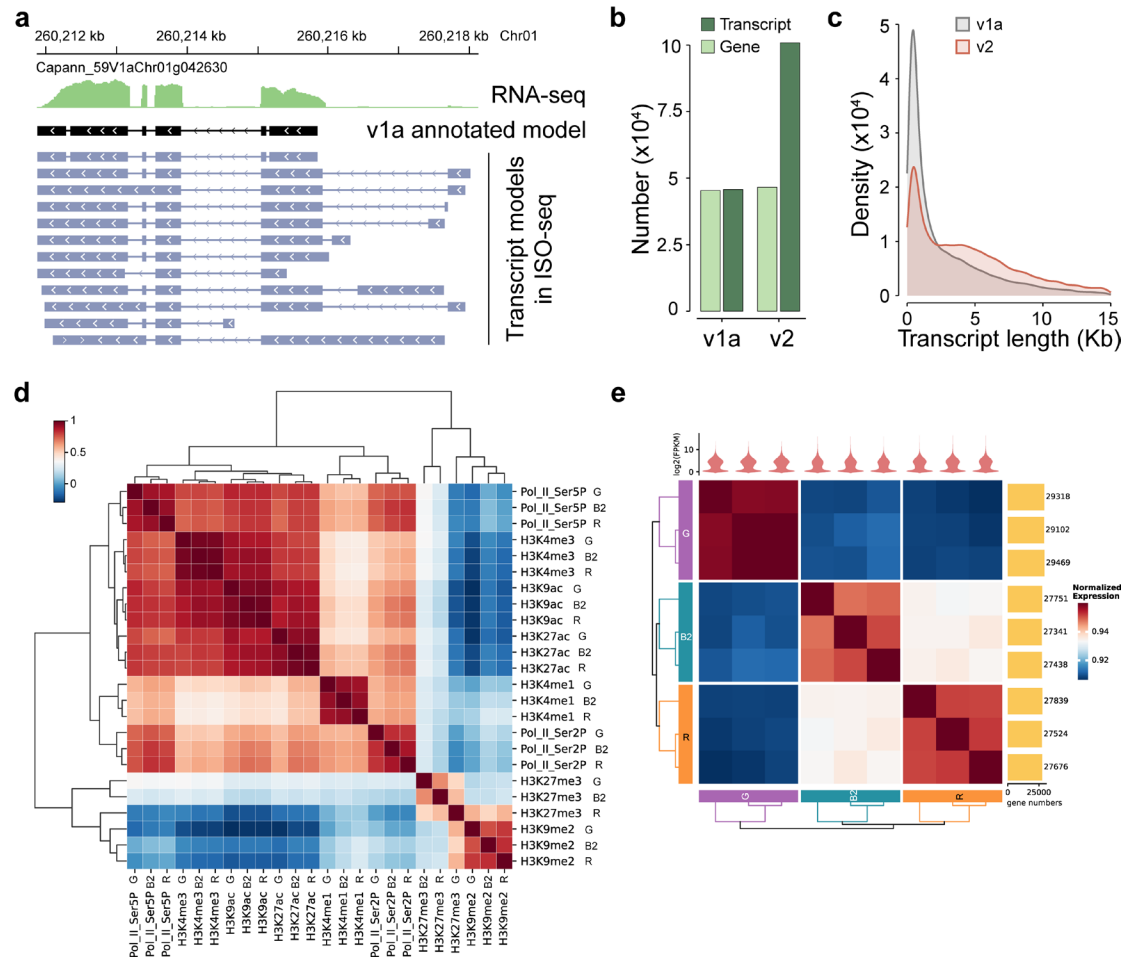
