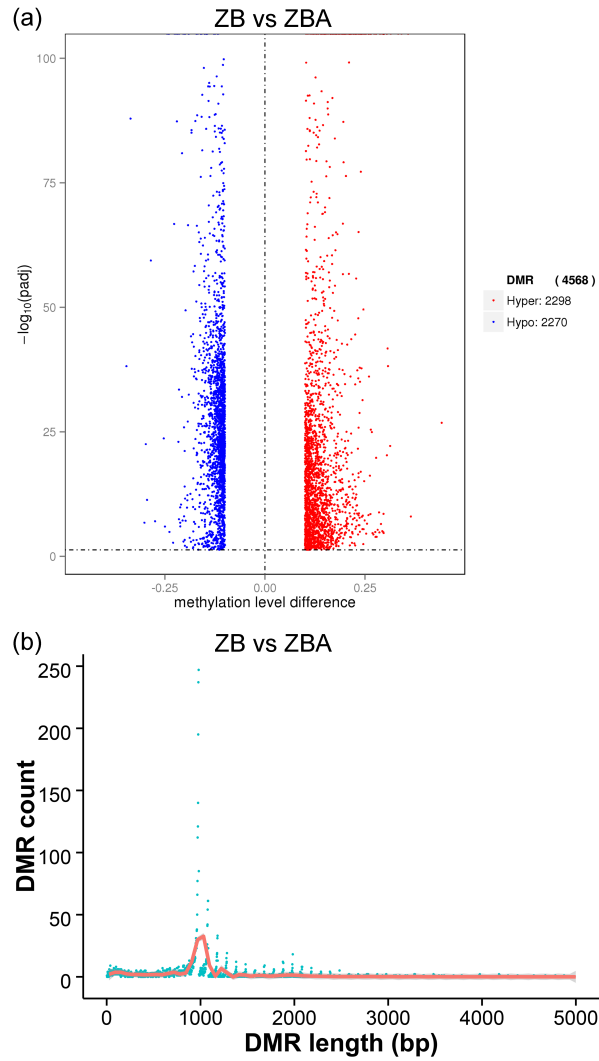
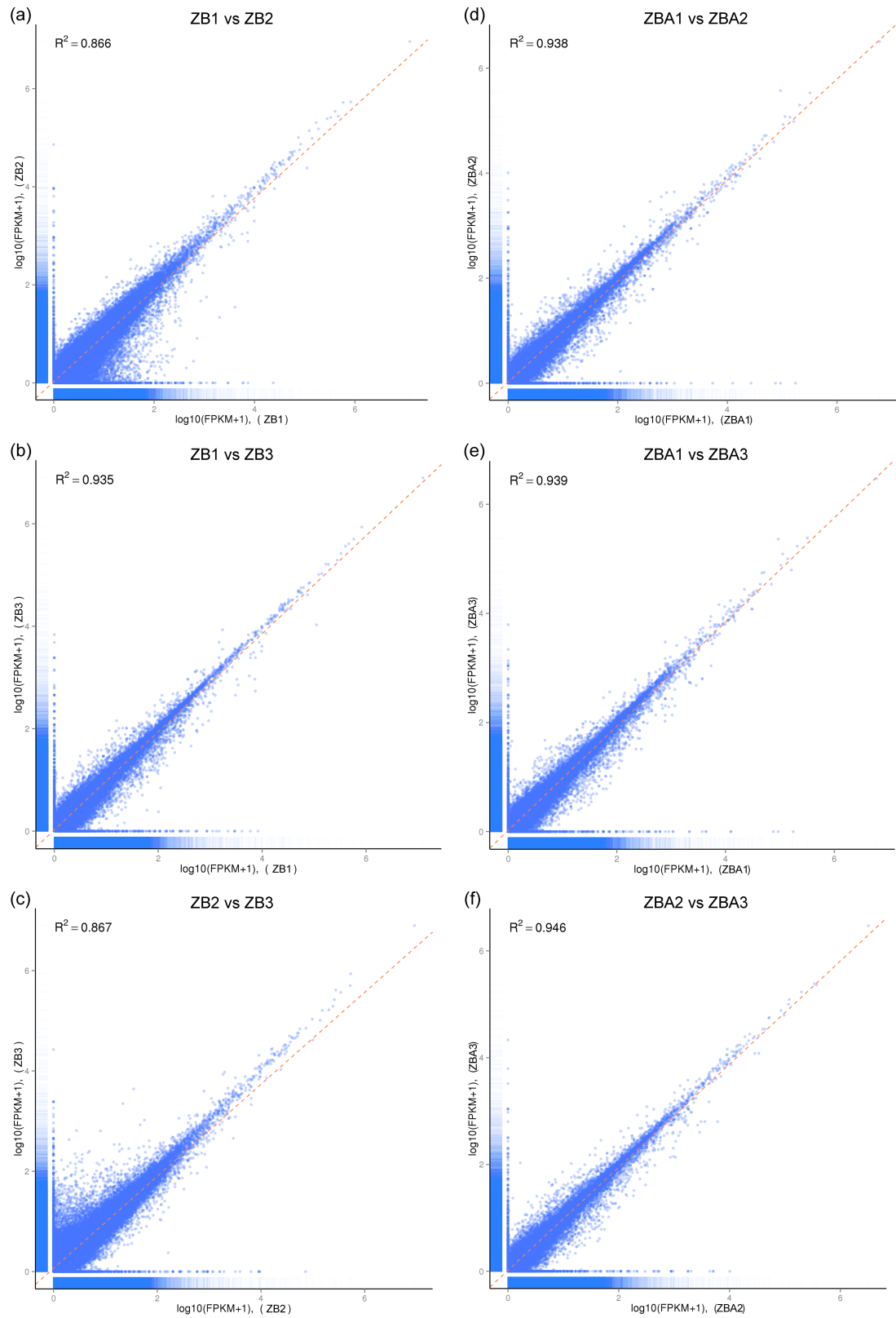


