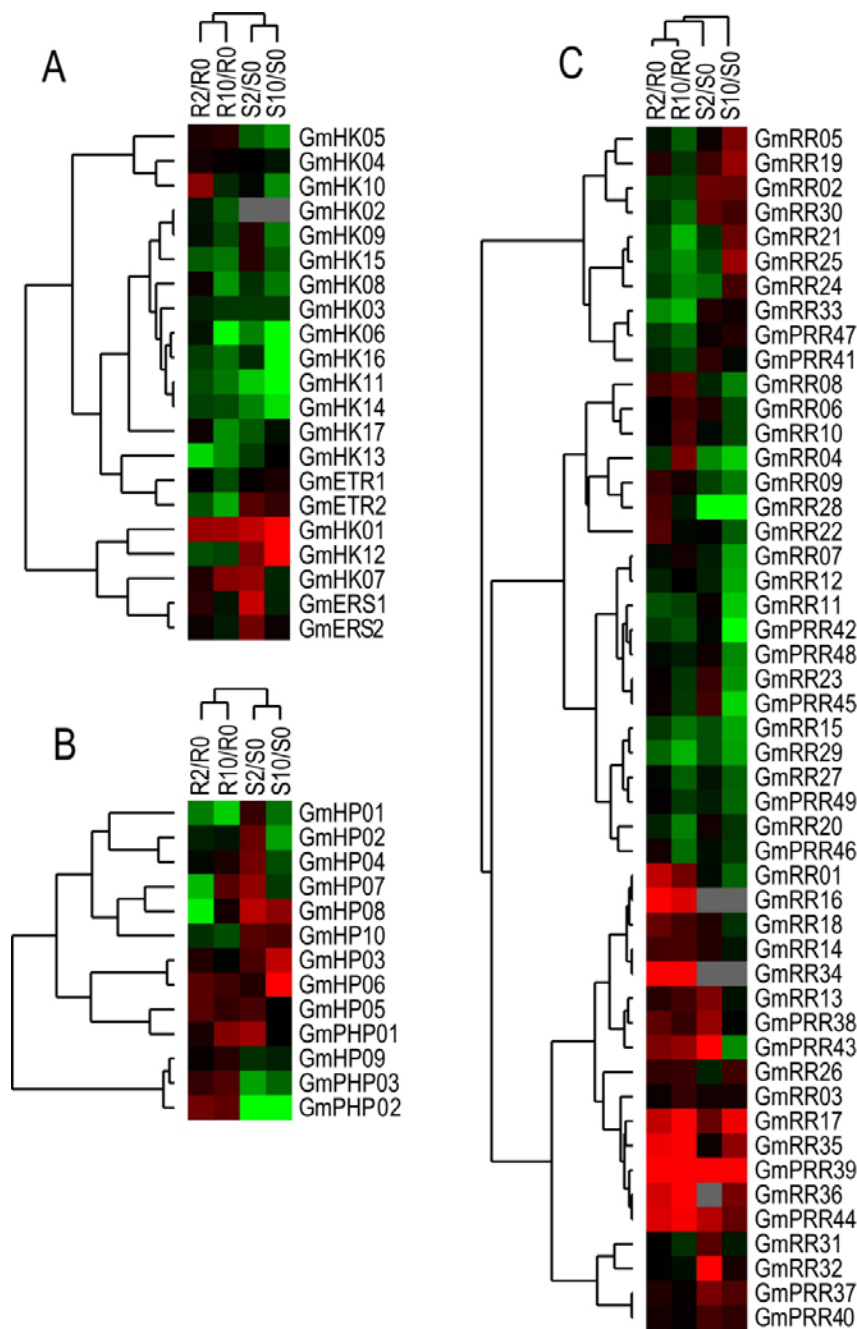
Supplementary Figure S1. Stress intensity of treated soybean plants. (A) Measurements of five independent plants were taken and averaged at indicated time points to determine the relative water content (%) and standardized water content (%). (B) Visual signs of the treated plants.



Supplementary Figure S2: Expression of the soybean TCS genes, whose mRNA levels were altered in dehydrated roots and shoots (upper panels), was examined in respective water-treated mock control tissues (lower panels). (A) TCS genes encoding HK proteins. (B) TCS genes encoding HPt proteins. Open and close columns indicate root and shoot tissues, respectively. Relative gene expression levels were normalized to a value at 1 in the untreated plant samples (0 h). Data represent the means and standard errors of three independent biological samples. Asterisks on top of bars indicate statistically significant differences when compared to 0 h with a p-value less than 0.05 (*) or 0.01 (**).



Supplementary Figure S3: Expression of the RR encoding soybean TCS genes, whose mRNA levels were altered in dehydrated roots and shoots (upper panels), was examined in respective water-treated mock control tissues (lower panels). Open and close columns indicate root and shoot tissues, respectively. Relative gene expression levels were normalized to a value at 1 in the untreated plant samples (0 h). Data represent the means and standard errors of three independent biological samples. Asterisks on top of bars indicate statistically significant differences when compared to 0 h with a p-value less than 0.05 (*) or 0.01 (**).



Supplementary Figure S4: Heat map presentation of the normalized expression data of the soybean TCS genes in response to dehydration. (A) TCS genes encoding HK proteins. (B) TCS genes encoding HPT proteins. (C) TCS genes encoding RR proteins. Expression levels of the soybean TCS genes at 0 h were normalized to 1, and the expression levels of the same gene at 2 h and 10 h after dehydration were calculated as a ratio to that at the 0 h. Genes clustered in this figure may be an indication of the same responsive patterns as a result of having similar dehydration-responsive *cis*-elements and/or transcription factors.