

## **SUPPLEMENTARY INFORMATION**

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## Supplementary Tables

**Table S1. Summary of RNA-Seq raw data.**

| Library type | Tissues     | Replicates | # of clean read pairs |
|--------------|-------------|------------|-----------------------|
| RNA-Seq      | anther      | R1         | 38,551,196            |
|              |             | R2         | 37,913,267            |
|              |             | R3         | 29,983,861            |
|              | cotyledon   | R1         | 41,881,249            |
|              |             | R2         | 43,279,246            |
|              |             | R3         | 37,058,227            |
|              | fiber_10DPA | R1         | 43,244,988            |
|              |             | R2         | 47,013,569            |
|              |             | R3         | 36,986,482            |
|              | fiber_20DPA | R1         | 42,001,464            |
|              |             | R2         | 37,883,818            |
|              |             | R3         | 32,194,818            |
|              | hypocotyl   | R1         | 45,111,164            |
|              |             | R2         | 39,419,967            |
|              |             | R3         | 28,115,163            |
|              | leaf        | R1         | 44,206,720            |
|              |             | R2         | 47,767,435            |
|              |             | R3         | 36,481,411            |
|              | ovule       | R1         | 38,425,382            |
|              |             | R2         | 37,841,423            |
|              |             | R3         | 29,599,001            |
|              | petal       | R1         | 44,857,597            |
|              |             | R2         | 42,785,437            |
|              |             | R3         | 41,505,125            |
|              | radicle     | R1         | 42,503,638            |
|              |             | R2         | 42,154,266            |
|              |             | R3         | 41,232,914            |
|              | root        | R1         | 42,650,994            |
|              |             | R2         | 36,285,594            |
|              |             | R3         | 43,302,321            |
|              | stem        | R1         | 38,760,659            |
|              |             | R2         | 39,013,650            |
|              |             | R3         | 30,608,459            |
|              | stigma      | R1         | 41,305,894            |
|              |             | R2         | 36,873,026            |
|              |             | R3         | 42,134,761            |

**Table S2. Summary of ChIP-Seq datasets.**

| Library type | Tissues     | Replicates | # of clean reads | FRiP  | Peaks (-p 0.005) | IDR ( $\leq 0.05$ ) | Recall | Merge  |
|--------------|-------------|------------|------------------|-------|------------------|---------------------|--------|--------|
| ATAC-Seq     | anther      | R1         | 61,917,396       | 29.38 | 145,750          | 16,026              | 26,142 | 26,209 |
|              |             | R2         | 38,429,311       | 31.34 | 257,985          |                     |        |        |
|              | fiber_10DPA | R1         | 50,698,456       | 21.81 | 134,158          | 11,920              | 24,992 | 27,388 |
|              |             | R2         | 51,027,903       | 22.61 | 171,989          |                     |        |        |
|              | fiber_20DPA | R1         | 68,917,655       | 22.63 | 178,108          | 13,459              | 28,796 | 30,627 |
|              |             | R2         | 62,227,336       | 23.42 | 159,134          |                     |        |        |
|              | hypocotyl   | R1         | 59,668,870       | 22.69 | 203,760          | 15,834              | 25,256 | 25,468 |
|              |             | R2         | 57,582,330       | 22.15 | 192,821          |                     |        |        |
|              | ovule       | R1         | 60,231,006       | 47.61 | 212,240          | 15,663              | 18,819 | 26,054 |
|              |             | R2         | 59,583,146       | 46.83 | 192,670          |                     |        |        |
|              | petal       | R1         | 62,338,132       | 41.01 | 221,683          | 28,597              | 19,977 | 30,413 |
|              |             | R2         | 56,425,009       | 40.49 | 197,113          |                     |        |        |
|              | radicle     | R1         | 63,960,987       | 18.81 | 144,162          | 18,242              | 23,267 | 26,051 |
|              |             | R2         | 56,748,596       | 19.94 | 176,769          |                     |        |        |
|              | stigma      | R1         | 64,080,377       | 29.51 | 233,145          | 29,839              | 16,585 | 30,768 |
|              |             | R2         | 59,453,640       | 30.20 | 220,941          |                     |        |        |

P-values were computed by MACS2 using the default parameters. MACS2 computes a p-value for each peak by implementing a dynamic Poisson distribution.

**Table S3. Summary of ATAC-Seq datasets.**

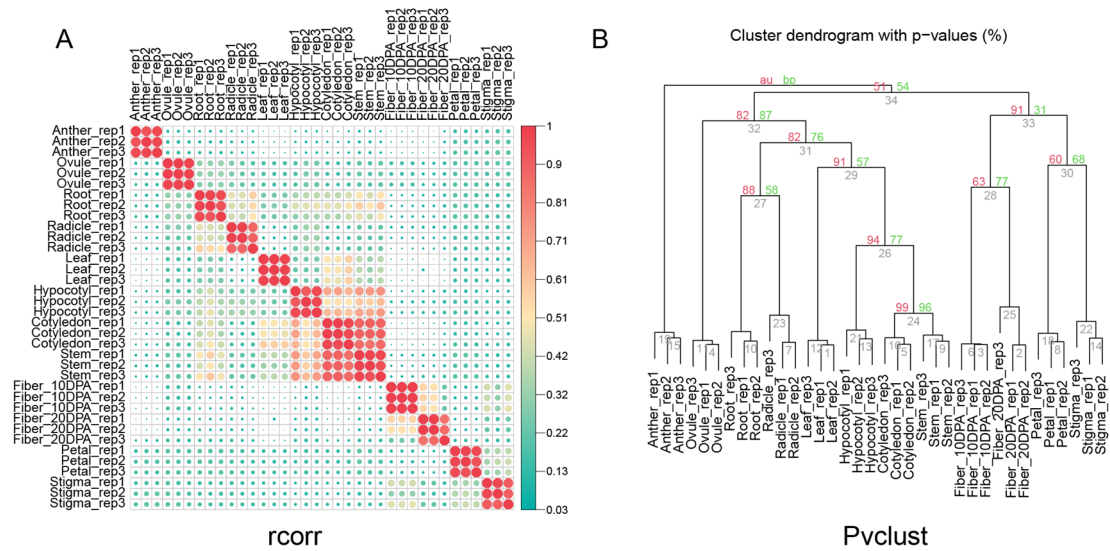
| Library type | Tissues     | Replicates | # of clean reads | FRiP  | Peaks (-p 0.005) | IDR ( $\leq 0.05$ ) | Recall | Merge  |
|--------------|-------------|------------|------------------|-------|------------------|---------------------|--------|--------|
| ATAC-Seq     | anther      | R1         | 61,917,396       | 29.38 | 145,750          | 16,026              | 26,142 | 26,209 |
|              |             | R2         | 38,429,311       | 31.34 | 257,985          |                     |        |        |
|              | fiber_10DPA | R1         | 50,698,456       | 21.81 | 134,158          | 11,920              | 24,992 | 27,388 |
|              |             | R2         | 51,027,903       | 22.61 | 171,989          |                     |        |        |
|              | fiber_20DPA | R1         | 68,917,655       | 22.63 | 178,108          | 13,459              | 28,796 | 30,627 |
|              |             | R2         | 62,227,336       | 23.42 | 159,134          |                     |        |        |
|              | hypocotyl   | R1         | 59,668,870       | 22.69 | 203,760          | 15,834              | 25,256 | 25,468 |
|              |             | R2         | 57,582,330       | 22.15 | 192,821          |                     |        |        |
|              | ovule       | R1         | 60,231,006       | 47.61 | 212,240          | 15,663              | 18,819 | 26,054 |
|              |             | R2         | 59,583,146       | 46.83 | 192,670          |                     |        |        |
|              | petal       | R1         | 62,338,132       | 41.01 | 221,683          | 28,597              | 19,977 | 30,413 |
|              |             | R2         | 56,425,009       | 40.49 | 197,113          |                     |        |        |
|              | radicle     | R1         | 63,960,987       | 18.81 | 144,162          | 18,242              | 23,267 | 26,051 |
|              |             | R2         | 56,748,596       | 19.94 | 176,769          |                     |        |        |
|              | stigma      | R1         | 64,080,377       | 29.51 | 233,145          | 29,839              | 16,585 | 30,768 |
|              |             | R2         | 59,453,640       | 30.20 | 220,941          |                     |        |        |

\* P-values were computed by MACS2 using the default parameters. MACS2 computes a p-value for each peak by implementing a dynamic Poisson distribution.

