Figure S1

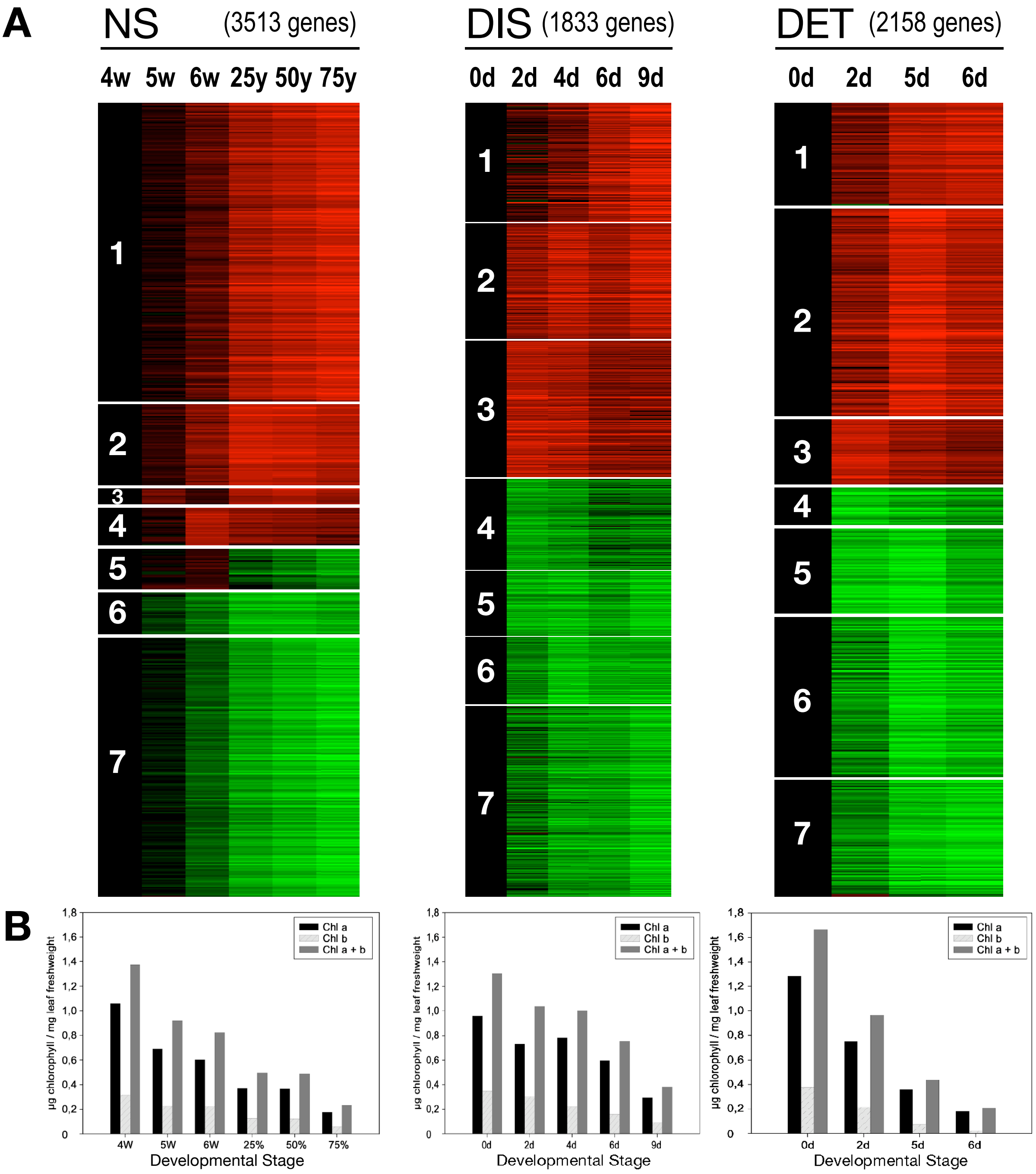

Figure S1: **A**: k-means clustering of the significantly regulated genes. The genes regulated during NS (3513 genes), DIS (1833 genes) and DET (2158 genes) were sorted into clusters one to seven (indicated in white letters in the 4w/0d columns). Bars in red indicate upregulation, bars in green indicate downregulation and bars in black indicate no significant regulation. **B**: Chlorophyll a and b content of the leaf material harvested at subsequent senescence stages for RNA preparation was determined.