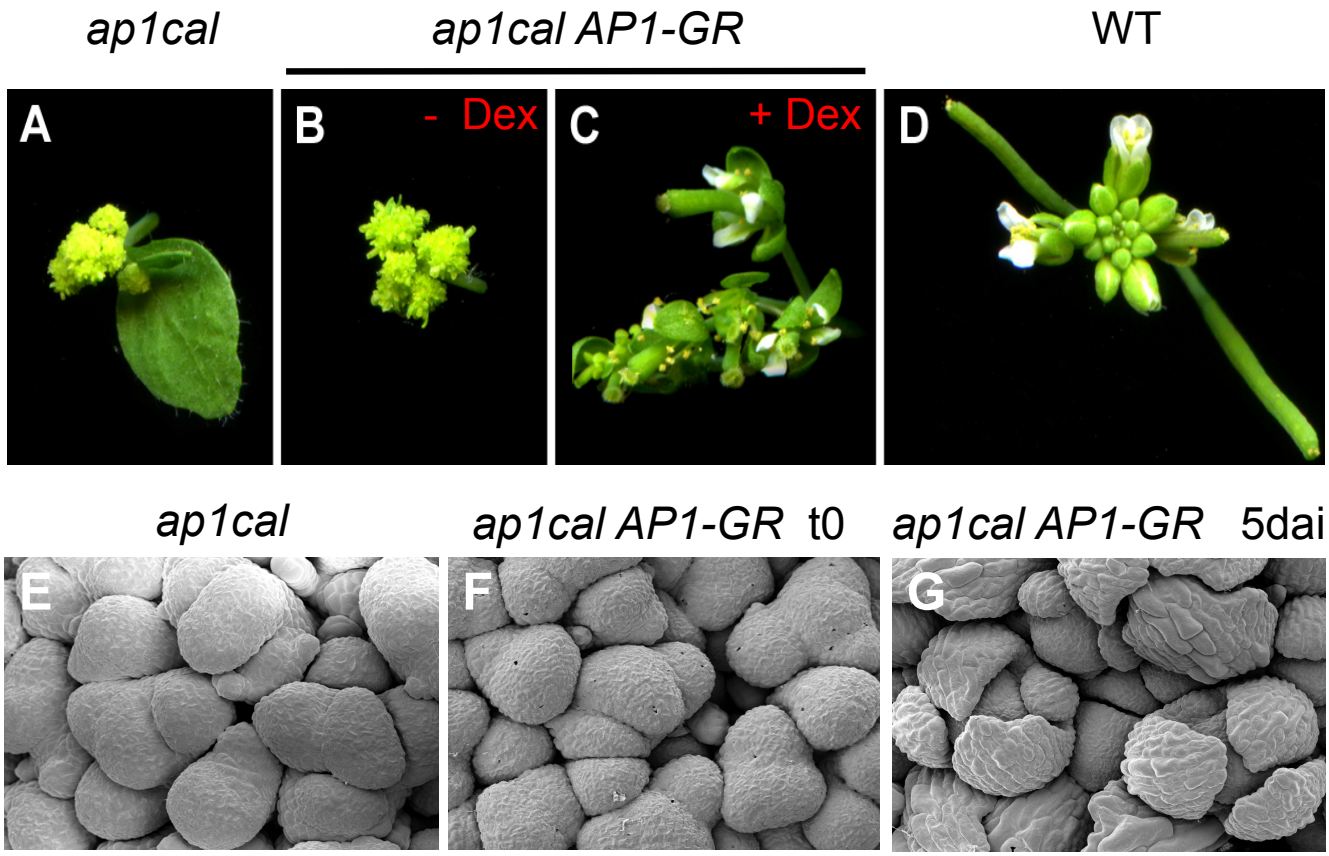

Figure S1: **Validation of the *ap1cal AP1-GR* induction system for the analysis of early events of gene activation, *in situ*.** **(A)** - **(D)** Floral induction in *ap1cal* double mutants by *AP1-GR* activation. Top viewed inflorescences of (A) *ap1cal*, (B-C) *ap1cal 35S::Ap1-GR* and (D) L*er* wild type (WT). Pictures were taken 12 days after single treatment with (A, C, D) 1μM of dex solution or (B) mock. Activation of the AP1-GR protein in the *ap1cal* led to the production of WT looking flowers. **(E)** - **(H)** Scanning electron micrographs of inflorescence-like meristems of (E) and *ap1-1 cal-1* double mutant, (F) an untreated *ap1cal 35S::AP1-GR* plant and (G) an *ap1cal 35S::AP1-GR* plant five days after single treatment with 1μM of dex solution. Scale bars: 100 nm.

