Supplementary data

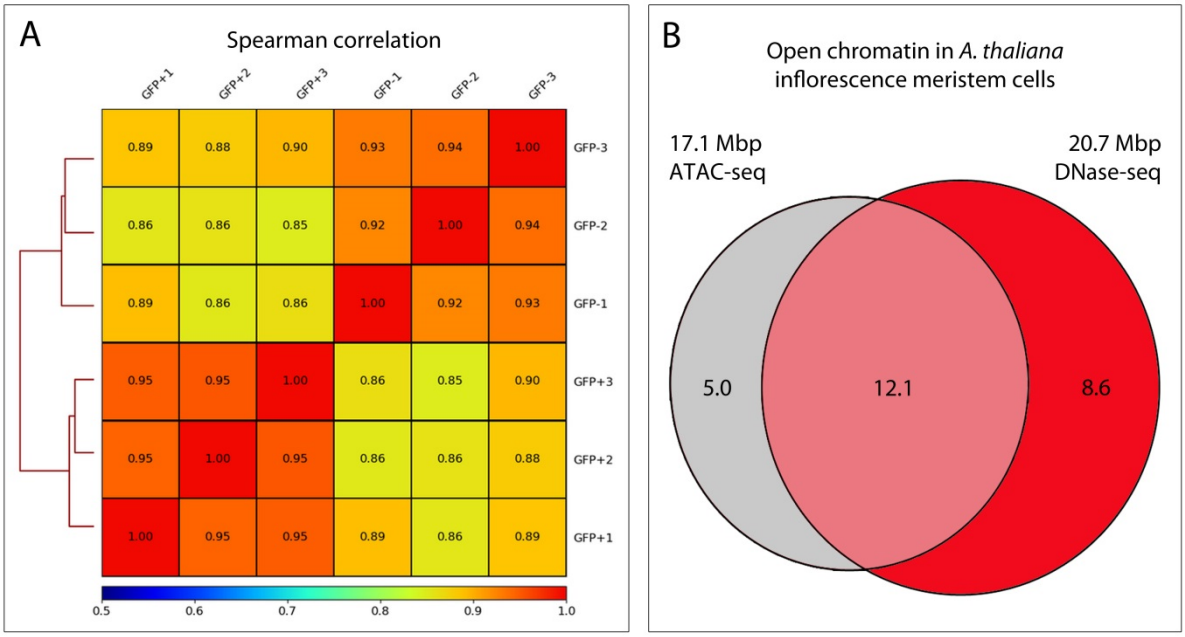

Figure S1. Comparison of biological replicates within the ATAC-seq analysis and overlap with available DNase-seq data

A) Spearman correlation of THSs between the three biological replicates and the GFP+ LOFCs and GFP– meristematic cells. **B**) Open chromatin regions in *ap1 cal* inflorescence meristem cells detected by ATAC-seq (grey) or DNase-seq (red) according to Pajoro *et al*. (2014); note the central 12.1 Mbp overlap (70 or 58%). (Mbp = megabase pairs).

