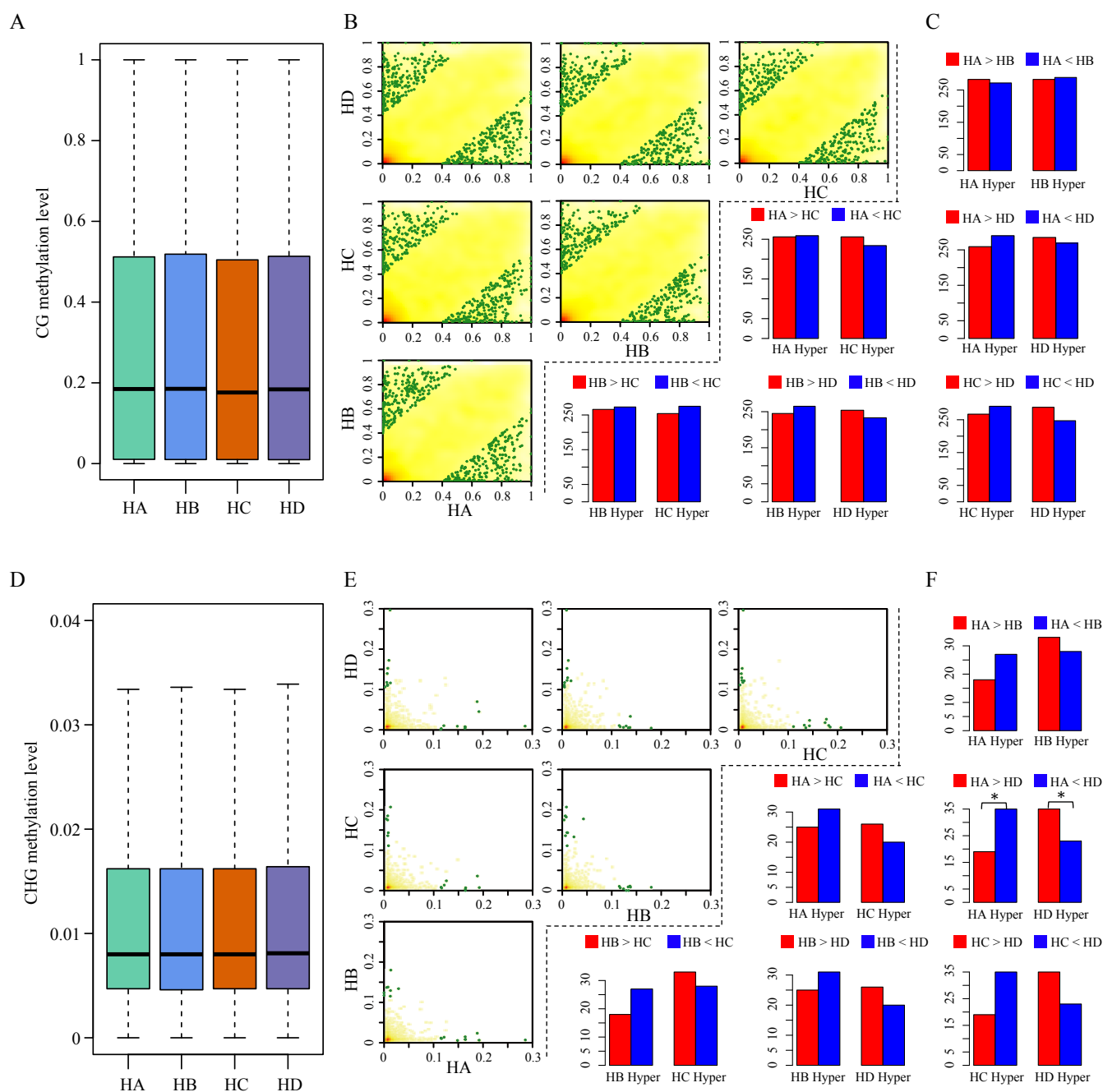
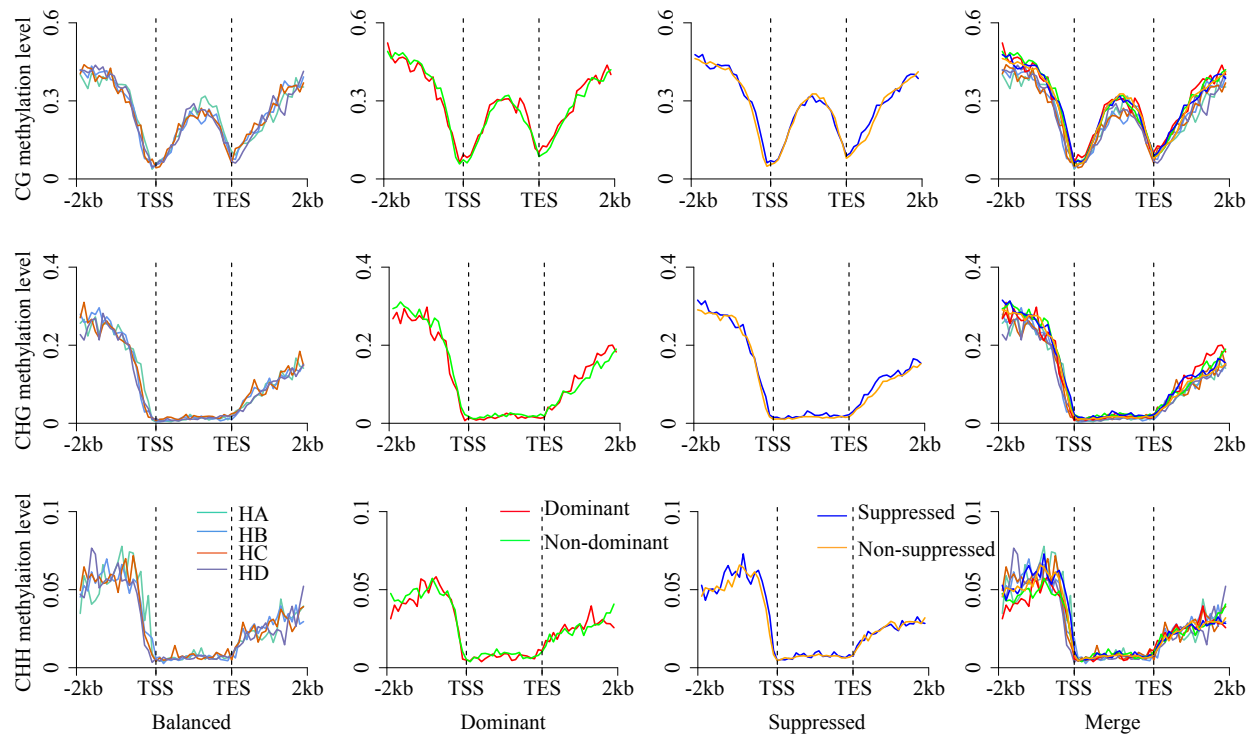


**Figure S1.** Pairwise expression comparison between homologous alleles of different subgenomes. **(A)** The expression patterns of each genes derived from the RT-PCR and RNA-seq are shown in a histogram a line chart, respectively. **(B-F)** Homologous alleles expression bias and location preference of comparison between HA and HC **(B)**, HA and HD **(C)**, HB and HD **(D)**, HB and HD **(E)**, HC and HD **(F)**.



**Figure S2.** Association between DNA methylation and gene expression of homologous alleles. Boxplot showing methylation level of tetrad alleles of different haplotype chromosomes in CG (**A**) and CHH (**D**) contexts. Pairwise comparison of homologous four groups of homologous chromosomes in CG (**B**) and CHH (**E**) contexts. Comparison of the number of homologous alleles with difference in expression and gene body methylation in CG (**C**) and CHH (**F**) contexts. The differences between homologous alleles were tested using the Wilcoxon rank-sum test. \* $P$  value < 0.05.



**Figure S3.** DNA methylation variation and association with expression of tetrad alleles. DNA methylation profiles of the tetrad alleles after excluding intronic TEs in CG, CHG and CHH sequence contexts.