

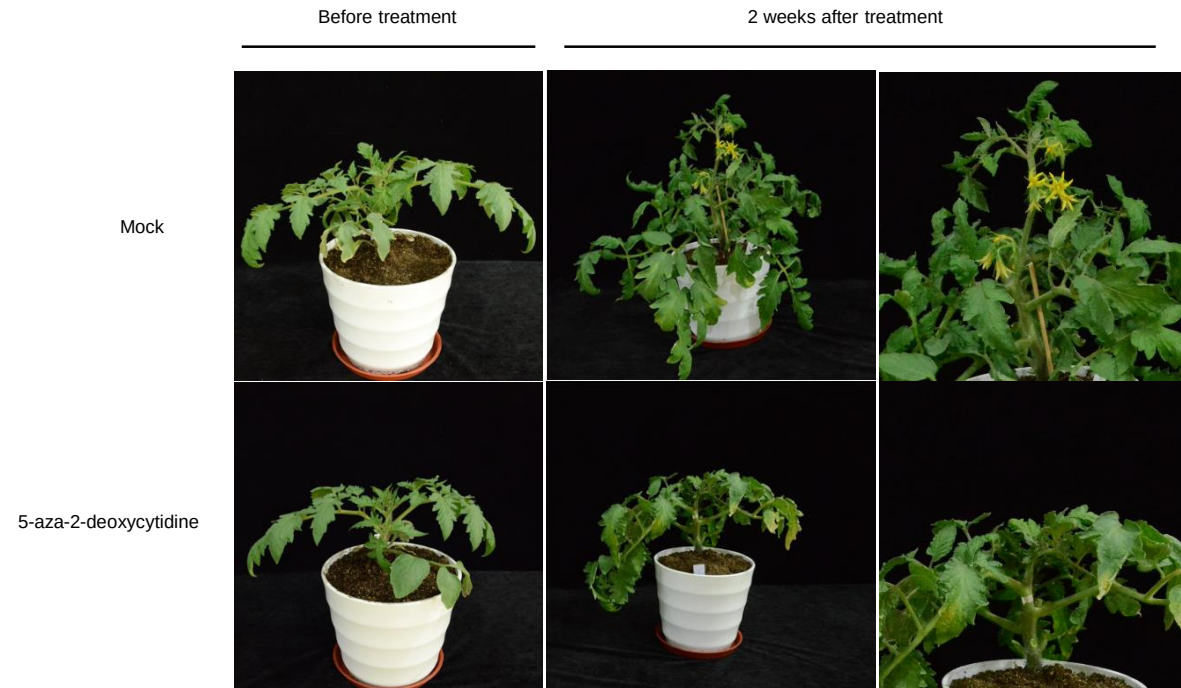


Figure S1. DNA methylation inhibitor 5-aza-2-deoxycytidine treatment inhibited the occurrence of inflorescence and caused growth retardation of tomato

100 μ l of 2mM 5-aza-2-deoxycytidine was added on the shoot apical meristem of 3-week-old tomato plants (Ohio8245), and the treatment was repeated after one week. Photos were taken two weeks after the initial treatment.