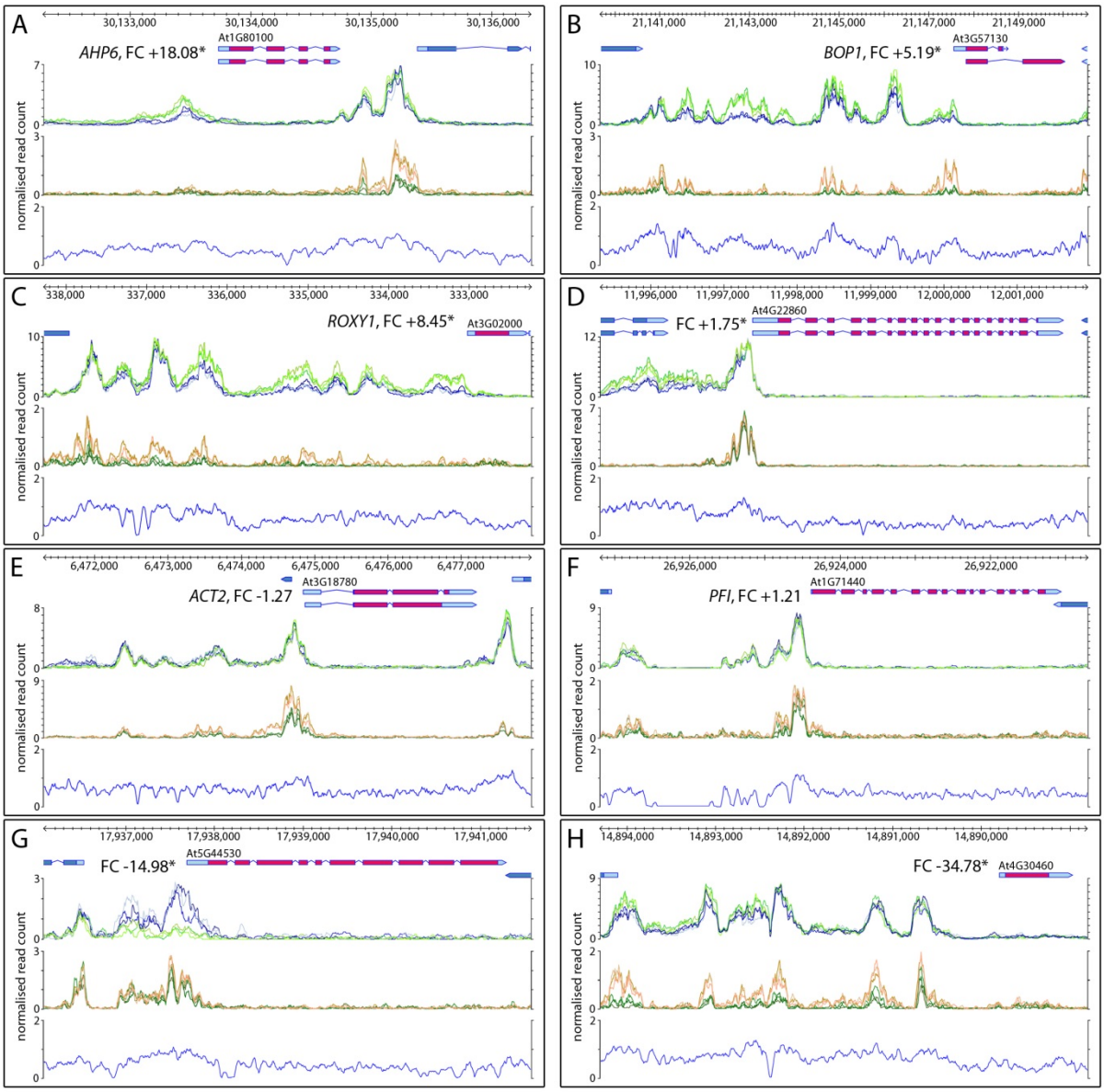

Figure S2. Comparison of the chromatin configurations of exemplary genes between ATAC-seq and DNase-seq, different cell types and enrichment methods

This comparison relates to Fig. 3 and genes extensively discussed in the main text. **A**) *AHP6*, **B**) *BOP1*, **C**) *ROXY1*, **D**) *At4g22860*, **E**) *ACT2*, **F**) *PFI*, **G**) *At5g44530* and **H**) *At4g30460*. It outlines experimental differences between the enrichment of protoplasts via FACS (top) or nuclei by the INTACT method (centre) or between peak calling in ATAC-seq and DNase-seq data in the *ap1 cal* IM (bottom). The Y-axis depicts normalised read counts and differs in scale between examples. The graphs depict mean values from three biological ATAC-seq replicates of GFP+ (green) and GFP– (blue) *ap1 cal* inflorescence meristem cells in the upper panels, vegetative stem (orange) and mesophyll (green) cells (Sijacic *et al.*, 2018) in the central panels and two biological replicates of *ap1 cal* IM chromatin subjected to DNaseI digestion (lower panels) (Pajoro *et al*., 2014). Note that the DNase data replicates were mapped as a pool due to the submission format of the data. Gene locus descriptions exactly follow the legend for Fig. 3 in the main text.

