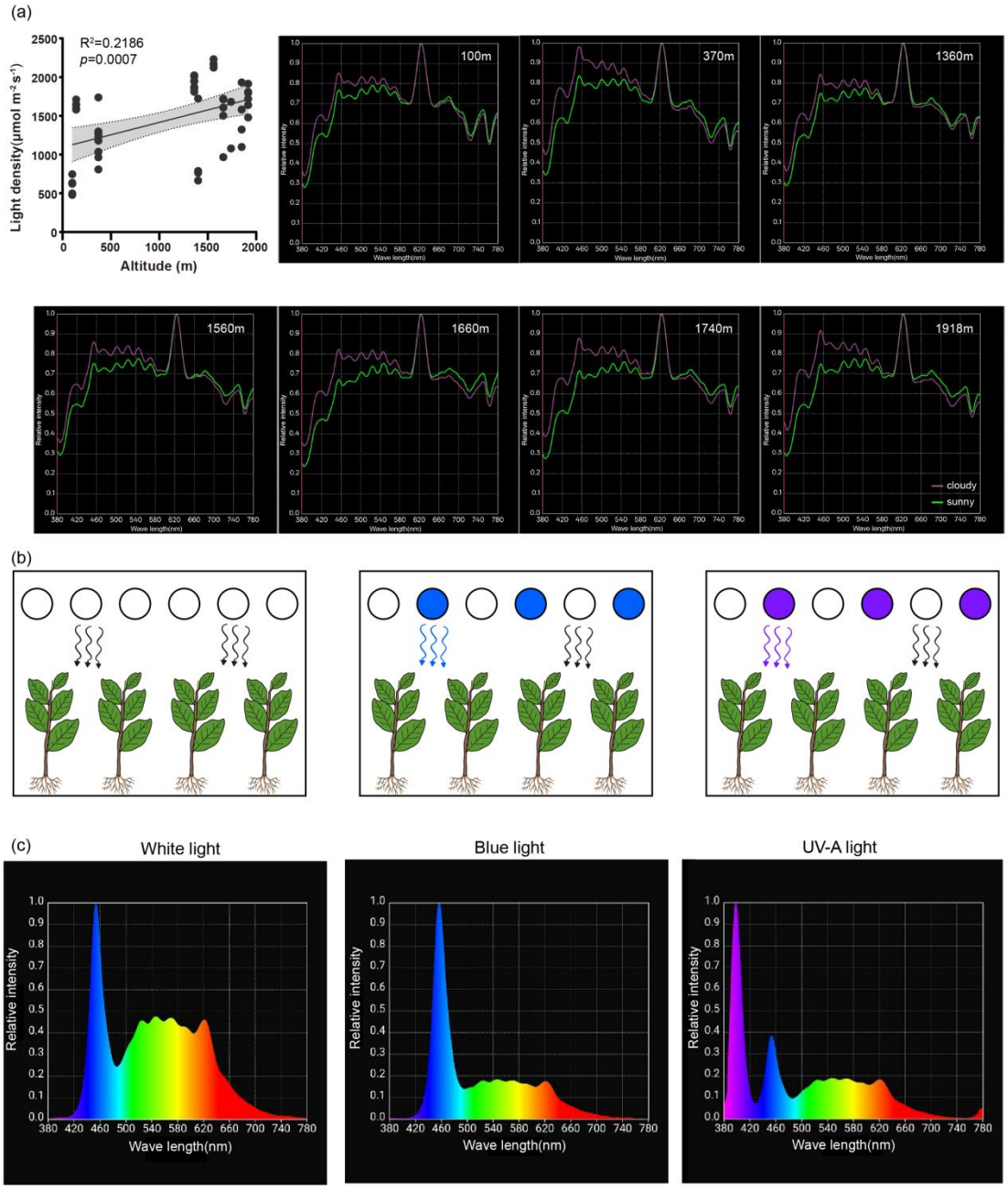

Fig. S1. Overview of different lights treatment of *C.sinensis*. (a) The correlation between altitude and light intensity and the spectrum plots of different altitudes with sunny or cloudy condition. (b) The schematic diagram of light treatment. (c) The measurement of the visible spectrum.