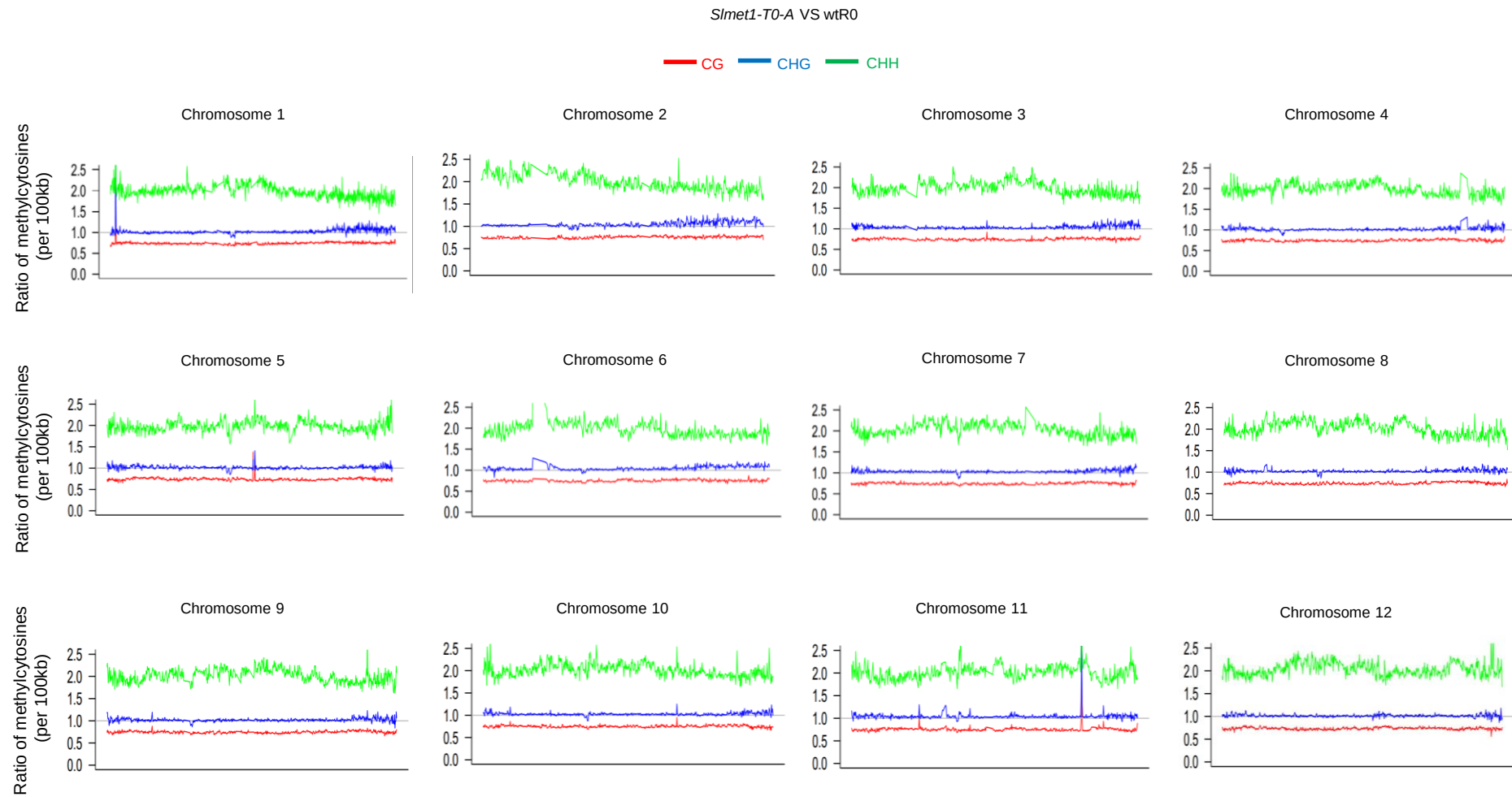


Figure S2. Comparison of methyl cytosine levels in *slmet1-T0-A* versus wtR0

Methyl cytosines were counted per 100kb in all the 12 chromosomes. The horizontal axis indicates chromosomal positions, and the plotted line represents the ratios of methyl cytosine numbers in *slmet1-T0-A* mutant versus that in wtR0. Cytosine levels in the CG, CHG, and CHH contexts are indicated by red, blue, and green colors, respectively.

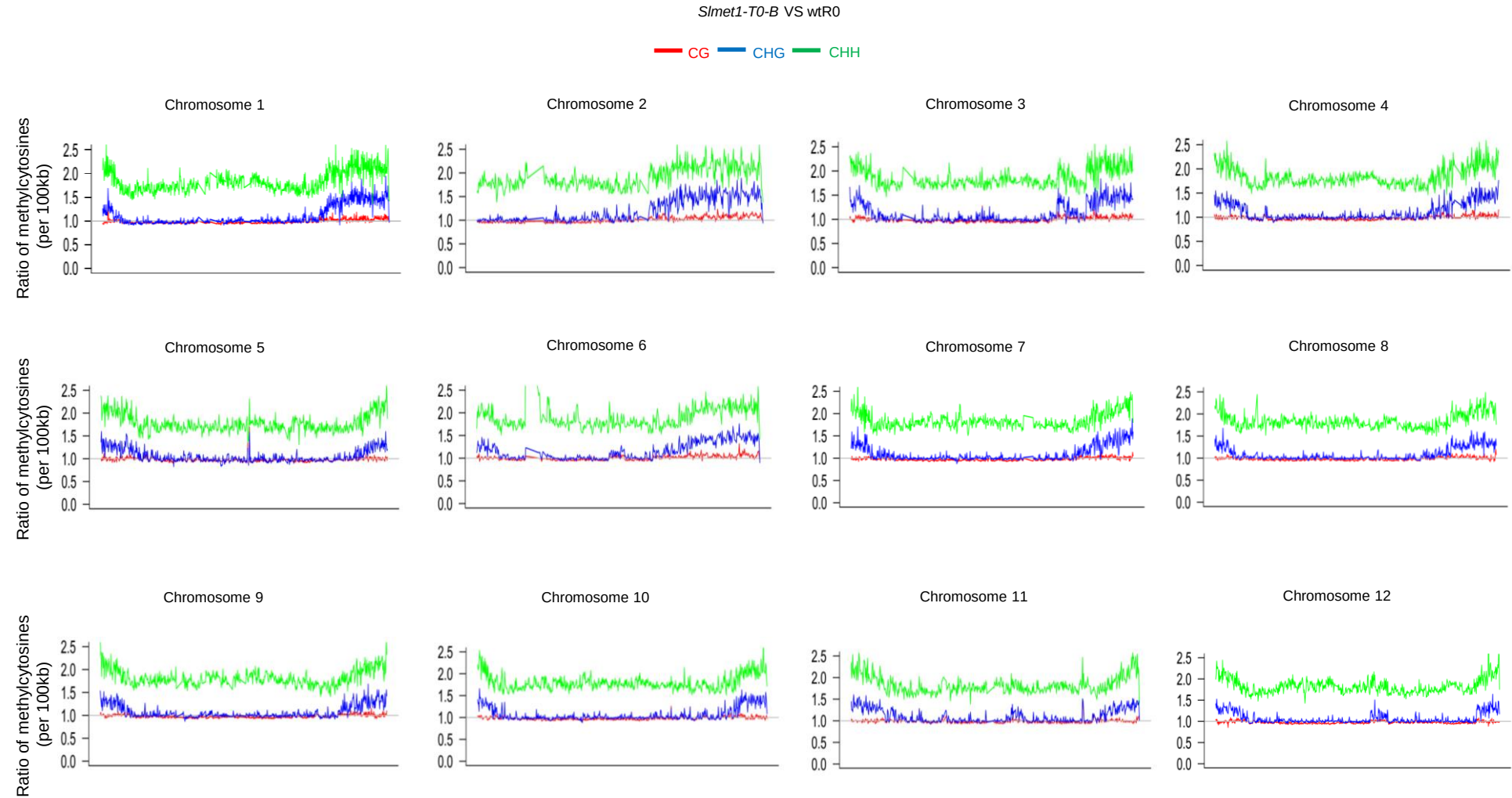


Figure S3. Comparison of methyl cytosine levels in *slmet1-T0-B* versus wtR0

Methyl cytosines were counted per 100kb in all the 12 chromosomes. The horizontal axis indicates chromosomal positions, and the plotted line represents the ratios of methyl cytosine numbers in *slmet1-T0-B* mutant versus that in wtR0. Cytosine levels in the CG, CHG, and CHH contexts are indicated by red, blue, and green colors, respectively.