**Table S4. Summary of the identified loops by multiple tools.**

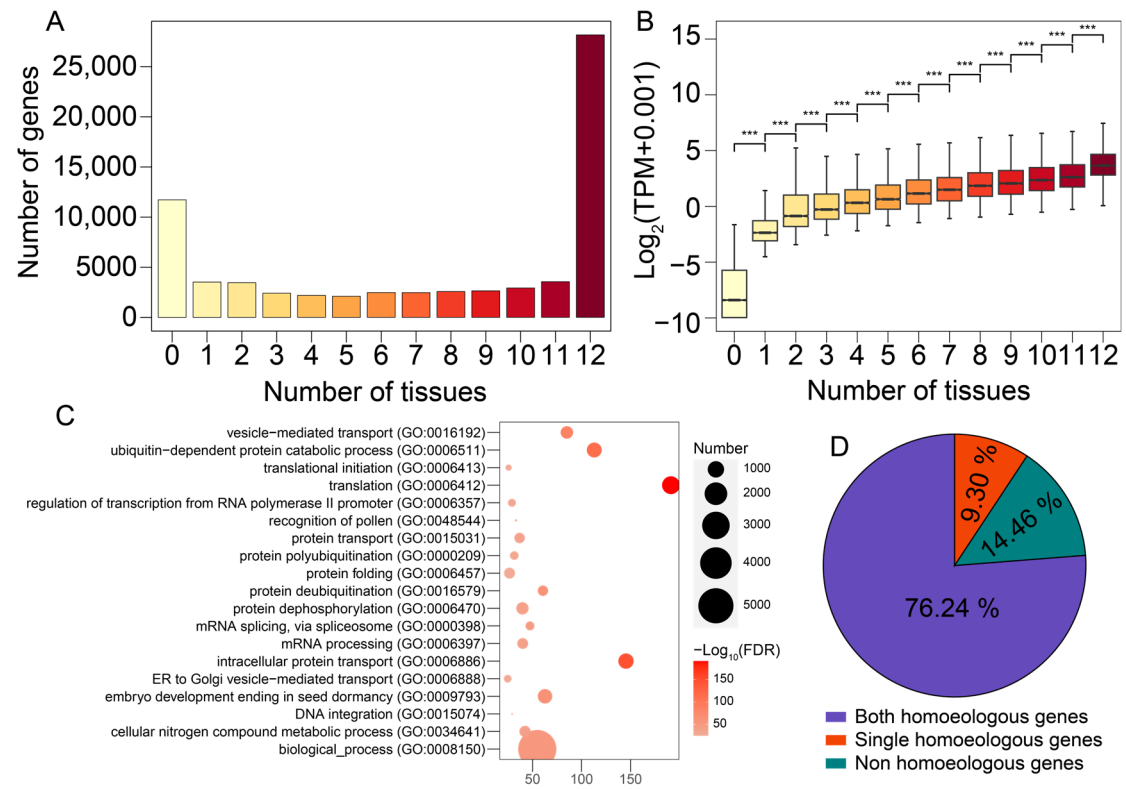
| <b>Tissues</b> | <b>Fit-Hi-C</b> | <b>Mustache</b> | <b>Chromosight</b> | <b>Peakachu</b> | <b>Top 25% loops</b> | <b>Overlap loops</b> | <b>Final loops</b> | <b>Gene loops</b> |
|----------------|-----------------|-----------------|--------------------|-----------------|----------------------|----------------------|--------------------|-------------------|
| Anther         | 174,675         | 103,114         | 134,213            | 229,961         | 145,886              | 64,175               | 173,942            | 52,550            |
| Leaf           | 154,371         | 144,151         | 71,241             | 206,234         | 125,287              | 83,521               | 163,830            | 67,119            |
| Hypocotyl      | 199,313         | 176,205         | 135,030            | 204,972         | 157,304              | 71,520               | 186,642            | 74,605            |
| Cotyledon      | 211,707         | 201,115         | 98,006             | 160,858         | 145,525              | 83,201               | 180,537            | 66,811            |
| Stem           | 127,377         | 146,784         | 114,093            | 210,975         | 119,594              | 74,264               | 154,797            | 63,778            |
| Root           | 213,878         | 146,955         | 62,552             | 148,382         | 125,958              | 81,492               | 165,406            | 57,897            |
| Radicle        | 299,967         | 151,060         | 71,714             | 112,889         | 141,554              | 72,420               | 175,759            | 75,238            |
| Ovule          | 253,313         | 94,981          | 46,523             | 129,398         | 117,690              | 74,889               | 157,033            | 71,686            |
| Fiber_10DPA    | 168,910         | 129,725         | 55,558             | 196,265         | 121,596              | 79,370               | 160,463            | 48,002            |
| Fiber_20DPA    | 129,923         | 141,891         | 58,534             | 225,934         | 120,622              | 77,265               | 156,524            | 43,930            |
| Petal          | 167,751         | 112,690         | 79,553             | 150,845         | 104,995              | 74,003               | 142,253            | 55,555            |
| Stigma         | 240,347         | 106,194         | 93,129             | 202,670         | 144,449              | 68,083               | 175,373            | 65,814            |

## Supplementary Figures



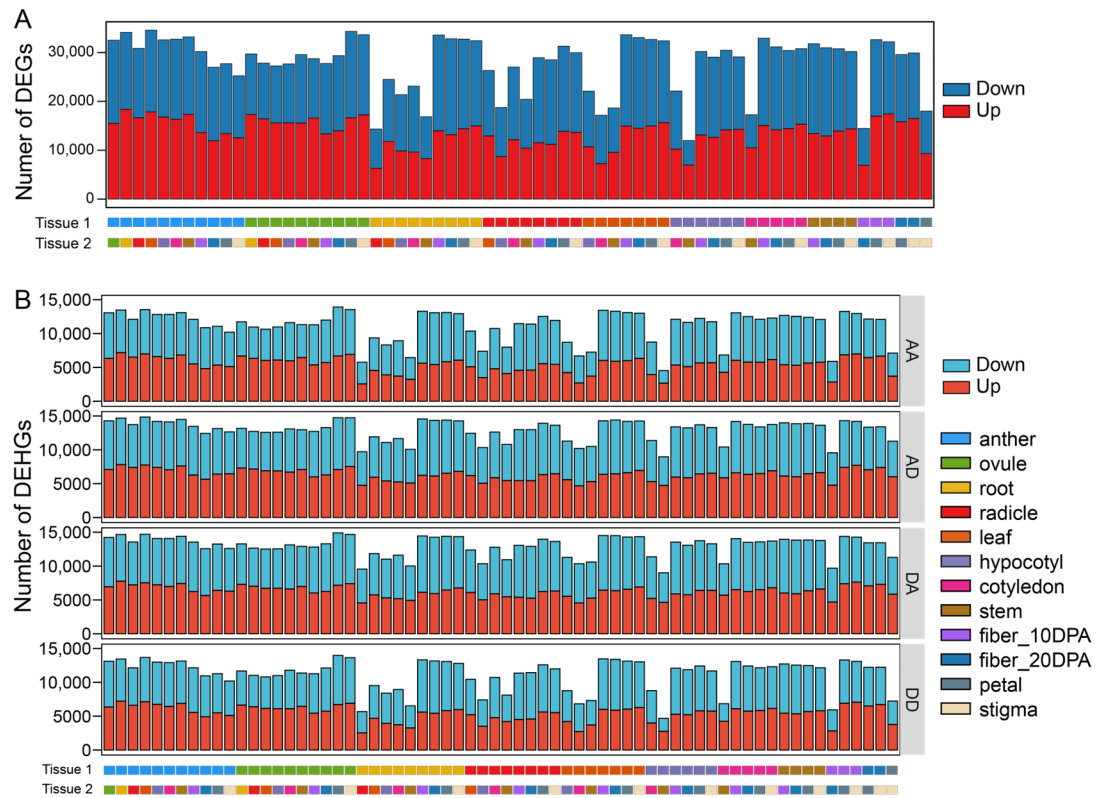
### Supplementary Fig. 1 Evaluation of consistency of transcriptome samples.

**A.** The heatmap displaying the correlation between transcriptome datasets of 12 tissues. The correlation coefficient was calculated by using the rcorr function from the Hmisc R package. **B.** Hierarchical clustering for transcriptome datasets using pvclust. The pvclust is an R package that generates two p values: approximately unbiased (AU) and bootstrap probability (BP).



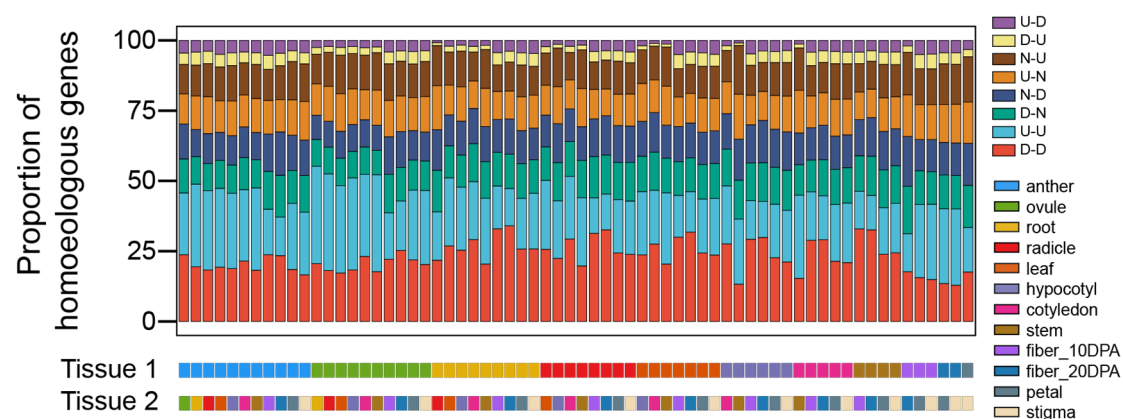
## Supplementary Fig. 2 Identification of core genes.

**A.** The bar plot shows the number of genes expressed in multiple tissues. **B.** The box plot illustrates the expression level of genes. Two-sided Wilcoxon signed-rank test, \*\*\* represents  $P < 2.2 \times 10^{-16}$ . **C.** The point plot shows the GO terms of core genes. **D.** The pie plot presents three types of core genes. The label both homoeologous genes indicates that the homoeologous gene pairs are core genes. The label single homoeologous genes indicates that only one of the homoeologous genes is a core gene, while the label non homoeologous genes indicates that the core genes are not homoeologous.



