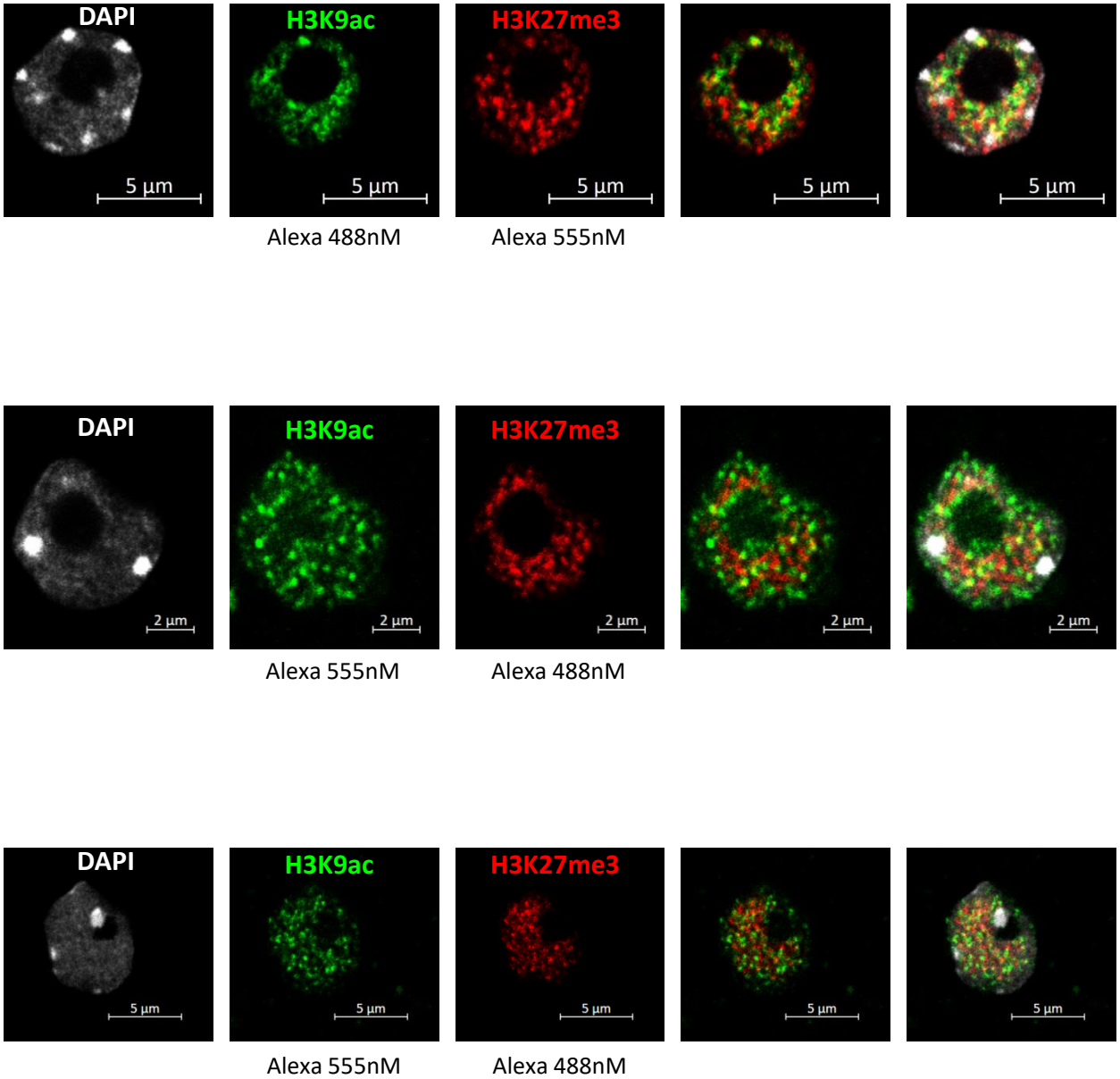
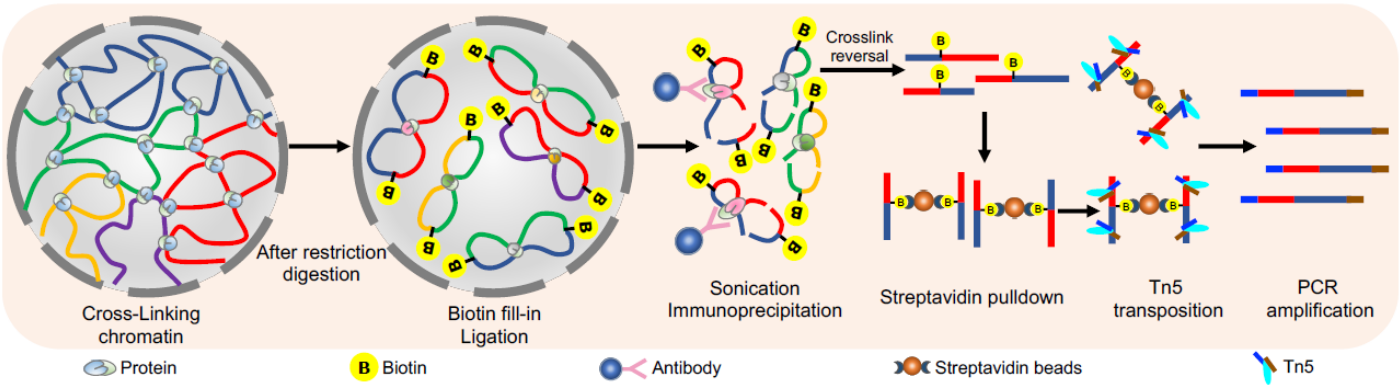
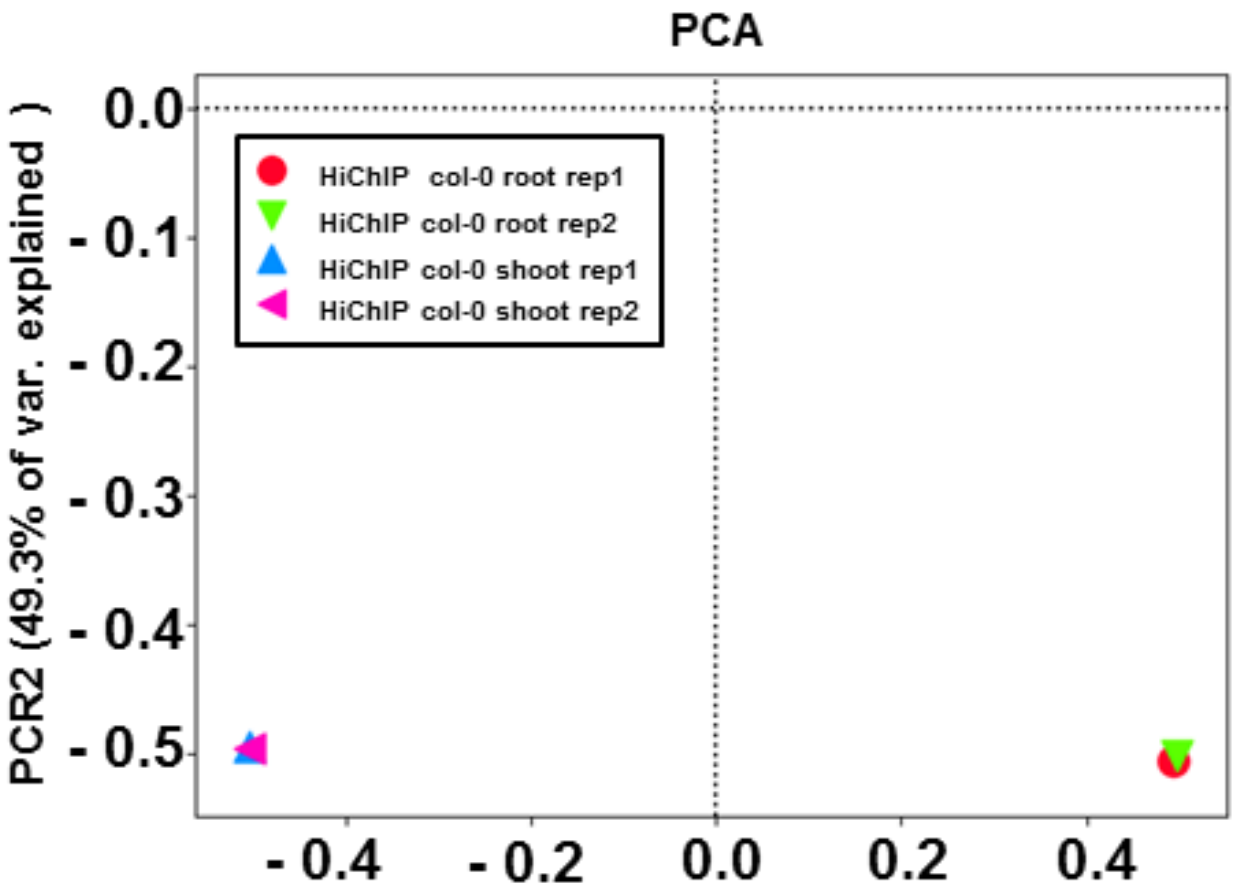