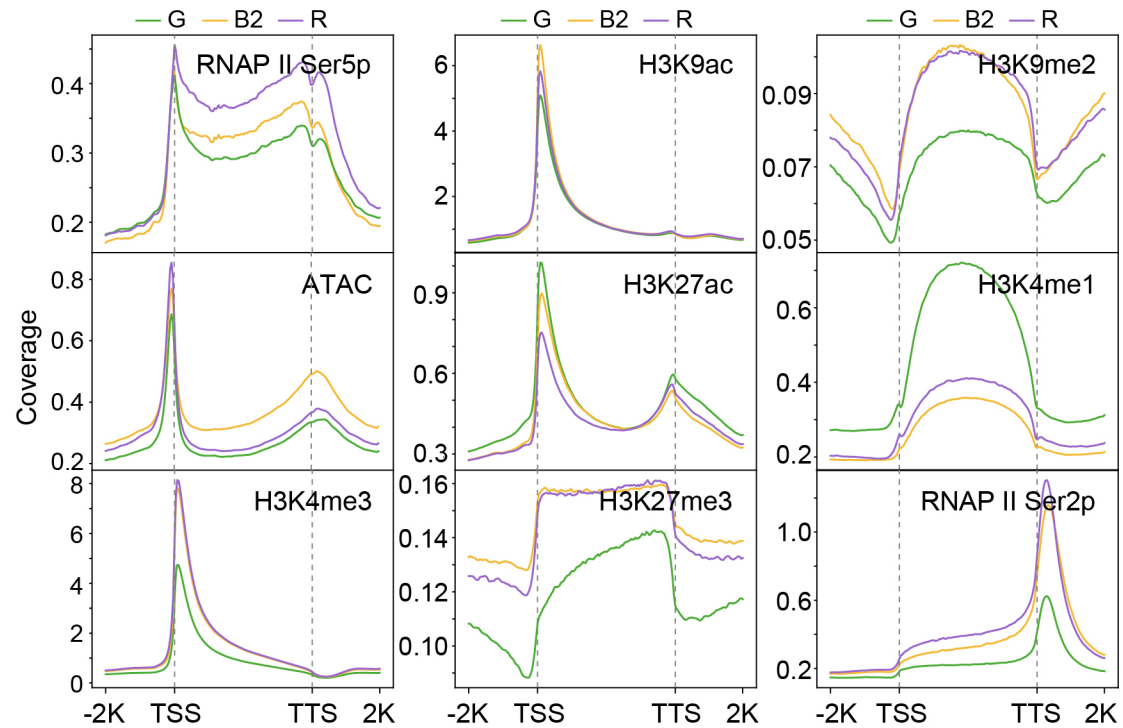
