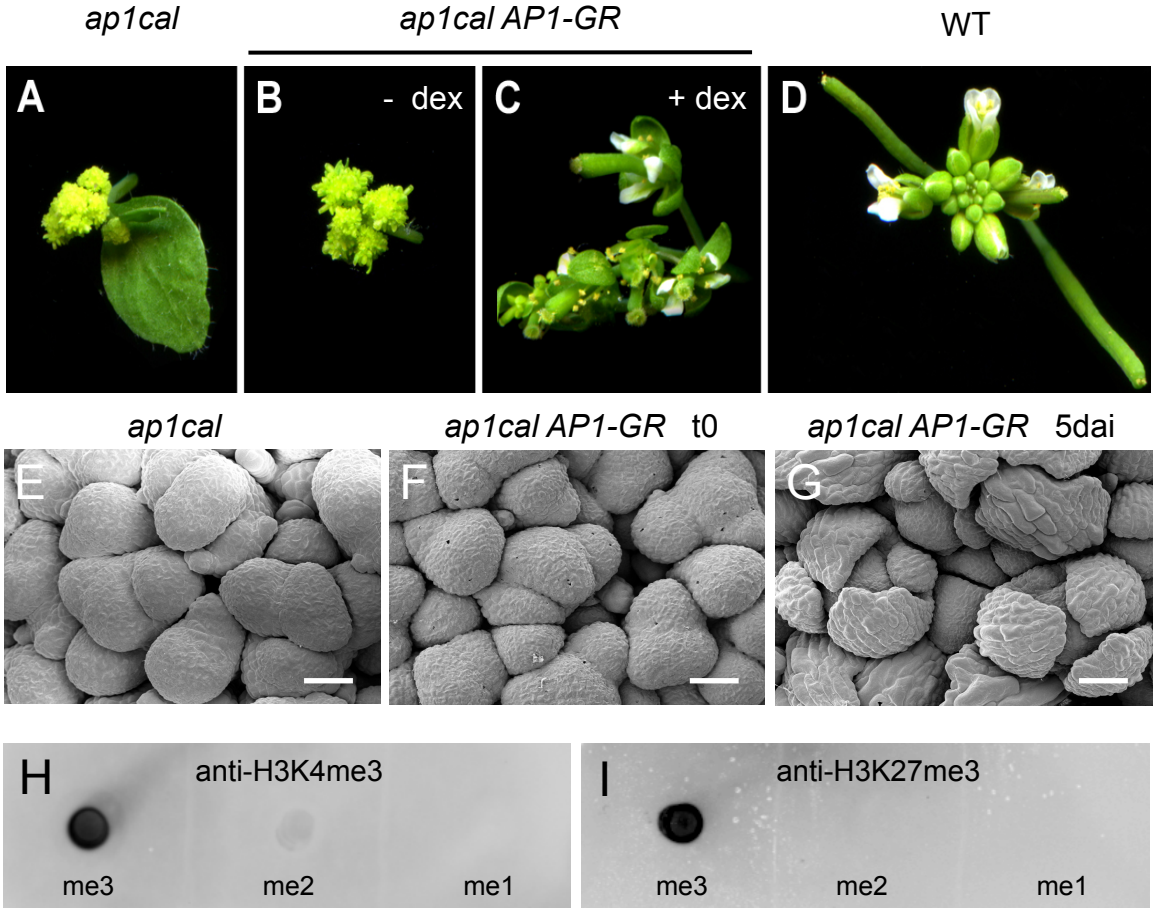

Figure S1. Validation of the material used for the analysis of early events of gene activation, *in situ*. (A-G) Validation of the *ap1cal AP1-GR* induction system. To verify the morphological effect of *AP1* induction and assess its blockage by the GR system, we compared inflorescence tissue of *ap1cal* plants and *ap1cal 35S::AP1-GR* plants, pre- and post-induction. (A) - (D) Floral induction in *ap1cal* double mutants by AP1-GR activation. Top viewed inflorescences of (A) *ap1cal*, (B-C) *ap1cal 35S::AP1-GR* and (D) L*er* wild type (WT). Pictures were taken 12 days after single treatment with (A, C, D) or (B) without 1 μM of dex solution. Activation of the AP1-GR protein in the *ap1cal* led to the production of WT looking flowers. (E) – (G) Scanning electron micrographs of inflorescence-like meristems of (E) *ap1-1 cal-1*, (F) untreated *ap1cal 35S::AP1-GR* and (G) *ap1cal 35S::AP1-GR*, five days after a single treatment with 1 μM of dex solution. Scale bars: 10 μm. While *ap1cal* and non-induced *ap1cal 35S::AP1-GR* plants show over-proliferated inflorescence meristems with no difference in floral organ formation, *ap1cal 35S::AP1-GR* plants had formed full flower buds with clearly visible sepals five days after induction. (H-I) Specificity assessment of antibody lots used in the chromatin immuno-precipitation experiments. Dot-Blots using anti-H3K4me3 and anti-H3K27me3 antibodies were performed on peptides containing mono- (me1), di (me2) and tri (me3)-methylated versions of the respective residue.