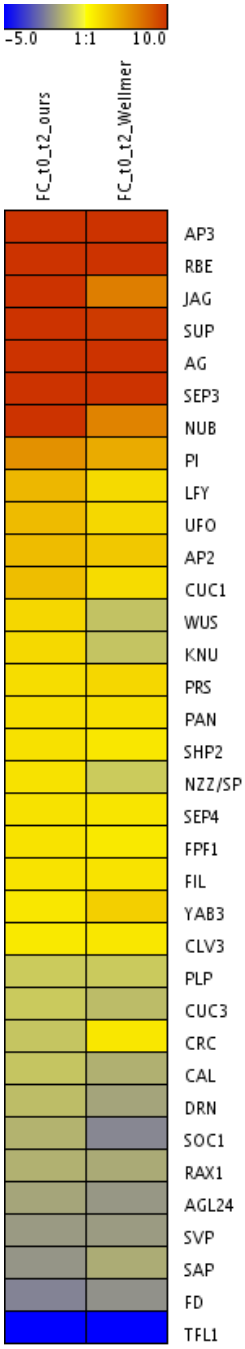

Figure S2: **Comparison of expression changes from t0 to t2 in this study and in Wellmer et al. (2006)** Fold changes (FC) in expression are depicted by a heat map reaching from genes expressed 5 times lower in t2 than t0 (blue) to genes expressed 10 times higher in t2 than t0 (red).

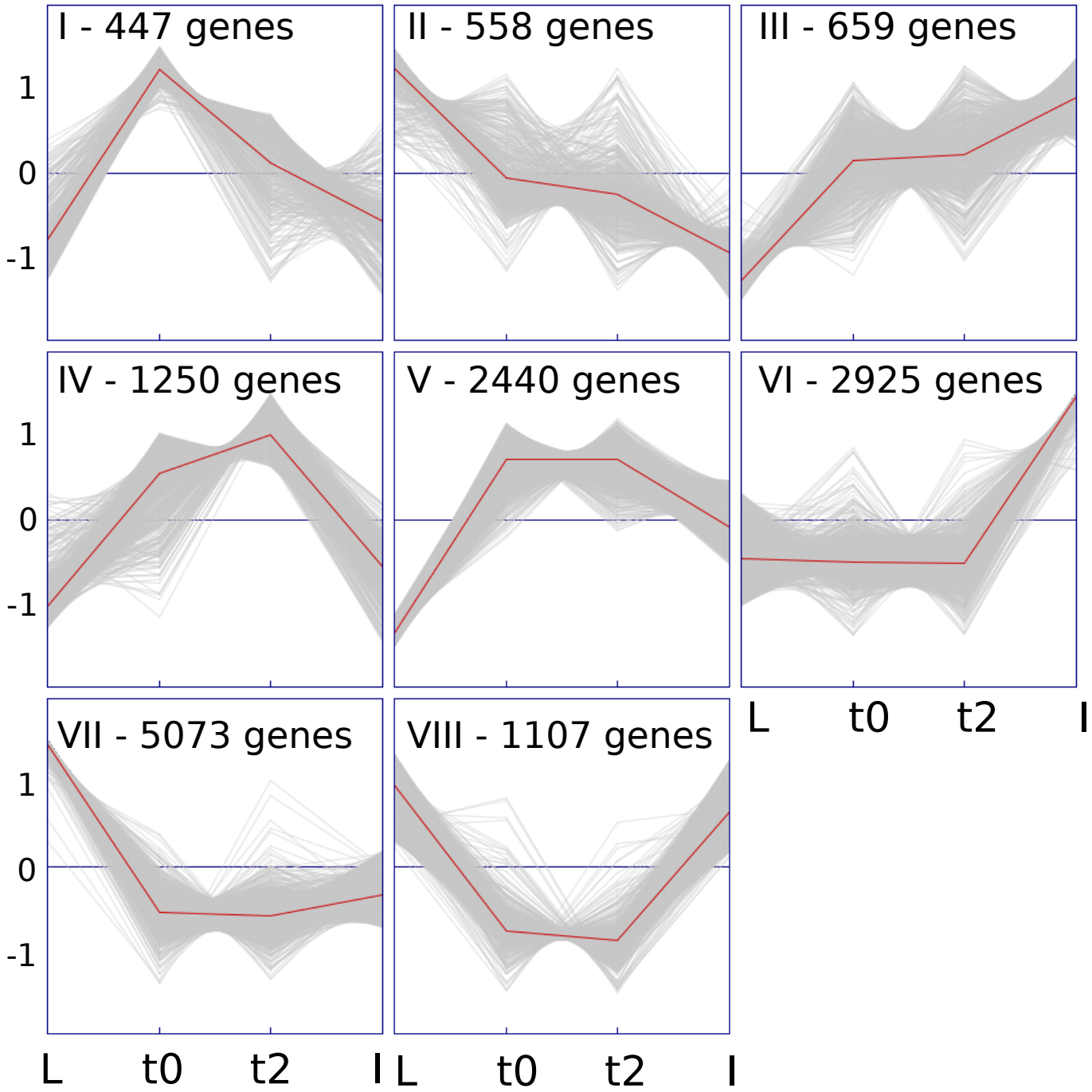

Figure S3: **Major expression patterns present among DEG** K-means clustering with k=8 for all differentially expressed genes. Overview of expression profiles in the 8 clusters. Relative expression values are expressed as z-scores to reveal similarities in expression patterns. Averages of z-scores in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