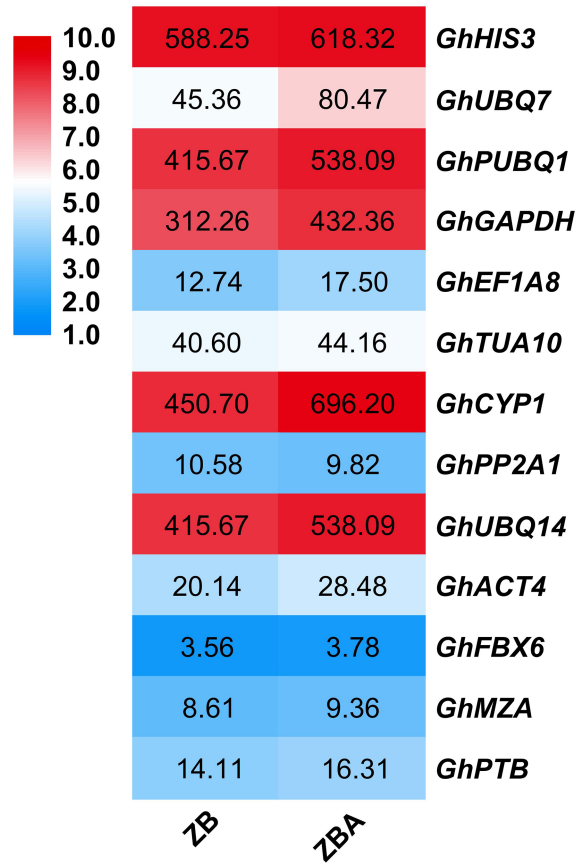
**Figure S1.** Levels of C, CG, CHG, and CHH methylation in 26 chromosomes. The X-axis represents all 26 chromosomes of upland cotton; the Y-axis represents methylation levels (MLs) in different sequence contexts.



**Figure S2.** Volcano map of identified differentially methylated regions (DMRs) (a) and their length distribution (b) in ZB versus ZBA. In the volcano map, each dot signifies one DMR. Among them, the red and blue dots represent hyper- and hypomethylated DMRs, respectively. The X-axis represents the ML difference; the Y-axis represents the opposite number of log<sub>10</sub> value of the *P*-value.