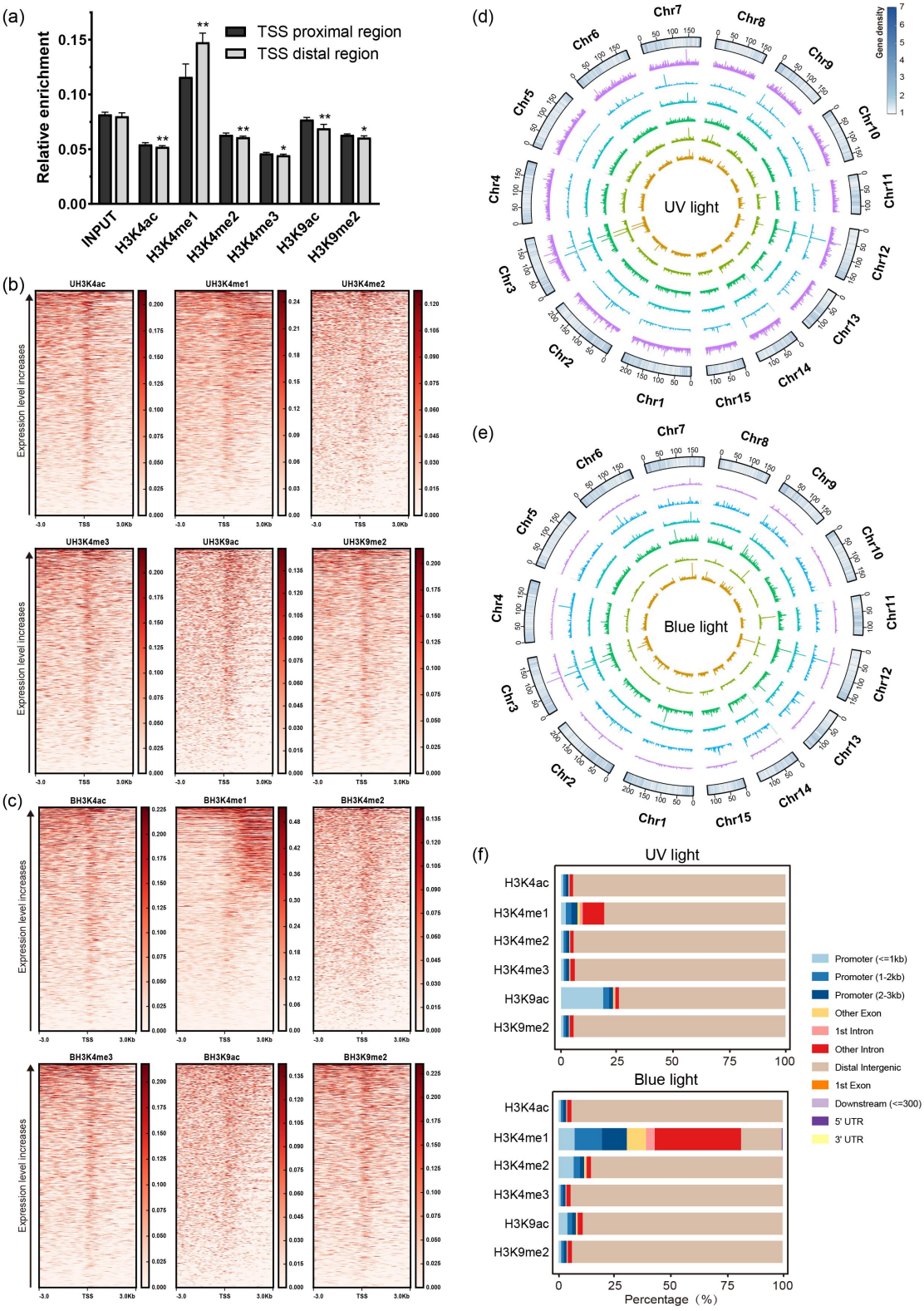

Fig. S2. Genome-wide mapping of histone modification markers under blue and UV-A light in *C.sinensis*. (a) The cumulative signal abundance of different histone modifications on TSS proximal region (the 15 % region near TSS in the gene body)

and TSS distal region. (b-c) Heatmaps of six histone modifications around the TSSs in leaves treated by UV-A light (b) and blue light (c). The genes were sorted according to the expression level. Regions 3Kb upstream and downstream of the gene are shown. (d-e) Circos plot of gene density and the peak distribution of six histone modifications of leaves treated by UV-A light (d) and blue light (e) on the genome. (f) The distribution of peaks in different genomic functional regions of leaves treated by UV-A light and blue light. U, UV-A light; B, blue light; W, white light.

Fig. S3. GO enrichment analysis of histone modifications related genes. U, UV-A light; B, blue light; W, white light.

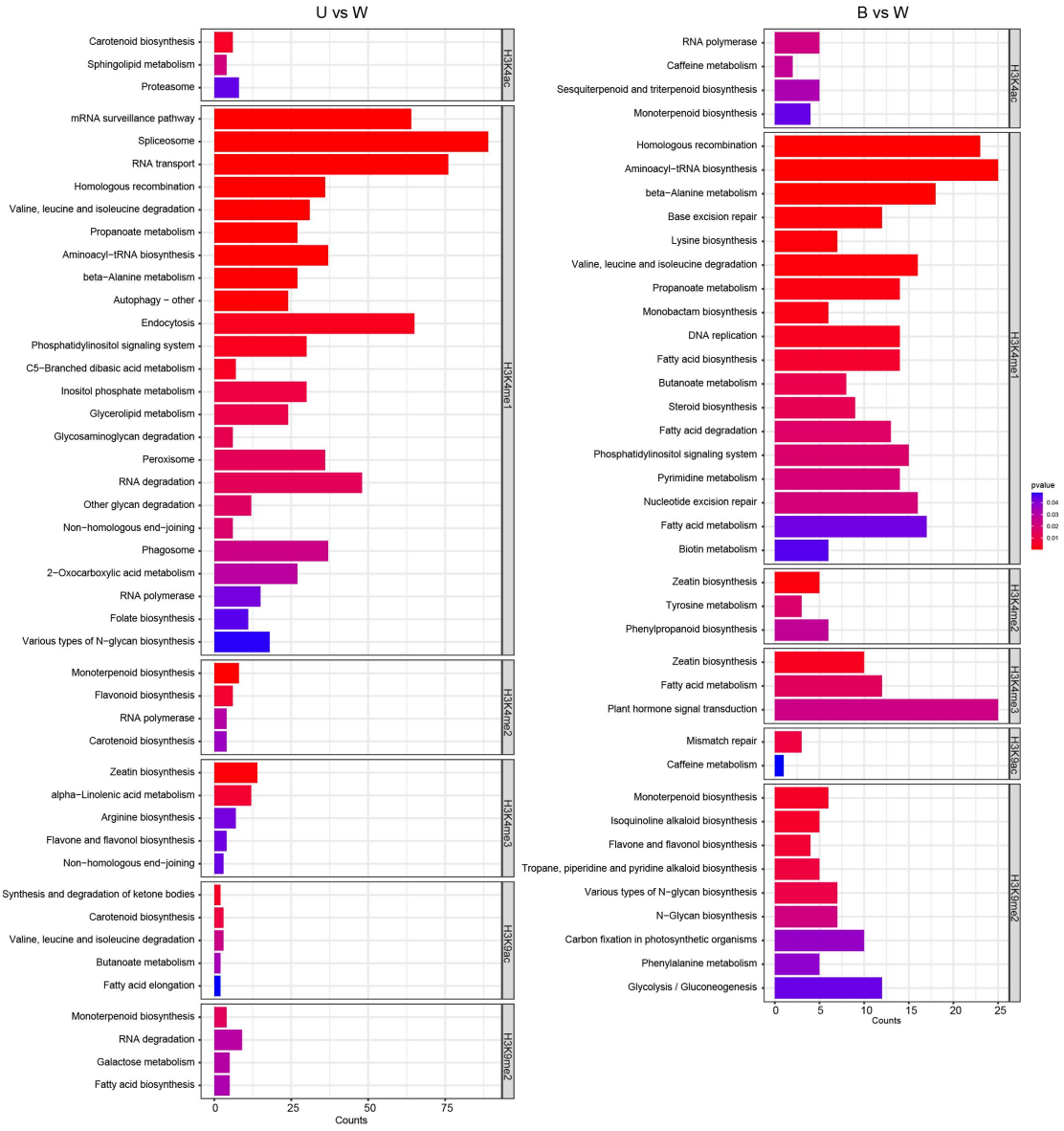

Fig. S4. KEGG enrichment analysis of histone modifications related genes. U, UV-A light; B, blue light; W, white light.

