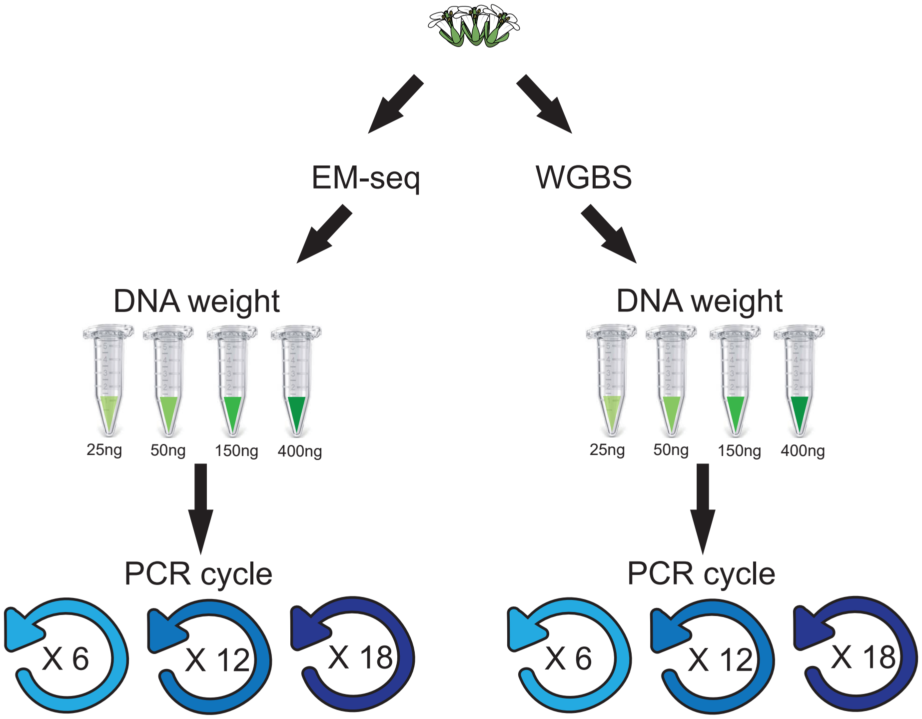


Figure S1 Schematic diagram of experimental design.

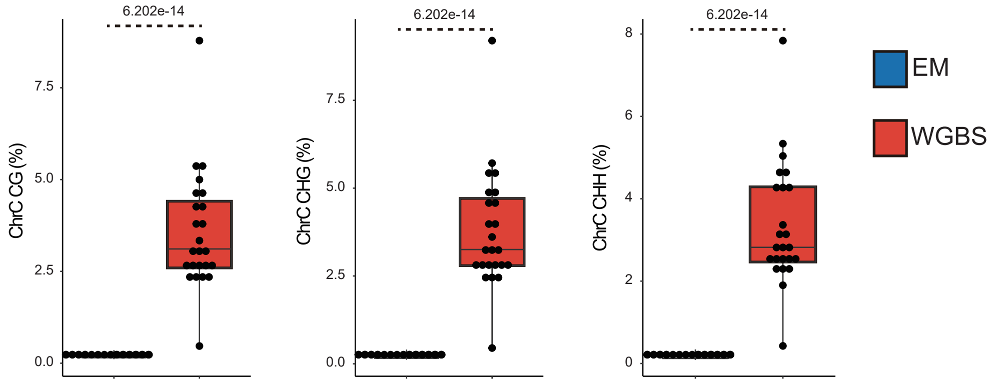


Figure S2 CG, CHG, and CHH methylation levels detected in chloroplast genome by EM-seq and WGBS. Blue box represents EM-seq and red box represents WGBS. The P values, shown at the top of the plots, were estimated with a Student's t-test.