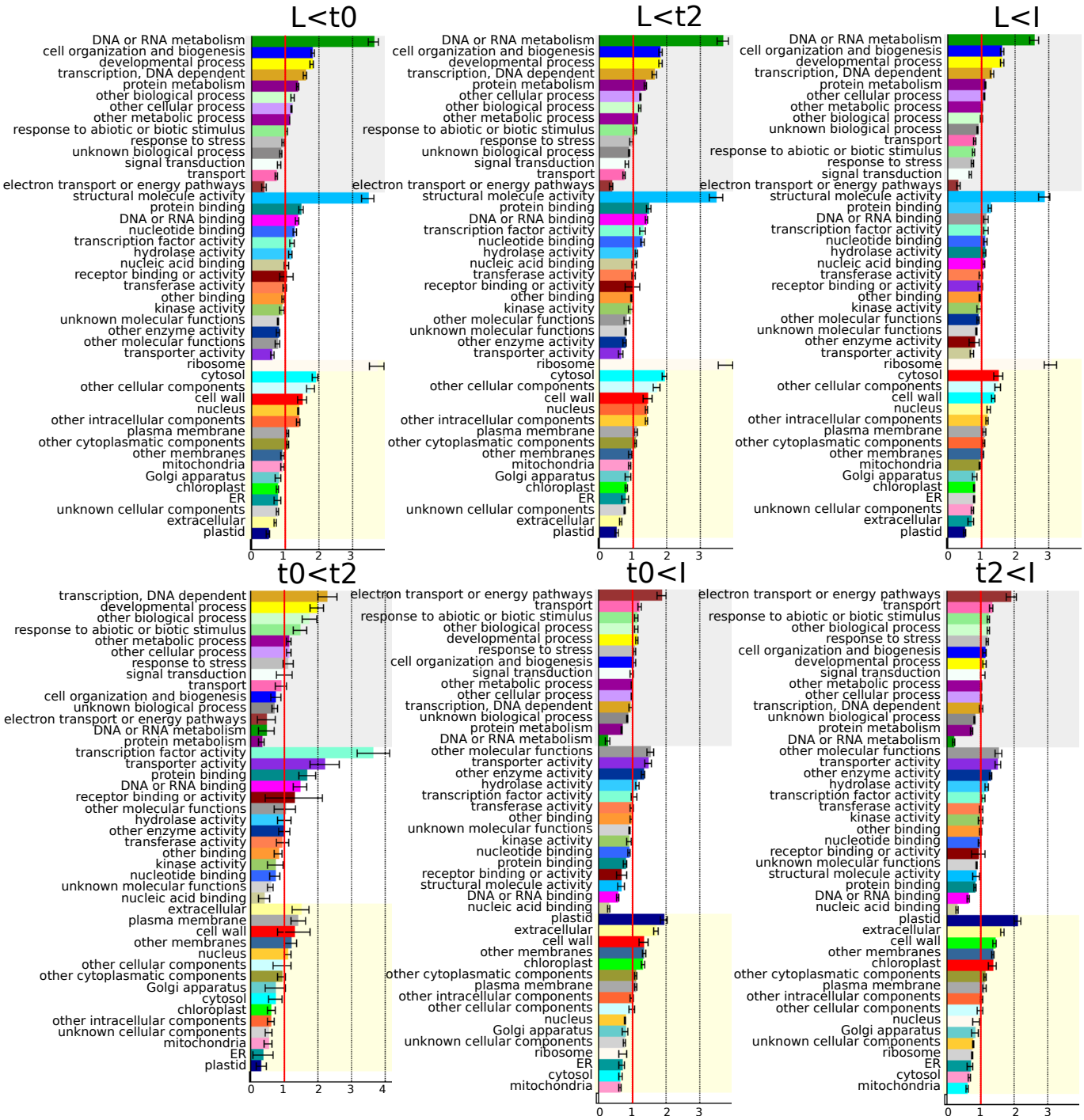

Figure S4: **Functional characterisation of up-regulated DEGs.** Figures were generated with the Classification Super Viewer from the BAR website (http://bar.utoronto.ca) using default parameters. The expected background is calculated by bootstrapping 100 sets of the same size from the whole genome.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