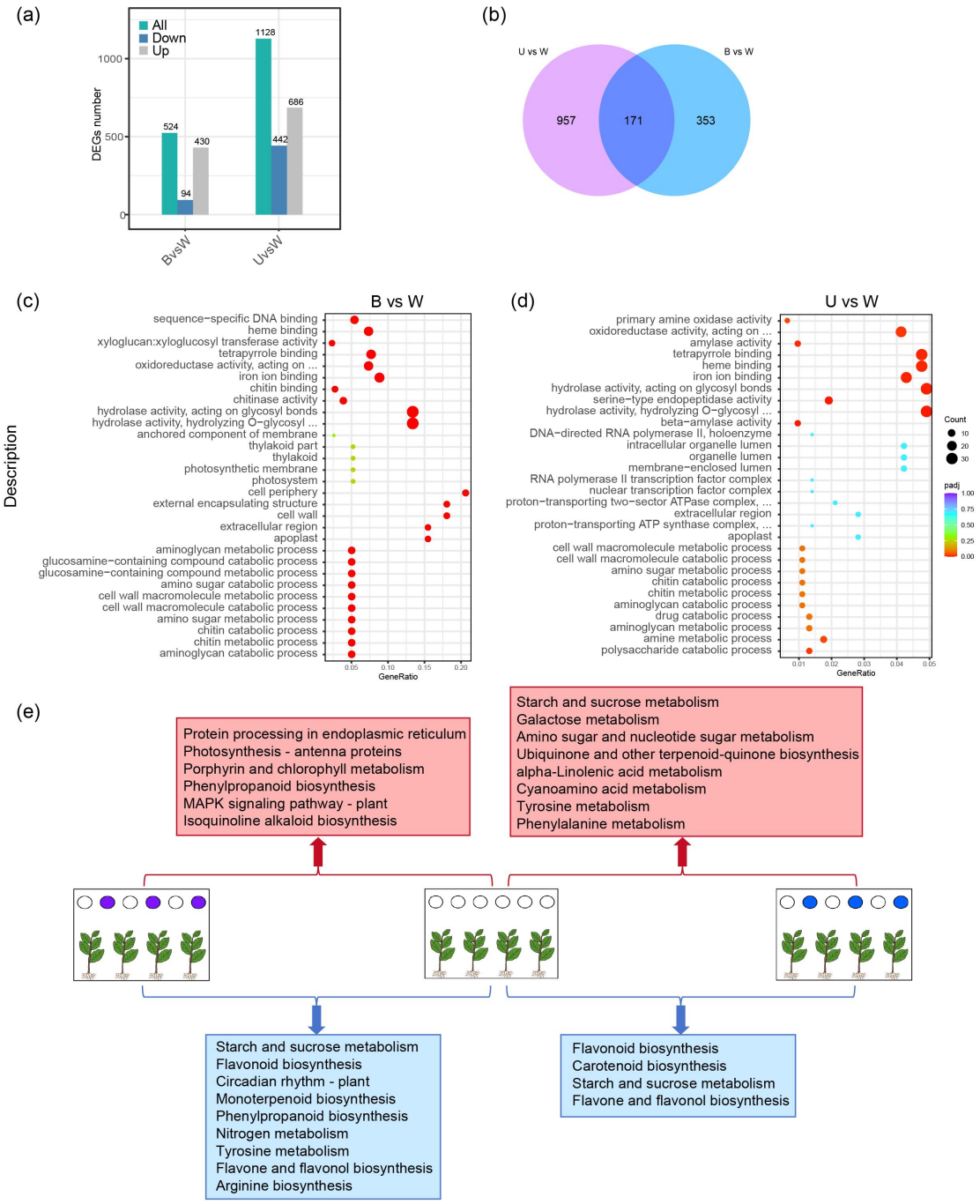

Fig. S5. Transcriptome analysis of different lights. (a) Number of DEGs identified by pairwise comparison of B versus W and U versus W. (b) Venn analysis of B versus W and U versus W about DEGs. (c-d) GO enrichment analysis among DEGs of B versus W (c) and U versus W (d). (e) KEGG enrichment analysis among DEGs of B versus W and U versus W. U, UV-A light; B, blue light; W, white light.

