Figure 7. Regulatory network analysis. A) Network representation of predicted regulatory interactions between Transcription Factors (TF) and cold responsive (COR) genes. TFs are represented by diamonds and their family by colors. COR genes are represented by circles and colored according to the tissue in which they are differentially regulated. **B)** Network Degree distribution in Log10/Log10 scale. **C)** Sub-network of the 10 genes with the highest centrality. Gene Ontology (GO) enrichments in the hub neighborhoods are available in Supplemental Table S12 and topology information and gene aliases are available in Supplemental Table S13.