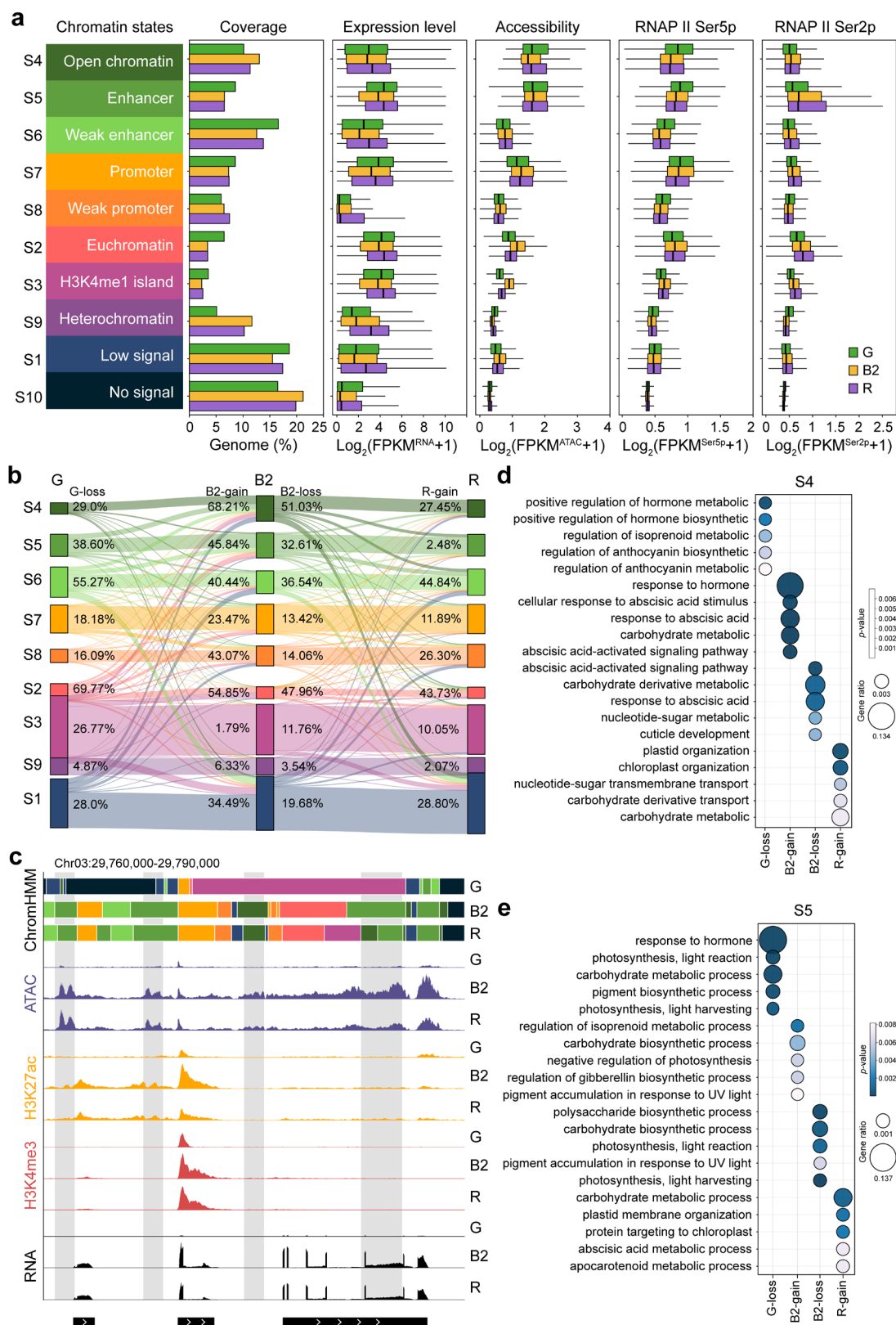