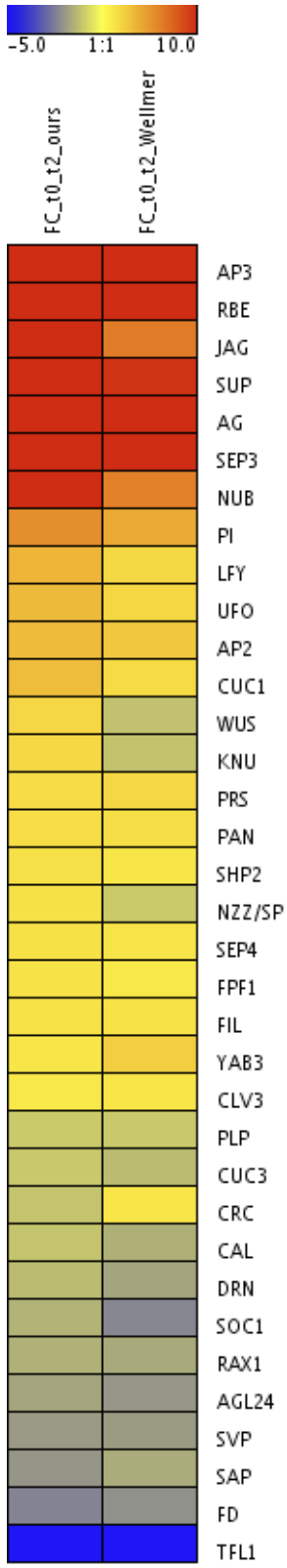

Figure S2. Comparison of expression changes from t0 to t2 in this study and in Wellmer *et al.* (2006). Fold changes (FC) in expression are depicted by a heat map reaching from genes expressed 5 times lower in t2 than t0 (blue) to genes expressed 10 times higher in t2 than t0 (red).