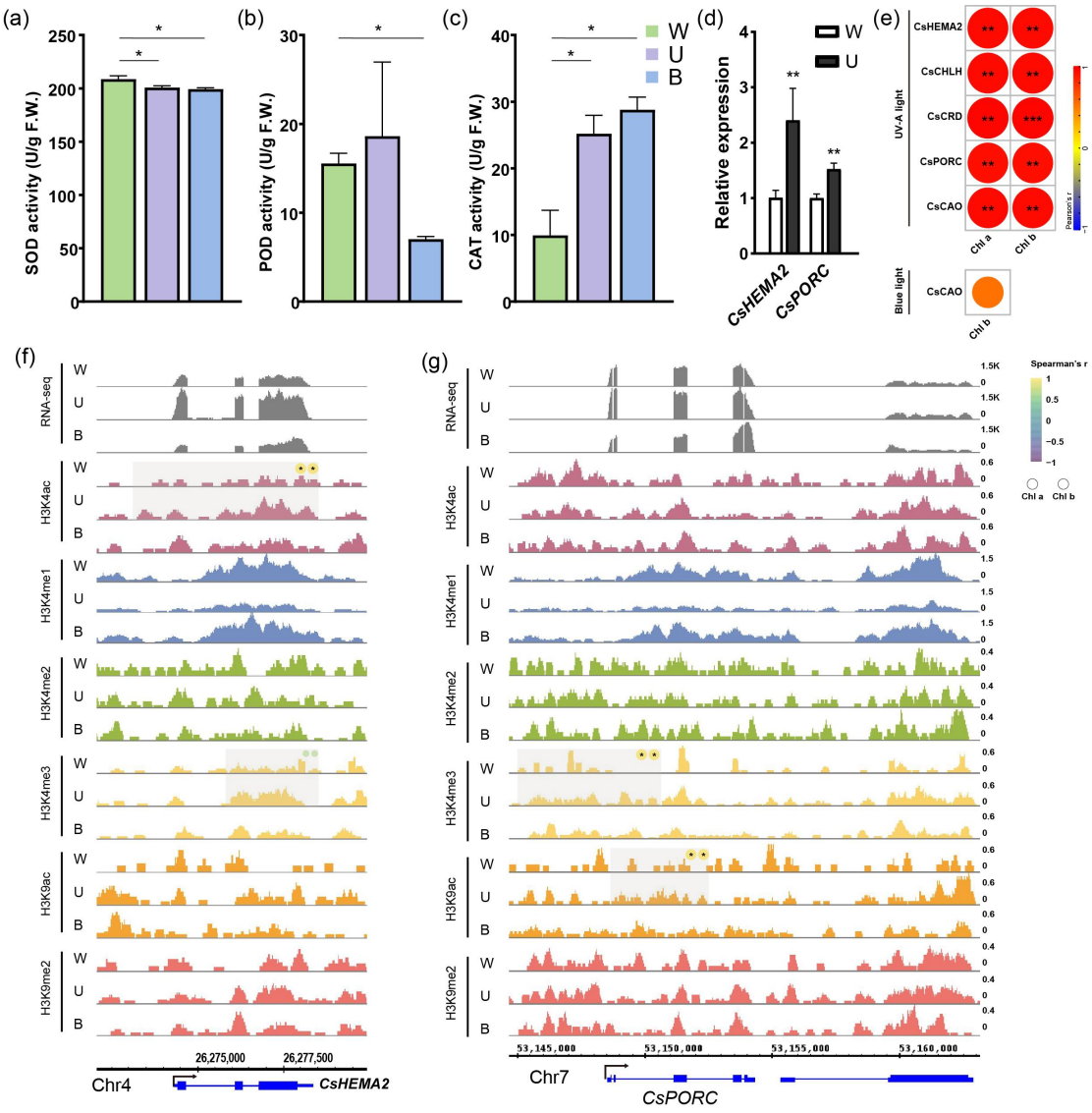

Fig. S6. Measurement of root enzyme activity and genome tracks of RNA-seq and ChIP-seq data for *CsHEMA2* and *CsPORC*. (a-c) The enzyme activity of SOD (a), POD (b), and CAT (c) in root. (d) RT-qPCR of *CsHEMA2* and *CsPORC* in leaves treated by UV-A light and blue light. (e) Pearson correlation analyses of metabolites and DEGs. (f-g) Genome tracks of RNA-seq and ChIP-seq data for *CsHEMA2*(f), and *CsPORC*(g). Y-axis values show normalized read counts. The different colors represent various histone modifications. The gray boxes represent the difference in histone modifications. The upper corner of the gray box shows the Spearman

correlation analysis between metabolites and histone modification abundance. The right side represents the product and the left side represents the substrate. Asterisks represent statistical significance (*P < 0.05, **P < 0.01). U, UV-A light; B, blue light; W, white light.

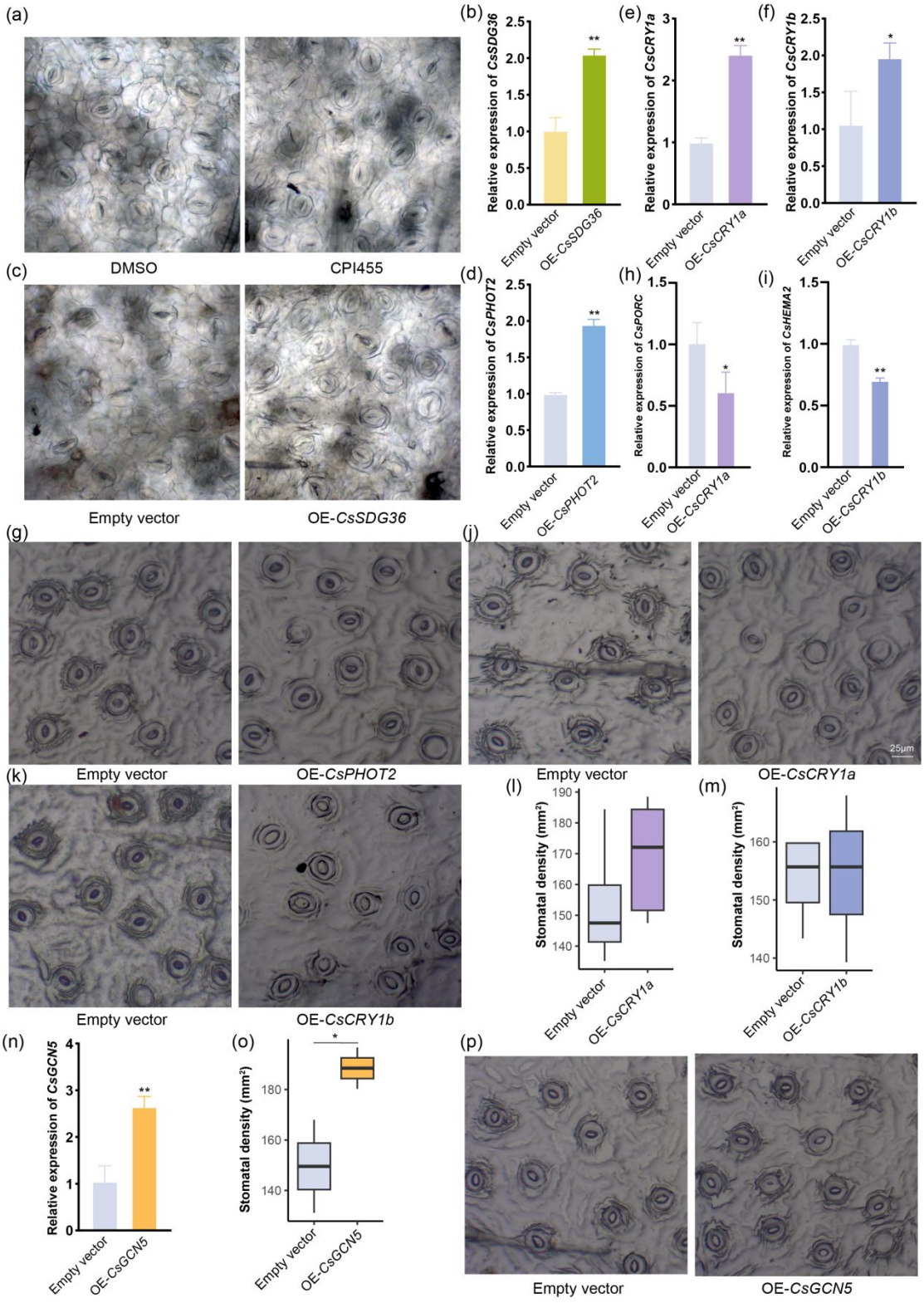

Fig. S7. The photoreceptor and histone modifications participate in regulation of stomatal development in *C. sinensis*. (a) The images of stomatal density treated with histone demethylase inhibitor. (b) Transient overexpression of *CsSDG36* genes in *C.*

