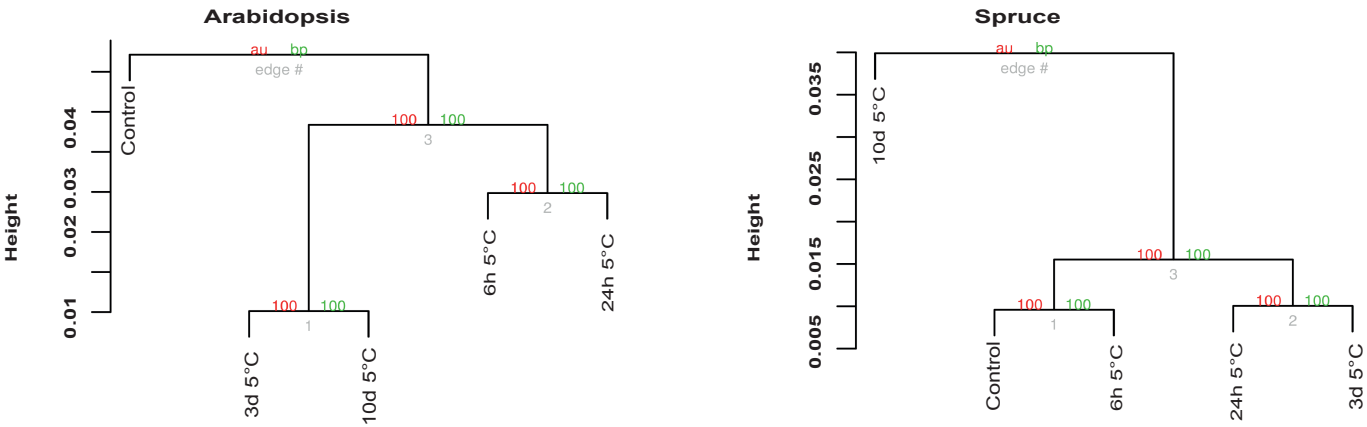
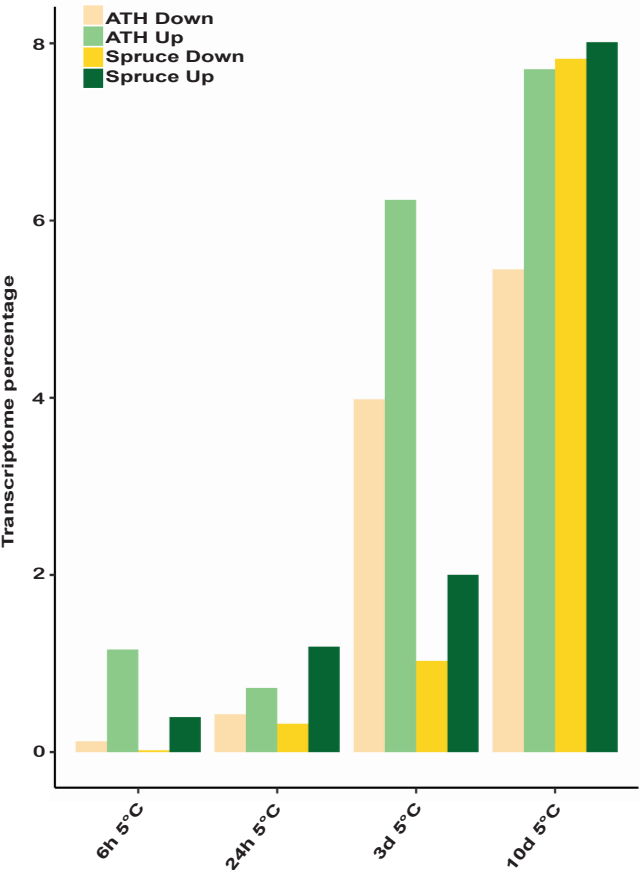


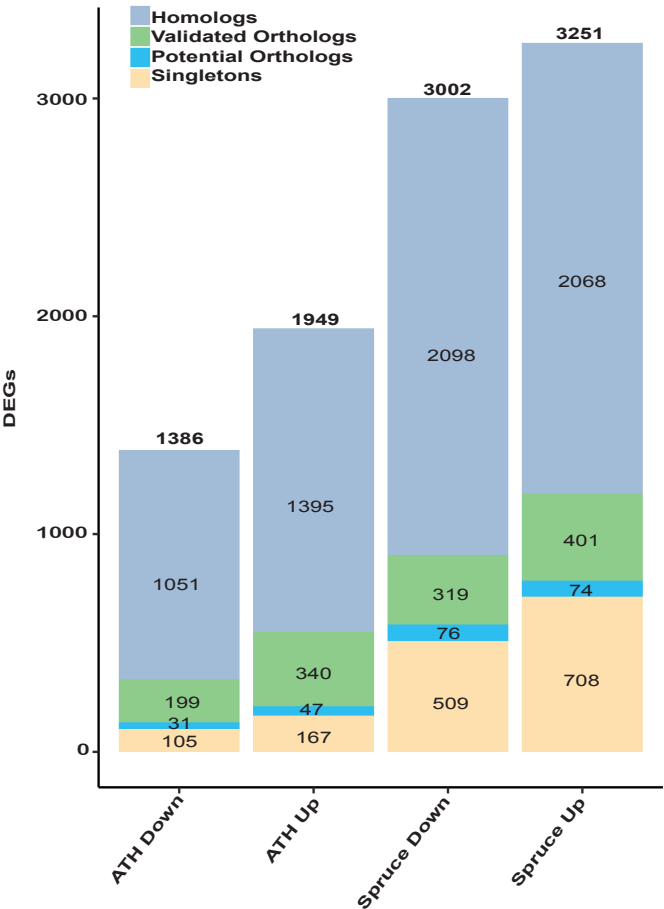
A



B



C



**Figure 1. Comparing the response of *Arabidopsis thaliana* leaf and *Picea abies* (Norway spruce) needle transcriptomes exposed to 5°C.** **A)** Hierarchical clustering using normalized data (see methods). The red numbers correspond to Approximately Unbiased (AU) values and the green ones to Bootstrap Probability (BP) values. **B)** Analysis of transcriptome progression in response to cold. Differentially expressed gene lists (DEGs) were obtained at each point in the time series, compared against the control, and then represented as a percentage of the transcriptome. DEGs significantly induced in *Arabidopsis* (green) and *Spruce* (dark green) and significantly repressed DEGs in *Arabidopsis* (yellow) and *Spruce* (dark yellow) were obtained by filtering the data by corrected Pvalue  $\leq 0.01$  and Fold Change  $\geq 2$ . **C)** Orthologs, Homologs and Species-specific DEGs for both species (down and up-regulated). Validated orthologs correspond to orthologous genes that are differentially regulated by cold in both species. Gene lists for each group and functional information are available in Supplemental Table S1.