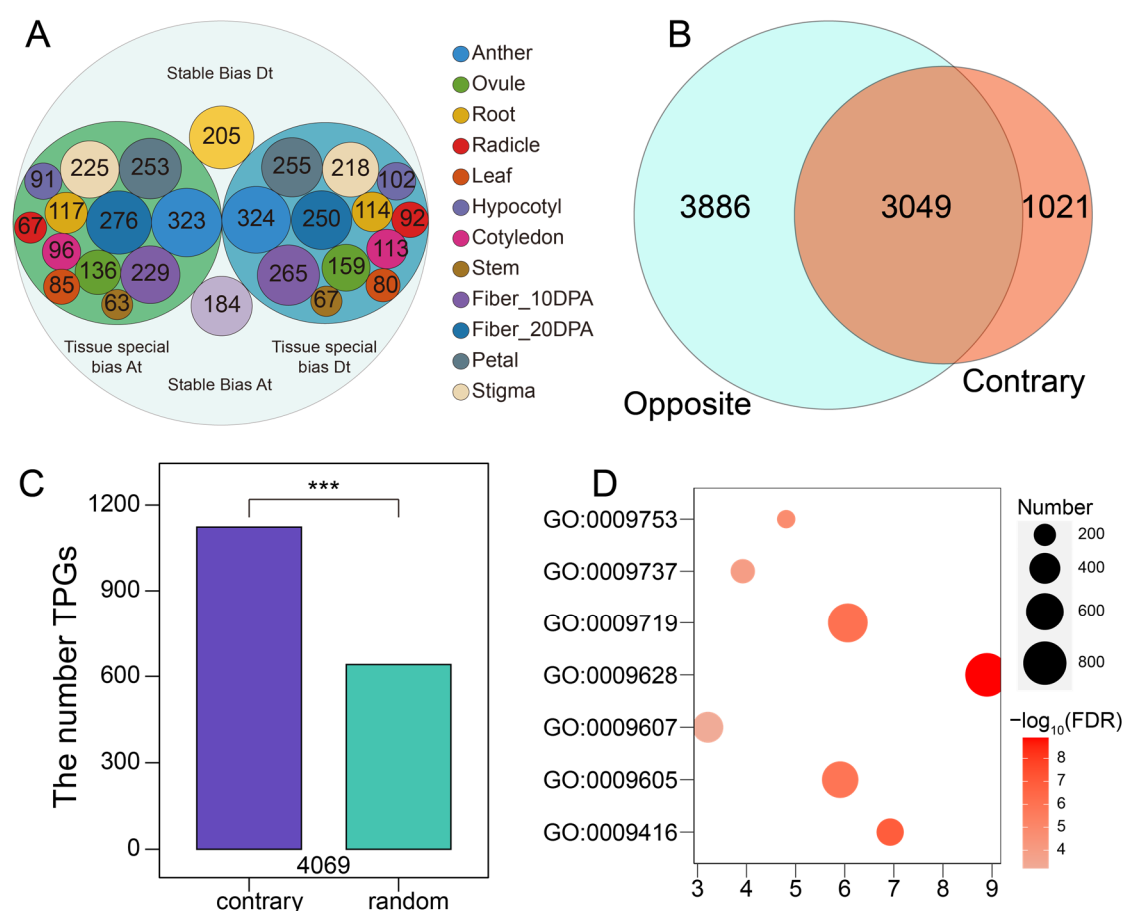
**Supplementary Fig. 3 Statistics of the differentially expressed genes between tissues.**

**A.** The bar plot shows the number of DEGs among tissues. **B.** The bar plot shows the number of homoeologous genes with differential expression between tissues.



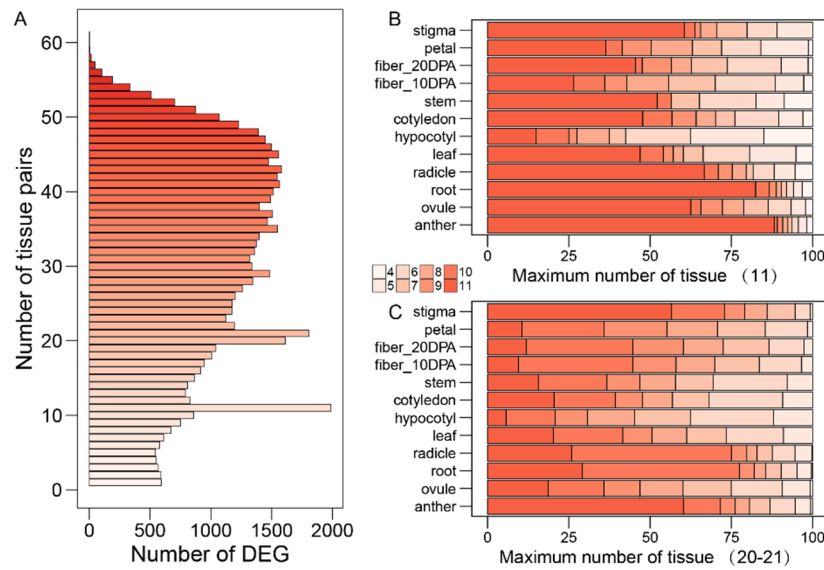
**Supplementary Fig. 4 Analysis of the opposite patterns (U–D and D–U) of homoeologous genes.**

The bar plot shows the proportion of eight different patterns among DEHGs that have an opposite pattern (U–D and D–U). D–D and U–U indicate that the homoeologous gene pairs have the same patterns of differential expression, either both upregulated or both downregulated. D–U and U–D indicate that the homoeologous gene pairs have opposite patterns of differential expression. D–N, N–D, U–N, and N–U indicate that only one homoeologous gene exhibits differential expression.



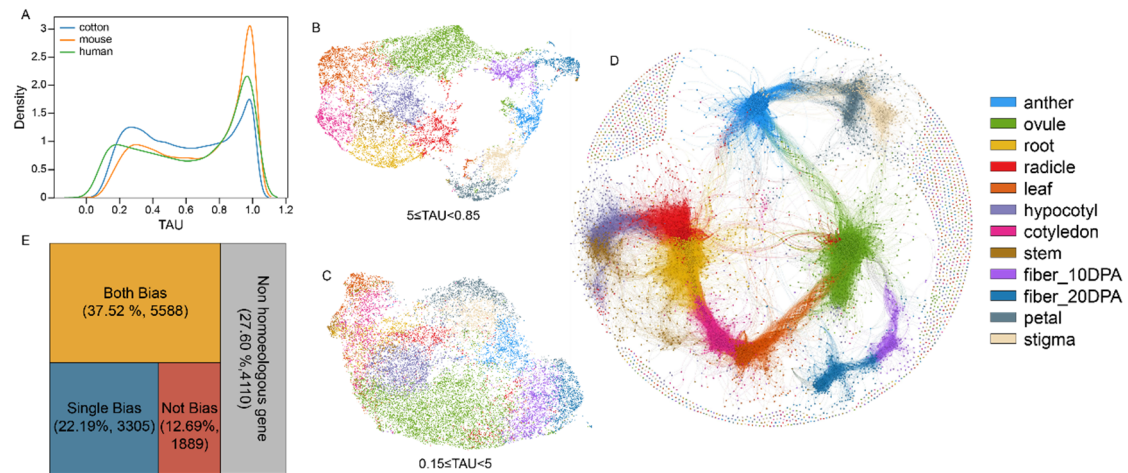
**Supplementary Fig. 5 Statistical analysis of homoeologous genes with biased expression.**

**A.** The circular packing plot displays the number of genes that exhibit consistently biased expression across twelve tissues or a single tissue. **B.** The Venn diagram shows the overlap between the homoeologous genes with contrary biased expression patterns and the homoeologous genes exhibiting opposite DE patterns. **C.** The bar plot showing a comparison in the number of TPGs contained in contrary biased genes and random homoeologous genes, respectively. Two-sided Pearson's chi-squared test,  $***P < 2.2 \times 10^{-16}$ . **D.** The point plot displays the GO terms of contrary biased genes.



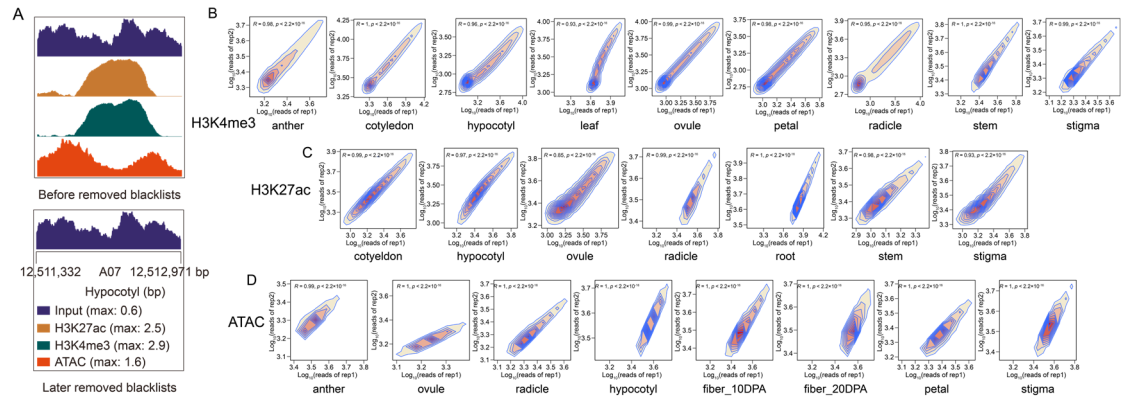
### Supplementary Fig. 6 Analysis of DEGs in multiple tissues.

**A.** The bar plot displays the accumulated number of DEGs across various tissues. **B** and **C.** Bar plots showing the ratio of DEGs. The color represents the frequency at which a gene can exhibit differential expression across tissues. The horizontal axis indicates the tissue with the highest expression level for that gene.



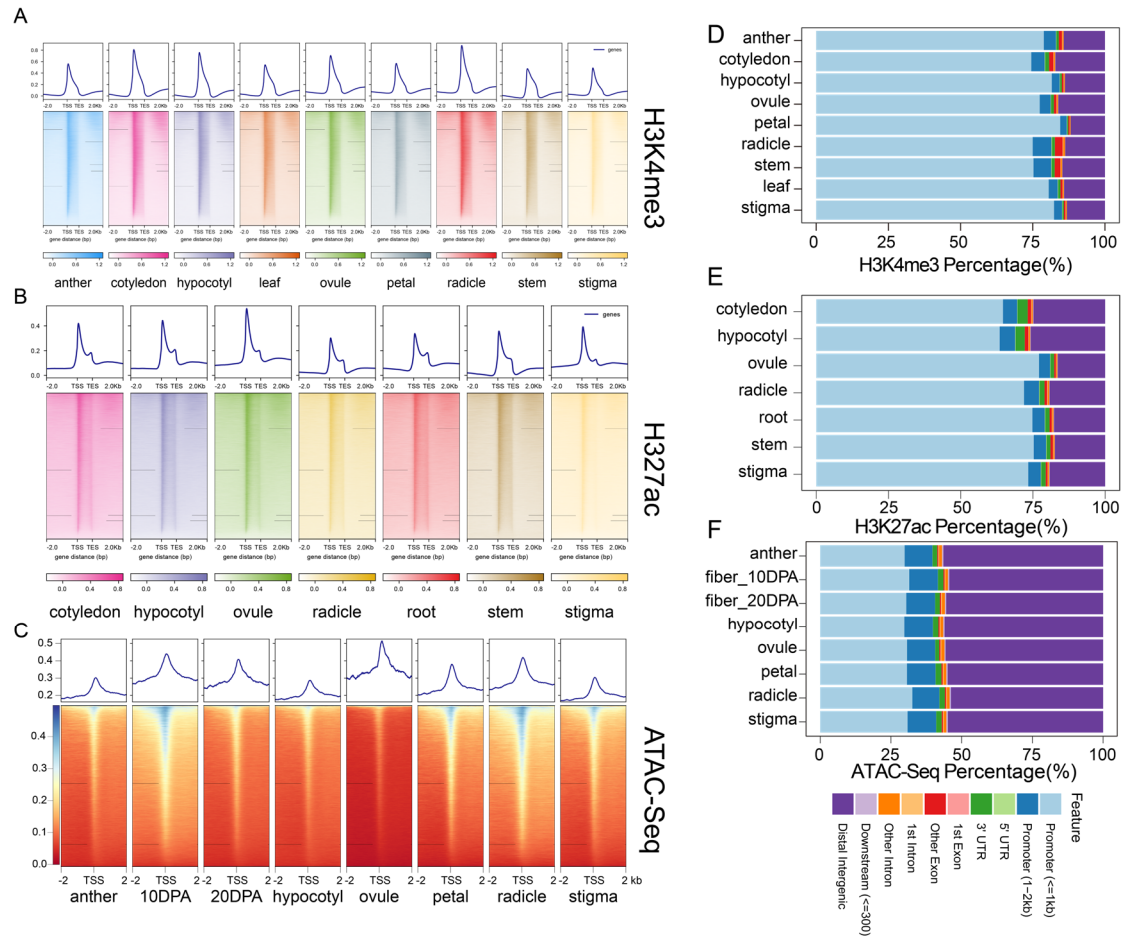
### Supplementary Fig. 7 Comprehensive evaluation of the TPGs.