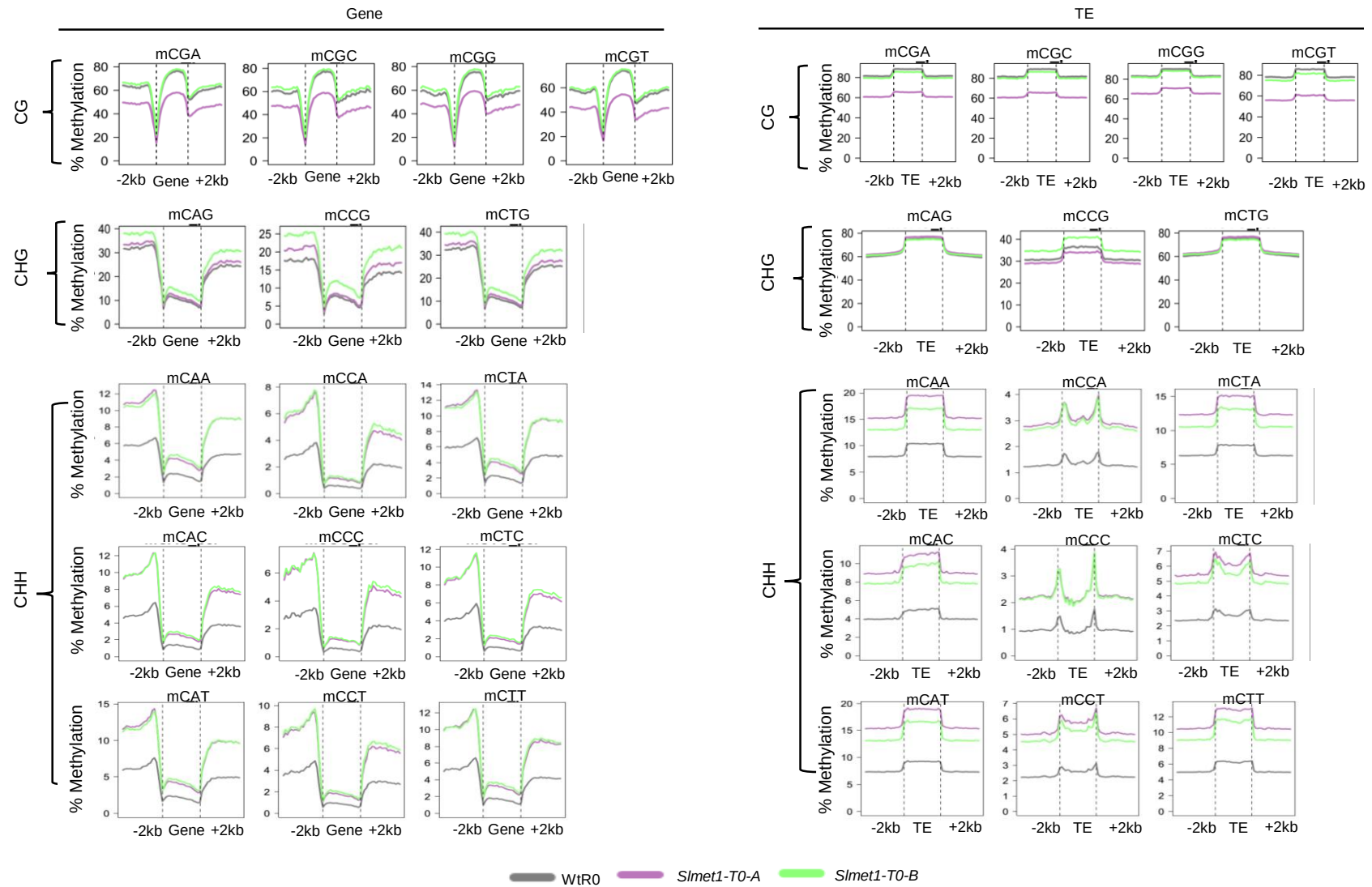


Figure S4. Genome-wide average methylation levels of subcontexts of CG, CHG, CHH and total C in gene regions and TE regions, each with their contiguous 2kb upstream and downstream flank regions

Data of *wtr0*, *slmet1-T0-A*, and *slmet1-T0-B* are presented in gray, purple, and green colors, respectively.

Slmet1-T0-A VS wtR0 (CHH subcontexts)