Supplemental Fig S1. Immunofluorescence detection of H3K9ac (green) and H3K27me3 (red) chromatin marks and DAPI staining in isolated *Arabidopsis* nuclei. Three independent nuclei are shown, complementary to Figure 1A.

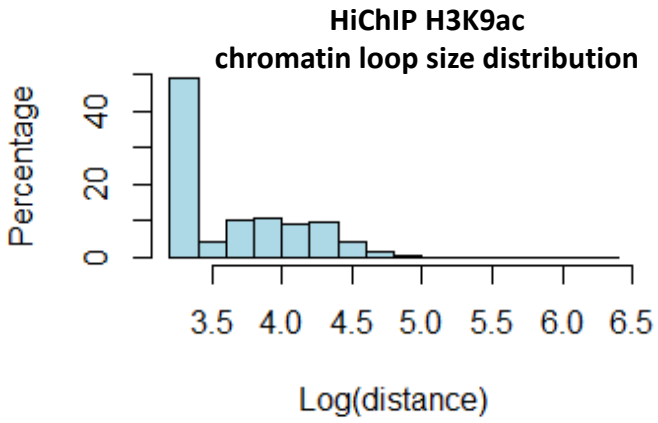


Supplemental Fig S2. Schematic representation of the HiChIP method.

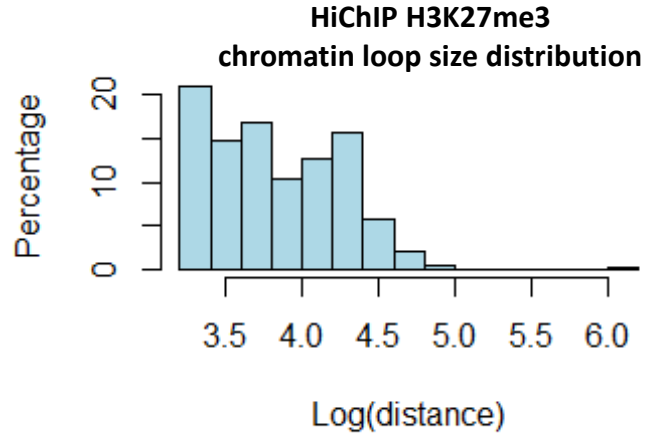


Supplemental Fig S3. PCA (principal component analysis) plot for different replicates of HiChIP-shoot and root of wild-type *Arabidopsis*. High reproducibility is observed between the replicates in HiChIP experiments.