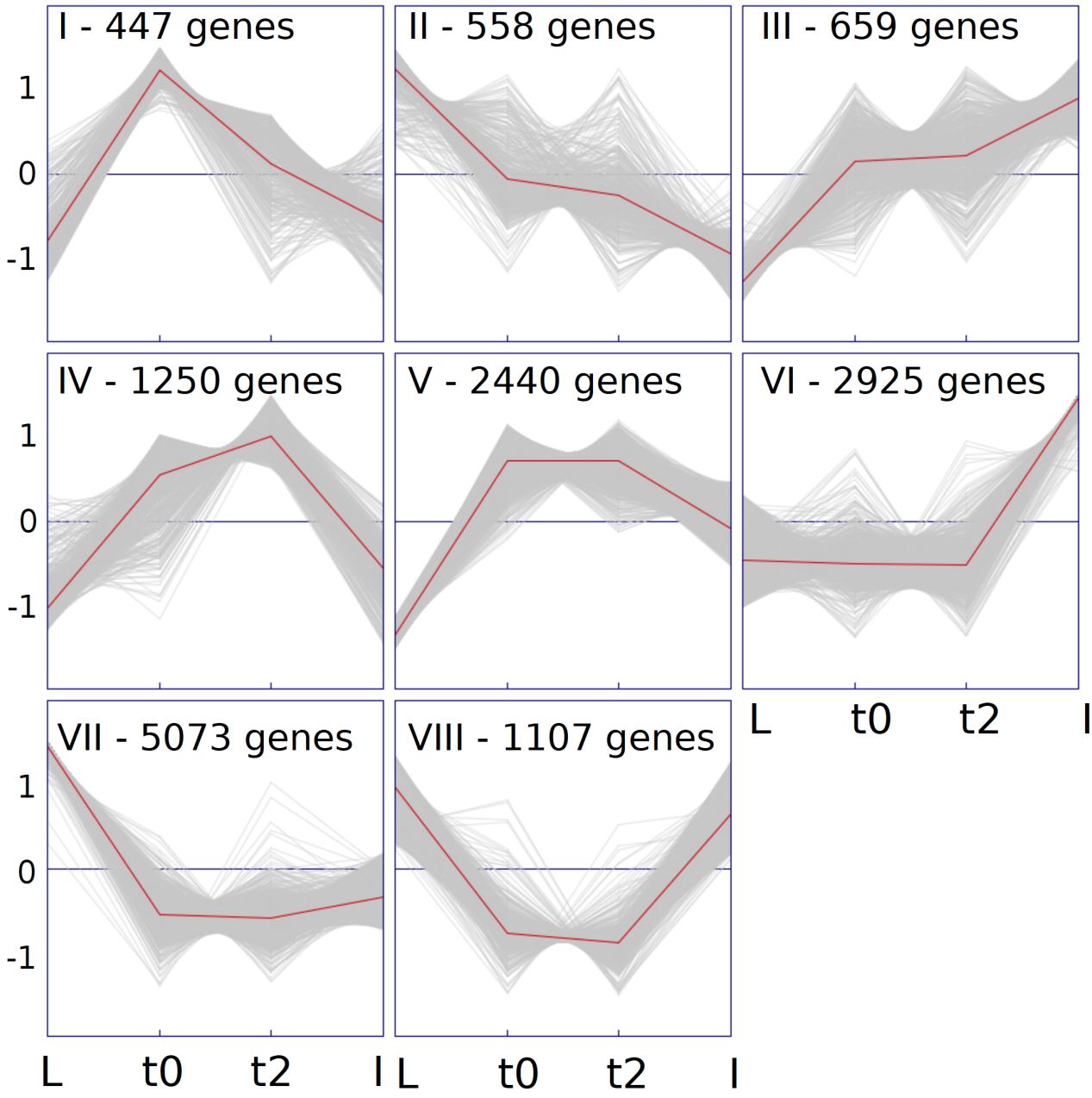

Figure S3. Major expression patterns present among differentially expressed genes (DEG). K-means clustering with k=8 was performed for all DEGs yielding an overview of expression profiles in the 8 clusters. Relative expression values are expressed as z-scores to reveal similarities in expression patterns. Averages of z-scores in each cluster are depicted in red. The grey lines represent the single genes in the cluster.