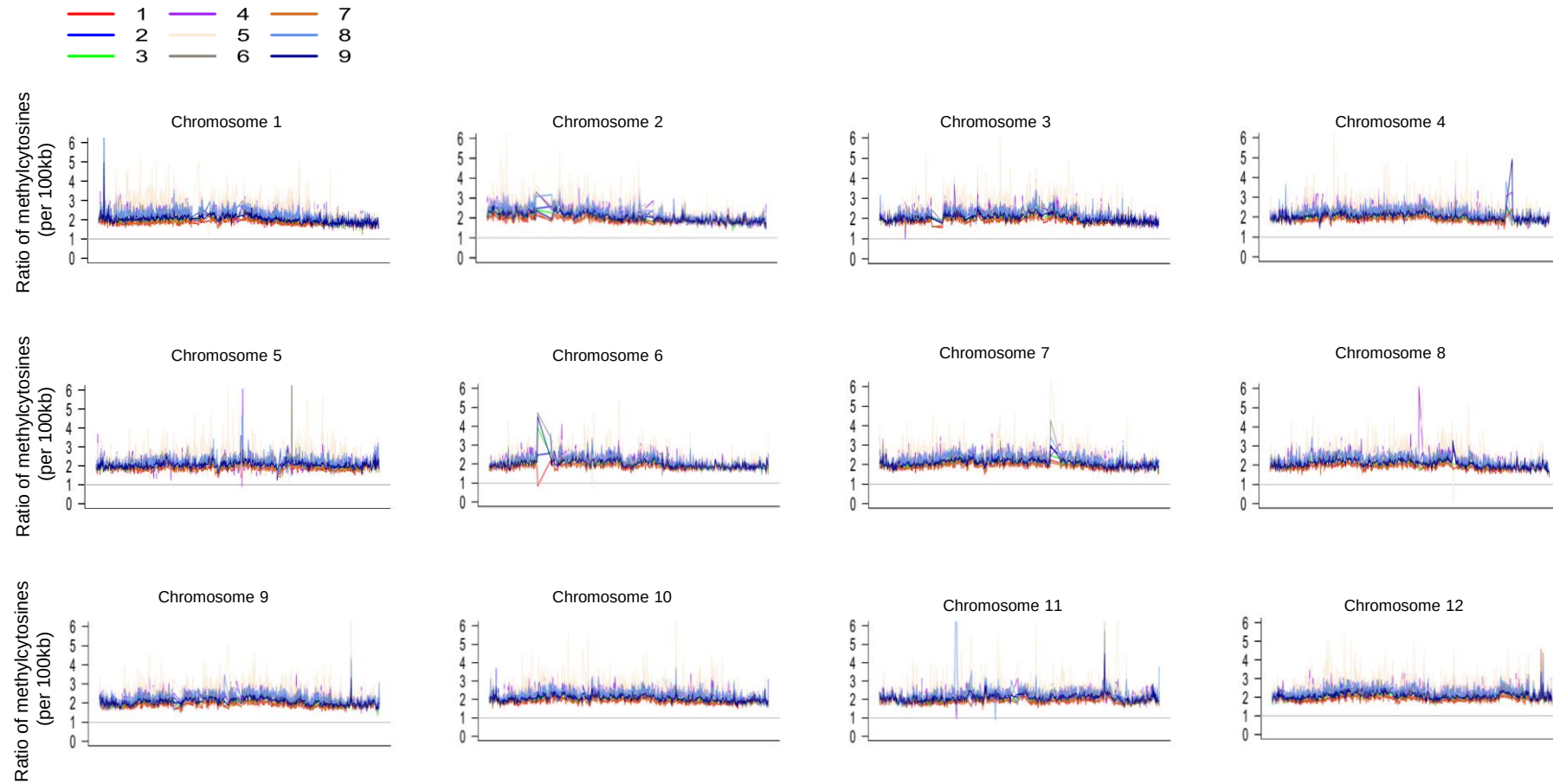


Figure S5. Comparison of methyl cytosine levels of all CHH subcontexts in *slmet1-T0-A* mutant versus wtR0

Methyl cytosines were counted per 100kb in all the 12 chromosomes. The horizontal axis indicates chromosomal positions, and the plotted line represents the ratios of methyl cytosine numbers in *slmet1-T0-A* mutant versus that in wtR0. The color 1 indicates mCAA, color 2 indicates mCAC, color 3 indicates mCAT, color 4 indicates mCCA, color 5 indicates mCCC, color 6 indicates mCCT, color 7 indicates mCTA, color 8 indicates mCTC, color 9 indicates mCTT.

Slmet1-T0-B VS wtR0 (CHH subcontexts)

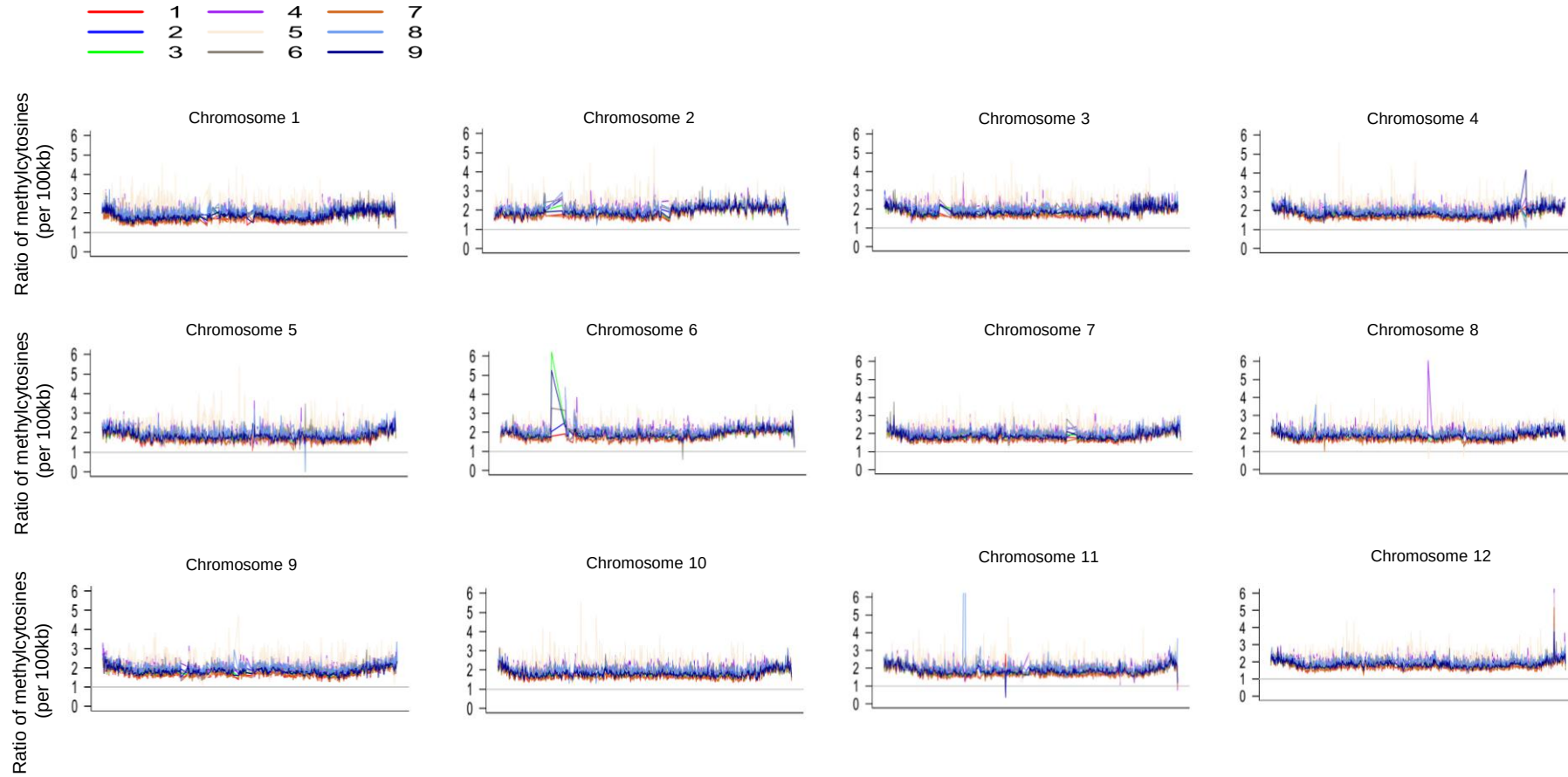


Figure S6. Comparison of methyl cytosine levels of all CHH subcontexts in *slmet1-T0-B* mutant versus wtR0

Methyl cytosines were counted per 100kb in all the 12 chromosomes. The horizontal axis indicates chromosomal positions, and the plotted line represents the ratios of methyl cytosine numbers in *slmet1-T0-B* mutant versus that in wtR0. The color1 indicates mCAA, color 2 indicates mCAC, color 3 indicates mCAT, color 4 indicates mCCA, color 5 indicates mCCC, color 6 indicates mCCT, color 7 indicates mCTA, color 8 indicates mCTC, color 9 indicates mCTT.