**A.** The line plot illustrates the gene density distribution across different TAU values. **B** and **C.** The point plots show the cluster of genes in different ranges of TAU values. **D.** The network plot shows the co-expression relationships between TPGs, with each point representing a gene and lines indicating Pearson correlation coefficients greater than 0.05. **E.** The treemap displays the proportions of the four types of TPGs.



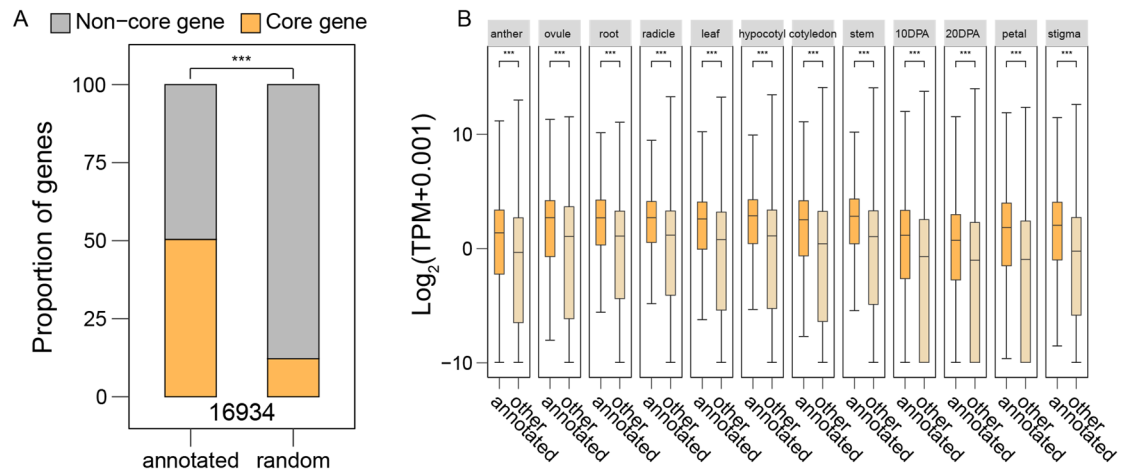
### Supplementary Fig. 8 Analysis for ChIP-Seq and ATAC-Seq datasets.

**A.** The genome region tracks plot illustrates the identified peaks before and after removing blacklisted regions. **B, C** and **D.** The density plots indicate the consistency between repeat datasets. We computed the correlation between repetitions using the Pearson correlation method and determined the p-values via the Two-sided T-test.



**Supplementary Fig. 9 Comprehensive evaluation of the ChIP-Seq and ATAC-Seq datasets.**

**A** and **B**. The heatmap and line plot show the regional signals of H3K4me3 and H3K27ac. **C**. The heatmap and the line plot show the point signal of ATAC-Seq. **D**, **E** and **F**. The bar plots show the annotation of peaks for H3K4me3, H3K27ac and ATAC-Seq libraries.

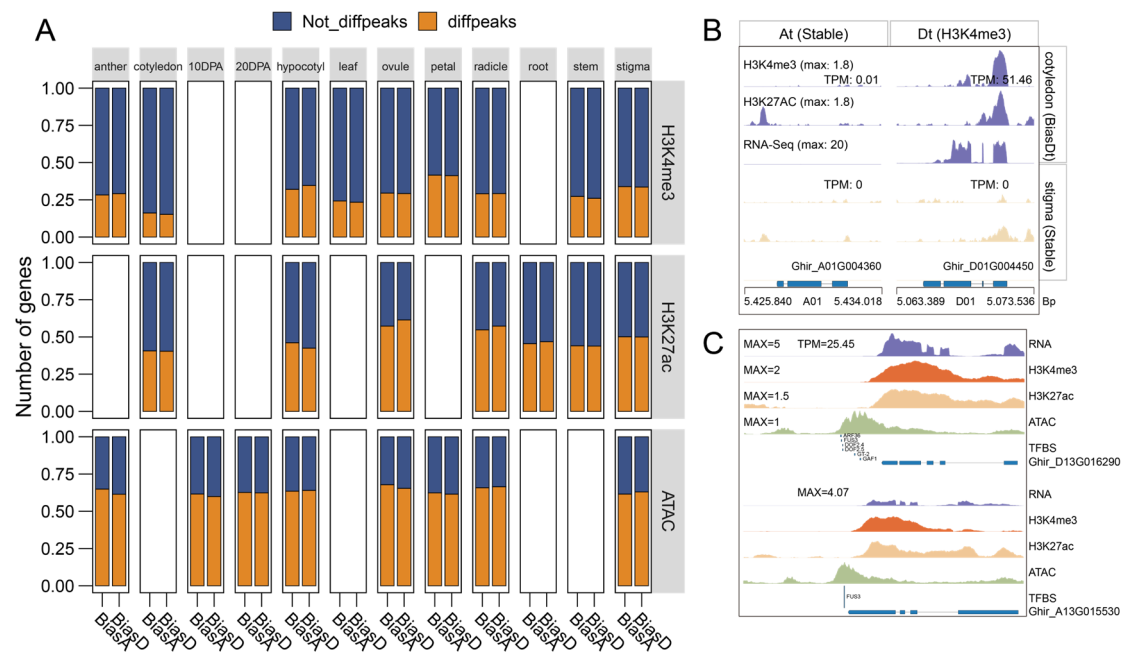


**Supplementary Fig. 10 Characterization of genes annotated by H3K4me3, H3K27ac, and ATAC peaks.**

**A.** The bar plot shows the proportion of core genes in genes annotated by H3K4me3, H3K27ac, and ATAC peaks. Two-sided Pearson's chi-squared test, \*\*\* $P < 2.2 \times 10^{-16}$ .

**B.** The box plot illustrates the comparison of expression levels between annotated genes and other genes. Two-sided Wilcoxon signed-rank test, \*\*\* $P < 2.2 \times 10^{-16}$ .



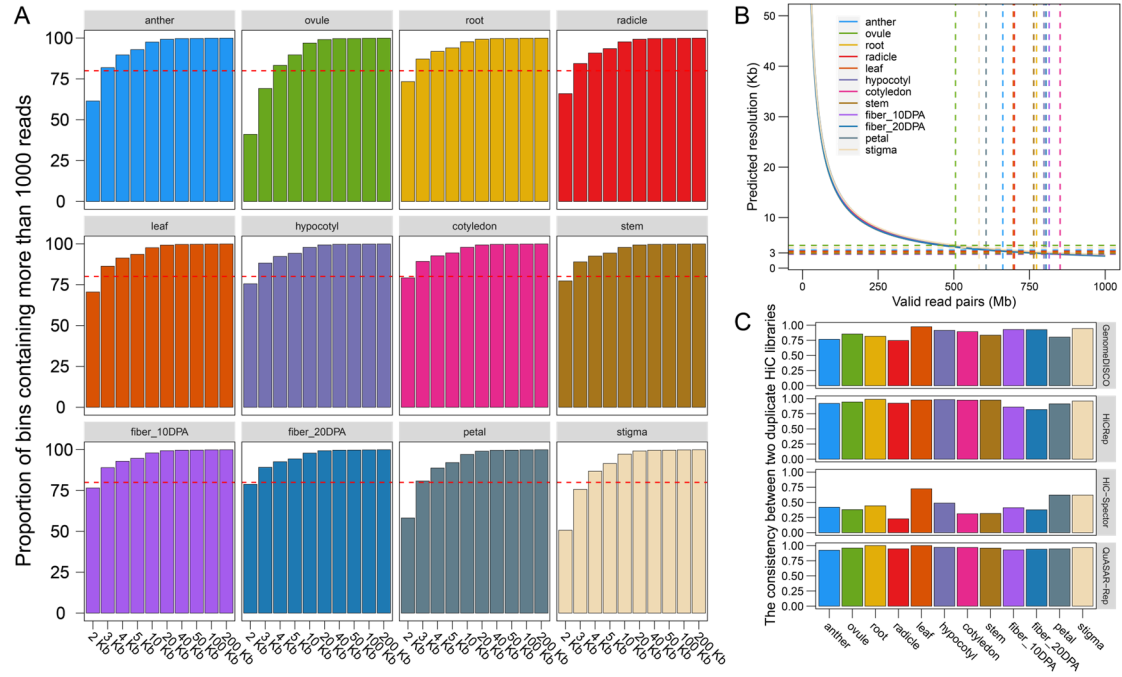


**Supplementary Fig. 12 Influence of multiple factors on homoeologous biased genes.**

**A.** The bar plot displays the proportion of homoeologous gene pairs with biased expression, in which at least one has presence peaks within 2 kb upstream of their TSS.