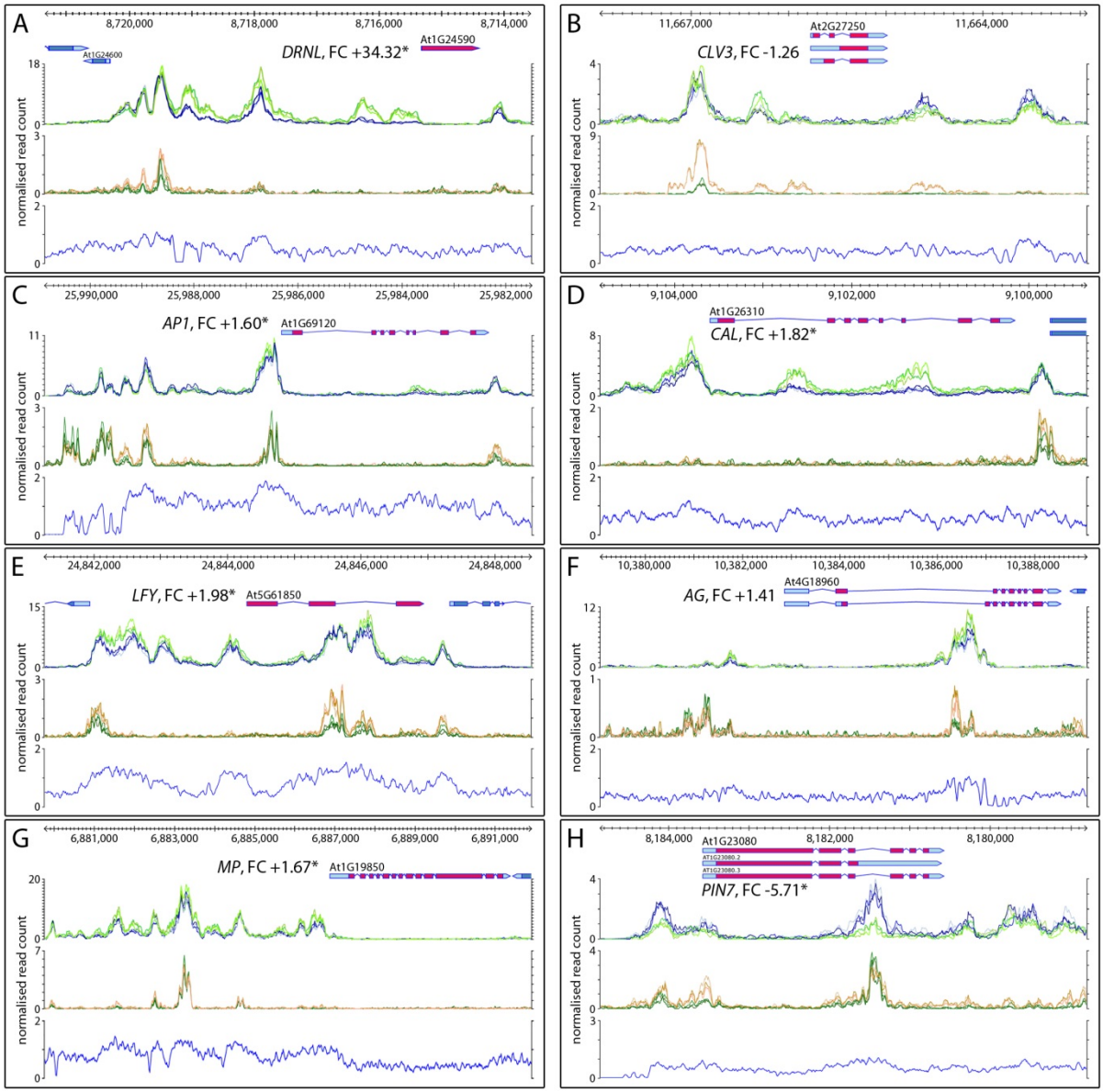

Figure S3. DNase-seq accessibility in genes and promoters used for cell type-specific enrichment or relating to developmental decisions

This figure provides DNase-seq data for individual genes in Fig. 5. **A**) *DRNL*, **B**) *CLV3*, **C**) *AP1*, **D**) *CAL*, **E**) *LFY*, **F)** *AG*, **G**) *MP* and **H**) *PIN7*. The arrangement of panels and colour code are the same as in supplementary Fig. S2. Note the different scale on the Y-axis between *DRNL* and *CLV3* with respect to LOFC- or stem cell-specificity and that peak calling in the DNase-seq data, similar to Fig. S2, results in poor peak resolution and a low signal-to-noise ratio.

