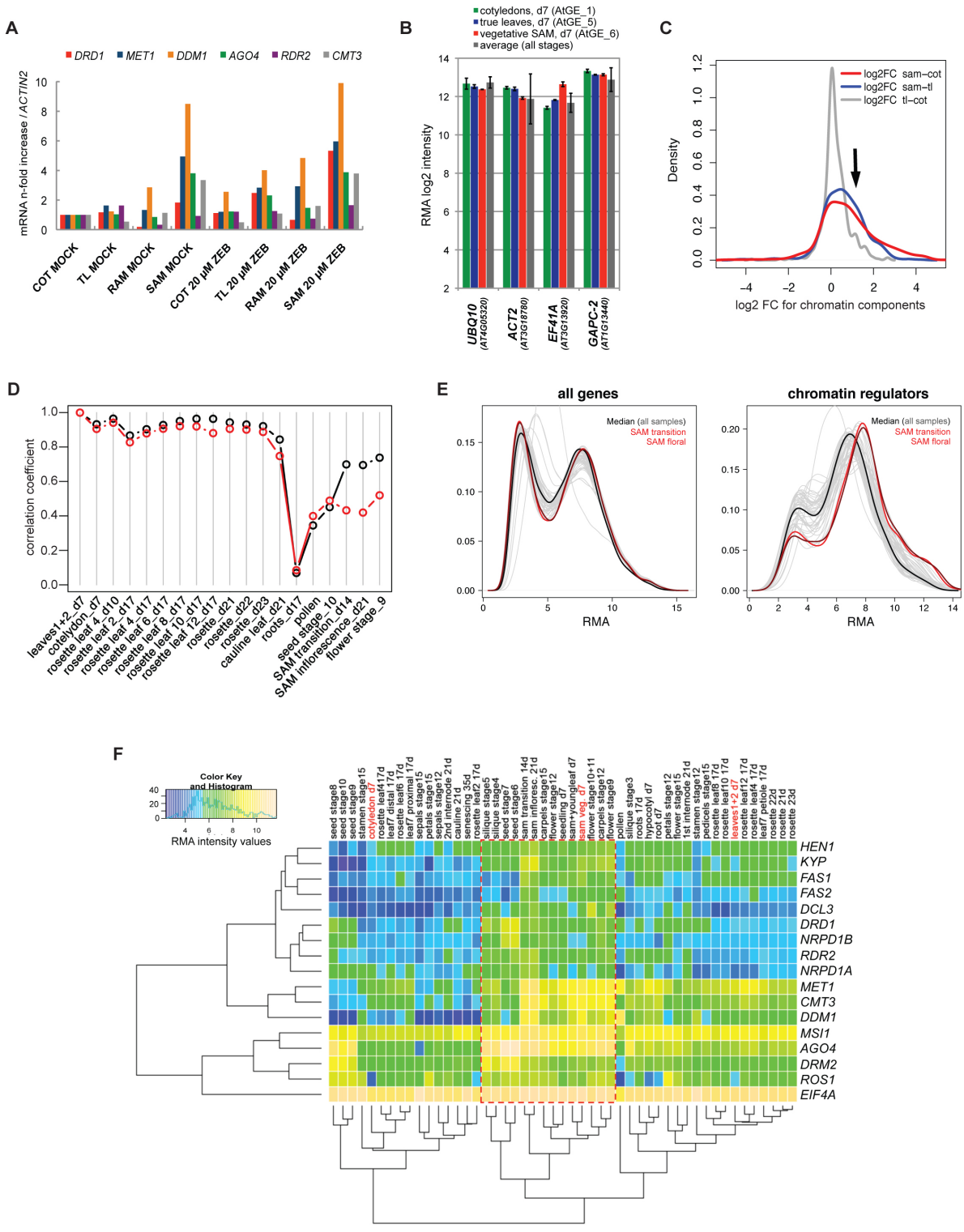

Supplementary Figure S4. Chromatin-related genes are up-regulated in the shoot apical meristem (SAM) tissues. (A) Zebularine treatments do not significantly affect transcription of genes involved transcriptional gene silencing - as shown by quantitative RT-PCR measurements in dissected cotyledons (COT), true leaves (TL), root apical meristem (RAM)-enriched or SAM-enriched tissues. Barplot indicates results from one experiment using pooled tissues from >20 plants per sample. **(B)** GC-Robust Microarray Analysis (RMA) normalized Affymetrix expression-array values from probes corresponding to different housekeeping genes in seven days-old cotyledons (green; AtGE_1), true leaves (blue;

AtGE_5) and vegetative SAM (red; AtGE_6), compared to average intensity in all available tissues from the AtGenExpress dataset (grey). Standard error of three independent replicates (cotyledons, true leaves and SAM) or across all tissues (average from three independent replicates) is indicated. **(C)** Density distribution of log2-fold changes between SAM and cotyledons (red), SAM and true leaves (blue) and true leaves and cotyledons (grey). Only probe sets corresponding to chromatin regulators (ChrDB) were used to generate this plot. **(D)** Pairwise correlation analysis for the first pair of true leaves (leaves1+2_d7) against various tissues sampled in the AtGenExpress dataset indicates conserved and specific gene expression patterns in all leaf samples (R>=0.8). R was calculated for all chromatin regulators (red) and all genes excluding chromatin regulators (black). Difference in correlation coefficients between ChrDB genes (red, R≈0.45) and the remainder (black, R≈0.7) in SAM tissues, again illustrates the SAM-specific expression for this set. **(E)** Density distribution of transcript abundance for all genes and chromatin regulators (ChrDB) measured as RMA transformed probe intensities. Results from all AtGenExpress datasets utilized in this study are shown in grey, distribution of the median calculated from all sets is shown in black and sets corresponding to SAM tissues (transition and floral) are highlighted in red pointing out the elevated expression of ChrDB genes in these tissues. **(F)** Heatmap and hierarchical clustering visualizing tissue-specific expression of selected chromatin modifiers during *Arabidopsis* differentiation, based on RMA values generated by the AtGenExpress consortium. Tissue-wise clustering separates meristematic and young floral tissues with high expression of TGS regulators (red square) from the remaining tissues.