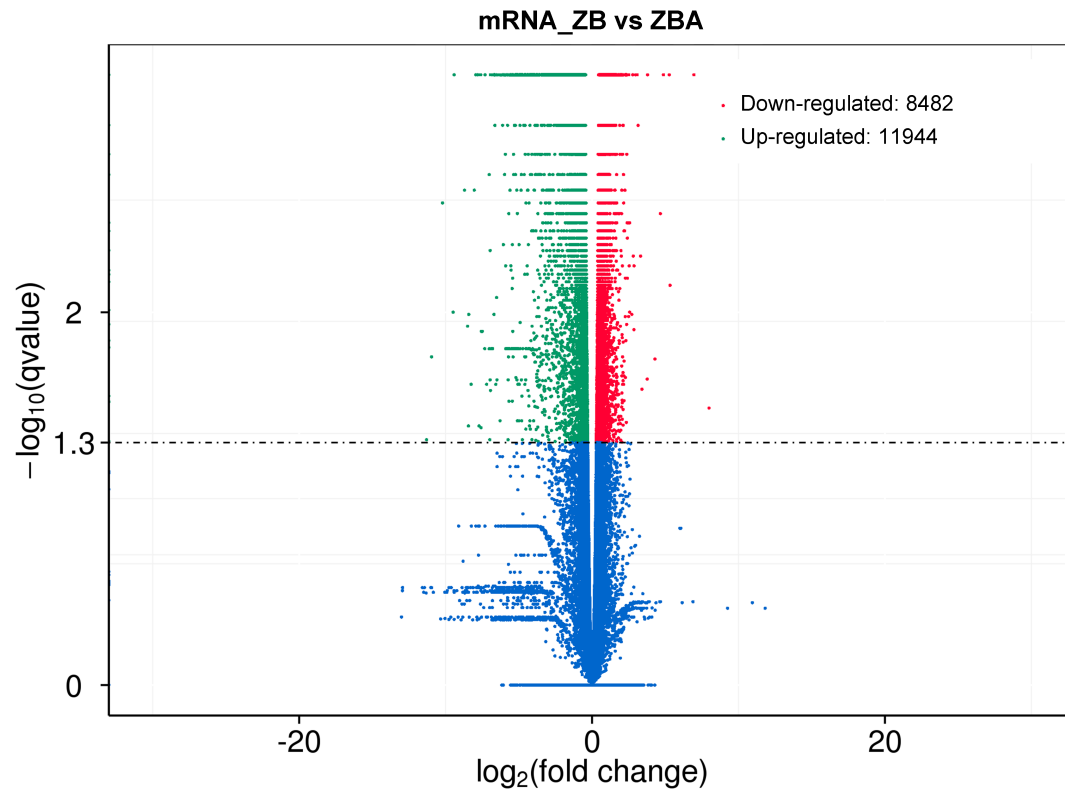


**Figure S3.** Evaluation of RNA sequencing data quality. (a) to (c) Pearson's Correlation coefficient testing the ZB dataset. (d) to (f) Pearson's Correlation coefficient testing the ZBA dataset.

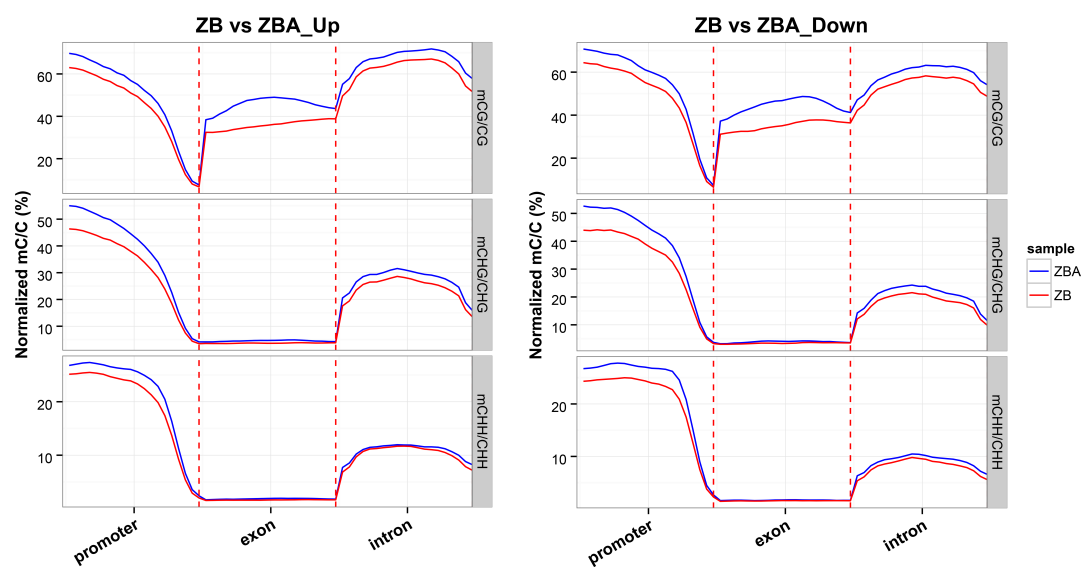


**Figure S4.** Heatmap of 13 selected cotton reference (housekeeping) genes with their respective FPKM values in ZB and ZBA. Log<sub>2</sub> expression (FPKM) values are used for the analysis and negative values are set to zero.

