



**Figure 4. The response of needles and root transcriptomes from Norway spruce to exposure to cold (5°C) and freezing (-5°C).** **A)** Hierarchical clustering of gene expression data from needles and roots samples (see methods). Red numbers correspond to Approximately Unbiased (AU) values and green ones to Bootstrap Probability (BP) values. **B)** Analysis of transcriptome progression in response to cold (5°C) and freezing (-5°C). Differentially expressed gene lists (DEGs) were obtained at each point in the time series, compared against the control. DEGs in Needles (dark green represents induced genes and light green represents repressed genes) and Roots (brown represents induced genes and tan represents repressed genes) were obtained by filtering the data by corrected Pvalue  $\leq 0.01$  and Fold Change  $\geq 2$ . **C)** The number of DEGs (counts) with different GOSlim tags assigned are represented by bubble size. GOSlim enrichments with Bonferroni corrected P-values  $\leq 0.05$  are represented with a red color scale. Non-significant P-values (corrected P-values  $> 0.05$ ) are in grey. A full list of GOSlim enrichments is included in Supplemental Table S6 and a complete description of each GOSlim category and the gene functions in Supplemental Table S7.