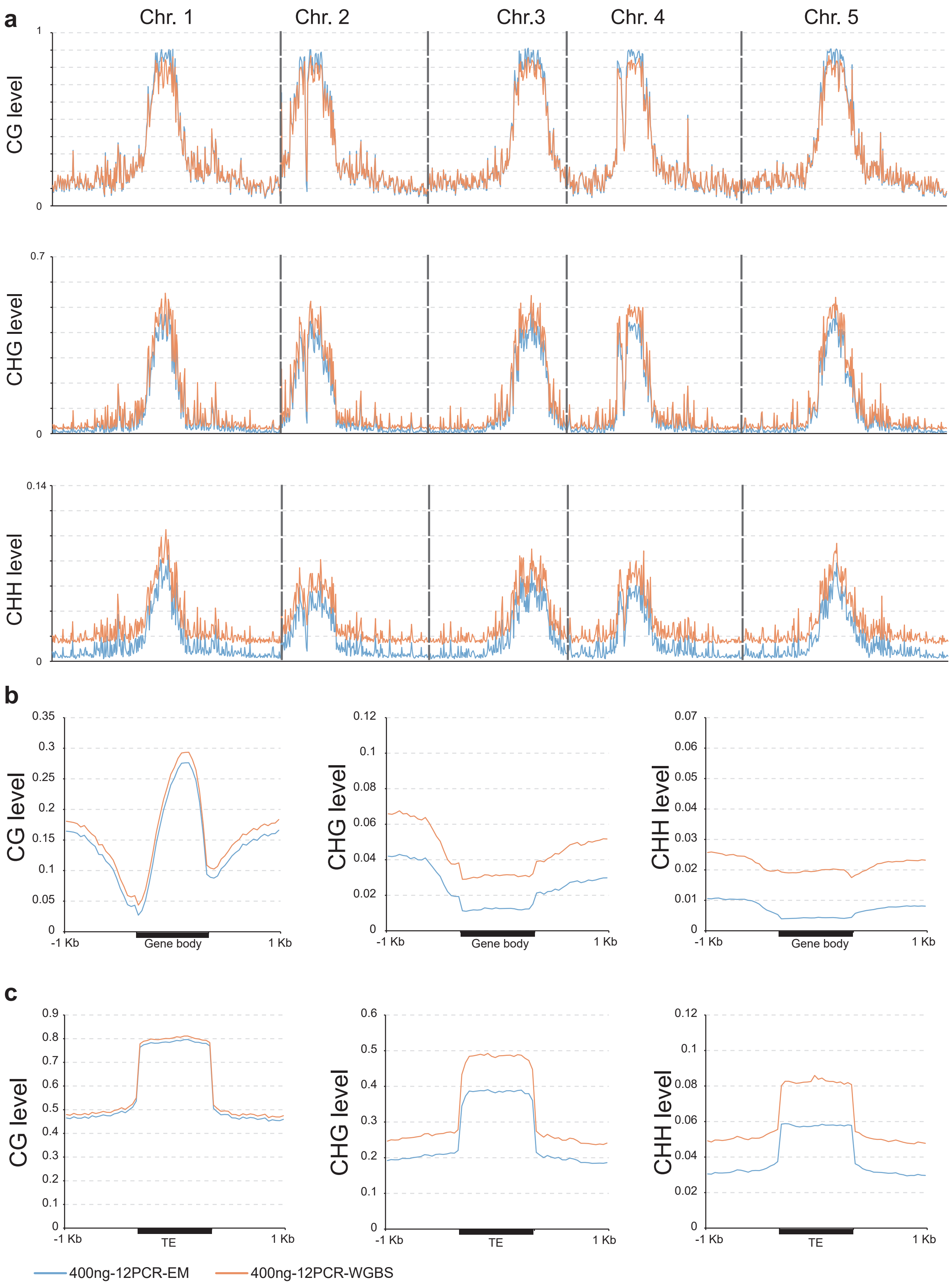
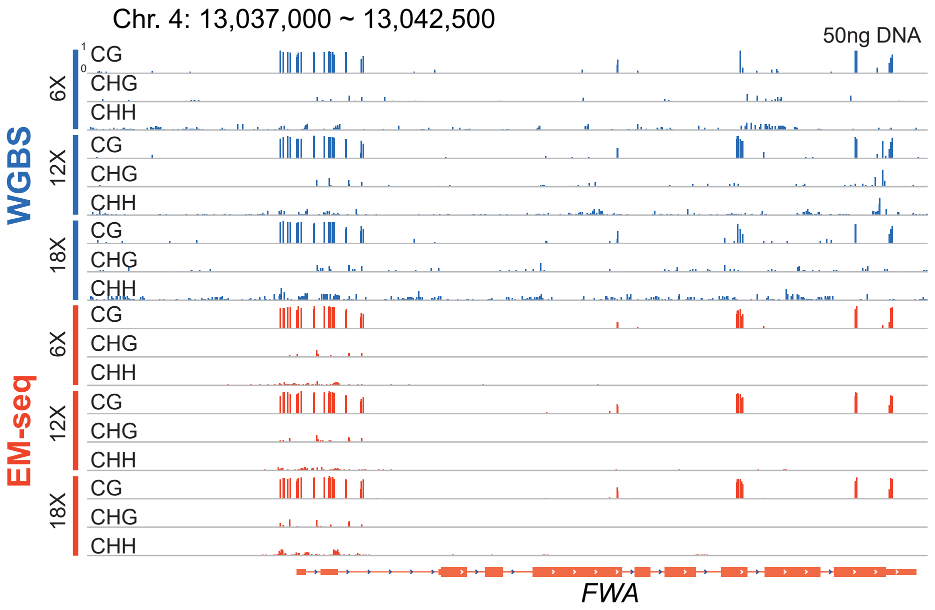