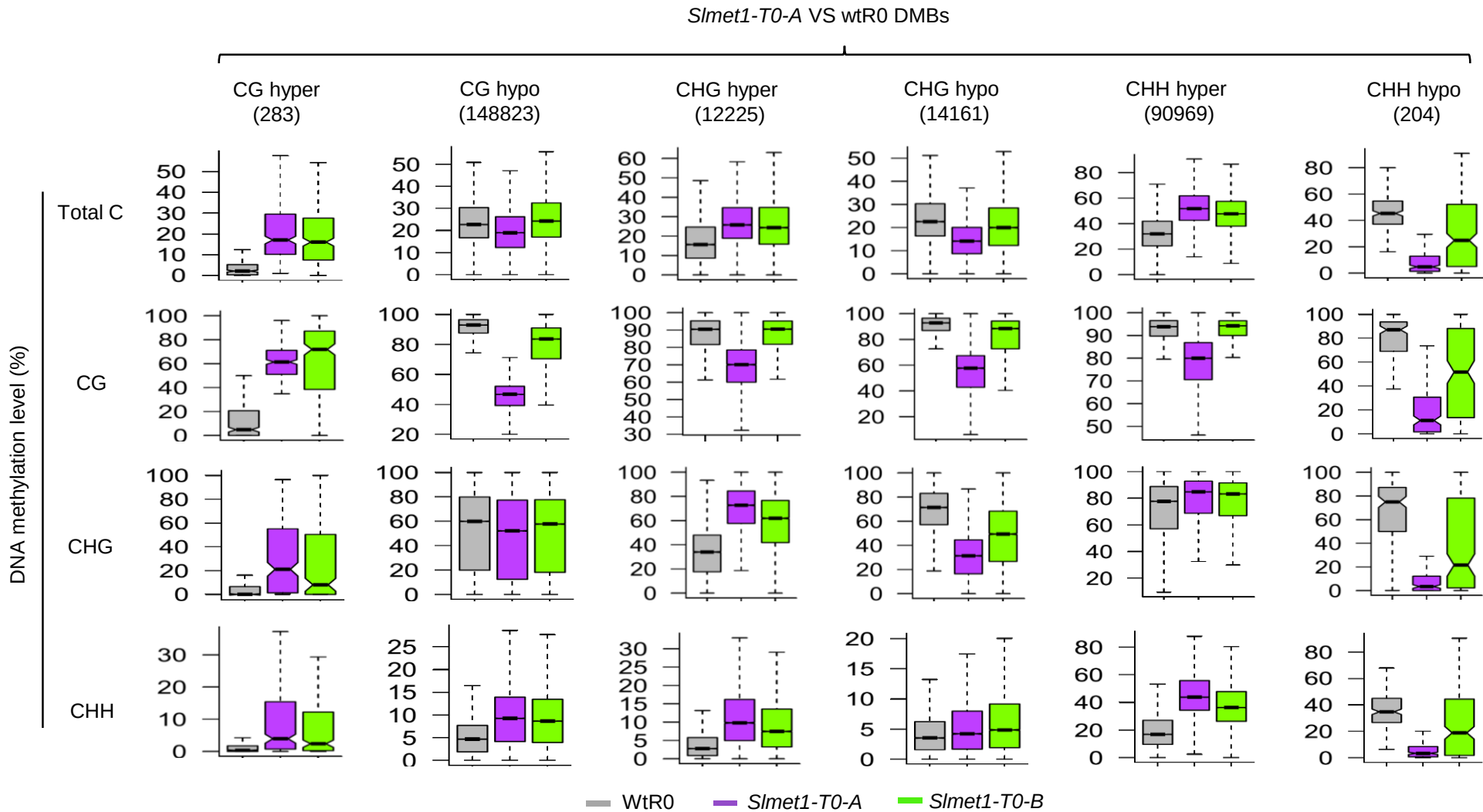


Figure S7. Overall DNA methylation levels in total C, CG, CHG and CHH contexts at CG, CHG and CHH hyper and hypo DMBS that were identified in *slmet1-T0-A* compared to wtR0