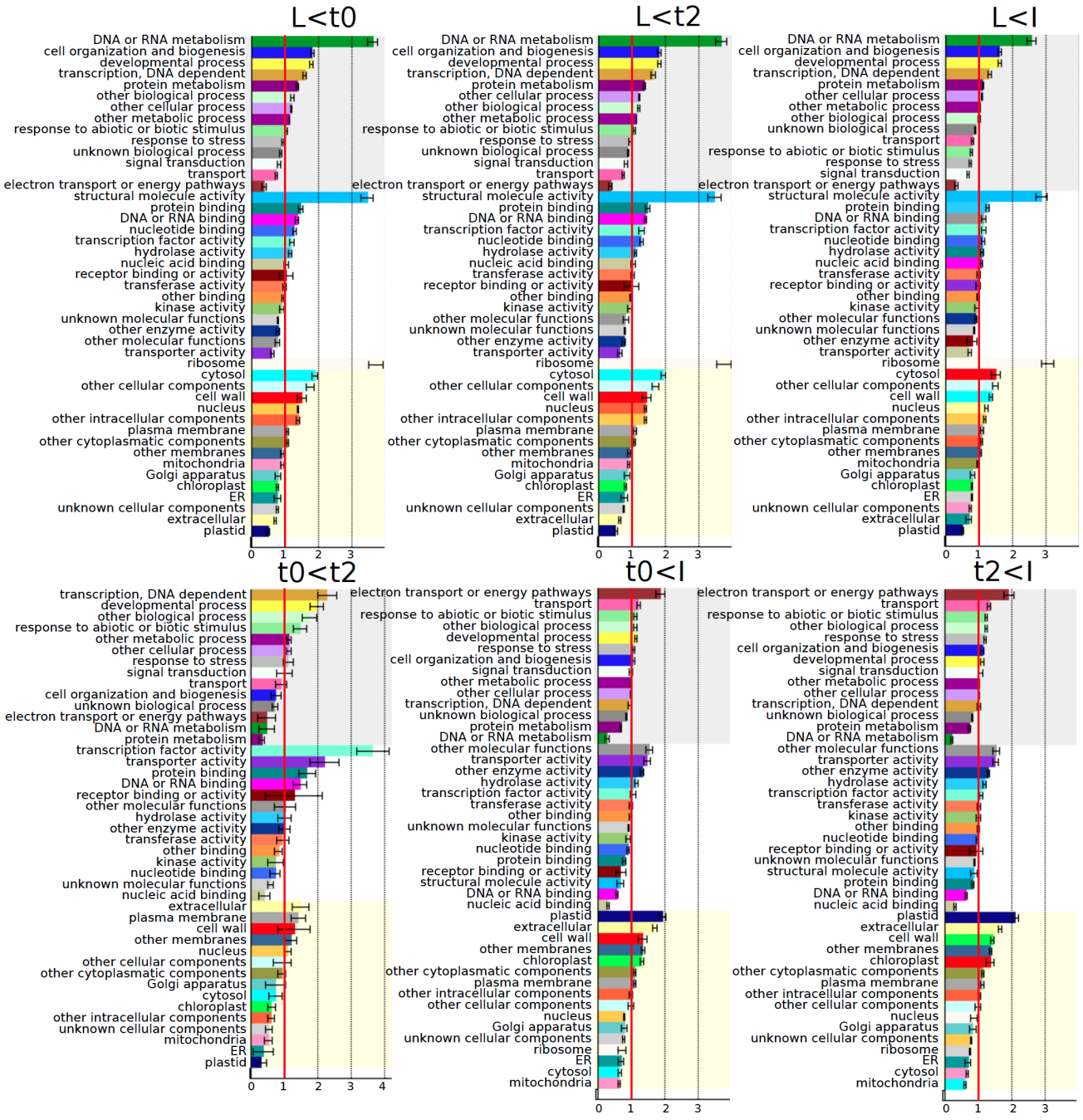

Figure S4. Functional characterisation of up-regulated DEGs. Panels were generated with the Classification Super Viewer from the BAR website (http://bar.utoronto.ca) using default parameters. The expected background is calculated by bootstrapping 100 sets of the same size from the whole genome. The y-axis displays normed frequencies with the expected frequency in the background distribution (whole genome) set to 1 (red line)