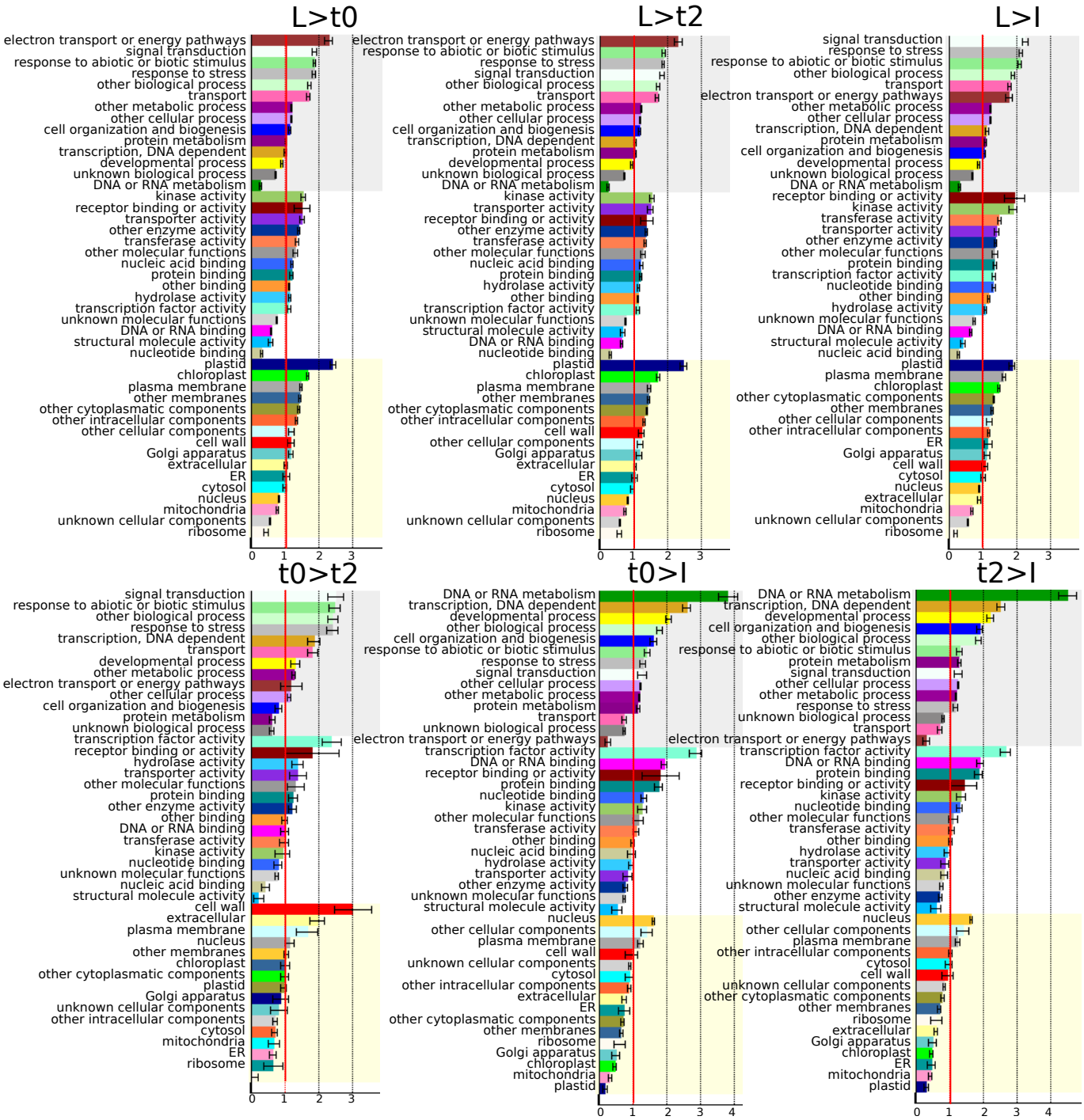

Figure S5: **Functional characterisation of down-regulated DEGs.** Figures were generated with the Classification Super Viewer from the BAR website (http://bar.utoronto.ca) using default parameters. The expected background is calculated by bootstrapping 100 sets of the same size from the whole genome.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

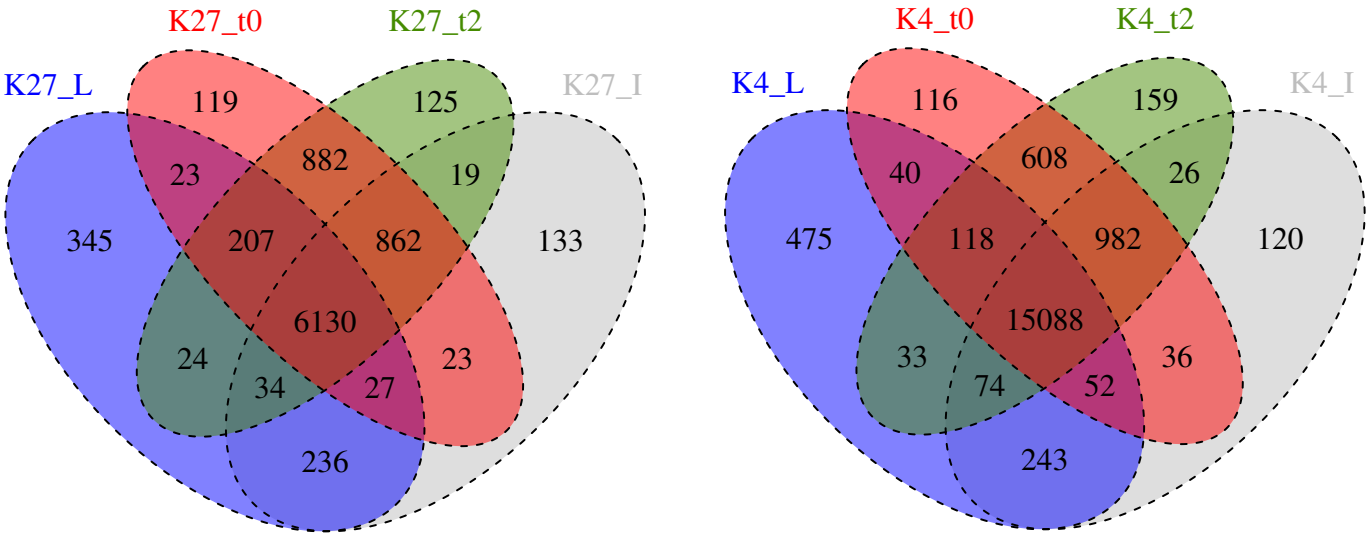

Figure S6: **Overlap between target genes in the four considered time points/tissues for H3K27me3 (K27) and H3K4me3 (K4).**