Supplementary Fig. 1 Overview of transcriptomic and epigenomic datasets during fruit color transition. **a**, IGV tracks showing the transcripts of *Chr01g042630* in Ca59 v1a and Ca59 v2 genome version, respectively. Ca59 v2 version is supported by full-length Iso-Seq transcripts. **b**, Numbers of annotated genes and transcripts in Ca59 v1a and the updated Ca59 v2. **c**, Distribution of transcript lengths in Ca59 v1a and updated Ca59 v2. **d**, Heatmap showing pairwise Pearson correlation coefficients for RNA polymerase II occupancy signals, including Pol II Ser5P and Pol II Ser2P, and histone modification signals, including H3K4me3, H3K9ac, H3K27ac, H3K4me1, H3K27me3, and H3K9me2. **e**, Spearman correlation analysis of all RNA-seq samples. The top violin plots show the distribution of $\log_2$ (TPM + 1) across all samples. The bottom heatmap shows pairwise Spearman correlation coefficients across RNA-seq samples. Red indicates higher correlation, whereas blue indicates lower correlation. The bar chart on the right shows the number of expressed genes in each sample.

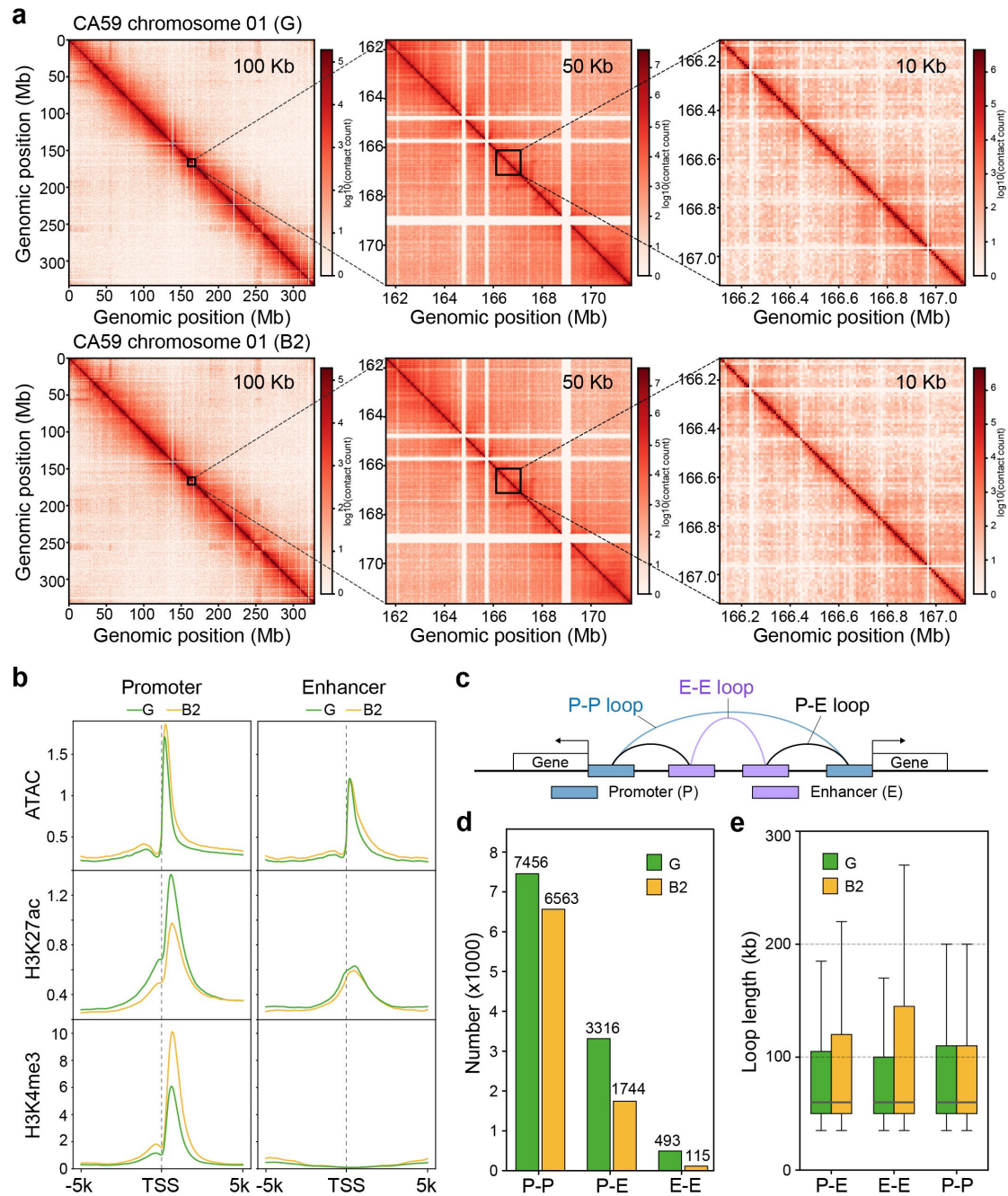


Supplementary Fig. 2 Dynamics of chromatin accessibility, histone modifications, and RNA polymerase II phosphorylation across gene bodies and regions surrounding the TSS and TTS. Signals include ATAC-seq, H3K9ac, H3K9me2, H3K27ac, H3K4me1, H3K4me3, H3K27me3, RNA polymerase II Ser5P, and RNA polymerase II Ser2P. TSS, transcription start site; TTS, transcription end site.