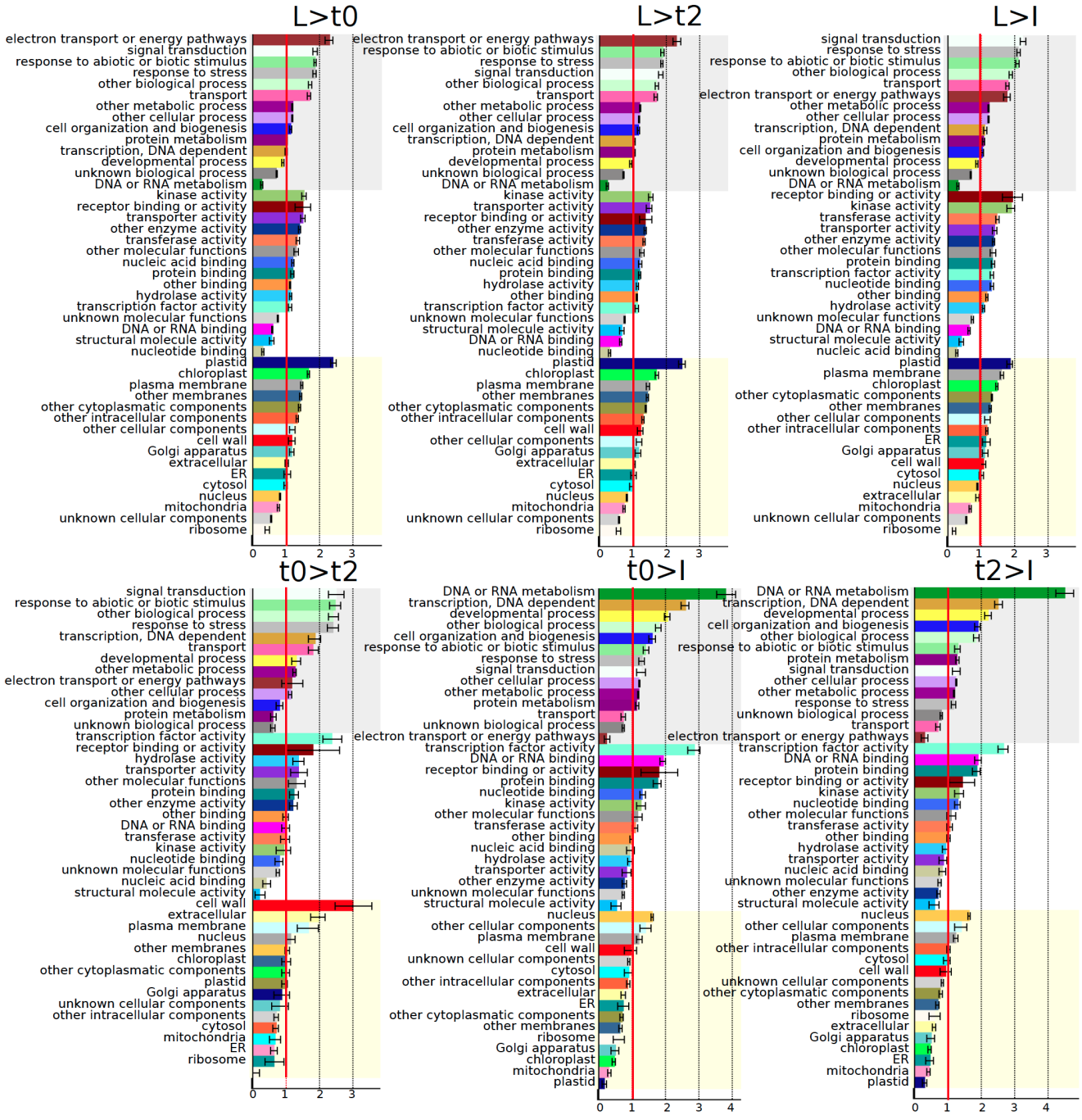

Figure S5. Functional characterisation of down-regulated DEGs. Panels were generated with the Classification Super Viewer from the BAR website (http://bar.utoronto.ca) using default parameters. The expected background is calculated by bootstrapping 100 sets of the same size from the whole genome. The y-axis displays normed frequencies with the expected frequency in the background distribution (whole genome) set to 1 (red line).

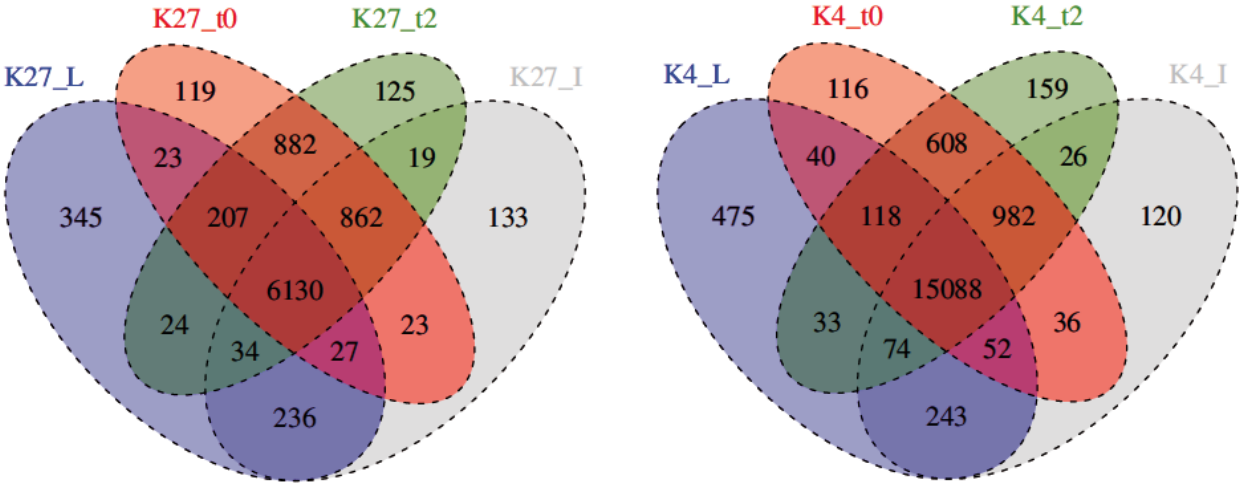

Figure S6. Overlap between target genes in the four considered time points/tissues for H3K27me3 (K27) and H3K4me3 (K4).