sinensis leaves resulted in increased *CsSDG36* expression. (c) The images of stomatal density in OE-*CsSDG36* plants. (d-f) Transient overexpression of *CsPHOT2*, *CsCTY1a*, and *CsCRY1b* genes in *C. sinensis* leaves increased expression. (g) The images of stomatal density in OE-*CsPHOT2* plants. (h-i) The expression of candidate genes in OE-*CsCRY1a*(h) and OE-*CsCRY1b*(i) plants. (j-k) The images of stomatal density in OE-*CsCRY1a*(j) and OE-*CsCRY1b*(k) plants. (l-m)The statistic data of stomatal density in OE-*CsCRY1a*(l) and OE-*CsCRY1b*(m) plants. (n) Transient overexpression of *CsGCN5* genes in *C. sinensis* leaves increased *CsGCN5* expression. (o-p) The statistic data(o) and images(p) of stomatal density in OE-*CsGCN5* plants. Asterisks represent statistical significance (*$P < 0.05$, **$P < 0.01$).

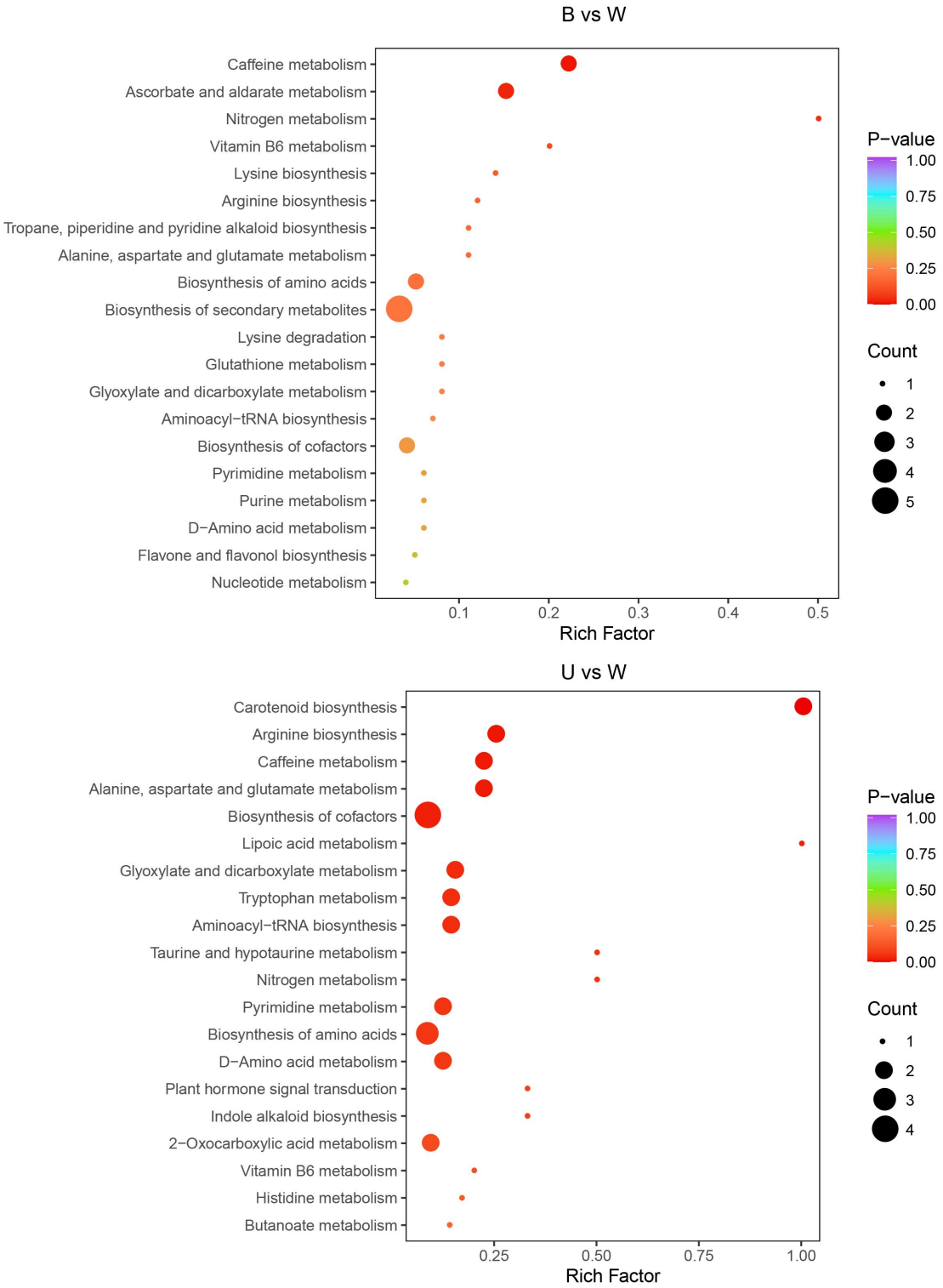

Fig. S8. KEGG enrichment analysis of metabolomics data of *C.sinensis*. U, UV-A light; B, blue light; W, white light.