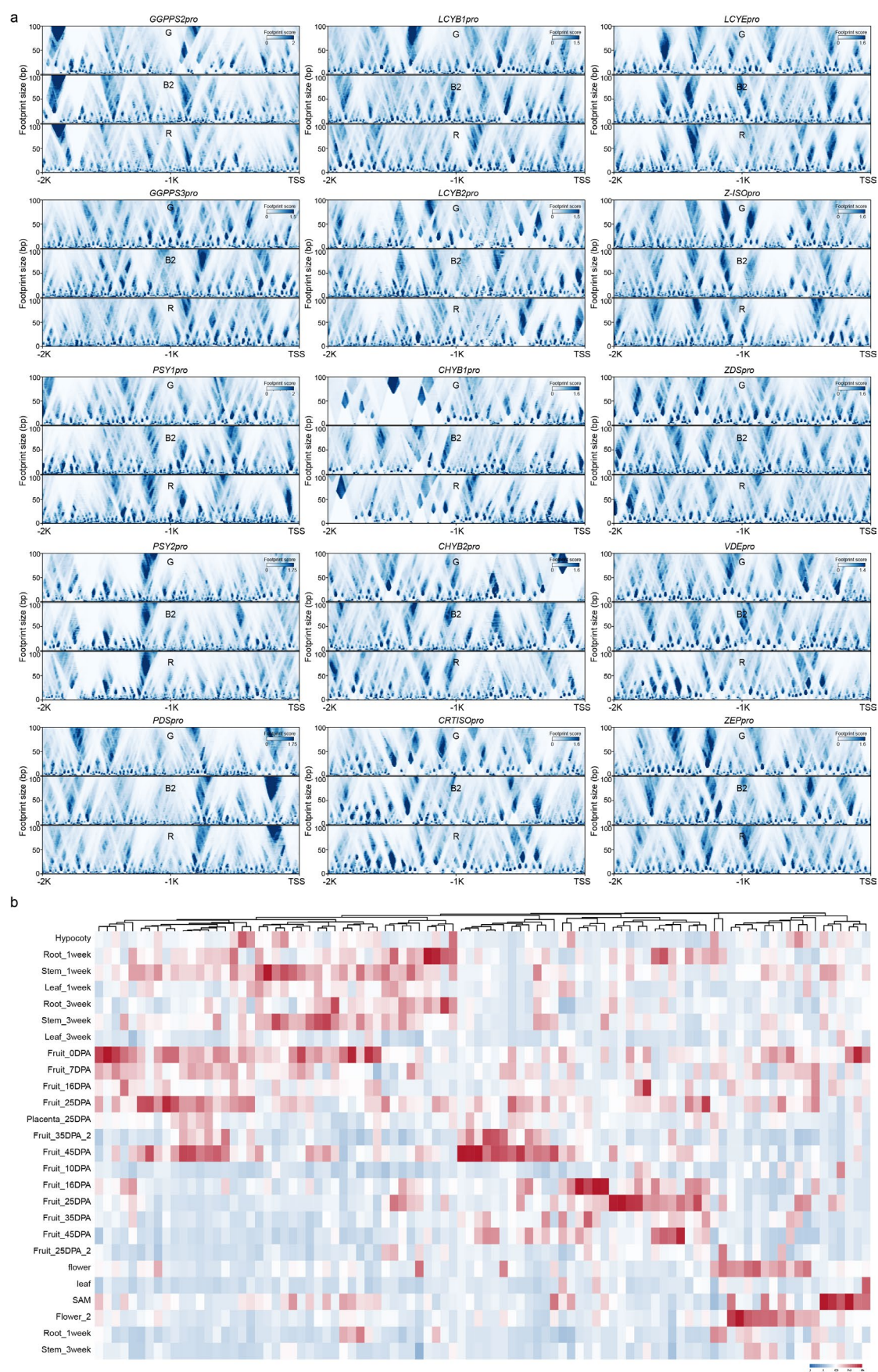


Supplementary Fig. 3 Chromatin dynamics coordinate transcriptional profiles during fruit color transition. **a**, Proportions of ChromHMM states and their associated RNA-seq, ATAC-seq, Pol II Ser5P, and Pol II Ser2P signal intensities during fruit color transition at the G, B2, and R stages. The left bar plot shows the proportion of each ChromHMM state, and

the boxplots show the distribution of $\log_2(\text{TPM} + 1)$ signals within each state. **b**, Sankey diagram showing chromatin state transitions during fruit color transition. Each node represents one ChromHMM state, and the number indicates the genomic length covered by that state. Link width is proportional to the genomic length undergoing each state transition. **c**, Genome browser tracks showing dynamic RNA-seq, ATAC-seq, and histone modification at the genomic interval chr03:29,760,000-29,790,000. **d**, GO enrichment analysis of genes associated with S4 open chromatin state transitions. G-loss indicates genes associated with regions losing the S4 state from G to B2, B2-gain indicates genes associated with regions gaining S4 from G to B2, B2-loss indicates genes associated with regions losing S4 from B2 to R, and R-gain indicates genes associated with regions gaining S4 from B2 to R. **e**, GO enrichment analysis of genes associated with S5 enhancer state transitions. G-loss indicates genes associated with regions losing the S5 state from G to B2, B2-gain indicates genes associated with regions gaining S5 from G to B2, B2-loss indicates genes associated with regions losing S5 from B2 to R, and R-gain indicates genes associated with regions gaining S5 from B2 to R.