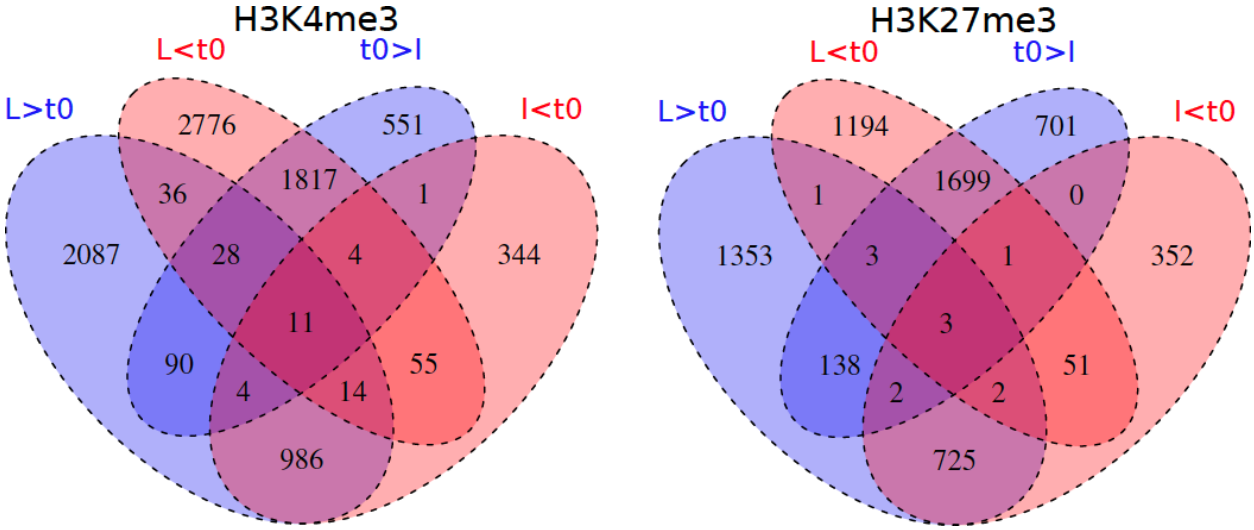

Figure S7. Overlap between differentially marked genes for H3K27me3 and H3K4me3 for changes from leaf to meristematic tissue (L-t0) and from meristematic tissue to inflorescences (t0-I).