Figure S3 Comparison of methylation pattern between EM-seq and WGBS libraries prepared with 400ng DNA input and 12 cycles of PCR. **a** Chromosomal distribution of CG, CHG, and CHH methylations. Methylation levels were calculated with Arabidopsis chromosomes divided into 100 Kb bins. **b** Metaplots of CG, CHG, and CHH methylations over genes and 1 Kb flanking sequences. **c** Metaplots of CG, CHG, and CHH methylation over TEs and 1 Kb flanking sequences.

a



b

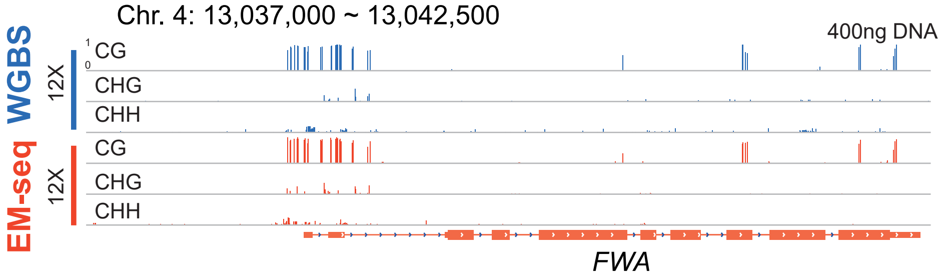


Figure S4 Genome browser screenshots of FWA locus. **a** Comparison of methylation detected by EM-Seq and WGBS in libraries prepared with 50ng DNA input. **b** Comparison of methylation detected by EM-Seq and WGBS in libraries prepared with 400ng DNA input and 12 cycles of PCR.