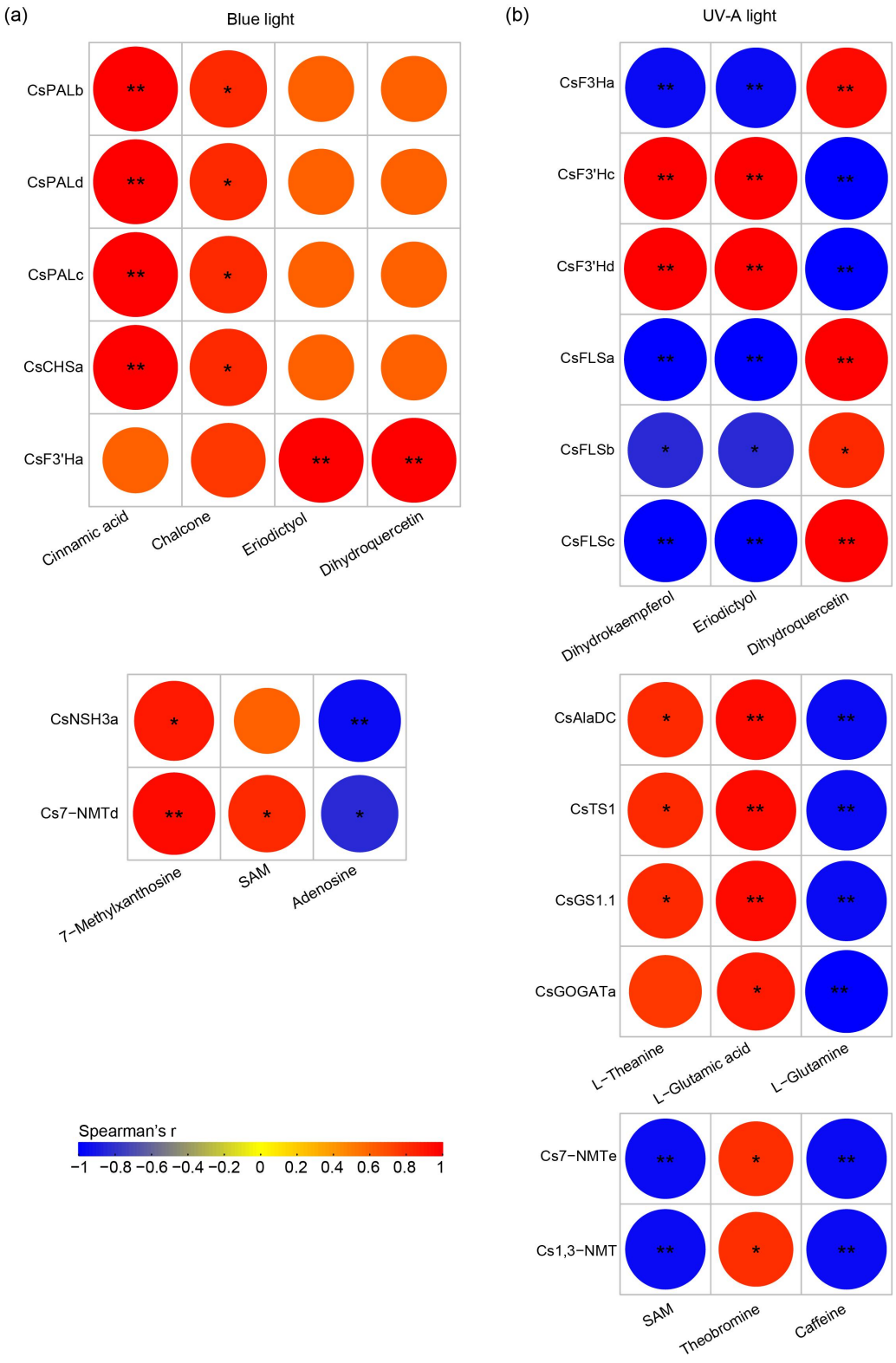

Fig. S9. The Spearman correlation analyses of critical metabolites and DEGs in blue light and UV-A light. Asterisks represent statistical significance (*P < 0.05, **P < 0.01).