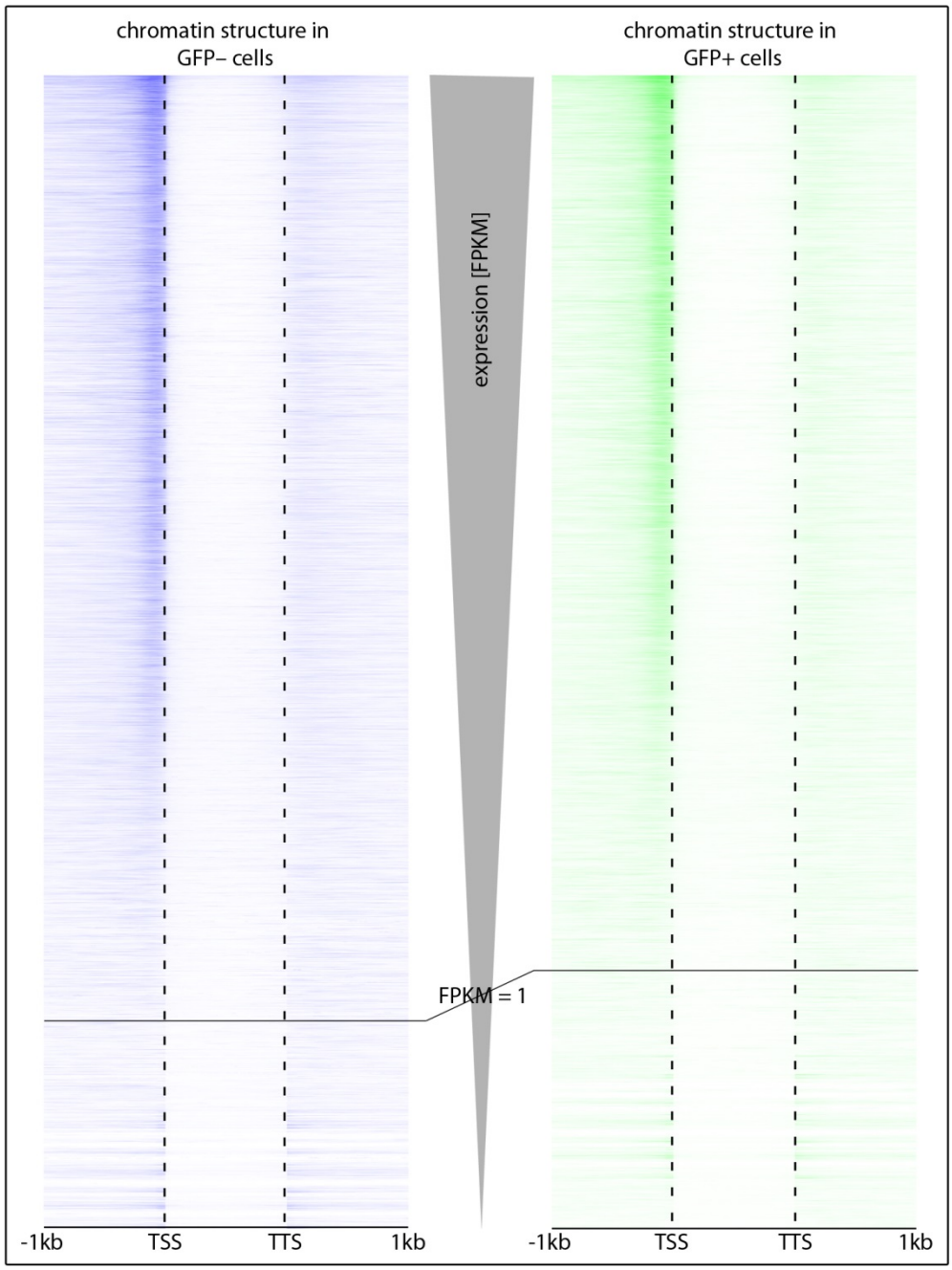

Figure S4. Correlation between ATAC-signal and gene expression

ATAC-seq signal distribution in GFP– (blue) and GFP+ (green) cells for all *Arabidopsis* genes sorted by increasing FPKM (Fragments Per Kilobase Million) values according to Frerichs *et al.* (2016).