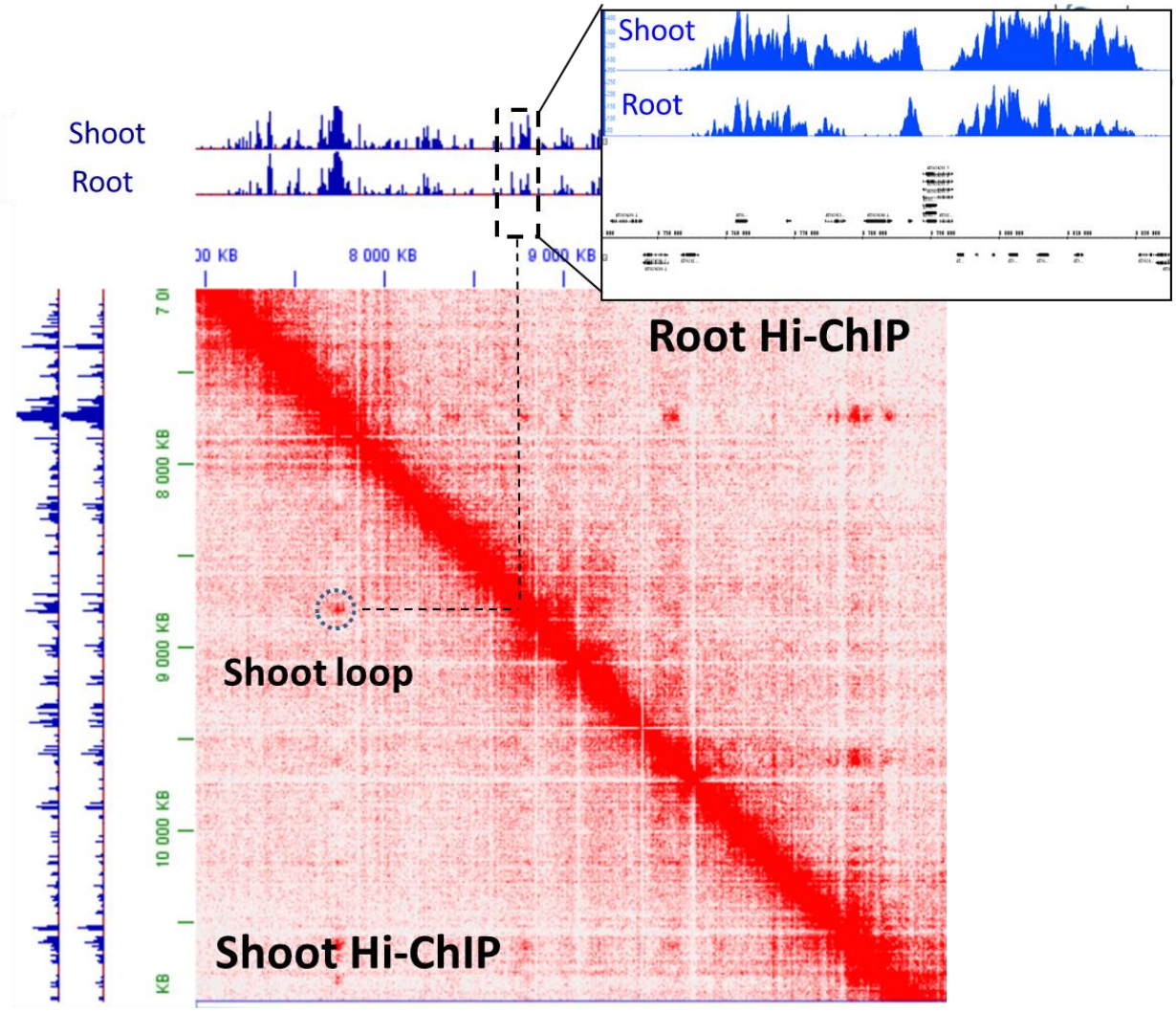
A



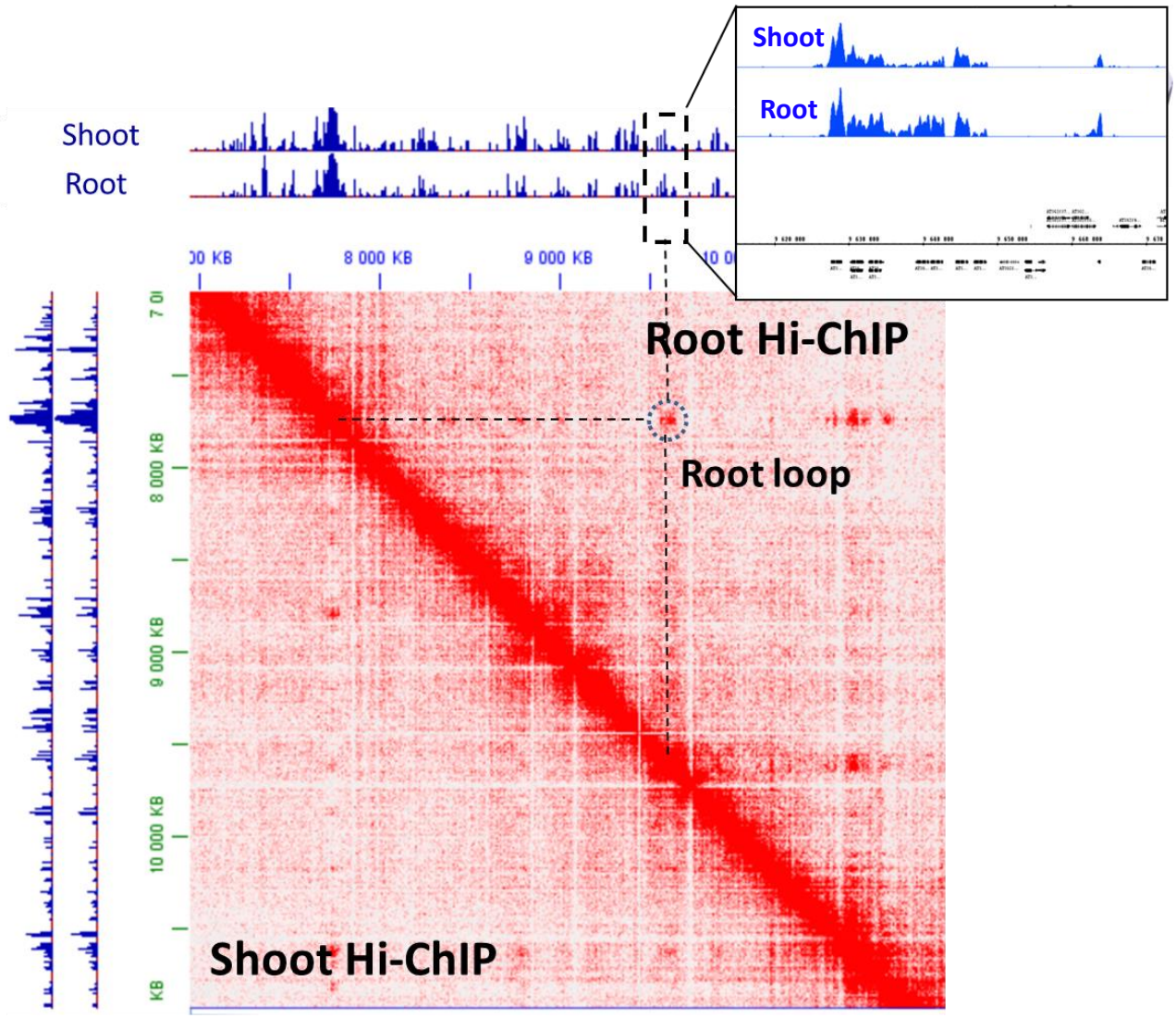
B



Supplemental Fig S4. Plots representing the H3K9ac **(A)** and H3K27me3 **(B)** chromatin loop size distribution



Supplemental Fig S5. Visualization of the interaction matrix of HiChIP in shoot and root of wild-type in *Arabidopsis* Chromosome 3 . An example of H3K27me3 HiChIP loops showing stronger interactions in shoot compared to root (SSRLs). A shoot loop showing higher signal of H3K27me3 in shoot than root is indicated in the map. ChIP-seq signals of H3K27me3 in shoot and root are shown as blue peaks.