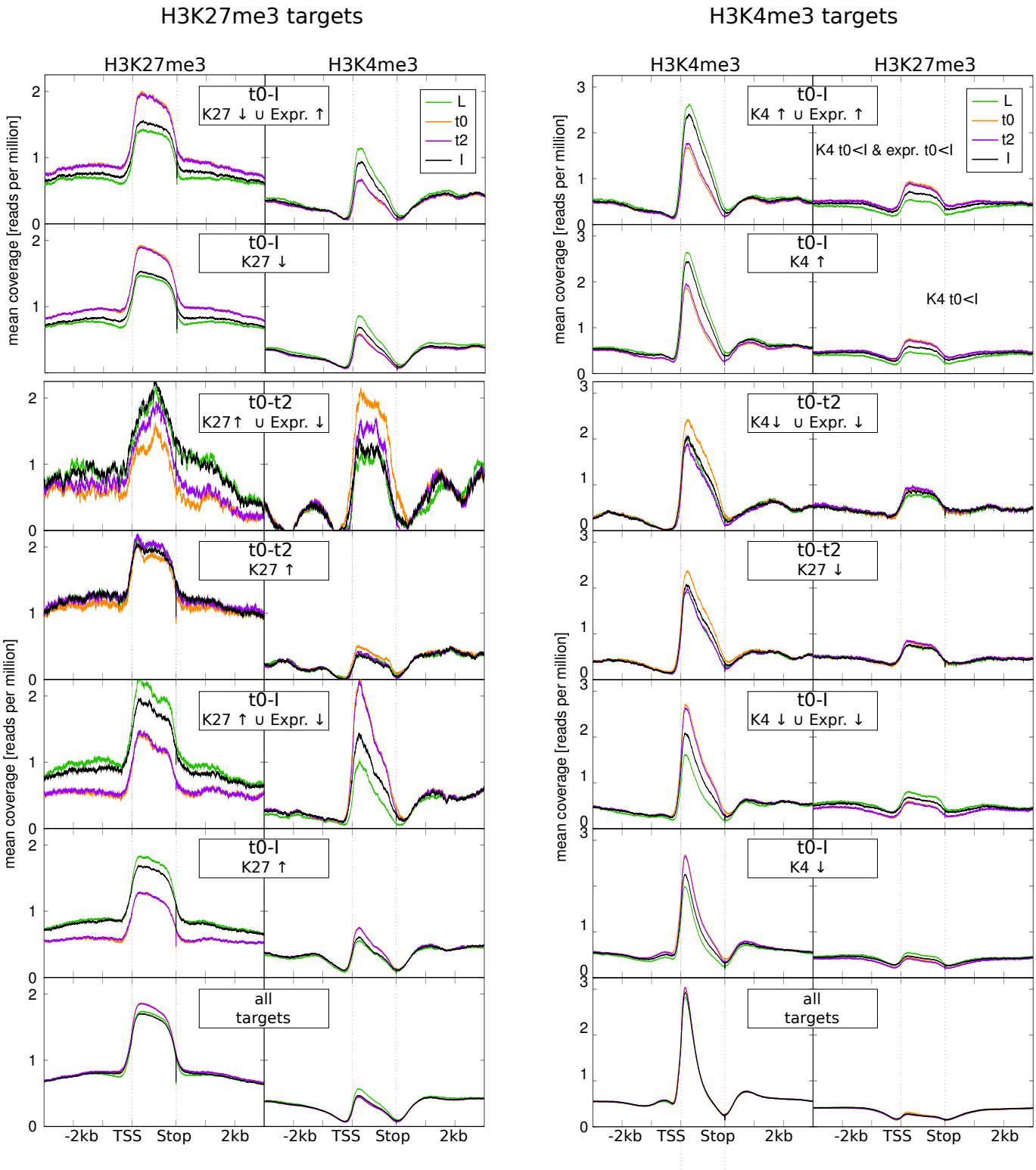

Figure S7: **Average distribution of H3K27me3 and H3K4me3 over DMGs and all target genes.** Genes are scaled to the same length (1500 bins), only the second replicate is displayed here. We saw the same tendencies in the first replicate.