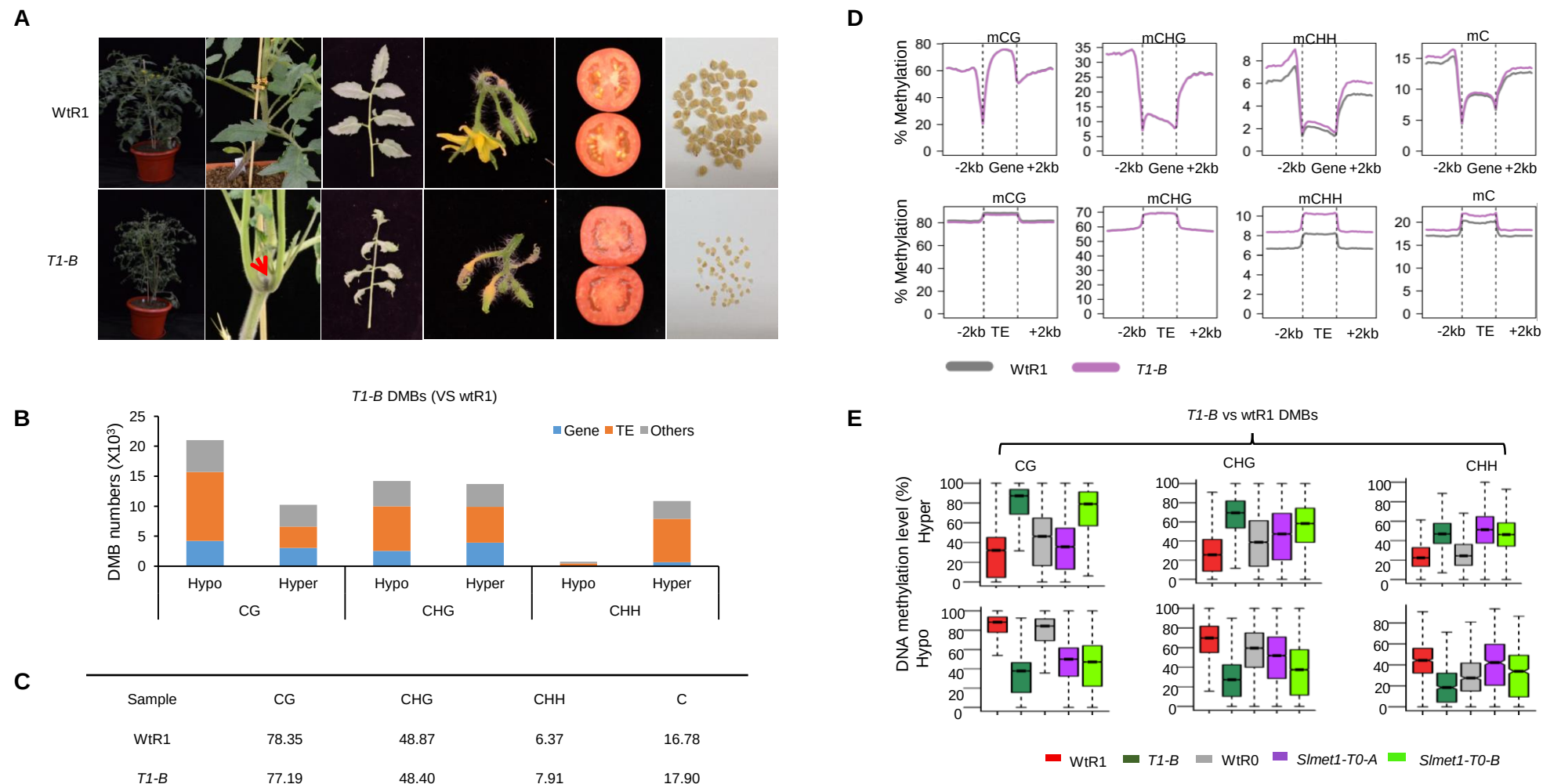


Figure S8. Morphological phenotypes and methylome of the *slmet1-1-T1-B* mutant.

(A) The *T1-B* mutant showed growth retardation, curly and thick leaves, reduced floral buds, and parthenocarpic fruits. **(B)** Numbers and composition of *T1-B* DMBs compared with wtR1 in the CG, CHG and CHH contexts. **(C)** Cytosine (C) methylation levels of CG, CHG, CHH, and total C in wtR1 and *T1-B*. **(D)** Genome-wide average methylation levels of CG, CHG, CHH and total C in gene regions and TE regions, each with their contiguous 2kb upstream and downstream flank regions. **(E)** Overall DNA methylation levels in the CG, CHG and CHH contexts at hyper and hypo DMBs identified in *T1-B* compared to wtR1.

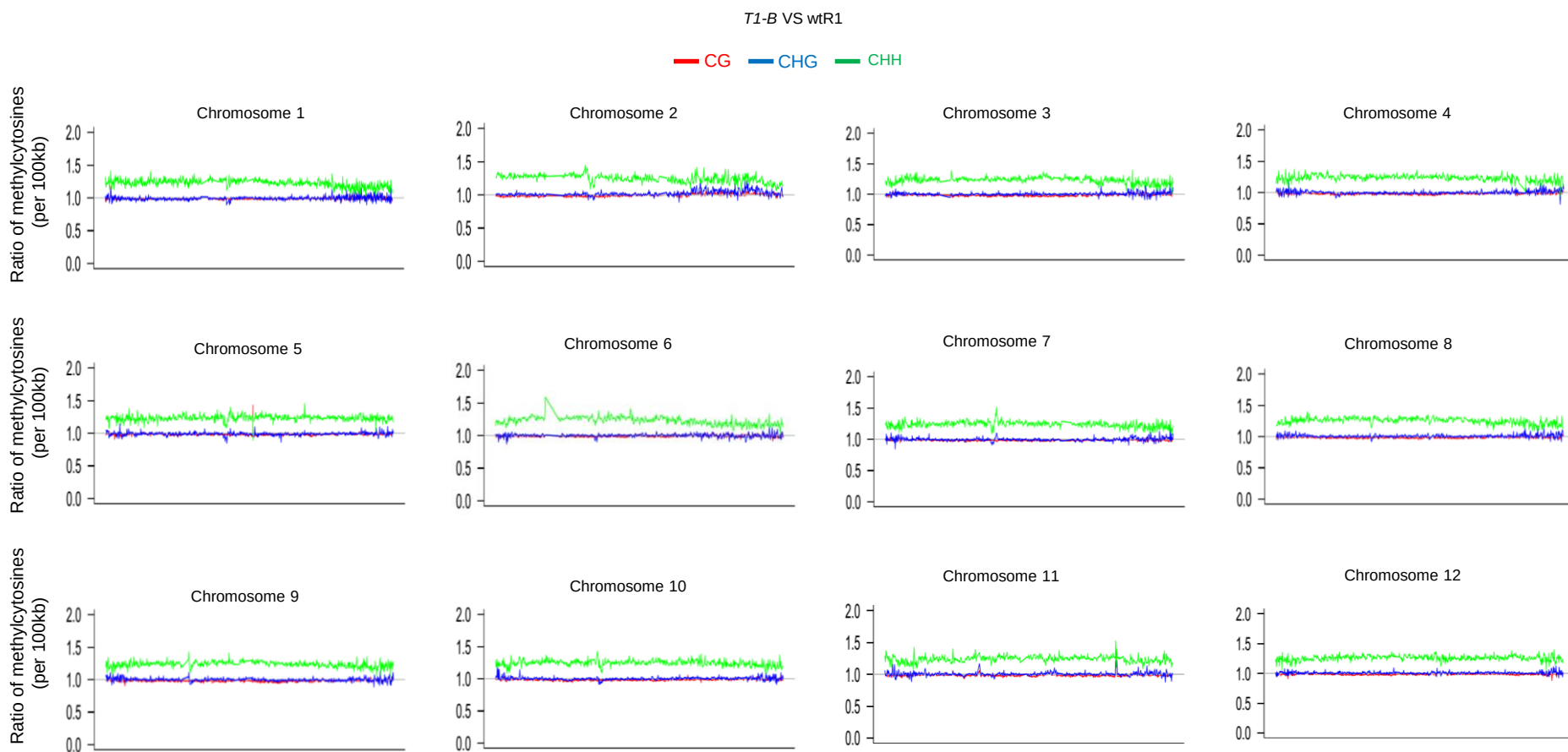


Figure S9. Comparison of methyl cytosine levels in *T1-B* versus wtR1

Methyl cytosines were counted per 100kb in all the 12 chromosomes. The horizontal axis indicates chromosomal positions, and the plotted line represents the ratios of methyl cytosine numbers in *T1-B* versus that in wtR1.