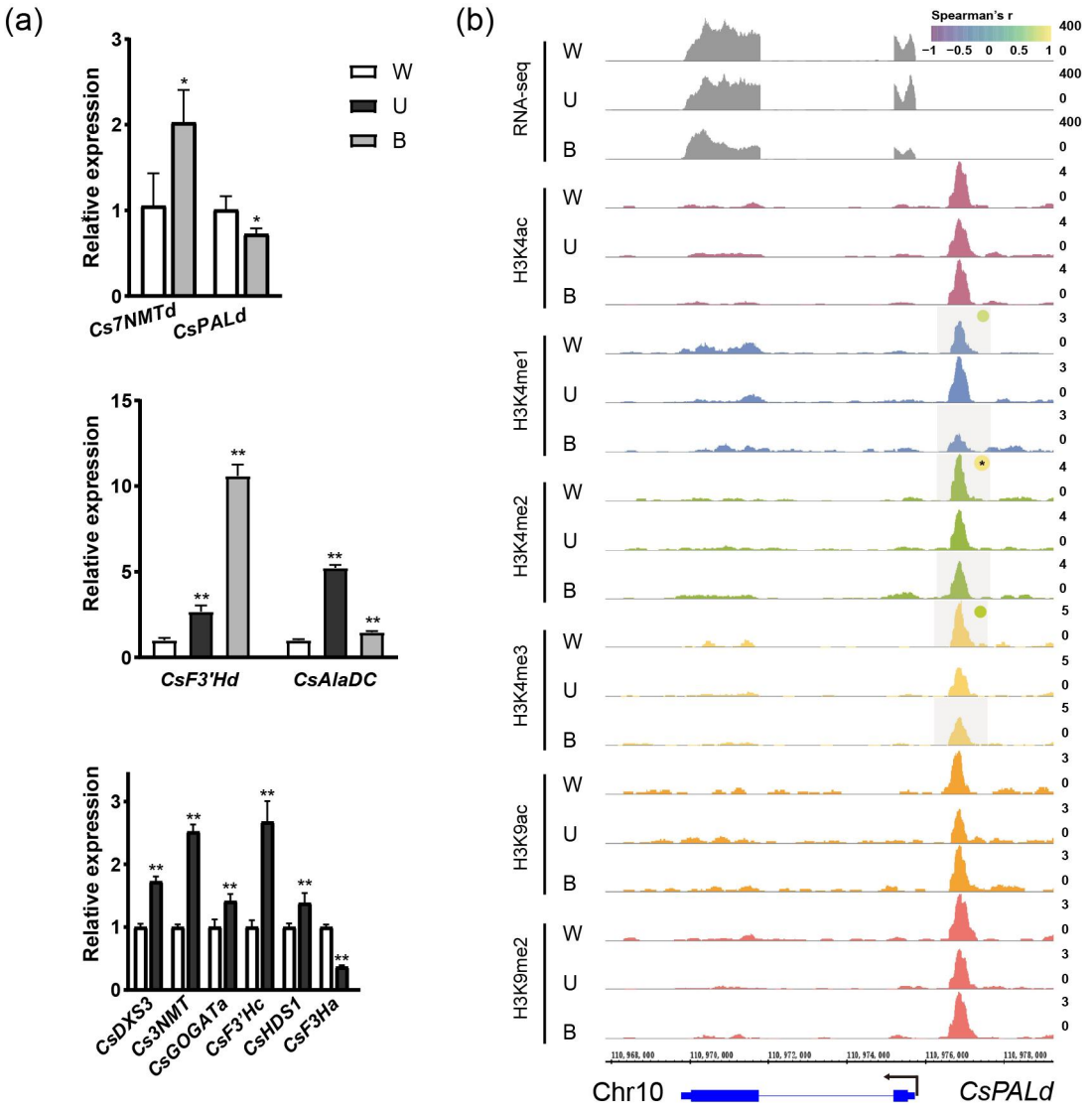

Fig. S10. The RT-qPCR validate and genome track analysis. (a)The expression of critical enzyme genes in leaves treated by UV-A light and blue light. (b) Genome tracks of RNA-seq and ChIP-seq data for *CsPALd*. Asterisks represent statistical significance (*P < 0.05, **P < 0.01). U, UV-A light; B, blue light; W, white light.

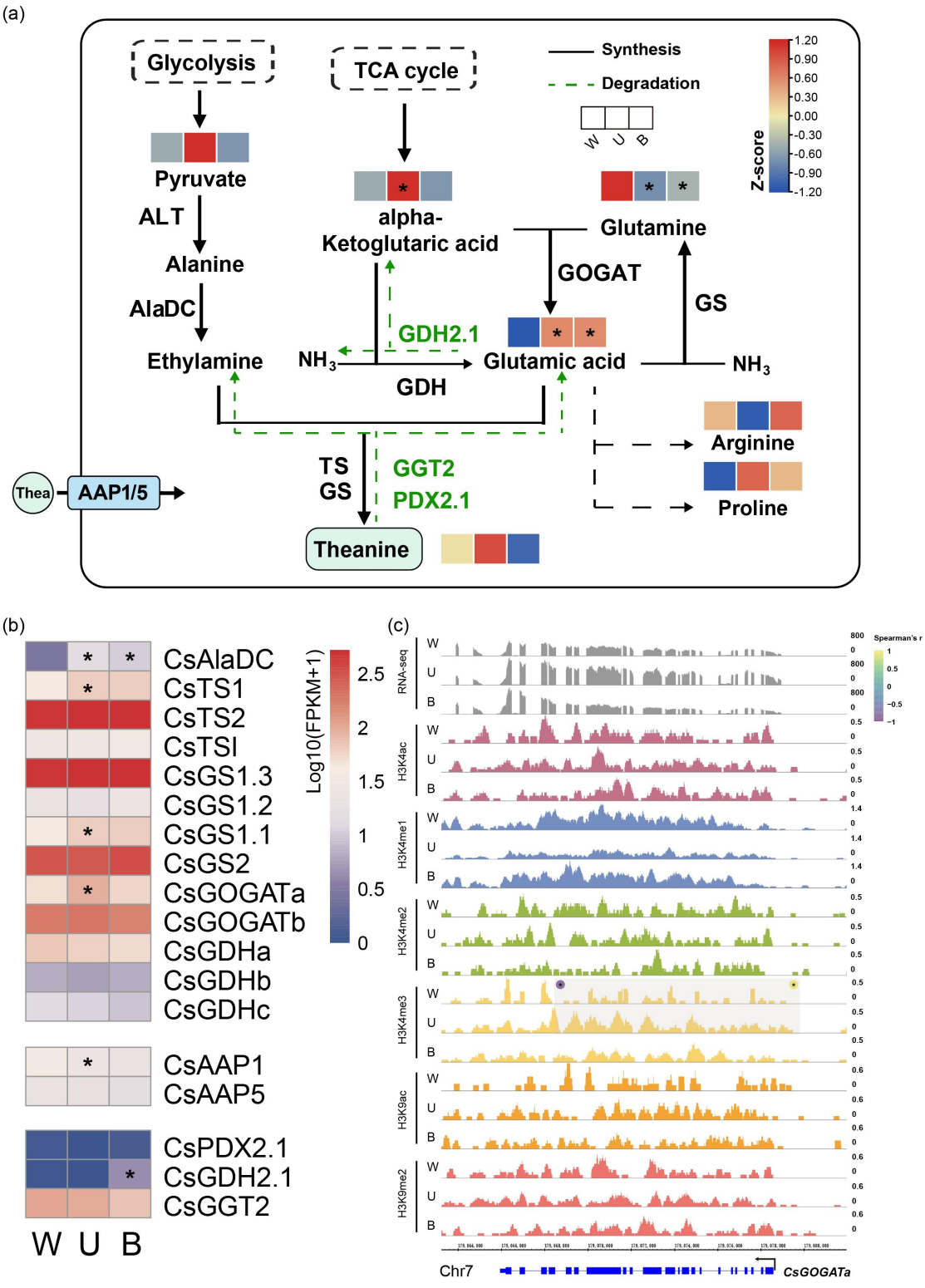

Fig. S11. Differences in gene expression, metabolites, and histone modifications of important genes for theanine biosynthesis, degradation, and transportation pathway from different lights. (a)The theanine biosynthesis and degradation pathway with the abundance of metabolites. The black arrows represented

biosynthesis pathway. The green arrows represent degradation pathway. The heatmap shows the relative abundance of metabolites. Asterisks represent DAMs compared with white light. (b) The heatmap shows the expression level of genes involved in theanine biosynthesis, degradation, and transportation pathways. Asterisks represent q value < 0.05. (c) Genome tracks of RNA-seq and ChIP-seq data for *CsGOGATa*. Y-axis values show normalized read counts. The different colors represent various histone modifications. The gray boxes represent the difference in histone modifications. The upper corner of the gray box shows the Spearman correlation analysis between metabolites and histone modification abundance. The right side represents the product and the left side represents the substrate. Asterisks of correlation analyses represent statistical significance (*P < 0.05). U, UV-A light; B, blue light; W, white light.