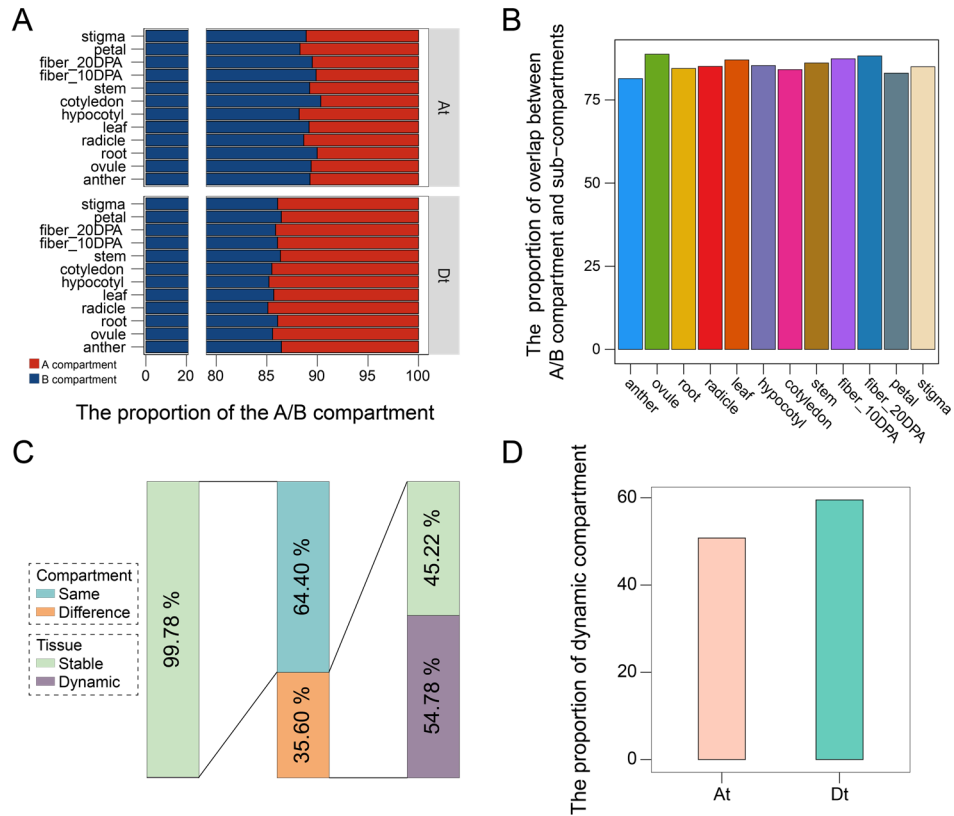
**B.** The genome region tracks plot illustrates that the different peaks influence the expression bias of homoeologous gene pairs and the differential expression of genes across tissues.

**C.** The genome region tracks plot illustrates the different TFBSs influencing the biased expression of homoeologous gene pairs in stigma.



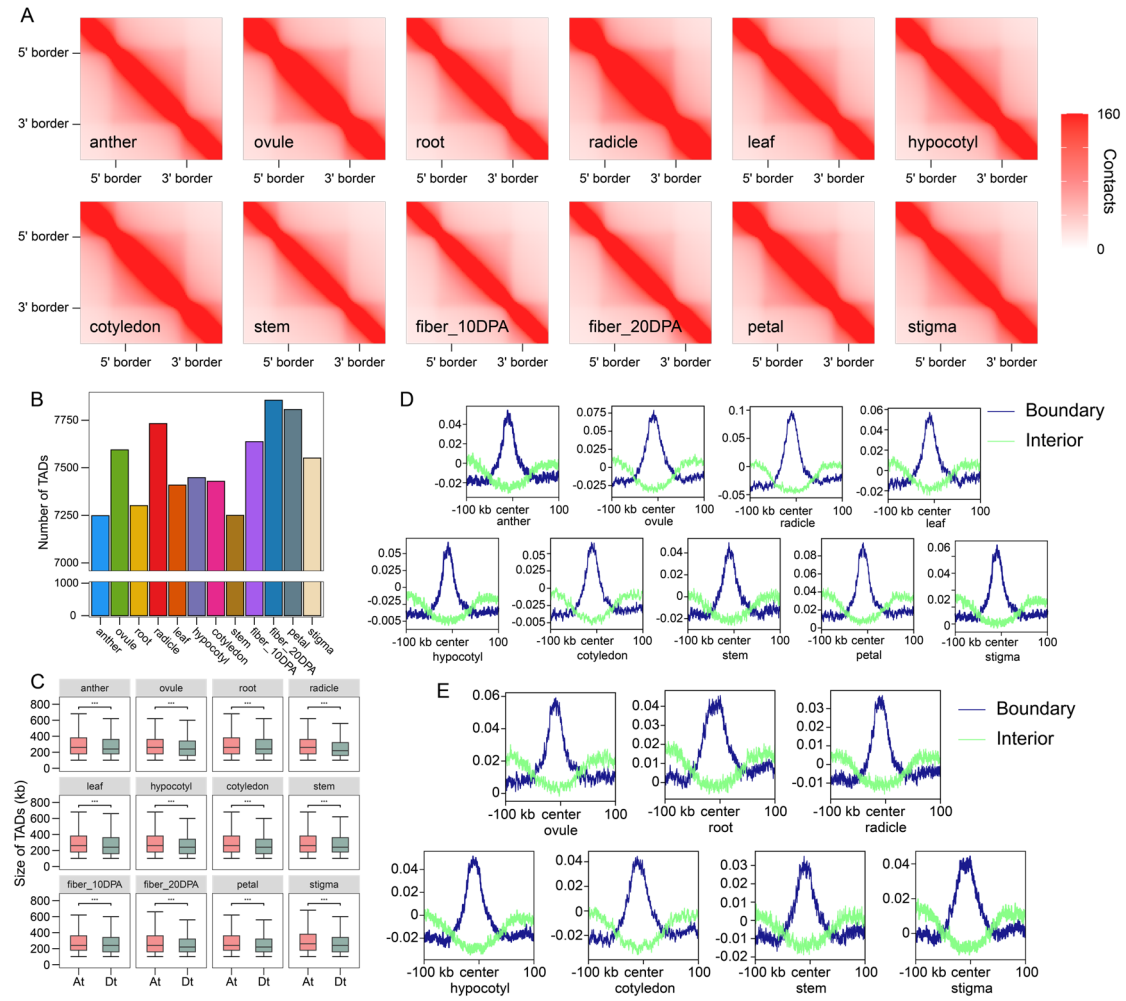
**Supplementary Fig. 13 Comprehensive evaluation of the *in situ* Hi-C libraries.**

**A.** The bar plot shows the proportion of bins that contain more than 1000 reads. **B.** The line plot displays the predicated resolution calculated by HiCRes. **C.** The bar plot illustrates the consistency between Hi-C replicate datasets calculated using the 3DChromatin\_ReplicateQC tool.



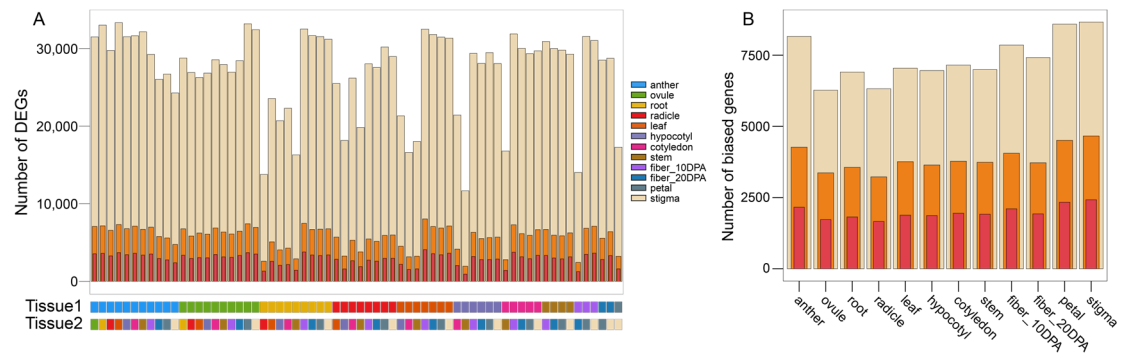
**Supplementary Fig. 14 Analysis of the chromatin status of the A/B compartment in noncoding regions.**

**A.** The bar plot shows the proportion of the A/B compartment in noncoding regions. **B.** The bar plot displays the ratio of overlap regions between A/B compartment and sub-compartments in 12 tissues. **C.** The bar plot presents an overview of overlapping regions of compartments across tissues. The middle bar illustrates the proportion of regions with the same or different A/B compartment and sub-compartments status in 12 tissues. The side bar displays the stable and dynamic compartment status across tissues. **D.** The bar plot shows the comparison of dynamic compartment status with different A/B compartment and sub-compartments status across tissues between two subgenomes.



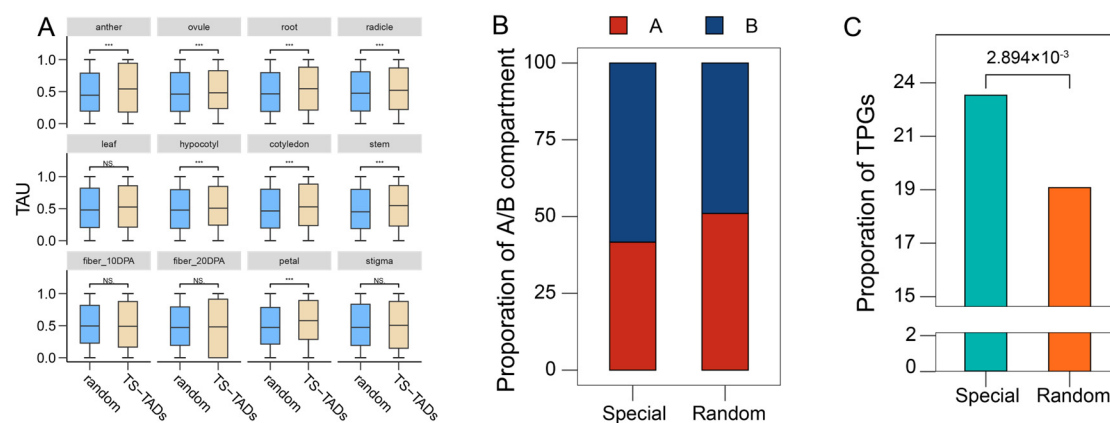
**Supplementary Fig. 15 Characterization of identified TAD-like domains.**

**A.** The Aggregate TAD Analysis (ATA) plot shows the characteristics of TAD-like domains identified in 12 tissues. **B.** The bar plot shows the number of identified TAD-like domains. **C.** The box plot shows the size of identified TADs. Two-sided Wilcoxon signed-rank test. \*\*\* represents  $P < 2.2 \times 10^{-16}$ . **D.** The line plot depicts the H3K4me3 signal in the 100 kb region surrounding TAD-like domain boundaries and interior. **E.** The line plot depicts the H3K27ac signal in the 100 kb region surrounding TAD-like domain boundaries and interior.