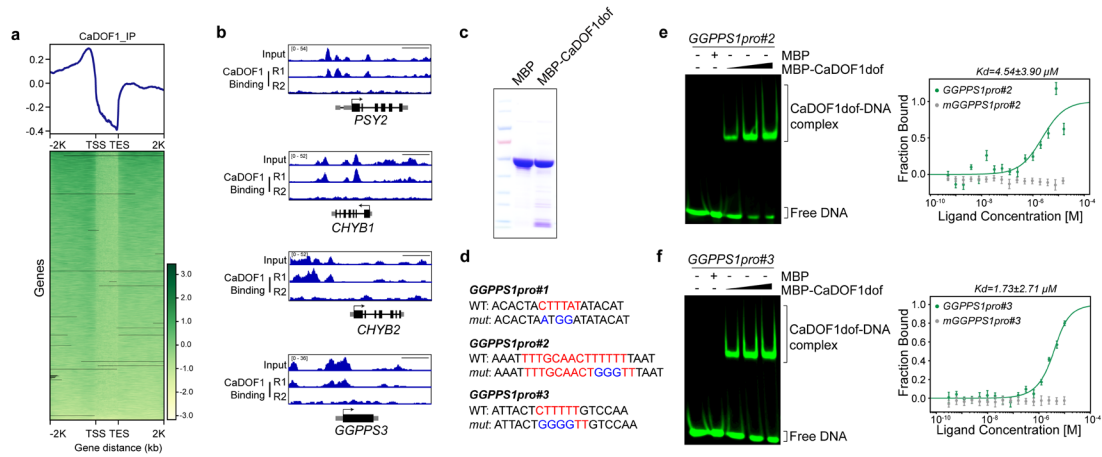


Supplementary Fig. 4 Regulatory-element-associated chromatin interactions during fruit color transition. **a**, Representative Hi-C chromatin interaction maps of chr01 at the G and B2 stages. The color scale on the right indicates interaction intensity. **b**, Average profiles of chromatin accessibility and histone modification signals, including ATAC-seq, H3K27ac, and H3K4me3, around promoter- and enhancer-associated regions. **c**, Schematic illustration of chromatin interaction types among regulatory elements. **d**, Bar chart showing the numbers of different regulatory-element-associated loop-feature pairs at the G and B2 stages. **e**, Boxplots showing the length distributions of promoter-enhancer, enhancer-enhancer, and promoter-promoter loops at the G and B2 stages.

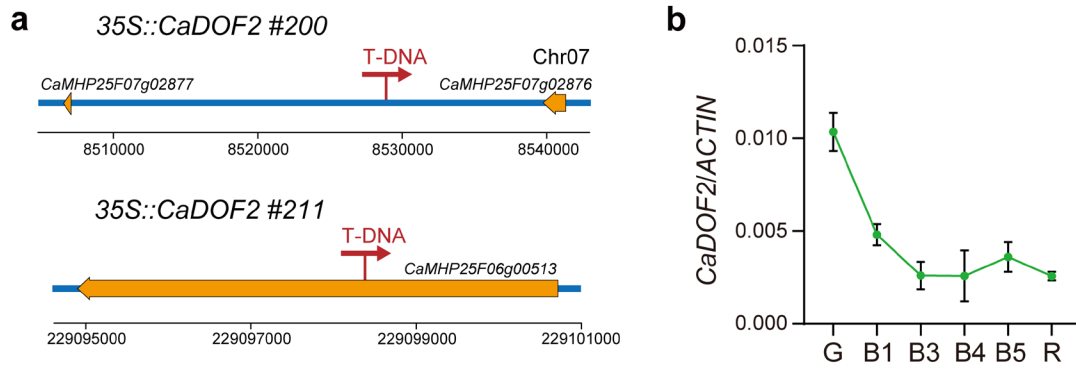


Supplementary Fig. 5 Dynamics of transcription factor footprints and the spatiotemporal profiling of representative transcription factors. a, PRINT-derived