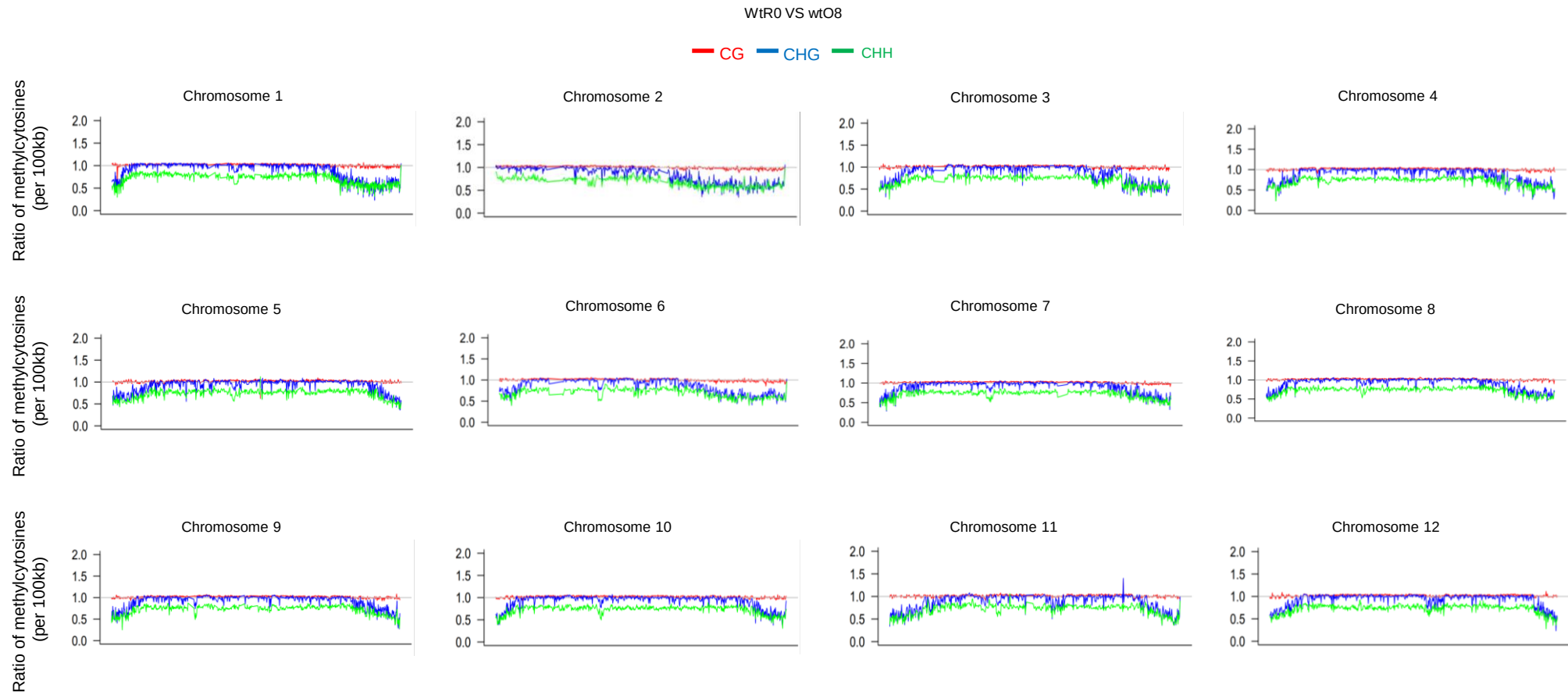


Figure S10. Comparison of methyl cytosine levels in wtR0 versus that in wtO8

Methyl cytosines were counted per 100kb in all the 12 chromosomes. The horizontal axis indicates chromosomal positions, and the plotted line represents the ratios of methyl cytosine numbers in *wtR0* versus that in *wtO8*.