Supplemental Fig S6. Visualization of the interaction matrix of HiChIP in shoot and root of wide-type in *Arabidopsis* Chromosome 3. An example of H3K27me3 HiChIP loops showing stronger interactions in root than in shoot. A root loop showing higher signal of H3K27me3 in root than shoot is indicated in the map. ChIP-seq signals of H3K27me3 in shoot and root are shown as blue peaks.

A

Shoot specific repressive loops (SSRL)	**Gene1-Log FC >0 induced**	**Gene1-Log FC_1<0 repressed**
Gene2-Log FC >0 induced	**194**	362
Gene2-Log FC_1<0 repressed	411	**1033***

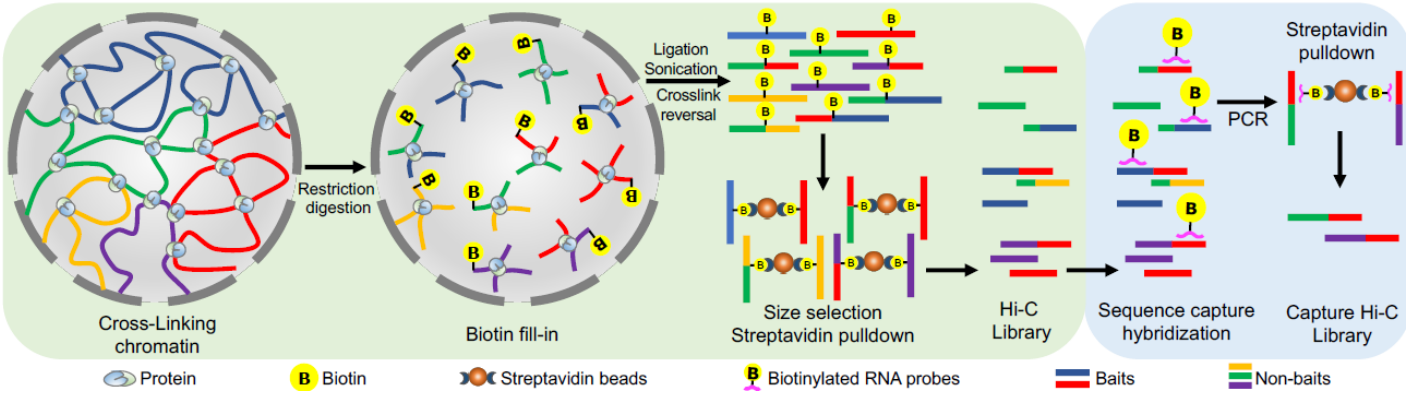
X^2 (3, N = 2000) = 809.38, p = 4.0E-175