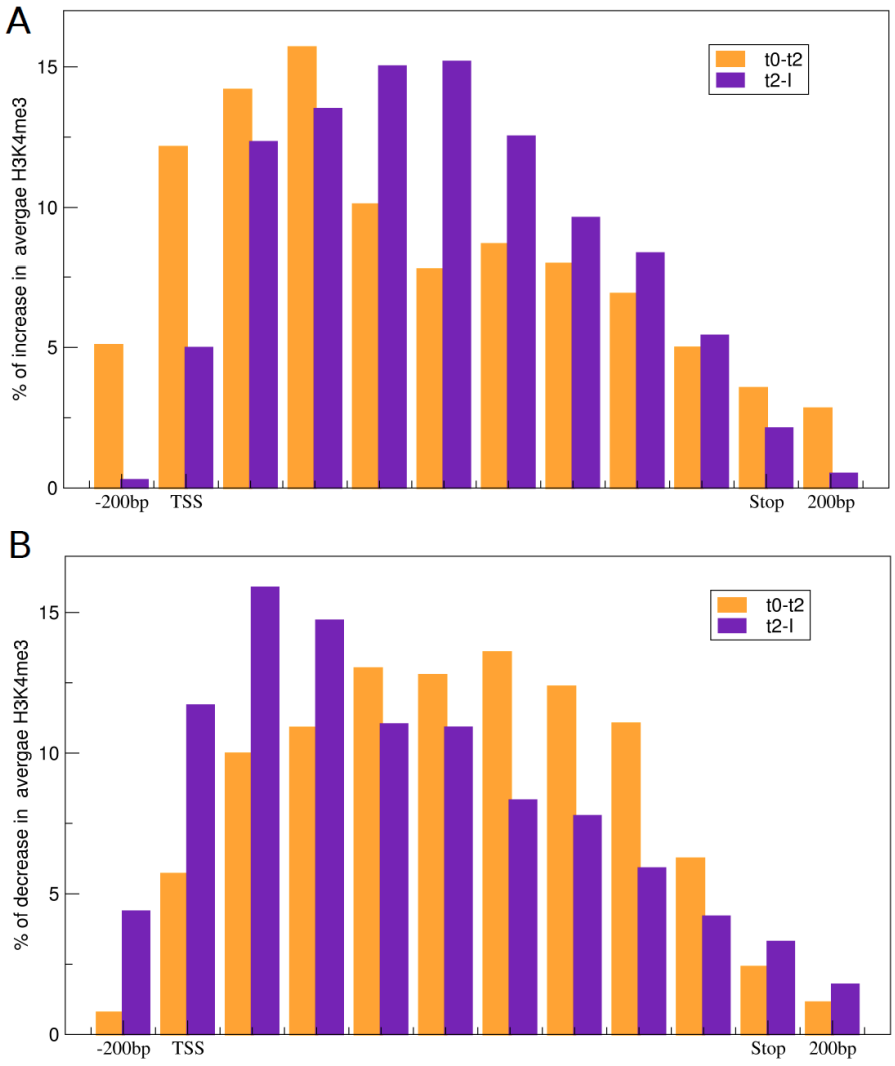

Figure S8. H3K4me3 signal shift between early and later expression changes. Only genes that are differentially expressed in both the t0 to t2 and t0 to I comparison, i.e. are activated or repressed early and stay activated/repressed after t2, are considered here (131 genes for activation and 105 genes for repression). Average differences in H3K4me3 signal (in reads per million) for genes are calculated in 200 bp windows/10% bins over genes from -200 bp to 200 bp downstream for each gene. For each bin, the percentage of the change on the whole change over the gene is displayed for t2 minus t0 and t2 minus I for both up-regulated (A) and down-regulated genes (B).

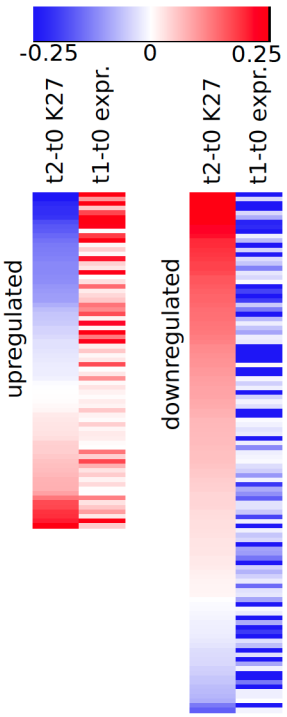

Figure S9. Expression changes of early DEGs during flower morphogenesis at t1. Heat maps showing the difference in expression from t0 to t1 as measured in a microarray experiment (Wellmer et al., 2006). Each line represents a DEG (from t0 to t2 comparison in our study). Genes are sorted by their average H3K27me3 change (T2-t0) as shown in the first column of the heat map with marks changing in the expected direction at the top. Note that only genes present on the microarray are shown and thus not all DEGs are considered.

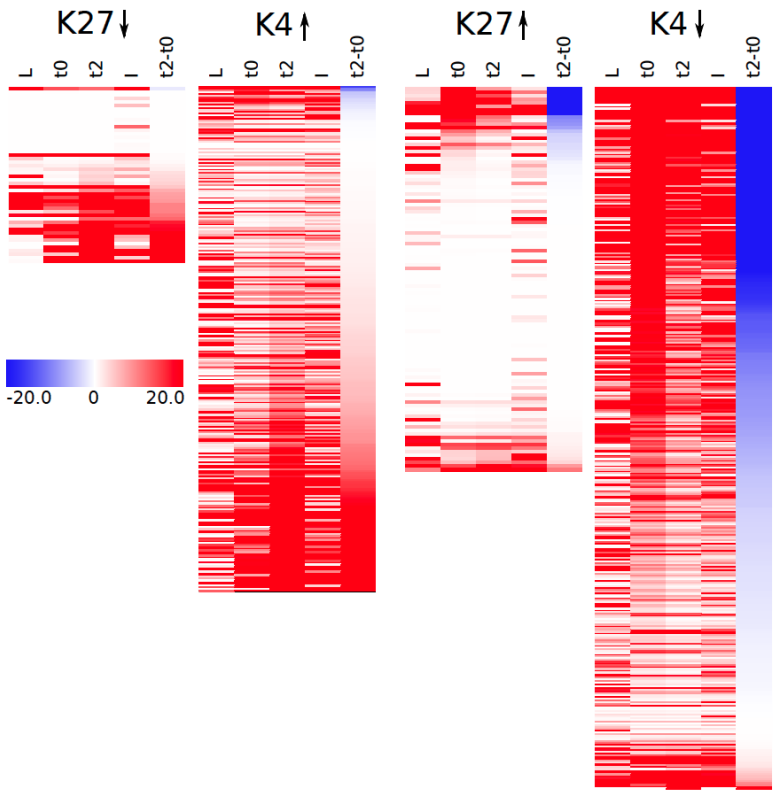

Figure S10. Expression of early DMGs during the time series. Heat maps showing expression values (FPKM) for significantly changing genes for H3K27me3 and H3K4me3. Each line represents a gene sorted by the expression changes during early flower morphogenesis (t2 minus t0, indicated as a column of the heatmap for orientation), with the highest negative expression change (down-regulation) at the top.

