



**Figure 5. Identification of coordinated responses to cold.** **A**) Venn diagram representing needle-specific, root-specific and common up-regulated differentially expressed genes (DEGs). A Gene Ontology (GO) enrichment analysis of these gene lists is available in Supplemental Table S8. **B**) Heat maps and main clusters of tissue specific and common up-regulated DEGs. Common DEGs were analyzed on both tissues and each identified cluster (C) was separated according clusters trends in needles (N) or in roots (R). **C**) Super clusters (SC) were defined by comparing clusters from Fig. B using Pearson correlation analysis. Common clusters (C) were separated by tissues to compare against tissue-specific clusters. So a cluster trend for a common cluster number “i” was called ‘C<sub>i</sub> in needles’ or ‘C<sub>i</sub> in roots’ according the tissue analyzed. For each SC, scaled gene expression mean values are represented with dotted lines. Grey areas represent variability by two standard deviation. An analysis of SC distribution in the network is available in Supplemental Figure S3. A GO enrichment analysis for these SC is available in Supplemental Table S9.