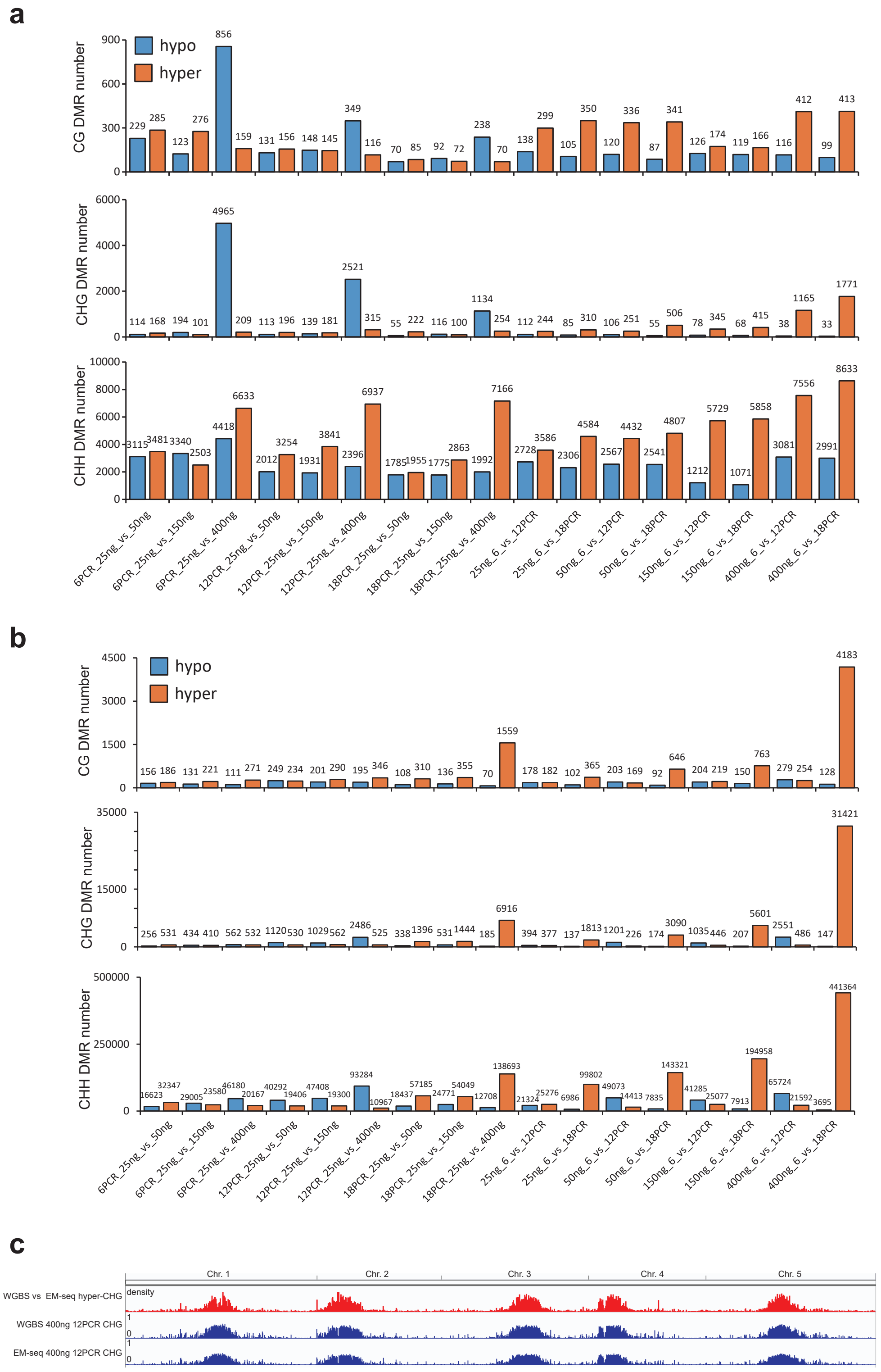


Figure S5 DMR numbers and chromosomal distribution. **a** DMR numbers between EM-seq libraries prepared with different conditions. **b** DMR numbers between WGBS libraries prepared with different conditions. **c** Chromosomal distribution of CHG methylation in EM-seq and WBGS libraries prepared with 400ng DNA input and 12 cycles of PCR and WGBS hyper-CHG DMRs.

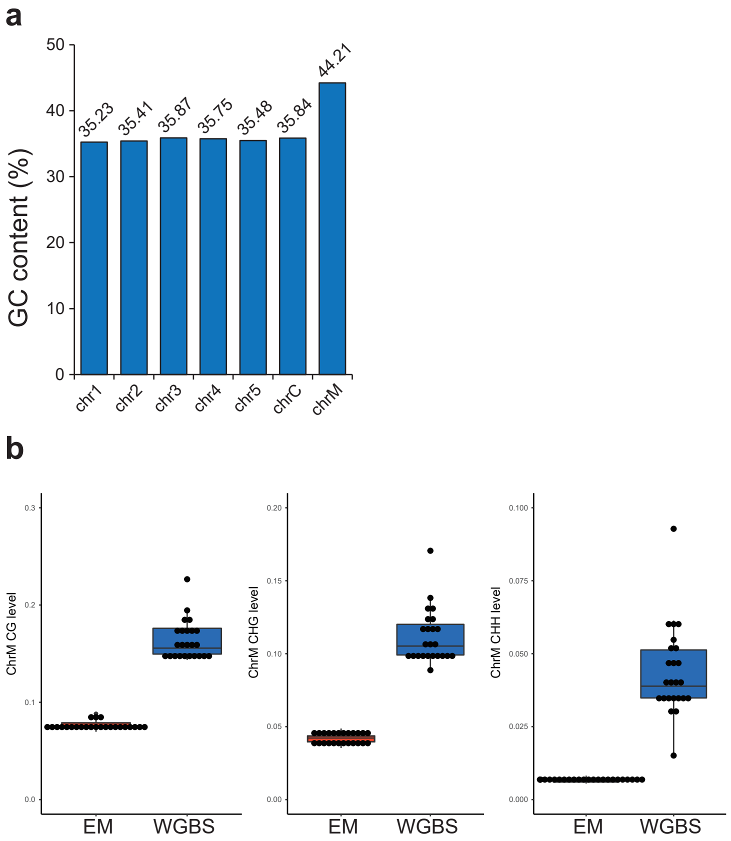


Figure S6 Methylation in mitochondrial DNA. **a** GC contents of Arabidopsis chromosomes. **b** CG, CHG, and CHH methylation levels in mitochondrial DNA.

