



Figure 4. Response of the Norway spruce bark transcriptome to methyl jasmonate (MeJA) treatment.

Expression profiles and functional characterisation of 6330 genes showing a significantly (adjusted p-value < 0.001) altered expression pattern, over a 28-day period, between bark tissues of 2-year-old spruce seedlings treated with water (control, blue) or 10 mM MeJA (red).

(a) Differentially expressed genes were grouped into 13 clusters (indicated by the coloured boxes with associated gene numbers (N)) using Spearman distances and Ward's method. The 13 clusters were assigned to one of four patterns (P) based on their general expression profile in MeJA relative to water treated plants: 1 – Upregulated; 2 – Upregulated, then downregulated; 3 – Downregulated; 4 – Downregulated, then upregulated. Read counts are displayed as per gene z-scores normalised for library size and transformed using the DESeq2 function `vst`.

(b) Per-cluster mean expression profiles with 95% confidence intervals. Variance-stabilizing transformation (VST) transformed counts are approximately on a \log_2 scale.

(c) Significantly overrepresented protein signatures (adjusted p-value \leq 0.05). If a cluster had more than five significantly enriched protein signatures, only the five with the highest fold enrichment are displayed. See Supplemental Data Set 3 for the full list of enriched protein signatures.