**Supplementary Fig. 16 The influence of rearrangement of the TAD-like domains on DEGs and homoeologous biased genes.**

**A.** The bar plot shows the number of DEGs. The beige color represents the number of DEGs, the orange color represents the number of DEGs located in the boundary and interior in different tissues, respectively, and the red color represents the number of DEGs whose genes are located in boundaries with higher expression levels. **B.** The bar plot shows the number of homoeologous biased genes. The beige color represents the number of homoeologous biased genes; the orange color represents the number of homoeologous biased genes located in the boundary and interior in different subgenomes, respectively; and the red color represents the number of homoeologous biased genes which are located in boundaries with higher expression levels.

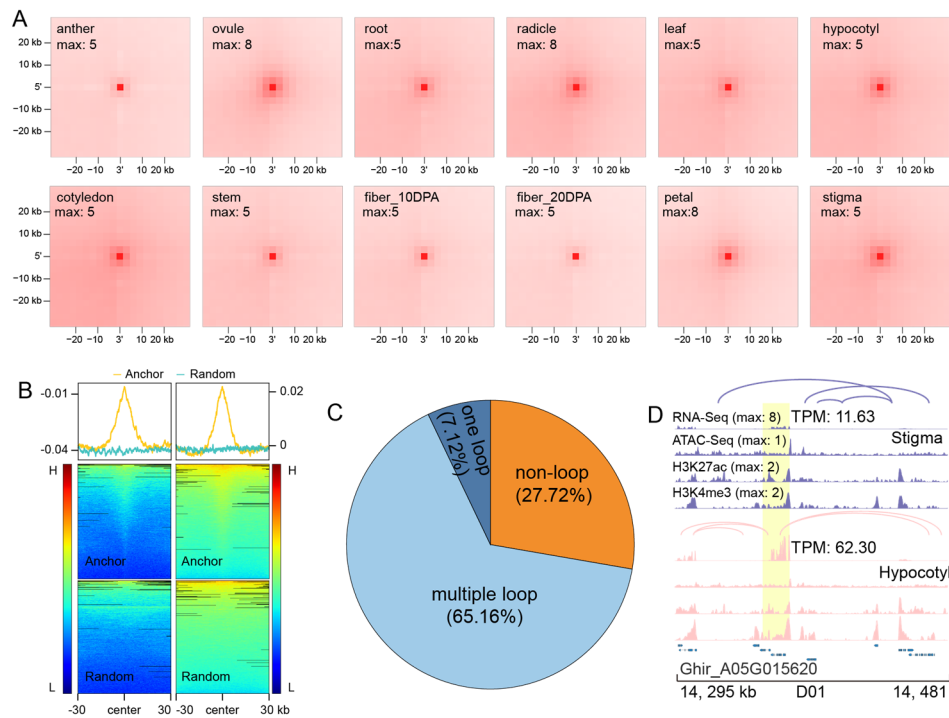


**Supplementary Fig. 17 Comparison of the TAU values between random genes and genes contained within TS-TADs.**

**A.** The box plot shows the TAU values of genes located in TS-TADs and random regions. Two-sided Wilcoxon signed-rank test. NS represents  $5 \times 10^{-2} \leq P$ , \* represents  $1 \times 10^{-3} \leq P < 5 \times 10^{-2}$ , \*\* represents  $2.2 \times 10^{-16} \leq P < 1 \times 10^{-3}$ , \*\*\* represents  $P < 2.2 \times 10^{-16}$ .

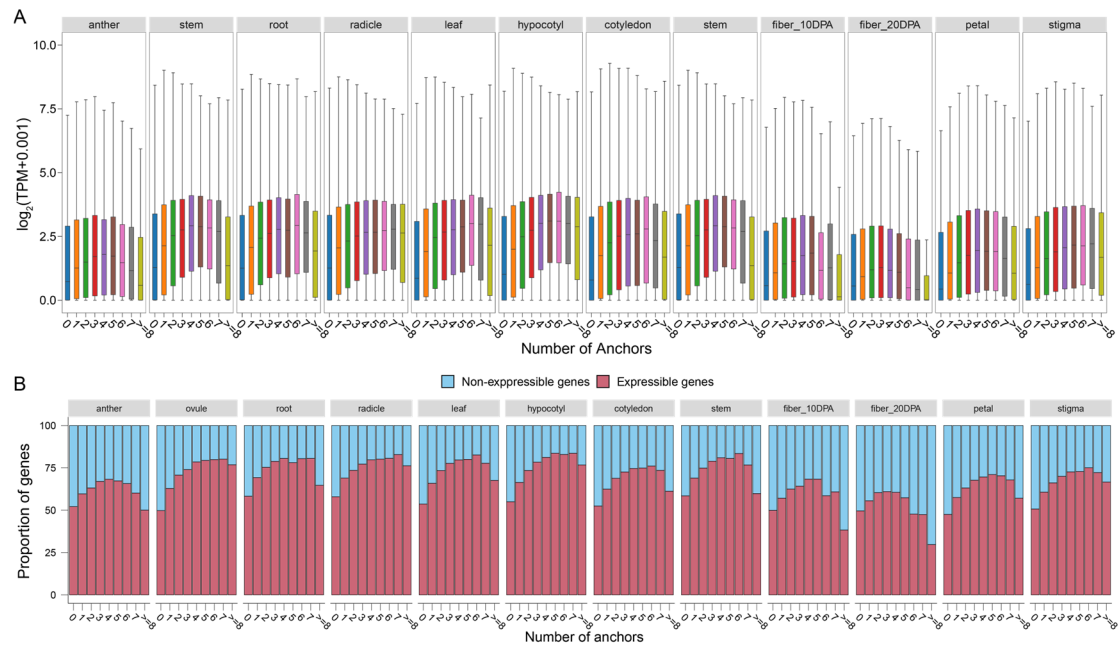
**B.** The bar plot shows the comparison of A/B compartment ratio between tissue-specific boundaries and random boundaries. **C.** The bar plot displays the proportion of TPGs among the genes located in the TAD boundaries, Two-sided Pearson's chi-squared test.

The set of random boundaries was sampled one hundred times.



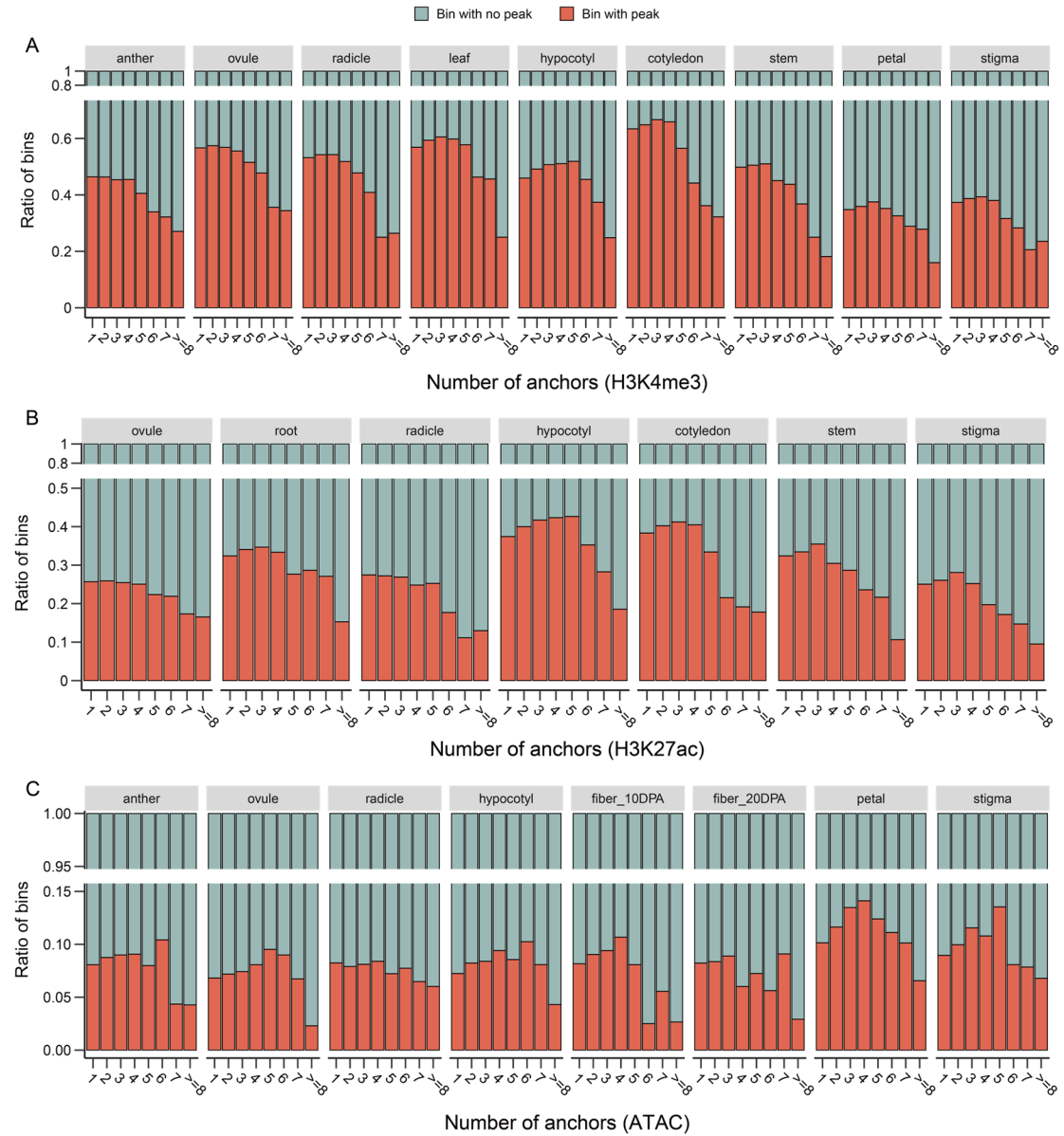
**Supplementary Fig. 18 Genes linked to different numbers of loops.**

**A.** The Aggregate Peak Analysis (APA) plot shows the averages of the signal surrounding the pixels making up the loops-linked to genes. The redder the color, the higher the frequency of interaction. **B.** The heatmap compares the signals of H3K4me3 and H3K27ac between the loop anchors and random bins (3 kb) in hypocotyl. **C.** The pie plot displays the proportion of genes associated with different numbers of loops in 12 tissues. "non-loop" refers to genes that are not located in any loop anchor across the 12 tissues. The term "one loop" indicates that the gene is connected by a maximum of one loop in 12 tissues. "multiple loops" refers to the scenario where a gene is connected by multiple loops. **D.** An example showing the influence of moderate loops for gene expression level. The yellow bar highlights the region with moderate loops.