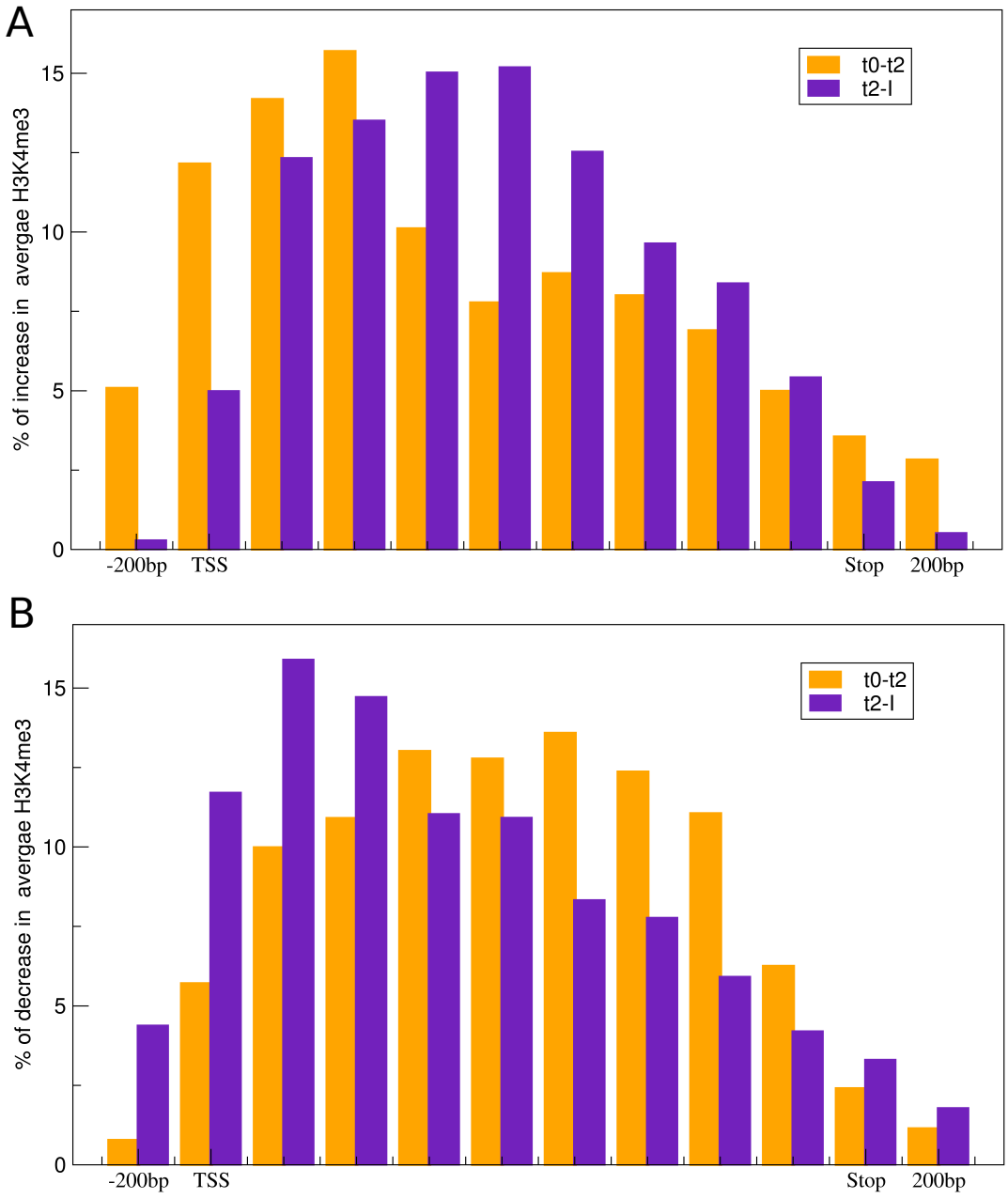

Figure S8: **H3K4me3 signal shift between early and later expression changes.** Average differences in H3K4me3 signal (in reads per million) for genes that are differentially expressed in both the t0 to t2 and t0 to I comparison are calculated in 200bp windows/10% bins over genes from -200bp to 200bp 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, I minus t2 and I minus t0) for both upregulated **(A)** and downregulated genes **(B)**.