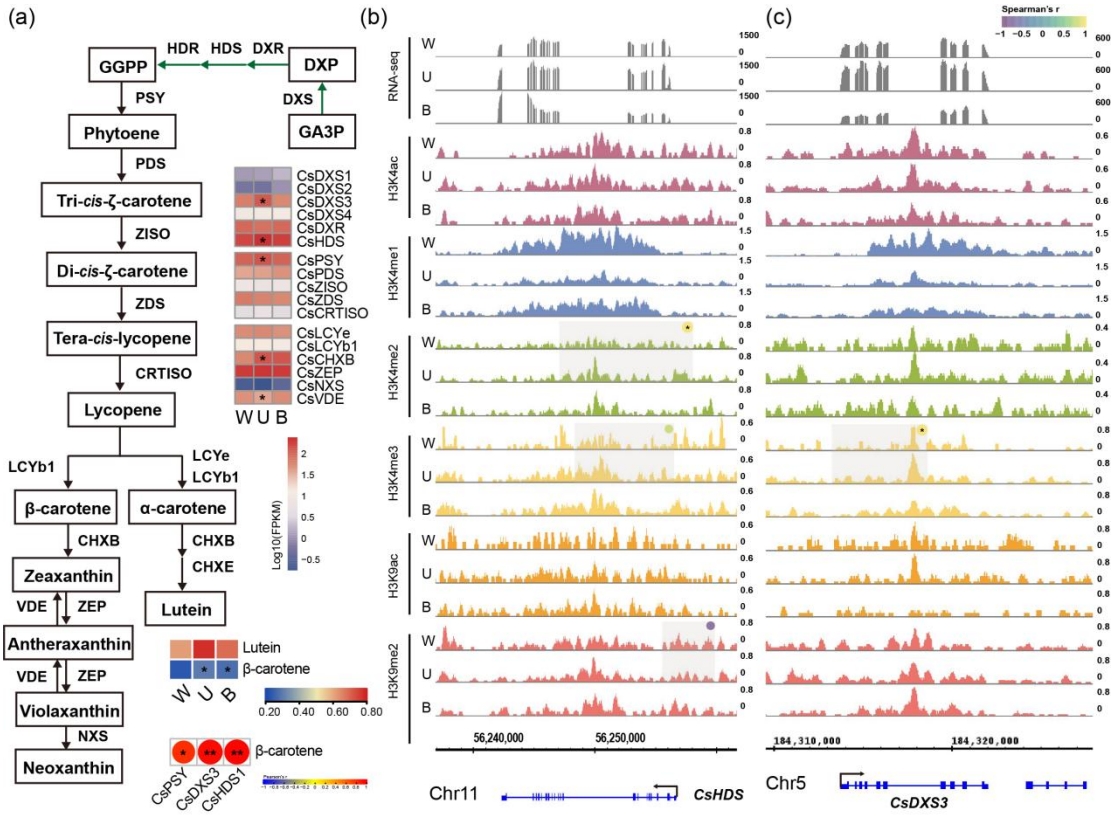

Fig. S12. Differences in gene expression, metabolites, and histone modifications of important genes for carotenoid biosynthesis pathway from different lights. (a) The β-carotene biosynthesis pathway with the content of β-carotene and lutein, the expression level of genes, and correlation analyses. Asterisks of expression heatmap represent $q < 0.05$. Asterisks of correlation analyses and metabolites content represent statistical significance (*$P < 0.05$, **$P < 0.01$). (b-c) Genome tracks of RNA-seq and ChIP-seq data for *CsHDS*(b), and *CsDXS3*(c). Y-axis values show normalized read counts. The different colors represent various histone modifications. The gray boxes represent the difference in histone modifications. The upper corner of the gray box shows the Spearman correlation analysis between metabolites and histone modification abundance. The right side represents the product and the left side represents the substrate. U, UV-A light; B, blue light; W, white light.

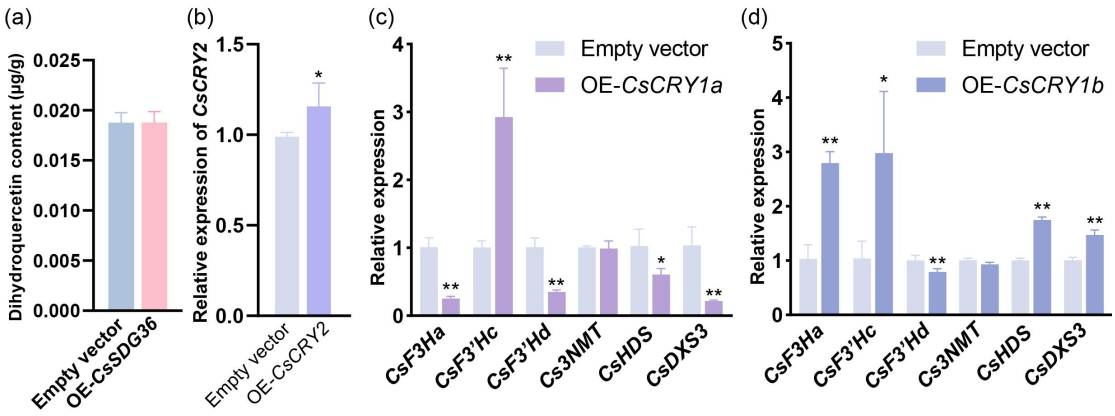

Fig. S13. The identification of genes expression and and metabolite content in transient overexpression plants. (a) The contents of dihydroquercetin in OE-*CsSDG36 C. sinensis* leaves for 5 days were detected by HPLC. (b) Transient overexpression of *CsCRY2* genes in *C. sinensis* leaves increased *CsCRY2* expression. (c-d) The expression of candidate enzyme genes in OE-*CsCRY1a*(c) and OE-*CsCRY1b*(d) plants. Asterisks represent statistical significance (*P < 0.05, **P < 0.01).