Supplemental Figure 1: Complete co-expression clustering results for genes with higher RPKM in Sha than in Ler (Sha/Ler RPKM ratio ≥5) after 10 h at -1.2 MPa. Edges represent genes having an expression correlation (Pearson correlation coefficient ≥ 0.6) over 2600 microarray data sets. Genes with higher RPKM in Sha that did not have a coexpression relationship with other genes higher in Sha are not shown here but are listed in Supplemental Table 2. Red color indicates genes recognized by a specific probe set in ATH1 arrays and having higher RPKM in Sha than in Ler. Lighter red indicates a greater difference in RPKM between Ler and Sha (see scale in lower right corner of figure). Uncolored nodes indicate cases where a gene was found to have higher RPKM in Sha but is part of a group of genes recognized by the same probe set in ATH1 arrays.
**Supplemental Figure 2: Complete co-expression clustering results for genes with Sha/Ler RPKM ratio ≤-5.** Analysis and data format are as described for Supplemental Figure 1. Green color indicates genes recognized by a specific probe set in ATH1 arrays and having lower RPKM in Sha than in Ler. Lighter green indicates a greater difference in RPKM between Ler and Sha (see scale in lower right corner of figure). Uncolored nodes indicate cases where a gene was found to have lower RPKM in Sha but is part of a group of genes recognized by the same probe set in ATH1 arrays.