Supplementary Figure 1: Clusters of similarly expressed genes

A) K-means clustering was performed with 1,471 normalized unique sequences that are composed of 5 or more ESTs. Expression levels are plotted after log base (2) transformation. The mean expression values are represented by magenta lines. Putative genes were grouped into 14 clusters with distinct expression profiles. The optimal number of clusters was determined by Figure of Merit Analyses (shown in B). The total number of putative genes that make up each cluster is shown in the upper left hand corner of each panel. On each cluster, Cold H4 library (c), Drought H4 library (d), Heat H4 library (h), Salt H4 (s), and Salt/Heat H4 library (s/h) are plotted on the x axis and expression levels on the y axis. B) Figure of Merit (FOM) analysis was performed with the Genesis Software. Ten iterations were used to produce the FOM graph.