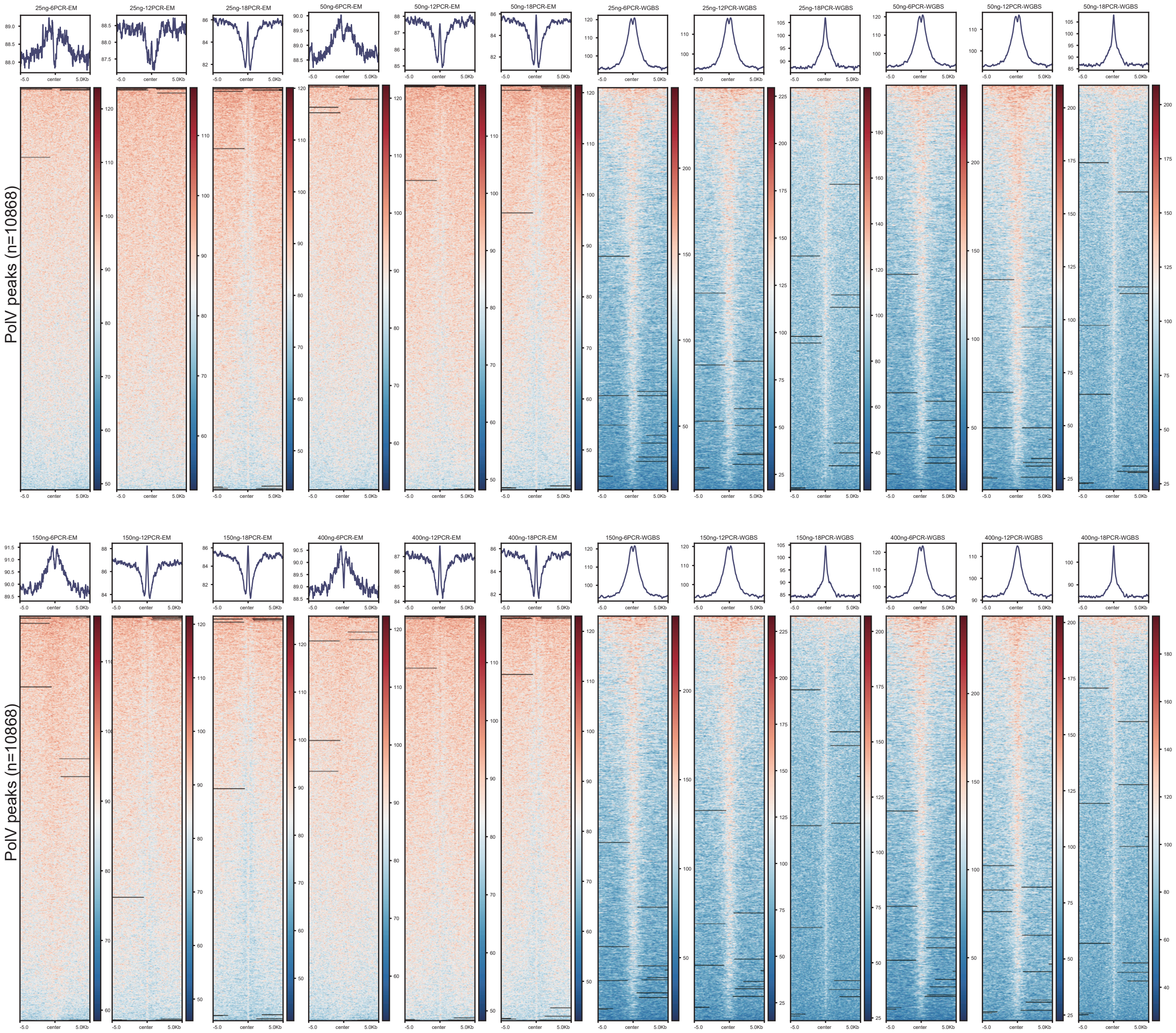


Figure S7 Heatmaps showing read coverage of EM-seq (left six columns both rows) and WGBS (right six columns both rows) over PolV ChIP-seq peaks.