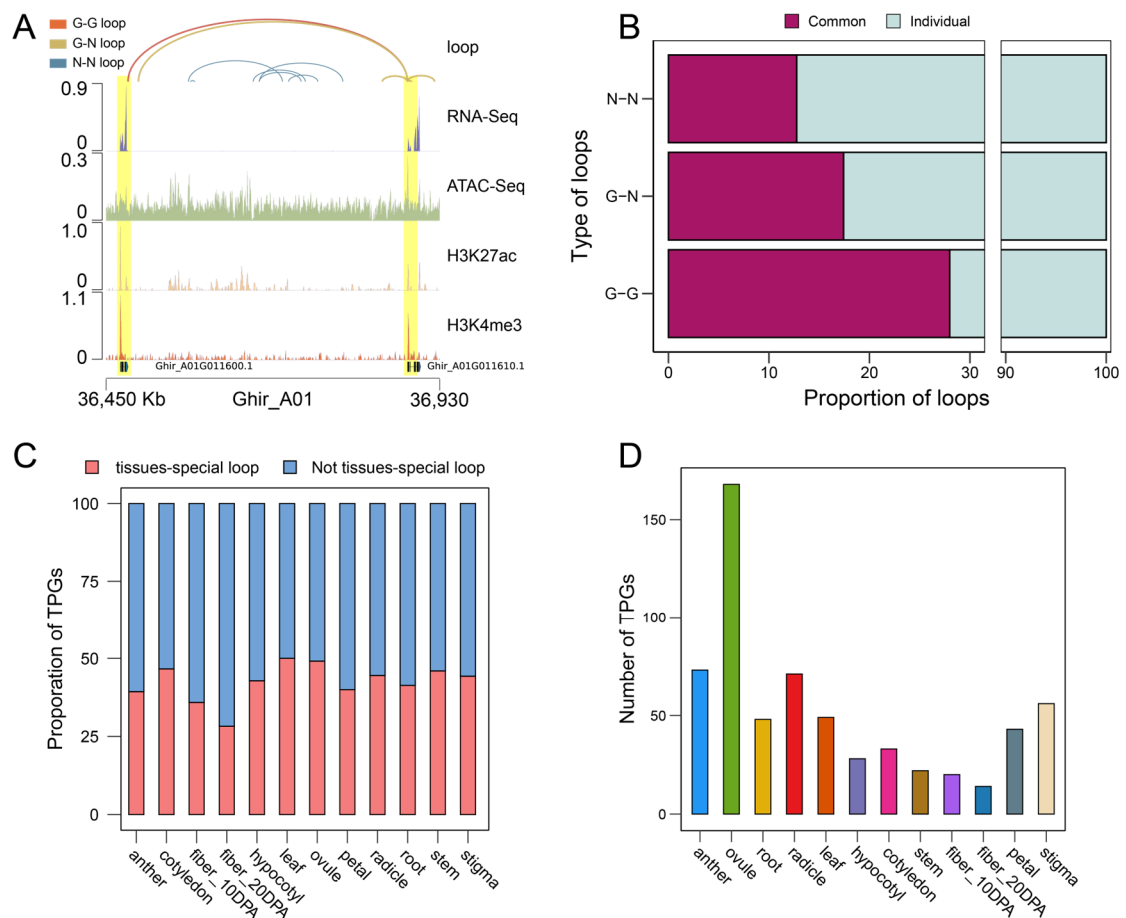
**Supplementary Fig. 19 Analysis of the expression level of genes located in anchors with various numbers of loops.**

**A.** The box plot displays the expression levels of genes located in the anchor with different loops. **B.** The bar plot shows the proportion of expressed genes located in the anchor with different loops.



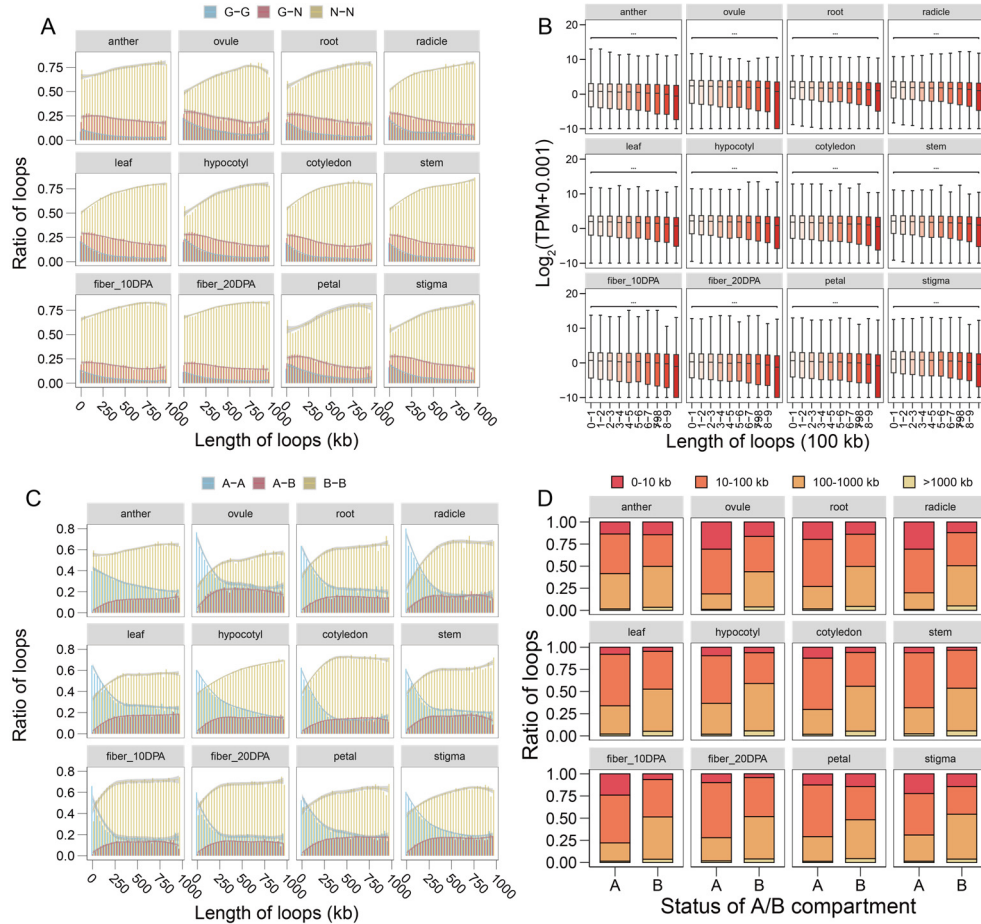
**Supplementary Fig. 20 Analysis of active histone modification and open chromatin status in anchors with various numbers of loops.**

**A, B and C.** The bar plots illustrate the proportion of bins with H3K4me3, H3K27ac and ATAC peaks, respectively. **A, B and C** share a common legend.



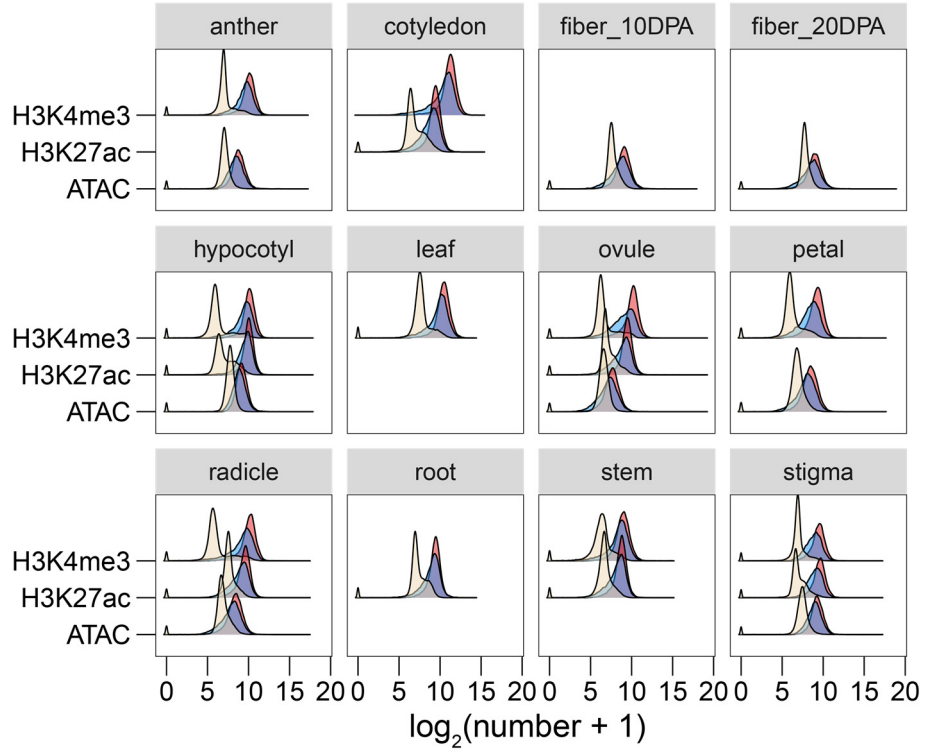
**Supplementary Fig. 21 Example and conservation analysis for multiple types of loops.**

**A.** The genome region tracks and interaction loops plot the three types of loops: G–G loops, G–N loops and N–N loops. **B.** The bar plot shows the ratio of conserved loops. **C.** The bar plot illustrates the proportion of TPGs associated with tissue-specific loops. **D.** The bar plot shows the number of TPGs regulated by putative functional elements that are connected by chromatin loops.