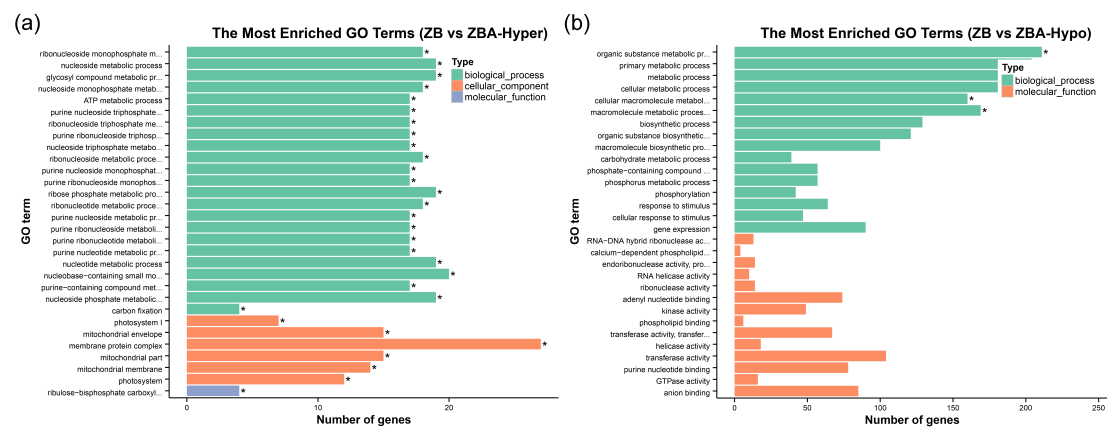




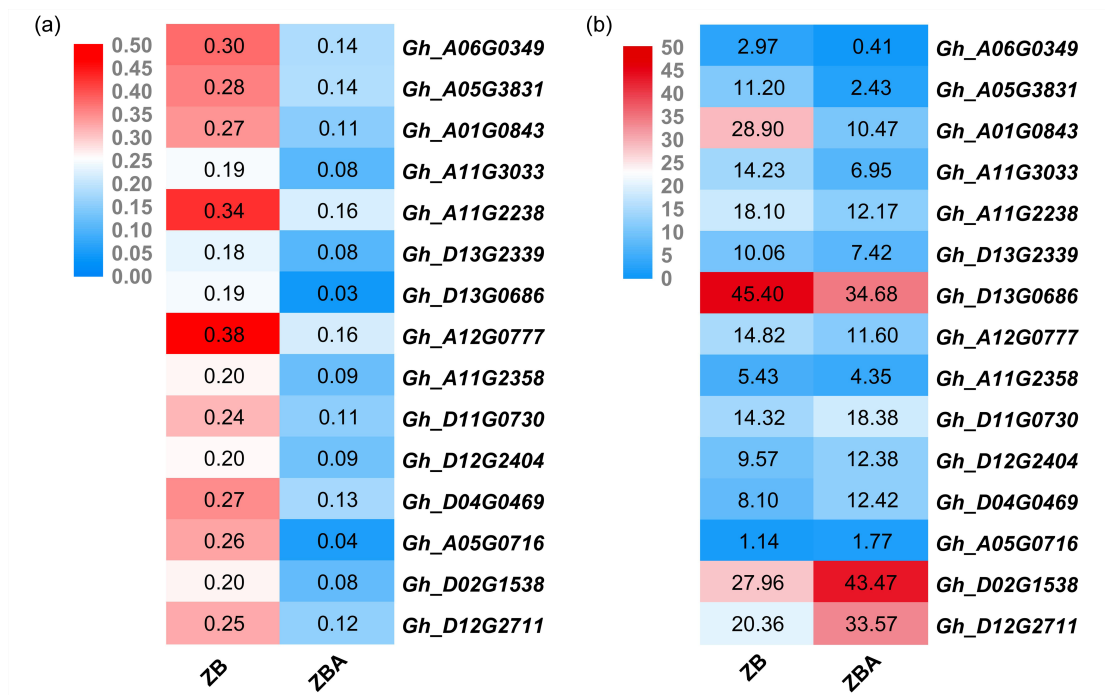
**Figure S5.** Numbers of differentially expressed genes (DEGs) in ZB versus ZBA. The X-axis is the  $\log_2$  value of fold change and the Y-axis is the opposite number of  $\log_{10}$  value of the  $q$ -value (adjusted  $P$ -value). Each dot represents one gene. Among them, the green and red dots represent up- and down-regulated genes, respectively, and the blue dots represent genes without differential expression.



**Figure S6.** Comparative analysis of methylation densities of C-sites in different gene regions of the up- or downregulated DEGs, including promoter, exon, and intron regions.



**Figure S7.** Gene ontology (GO) enrichment analysis of hyper- (a) or hypomethylated (b) DEGs in ZB versus ZBA. The bars followed by an asterisk are some significantly enriched GO terms.



**Figure S8.** Heatmaps showing the MLs (a) and the expression levels (i.e., FPKM values) (b) of hyper-DEGs involved in the “mitochondrial envelope” term in ZB versus ZBA.