Table S1. ATAC-seq read numbers compared to DNase-seq data

ATAC-seq read numbers in GFP+ and GFP– cells in the three biological replicates (1–3). Indicated are all reads mapping to the *Arabidopsis* genome, reads after removal of duplicates (deduplicated reads), reads mapping to the five *Arabidopsis* chromosomes excluding organelles (chromosomal reads) and their fraction relative to the mapped or deduplicated reads, respectively. The bottom row represents processed data according to Pajoro *et al*. (2014); note that the chromosomal read number substantially exceeds numbers in the individual ATAC-seq samples.

	Mapped reads	**Dedupli-cated reads**	**Dedupli-cated [%]**	**Chromosomal reads**	**Chromosomal reads [%]**
GFP+ 1	84,933,731	41,091,888	48.4	23,694,985	57.7
GFP– 1	82,537,762	41,196,912	49.9	25,662,021	62.3
GFP+ 2	96,093,332	46,976,856	48.9	29,838,420	63.5
GFP– 2	47,580,369	28,670,807	60.3	17,308,268	60.4
GFP+ 3	86,514,402	42,407,978	49.0	24,708,662	58.3
GFP– 3	89,808,530	44,347,953	49.4	27,084,948	61.1
DNase	-	45,130,287	28.4	44,137,107	97.8

Table S2. Statistical evaluation of dTHS relative to DEGs
The DEGs were taken according to Frerichs *et al.* (2016). Set1 consists of THS-up or THS-down; Set2 represents up- (717) or downregulated (3,356) DEGs. The column overlap indicates the fraction of Set 1 that overlaps with Set 2, the percentage [%] is calculated relative to Set1, i.e., THSs-up or down. Over- or under-representation and *p*-values were calculated assuming a total number of 28,496 *Arabidopsis* genes and a hypergeometric distribution.

Comparison (Set1/Set2)	**Set 1**	**Set 2**	**Over-lap**	**[%]**	**Over/Under-representation**	***p* value**
dTHS-up/expression up	121	717	37	30.6%	Over	6.556E-30
dTHS-up/expression down	121	3,356	3	2.5%	Under	0.0002118
dTHS-down/expression up	392	717	1	0.3%	Under	0.0004817
dTHS-down/expression down	392	3,356	189	48.2%	Over	2.617E-72

Table S3. Representation of GCC-boxes in genes carrying dTHSs and THSs
The column headings show the total number of GCC-boxes residing within genes (plus 1 kb upstream and downstream) in the *Arabidopsis* genome and distinguishes GCCGCC motifs from motifs allowing one mismatch at positions 2, 3 or 5 (perfect vs. relaxed). The sub-columns indicate motif frequency in genes carrying dTHS-up or dTHS-down, THSs of GFP+ or GFP– protoplasts or all genes and their percentages relative to the THS-category (1) or the number of motifs (2). Note the substantially fewer dTHSs compared to THSs for perfect and relaxed GCC-box sequences. The overlaps here are direct, i.e., genes are considered as overlapping when the motif and the THS/dTHS directly share one or more bases.

	2	Perfect GCC-boxes: 11,216			Relaxed GCC-boxes: 26,299		
	1		% of 1	% of 2		% of 1	% of 2
dTHS-up	121	5	4.13%	0.04%	15	12.4%	0.06%
dTHS-down	392	3	0.77%	0.03%	39	9.9%	0.14%
THS GFP+	20,736	2,807	13.54%	25.03%	10,243	49.4%	38.90%
THS GFP–	21,098	2,808	13.31%	25.04%	10,381	49.2%	39.50%
Genome	28,496	11,216	39.36%	100.00%	26,299	92.3	100.00