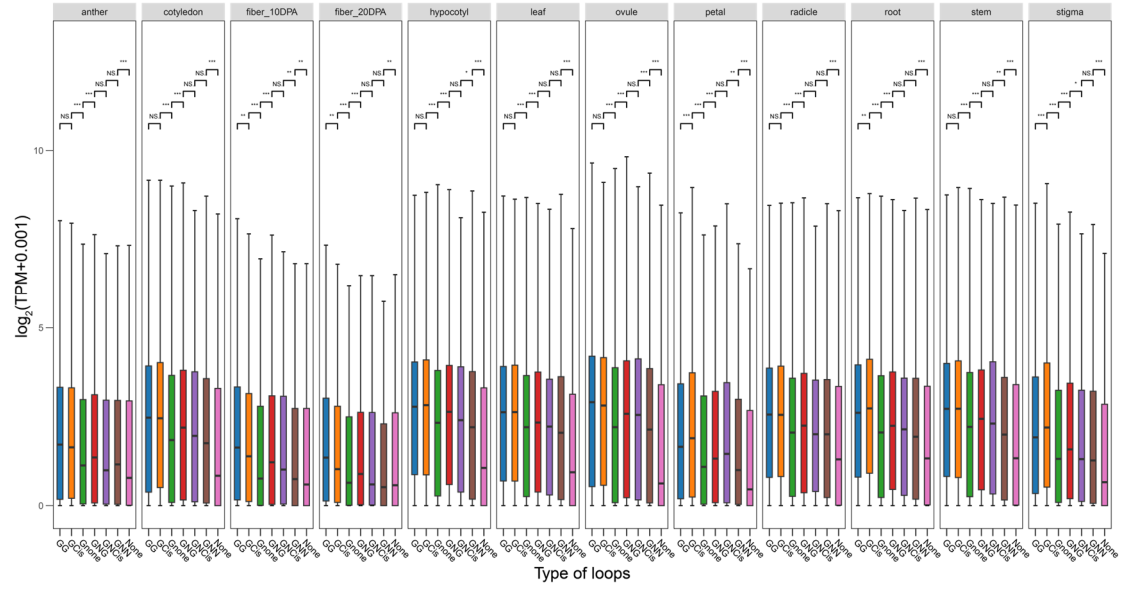
**Supplementary Fig. 22 Statistical analysis for multiple types of loops with various lengths.**

**A.** The bar plot displays the ratio of three types of loops (G–G, G–N and N–N) in different loop lengths. **B.** The box plot illustrates the expression level of genes located within loop anchors of various lengths. Two-sided Wilcoxon signed-rank test. \*\*\* represents  $P < 2.2 \times 10^{-16}$ . **C.** The bar plot displays the ratio of three types of loops (A–A, A–B and B–B) in different loop lengths. **D.** The bar plot shows the length ratio of loops within the A or B compartment.



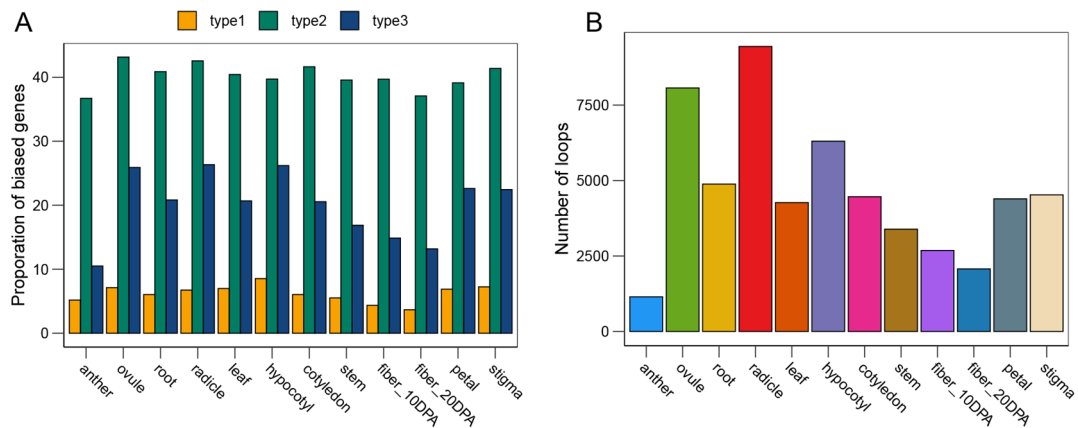
**Supplementary Fig. 23 Reads density analysis of ChIP-Seq and ATAC-Seq data in genes.**

The density plot shows the ChIP-Seq and ATAC-Seq signals in the regions of genes with unbalanced expression at the ends of loops and random expression. The number of random is consistent with ‘high’ and ‘low’.



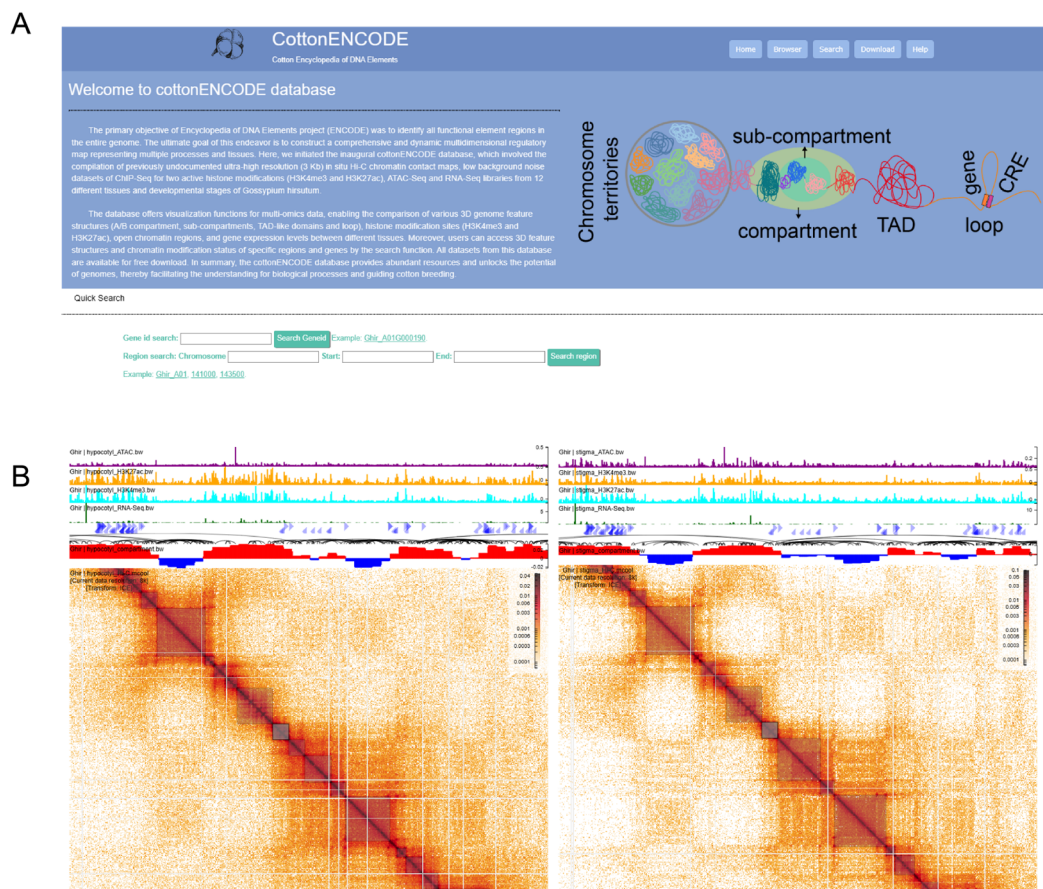
**Supplementary Fig. 24 The influence of different types of chromatin loops on gene expression.**

The box plot displays the expression level of genes located in various types of loop anchors. Two-sided Wilcoxon signed-rank test. NS represents  $5 \times 10^{-2} \leq P$ , \* represents  $1 \times 10^{-3} \leq P < 5 \times 10^{-2}$ , \*\* represents  $2.2 \times 10^{-16} \leq P < 1 \times 10^{-3}$ , \*\*\* represents  $P < 2.2 \times 10^{-16}$ .



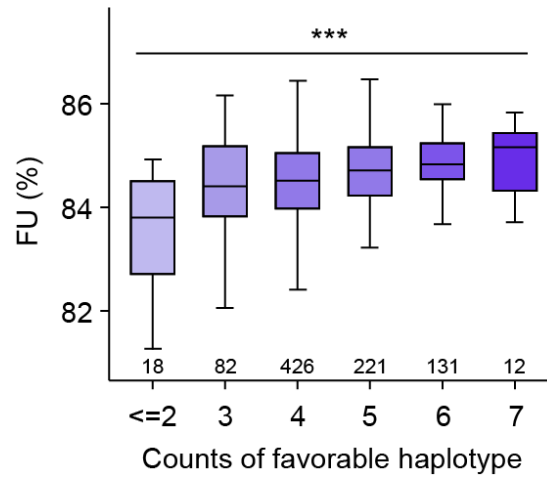
**Supplementary Fig. 25 The homoeologous loop anchors and expression of homoeologous genes.**

**A.** The bar plot displays the proportion of biased genes influenced by the absence of CREs (type 1), the loss of loops (type 2), and the distinct interaction patterns caused by loops (type 3) between two subgenomes. **B.** The bar plot illustrates the number of homoeologous loops (type4) between two subgenomes across 12 tissues.



**Supplementary Fig. 26 The home page of the CottonENCODE database.**

**A.** The home page of the CottonENCODE database which provides the data visualization (Browser), search and download functions. The cartoon elements in the figure were designed with the aid of Adobe Illustrator. **B.** Higlass, located on the browser page, facilitates the visual comparison of multi-omics data.



**Supplementary Fig. 27 The relationship between FU and counts of favorable haplotypes.**

The phenotypic value of accessions with different counts of favorable haplotypes. Two-sided Wilcoxon signed-rank test. \*\*\* $P < 0.001$ .