Figure 3. Treatment with methyl jasmonate (MeJA) induces a transient shift in the transcriptome of Norway spruce bark.

Principle component analysis (PCA) (a) and hierarchical clustering analysis (HCA) (b) plots displaying how treatment of 2-year-old spruce seedlings with water (blue) or 10 mM MeJA (red) impacts on the bark transcriptome over the subsequent 4 weeks. All genes with a total mRNA-seq read count of ≥ 100 across the 32 samples (n = 4 per treatment and time point) were included in the analyses. Both the PCA and the HCA utilised counts normalised with a variance-stabilizing transformation. Samples in the HCA were clustered using the Euclidean distances between samples (darker blue for lower distances) and the complete-linkage method.