B

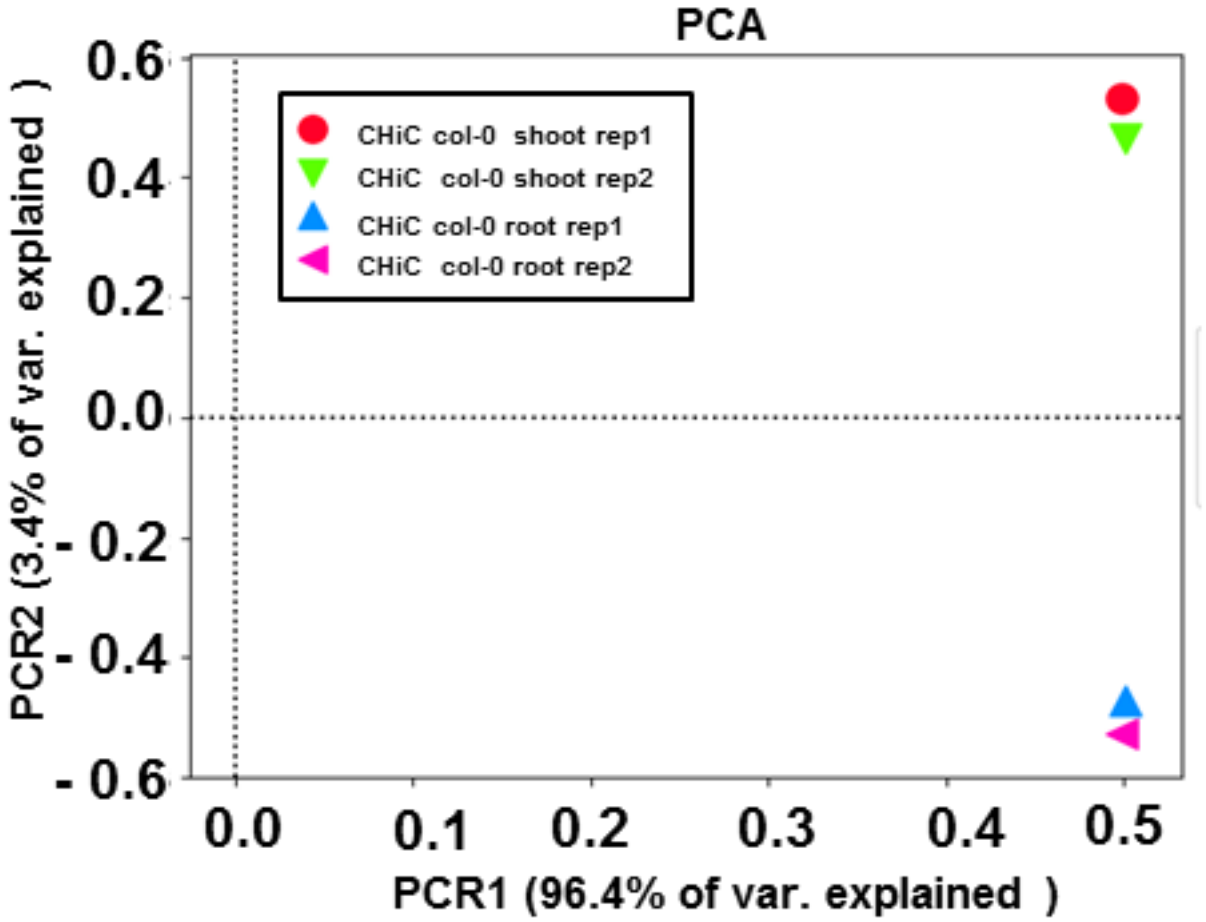
Root specific repressive loops (RSRL)	**Gene1-Log FC >0 induced**	**Gene1-Log FC_1<0 repressed**
Gene2-Log FC >0 induced	**801***	443
Gene2-Log FC_1<0 repressed	425	331

X^2 (3, N = 2000) = 256.072, p=3.2E-55

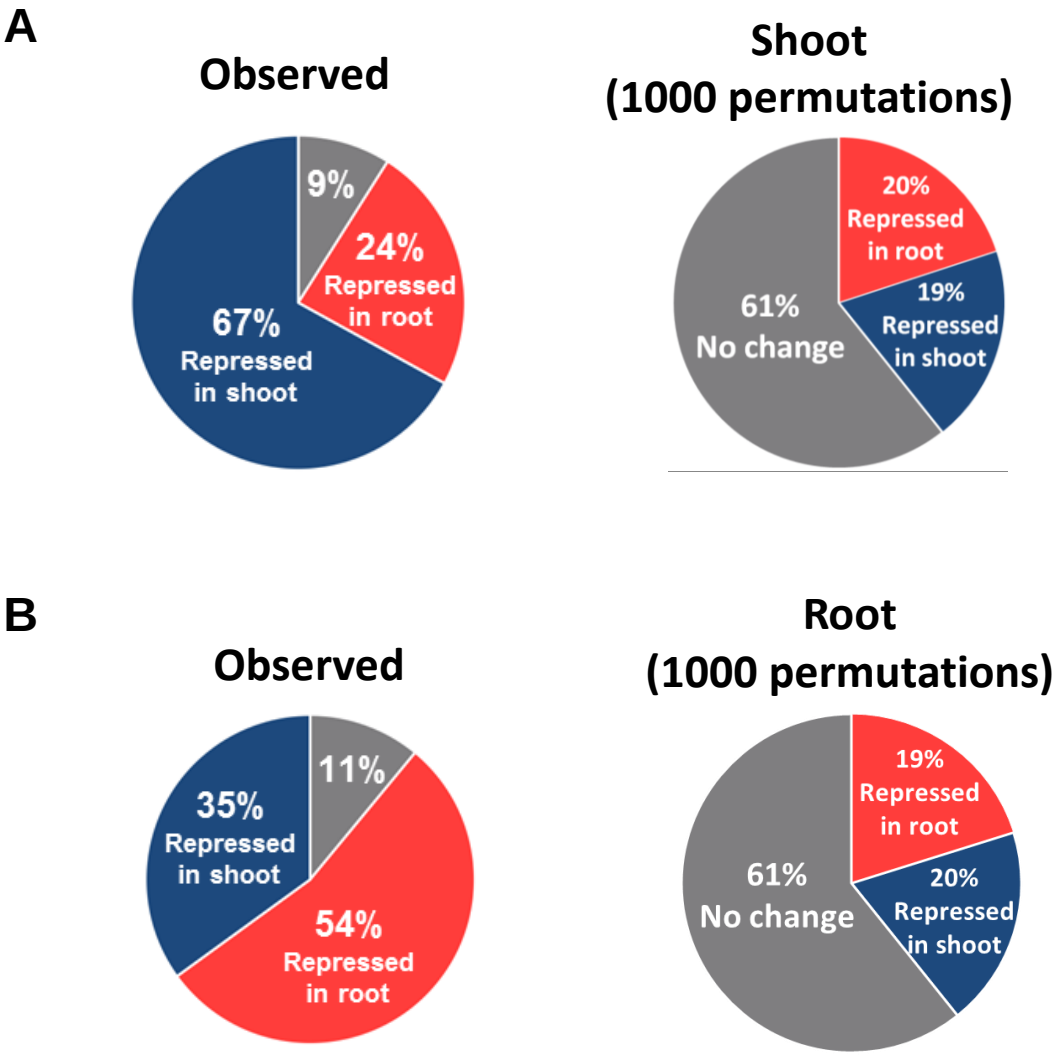
Supplemental Fig S7. Gene pairs connected in shoot specific repressive loops (SSRL) and root specific repressive loops (RSRL) in *Arabidopsis* wide-type. A higher number of gene pairs are repressed in SSRLs than expected randomly (p-value: 4E-175). For RSRLs, a higher number of gene pairs are induced (log FC shoot/root) than expected randomly (p-value: 3.2E-55).