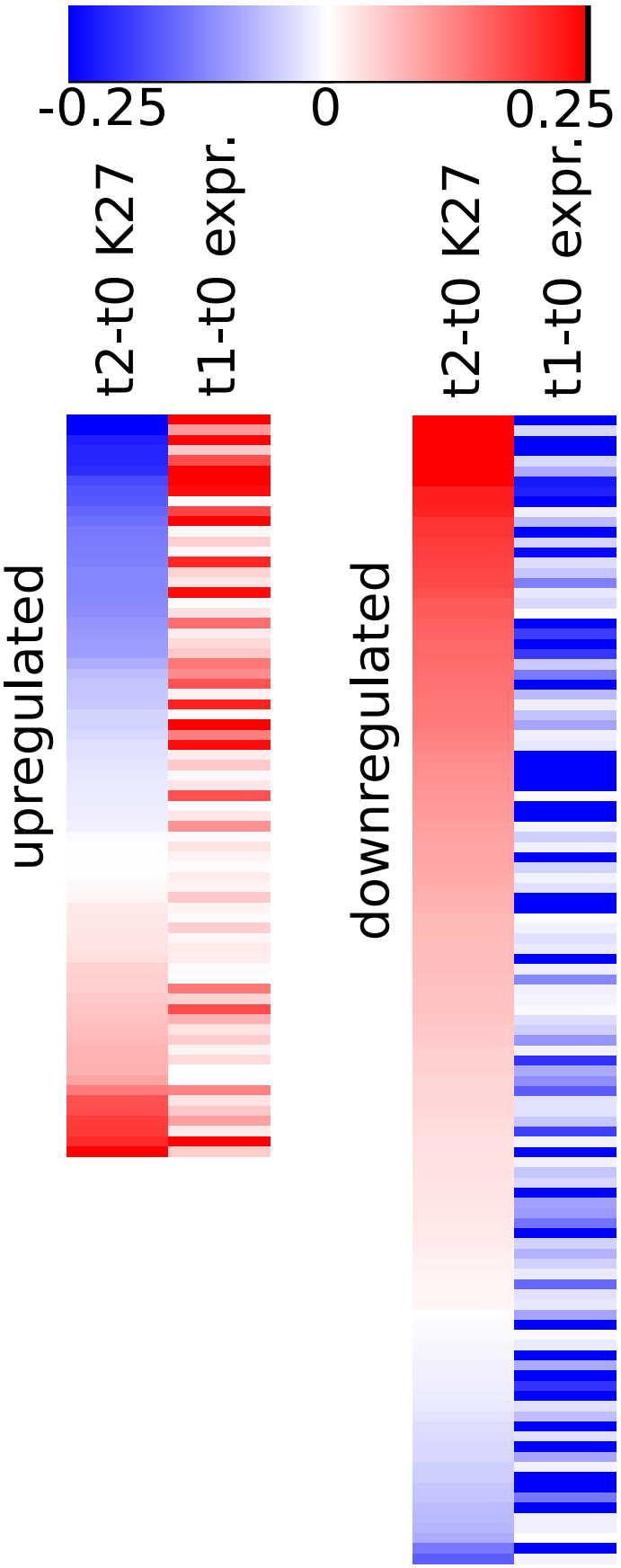

Figure S9: **Expression changes of early DEGs during flower morphogenesis at t1.** Heat maps showing the difference in expression from t0 to t1 as measured in a microarray experiment (Wellmer et al., 2006). Each line represents a DEG (from t0 to t2 comparison in our study). Genes are sorted by their 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.