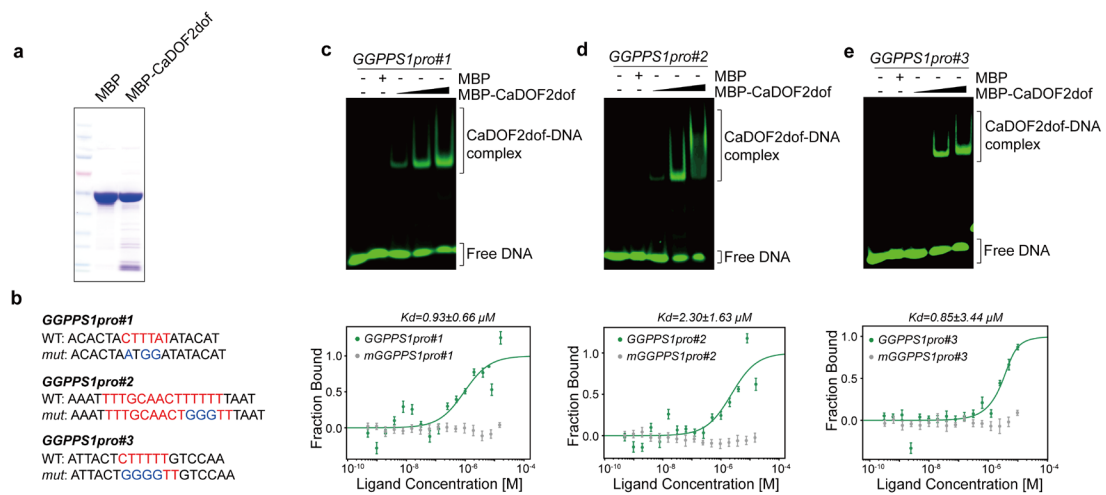
footprint score heatmaps showing dynamic changes in potential transcription factor occupancy and regulatory activity in the 2 kb upstream promoter regions of target genes during the G, B2, and R stages. Heatmaps were aligned relative to the TSS and oriented according to gene direction. Color intensity represents footprint score, with darker colors indicating stronger signals. **b**, Heatmap showing the expression of potential transcription factors across different cell types and developmental stages (10, 16, 35, and 45 DPA).



Supplementary Fig. 6 Mutations of the core motif in *GGPPS1* promoter significantly reduced the binding activity with CaDOF1. **a**, Metaplots and heatmaps of CaDOF1 DAP-seq reads over pepper genes. TSS, transcription start site; TTS, transcription terminal site; -2K, 2 kb upstream of TSS; 2K, 2 kb downstream of TTS. **b**, Genome tracks of CaDOF1 occupancy around *PSY2*, *CHYB1*, *CHYB2*, and *GGPPS3* genes. **c**, Coomassie blue-stained gel showing the purified recombinant proteins of MBP and MBP-CaDOF1dof. **d**, The sequences of wild-type (WT) and mutated probes of *GGPPS1* promoter. **e-f**, EMSA and MST assays showing the binding of MBP-CaDOF1dof proteins to the WT or mutated probes of *GGPPS1* promoter.



Supplementary Fig. 7 The T-DNA integration of 35S::*CaDOF2* plants and the dynamic *CaDOF2* expression during fruit color transition. a, Schematic diagram showing the T-DNA integration positions in pepper genomes of two independent transgenic lines. Yellow arrows represent the coding genes on the chromosome. Red line and arrow combination marked the positions of T-DNAs. **b**, qPCR analysis of *CaDOF2* expression in fruits at different growth stages. G, green mature; B1~5, breaker stages of 1~5 days; R, red ripening.



Supplementary Fig. 8 Mutations of the core motif in *GGPPS1* promoter significantly reduced the binding activity with CaDOF2. **a**, Coomassie blue-stained gel showing the purified recombinant proteins of MBP and MBP-CaDOF2dof. **b**, The sequences of wild-type (WT) and mutated probes of *GGPPS1* promoter. **c-e**, EMSA and MST assays showing the binding of MBP-CaDOF2dof proteins to the WT or mutated probes of *GGPPS1* promoter.