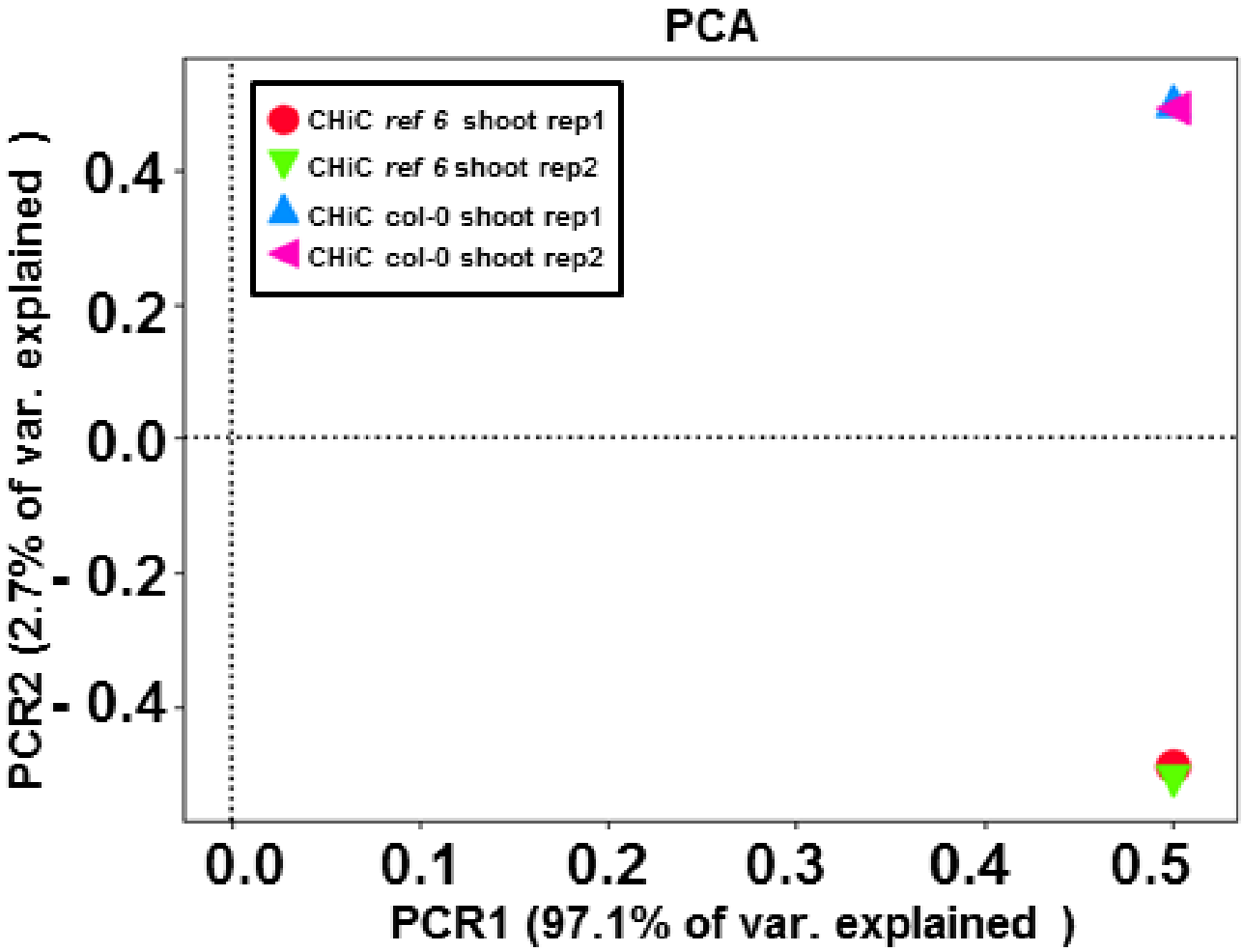
Supplemental Fig S8. Schematic representation of the Capture Hi-C (C-Hi-C) method.



Supplemental Fig S9. PCA (principal component analysis) plot for different replicates of Capture Hi-C in *Arabidopsis* wild-type shoot and root. High reproducibility was observed between the replicates in Capture Hi-C experiments.



Supplemental Fig S10. (A) Pie chart representing the observed and expected proportion of repressed genes in shoot (blue), repressed genes in root (red) and unchanged (grey) among the genes involved in loops detected both with HiChIP and C-Hi-C. **(B)** Pie chart representing the observed and expected proportion of repressed genes in shoot (blue), repressed genes in root (red) and unchanged (grey,) among the genes involved in loops detected both with HiChIP and C-Hi-C.
To obtain the expected proportion, we shuffled the gene expression signals 1000 times to obtain a randomized one. The mean of the 1000 permutations was used to determine the expected proportions.

