



Figure 8. Methyl jasmonate (MeJA) treatment alters the expression of regulators of multiple epigenetic modifications in Norway spruce bark, including DNA methylation.

(a) Bars show the number of annotated genes in different epigenetic regulator categories. Genes showing a significantly (adjusted p -value < 0.001) altered expression pattern across time as a result of treatment are indicated in grey. (b) The individual transcripts (faint lines with 95% confidence intervals) and category means (solid lines) for differentially expressed regulators of DNA methylation homeostasis in water (blue) and MeJA (red) treated bark (See Supplemental Data Set 6). Read counts were normalised using the variance stabilizing transformation (VST) in DEseq2. Epigenetic regulator categories are taken from Mageroy et al (2020b).