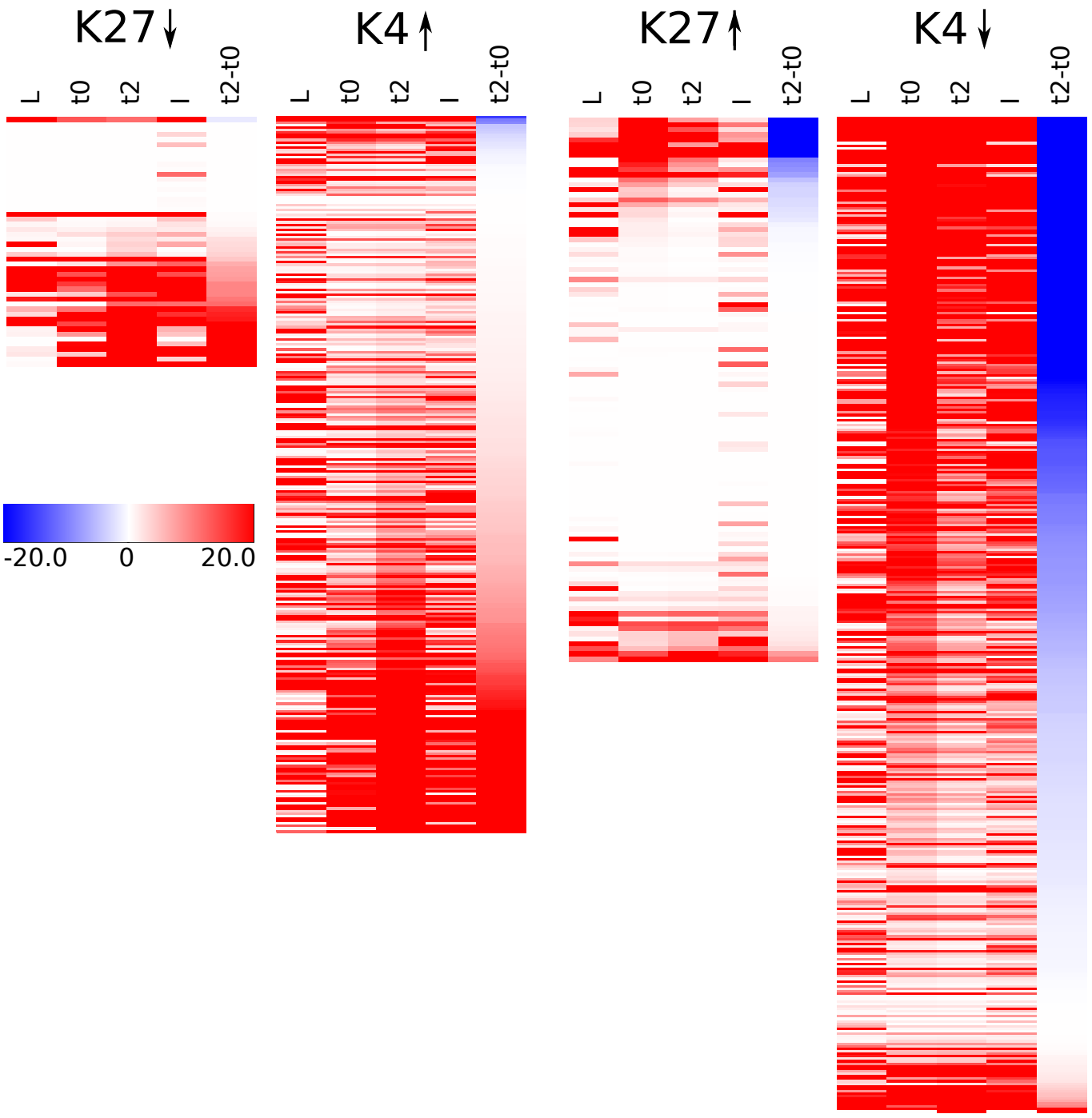

Figure S10: **Expression of early DMGs during the time series.** Heat maps showing expression values (FPKM) for significantly changing genes for H3K27me3 and H3K4me3. Each line represents a gene sorted by the expression changes during early flower morphogenesis (t2 minus t0, indicated as a column of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

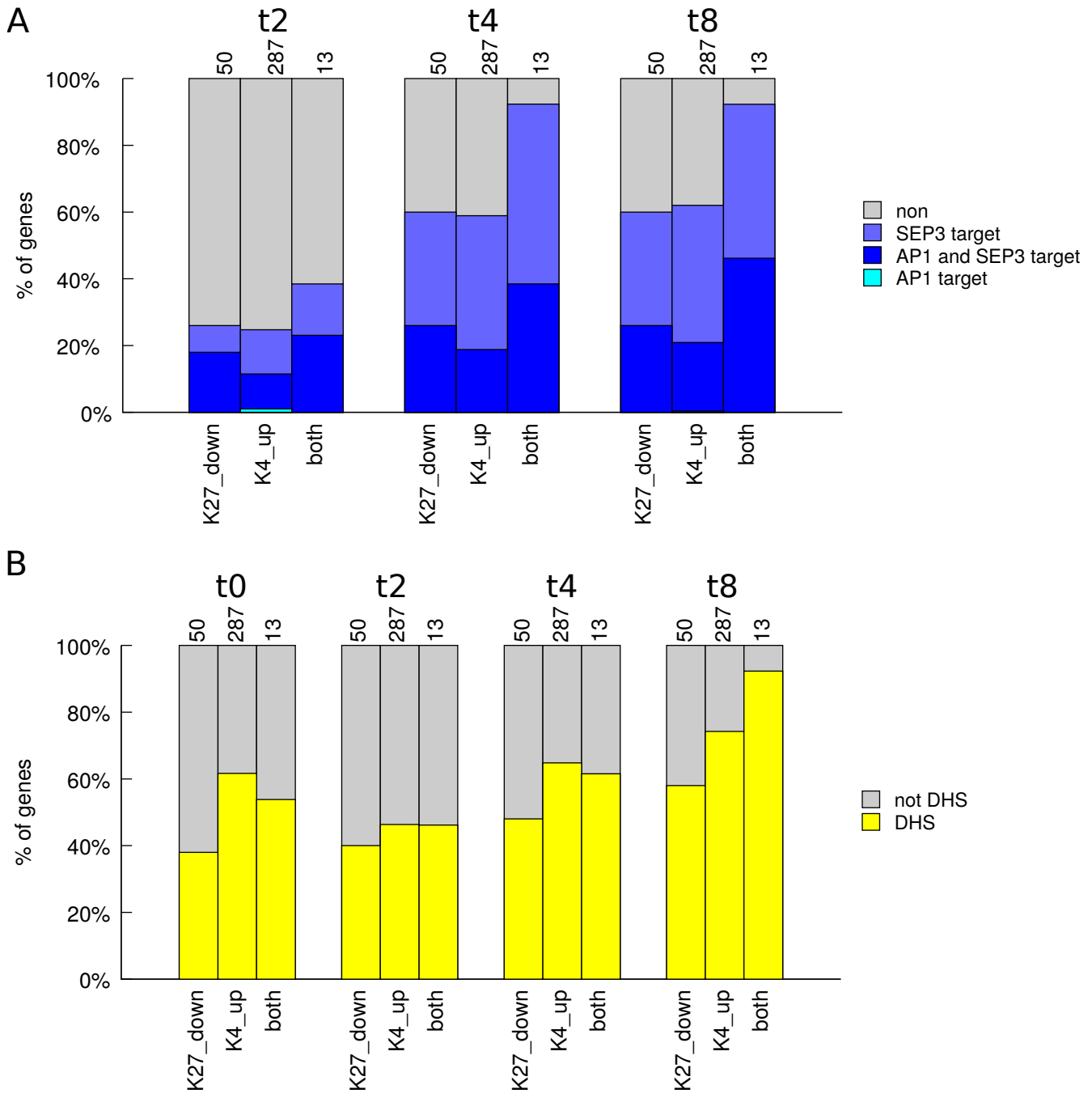

Figure S11: **Correlation of genome-wide changes in histone marks from t0 to t2 and binding of MADS TFs or DNase hypersensitivity during early flower development. (A)** Fraction of DMGs for H3K27me3, H3K4me3 and both marks from t0 to t2 (K27 down: H3K27me3 reduced t0-t2, K4 up: H3K4me3 elevated t0-t2, 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.