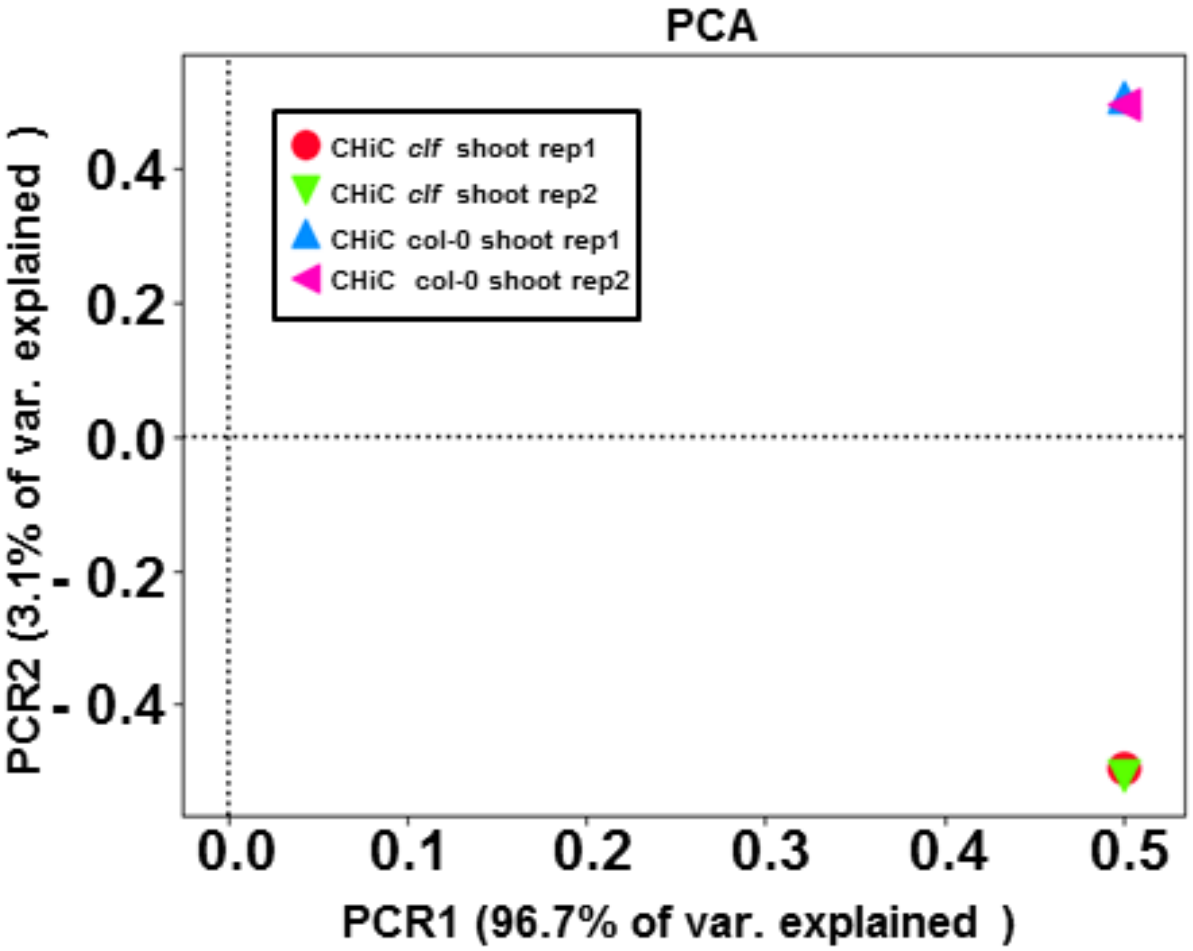


Supplemental Fig S11. PCA (principal component analysis) plots for different replicates of Capture Hi-C experiments of *ref6-5* mutant and wild-type shoot in *Arabidopsis*. A high reproducibility was observed between the replicates in Capture Hi-C experiments.

Interactions gained in *ref6-5*	Gene1-Log FC >0 induced	Gene1-Log FC_1<0 repressed
Gene2-Log FC >0 induced	**117**	116
Gene2-Log FC_1<0 repressed	113	**200***

X^2 (3, N = 2000) = 39.1, p = 4E-10

Supplemental Fig S12. Gene pairs connected in *ref6-5* specific loops (reSL) in *ref6-5* mutant compared to wild-type shoot in *Arabidopsis*. A higher number of gene pairs are repressed in reSLs than expected by chance (p-value = 4E-10).

