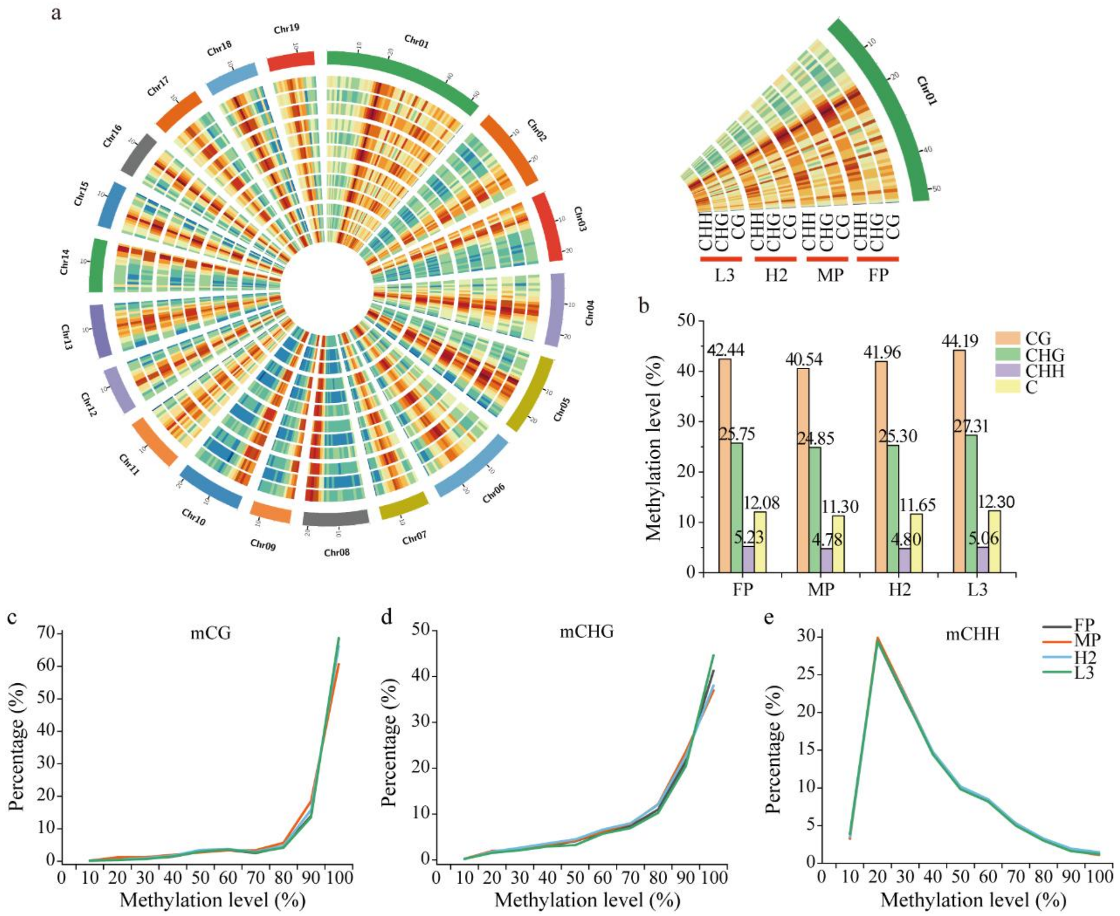
SUPPORTING INFORMATION



Supplementary Fig. 1 Distribution of different types of methylation levels and sources of hybrid methylation sites.

(a) Global methylome map of hybrids and their parents. (b) Genome-wide methylation levels of parents and hybrids in CG, CHG, and CHH cytosine contexts. (c-e) Distribution of the percentage of methylation at each cytosine context in the F1 hybrids and their parents. The x-axis shows the percentage of methylation in bins of 10%; The y-axis shows the percentage of total methylcytosines present in each bin.