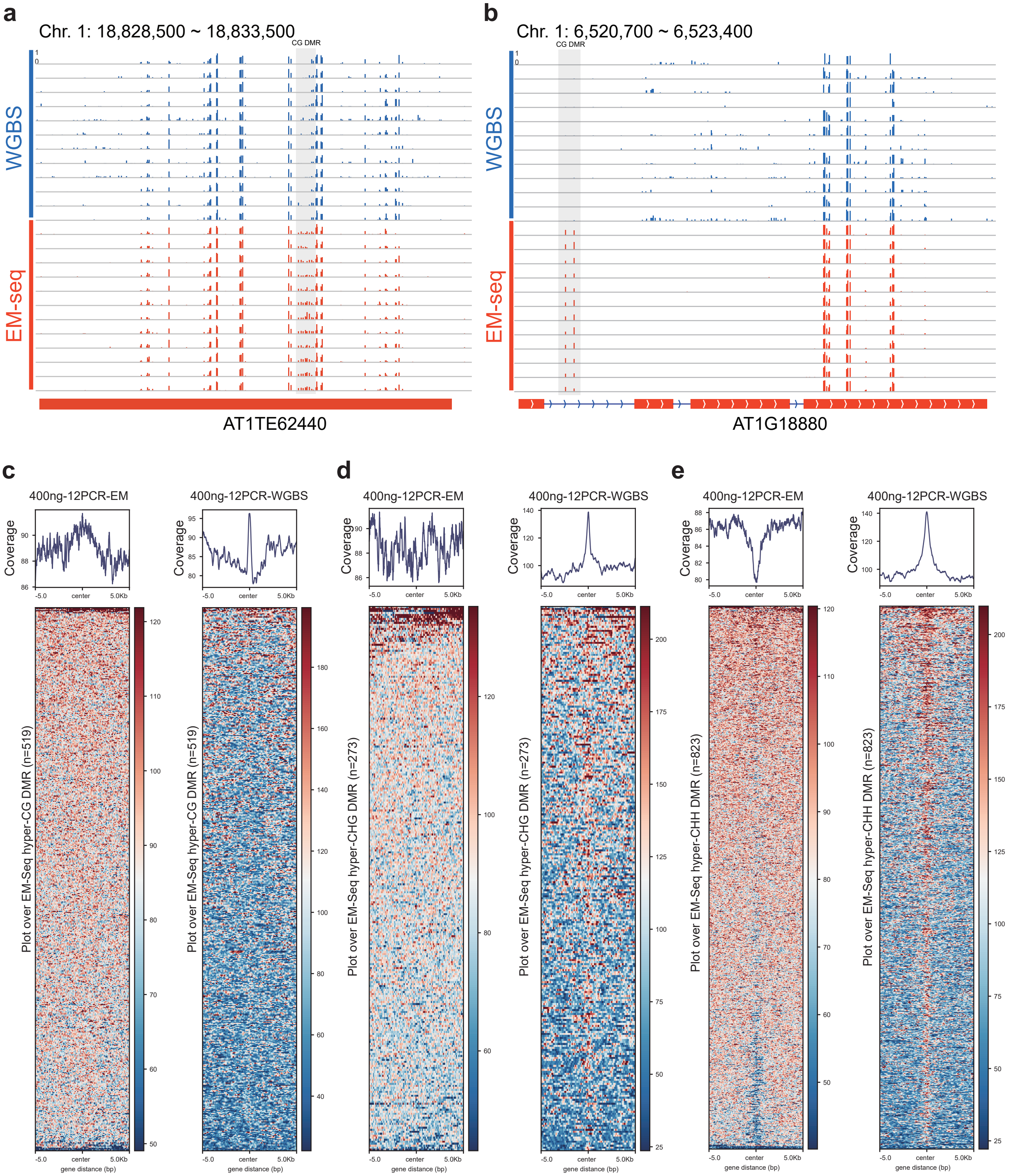


Figure S8 EM-seq hyper-DMRs. **a**,**b** Genome browser screenshots of EM-seq hyper-DMRs in pericentromeric TE (**a**) and in gene (**b**). **c**-**e** Heatmaps showing read coverage of EM-seq (left panels) and WGBS (right panels) over EM-seq hyper-CG (**c**), CHG (**d**), and CHH (**e**) DMRs.