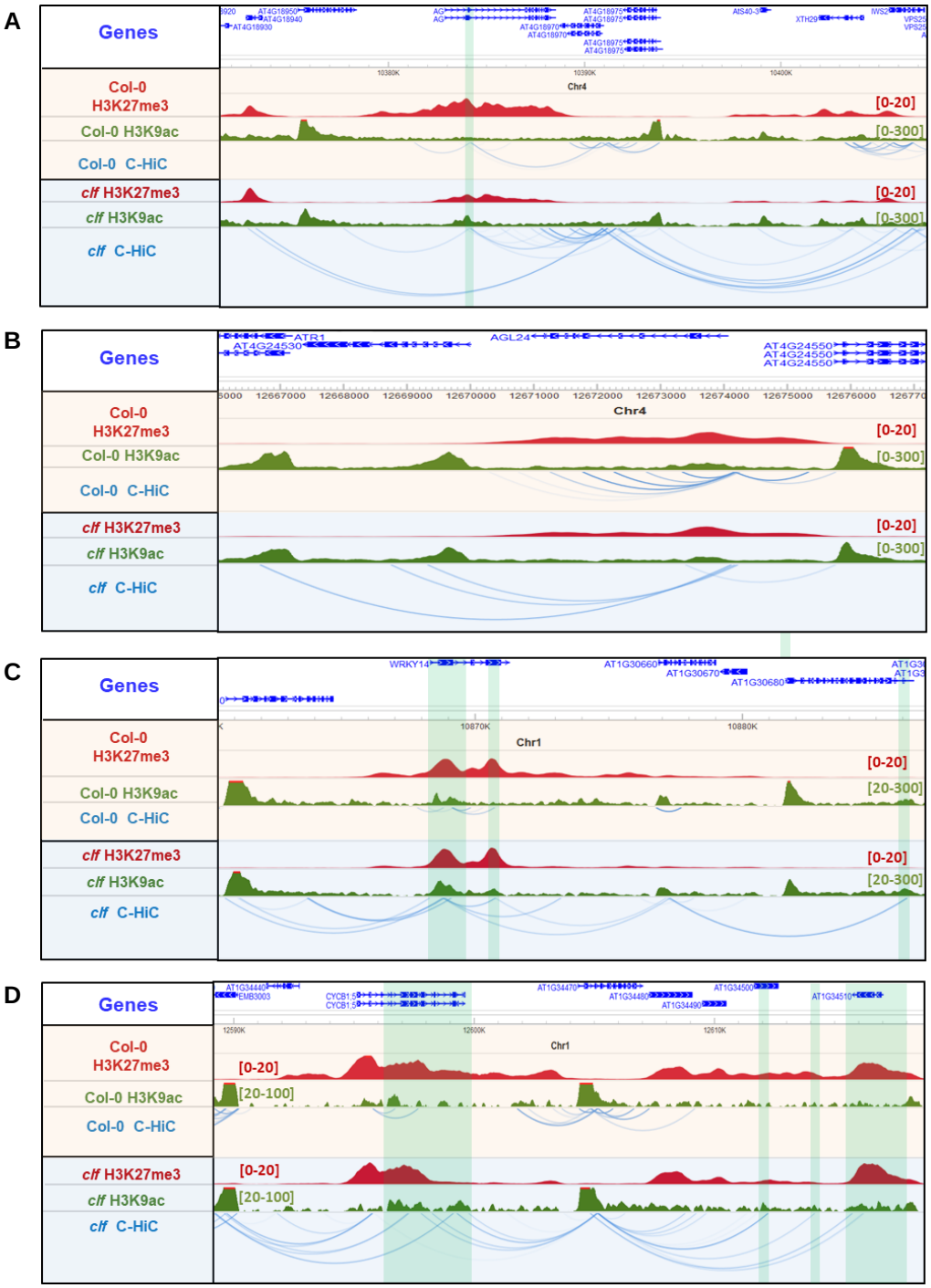


Supplemental Fig S13. PCA (principal component analysis) plot for different replicates of *clf* mutant and *Arabidopsis* wild-type. A high reproducibility was observed between the replicates in Capture Hi-C experiments.

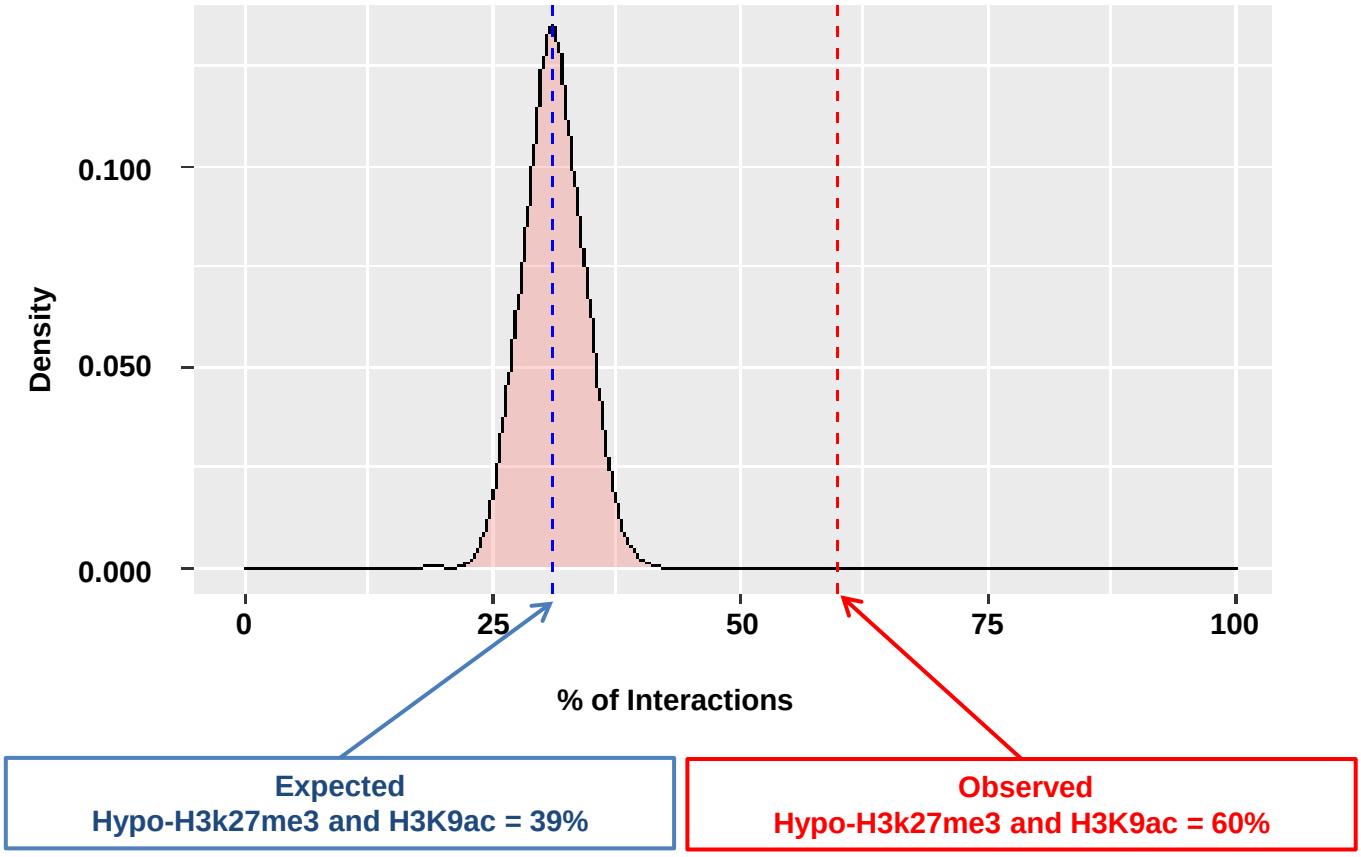
Interactions lost in *clf*	Gene1-Log FC >0 induced	Gene1-Log FC_1<0 repressed
Gene2-Log FC >0 induced	**185***	43
Gene2-Log FC_1<0 repressed	43	30

$$X^2\ (3,\ N = 2000) = 214.297,\ p = 4.33E\text{-}7$$

Supplemental Fig S14. Gene pairs connected in *clf* destabilized loops in *clf* mutant. A higher number of gene pairs are induced than expected randomly (p-value: 4.33E-7).



Supplemental Fig S15. Examples of important developmental genes AGAMOUS (AG), AGL24, WRKY14 and CYCB1;5 losing H3K27me3 in *clf* and that tend to establish interactions with regions marked with H3K9ac euchromatin mark. C-Hi-C interactions (blue lines), H3K9ac ChIP-seq signal in wild-type and *clf* (green peaks), H3K27me3 ChIP-seq signal in wild-type and *clf* (red peaks) are represented, respectively.



Supplemental Fig S16. Hypomethylated gene pairs interacting in *clf* are associated with H3K9ac. A density plot shows that interacting gene pairs in *clf,* which are hypomethylated, are also associated with the active mark H3K9ac in wild-type *Arabidopsis*. The frequency of observed Hypo-H3K27me3 and H3K9ac interactions is 60% and is greater than the expected frequency over 1000 permutations (39%).