

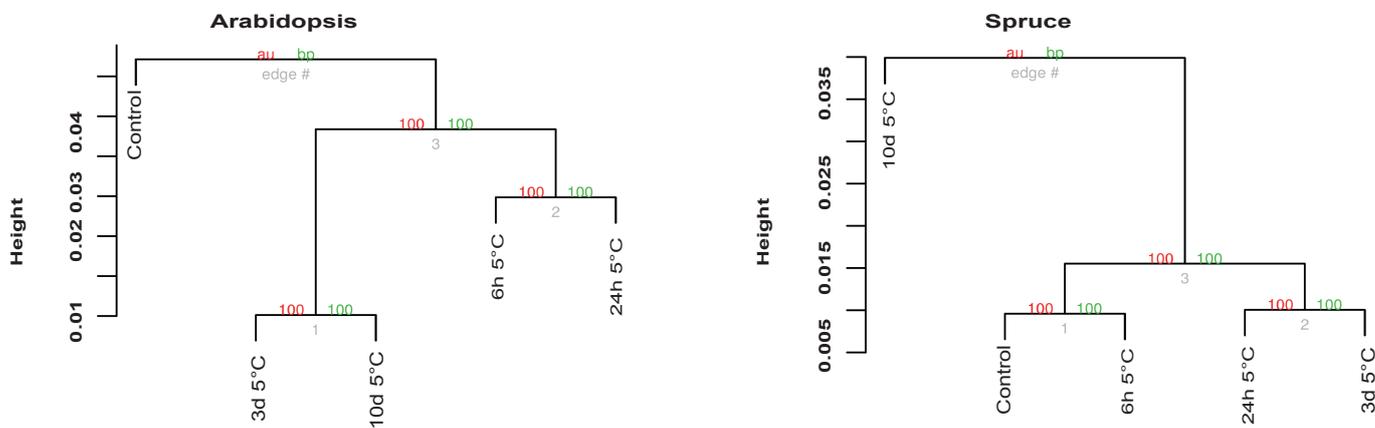
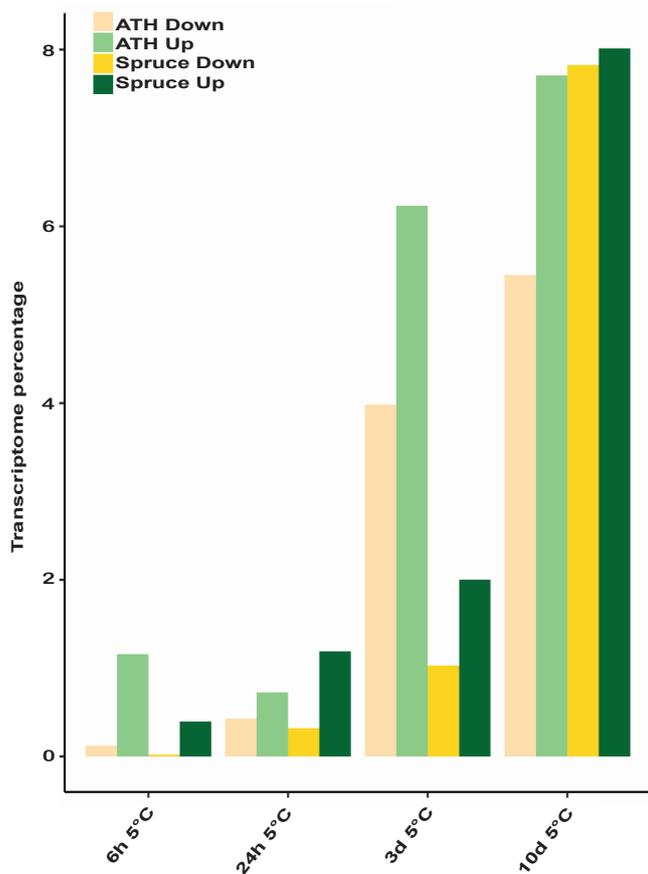
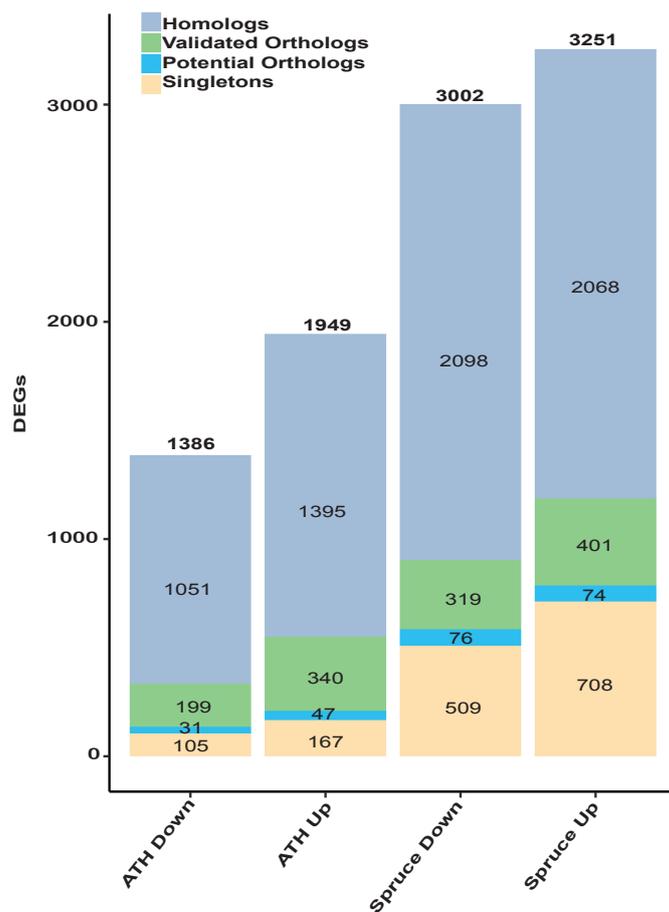
A**B****C**

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 ≤ 0.01 and Fold Change ≥ 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.