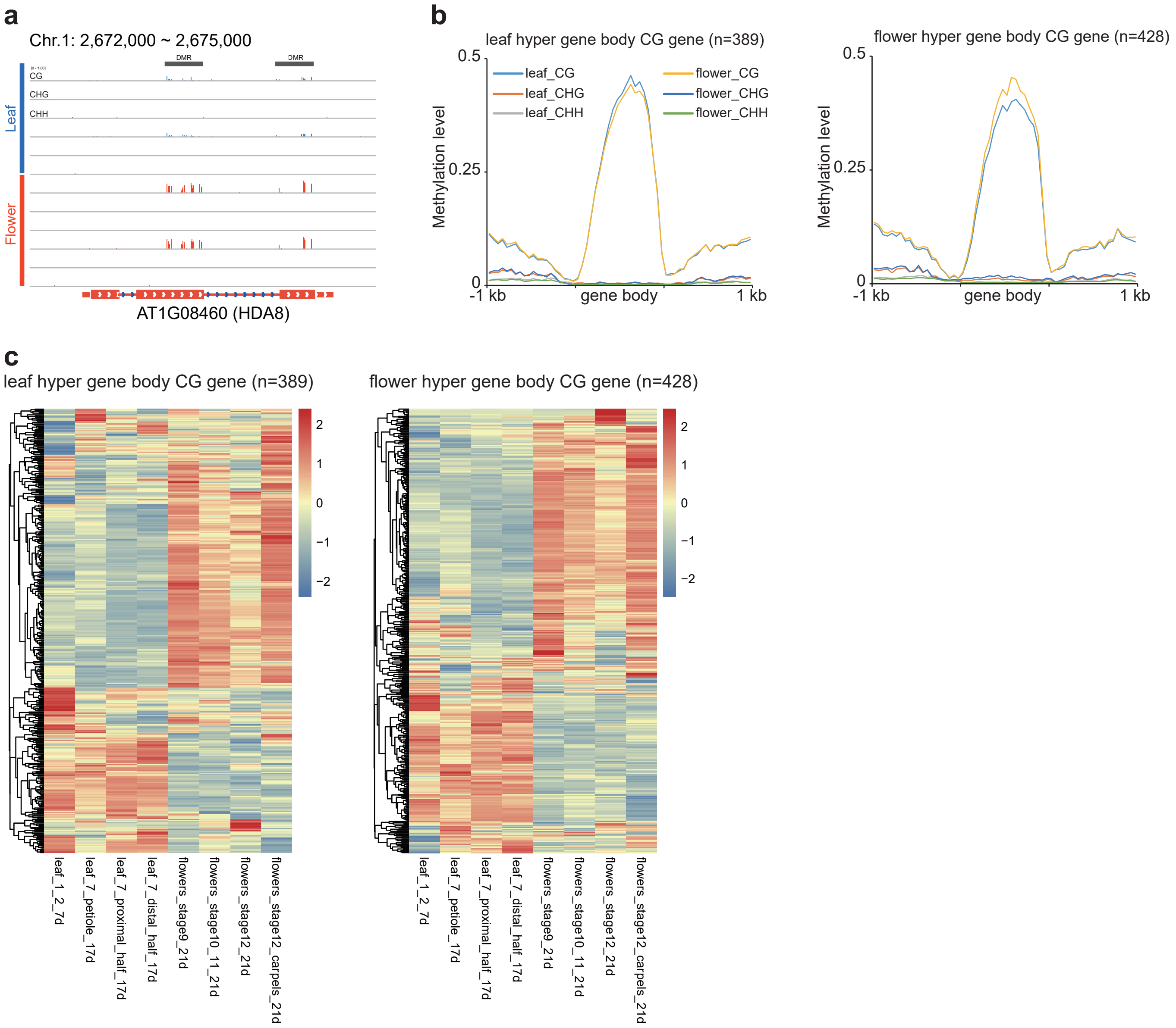


Figure S9 Gene body methylated genes. **a** Genome browser screenshots of flower hyper-CG DMRs in a gene body methylated gene. **b** Metaplots of CG, CHG, and CHH methylations in leaf and flower samples over genes containing hyper-CG DMRs and 1 Kb flanking sequences. **c** Clustering of expression patterns of gene body methylated genes containing hyper-CG DMRs.