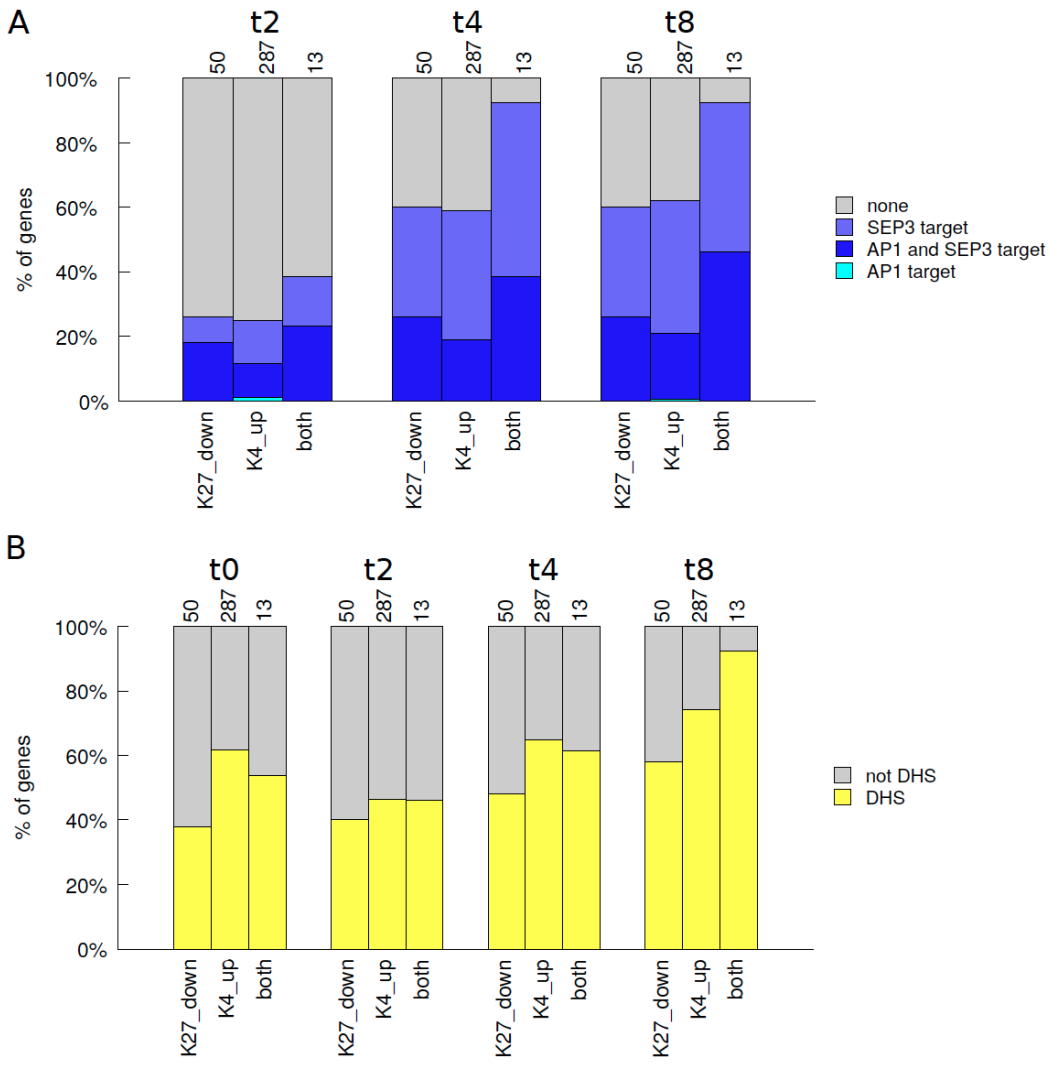

Figure S11. Correlation of genome-wide changes in histone marks from t0 to t2 and binding of MADS TFs or DNase hypersensitivity during early flower development. (A) Fraction of DMGs for H3K27me3, H3K4me3 and both marks from t0 to t2 (K27 down: H3K27me3 reduced t0-t2, K4 up: H3K4me3 elevated t0-t2, both: H3K27me3 reduced and H3K4me3 elevated t0-t2) that are bound by AP1 and/or SEP3 during early flower development. TF binding at three time points after dex-induction was considered: t2, t4 and t8 (Pajoro *et al.*, 2014). Numbers above each bar indicate the total number of DMGs for each respective comparison. (B) Fractions of same DMGs as in (A) that overlap with DNase I hypersensitive sites (DHS) during the same three time points as in (A) and at t0 (Pajoro *et al.*, 2014). Numbers on each bar indicate the total number of DMGs in the respective comparison.