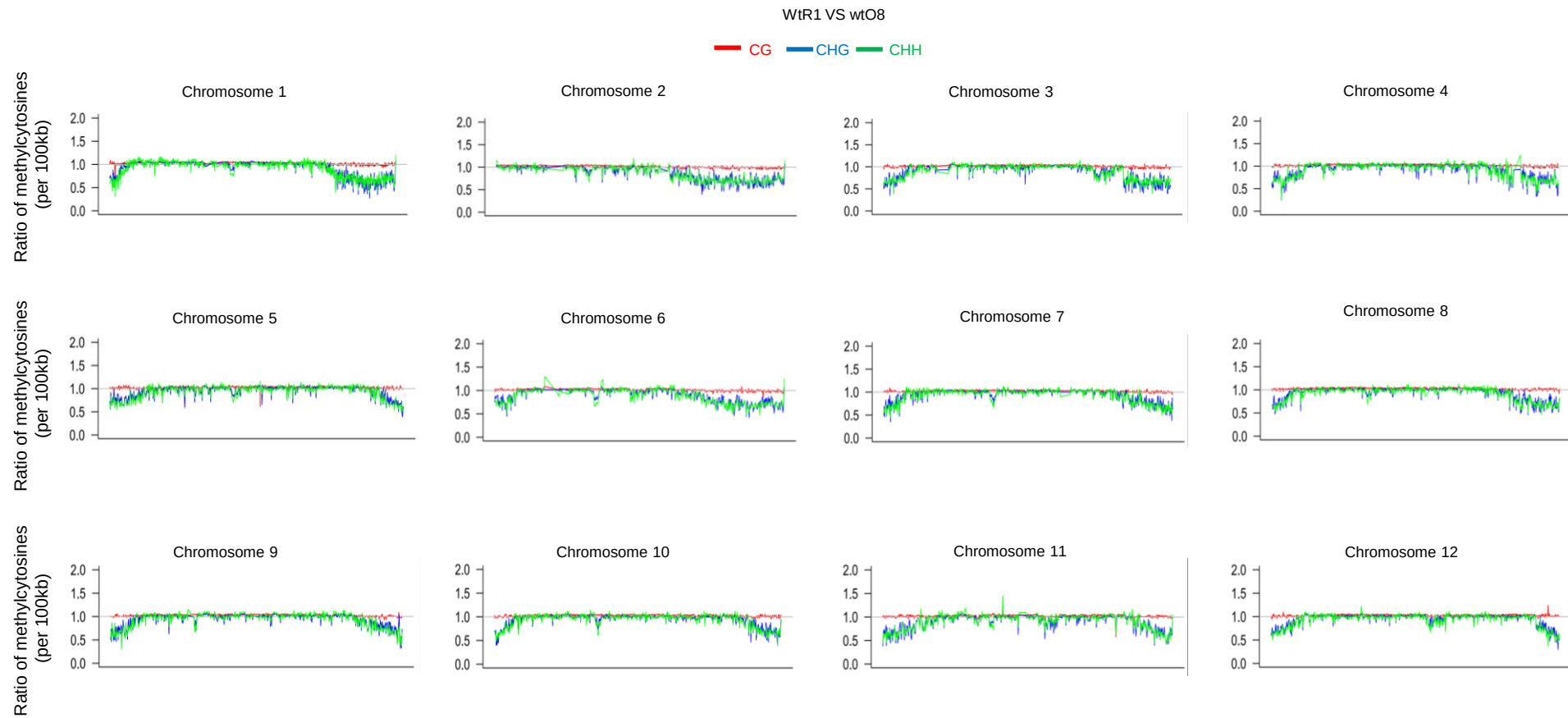


Figure S11. Comparison of methyl cytosine levels in wtR1 versus that in wtO8

Methyl cytosines were counted per 100kb in all the 12 chromosomes. The horizontal axis indicates chromosomal positions, and the plotted line represents the ratios of methyl cytosine numbers in *wtR1* versus that in *wtO8*.

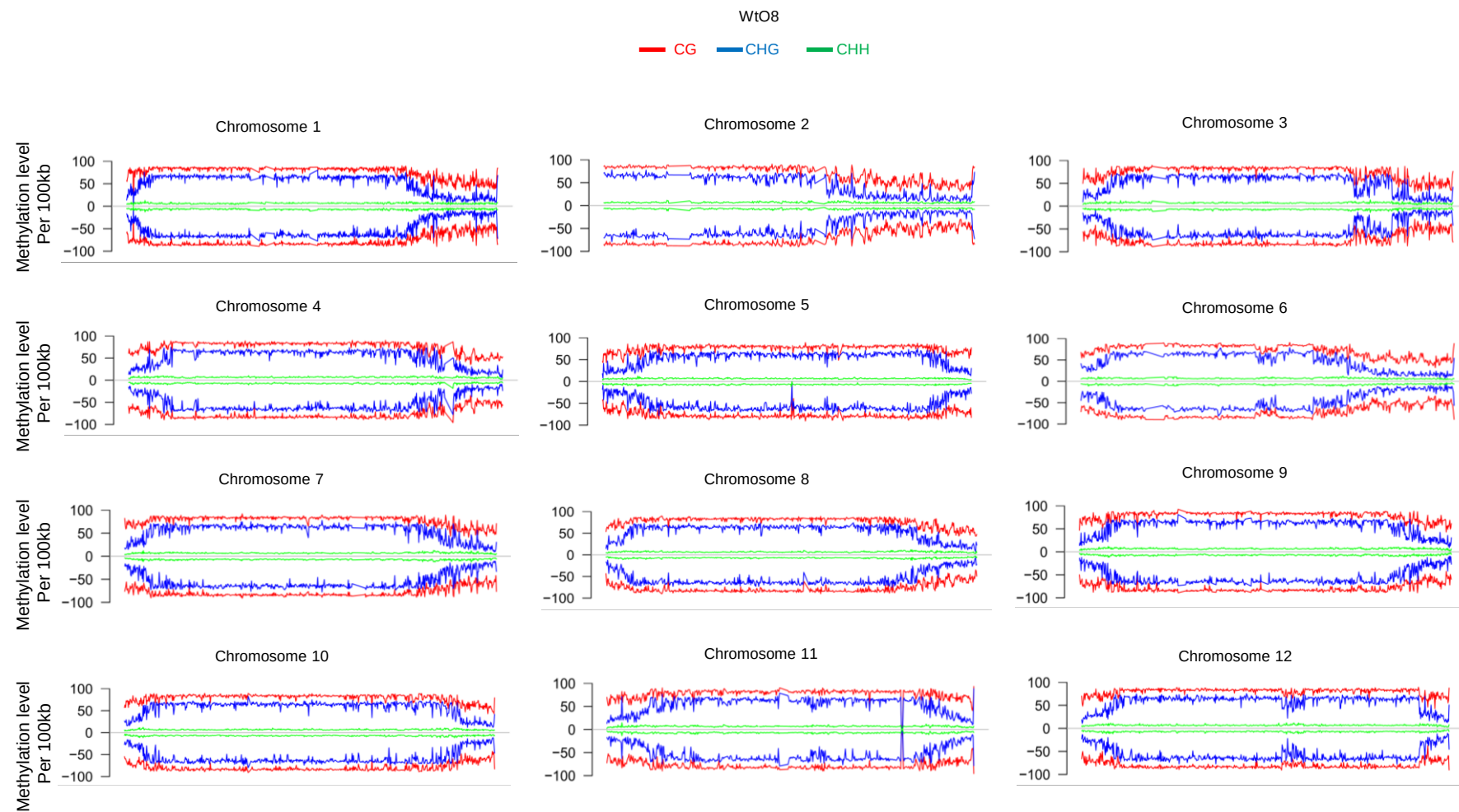


Figure S12. Distribution of methylcytosines in wtO8 on all the 12 chromosomes of tomato

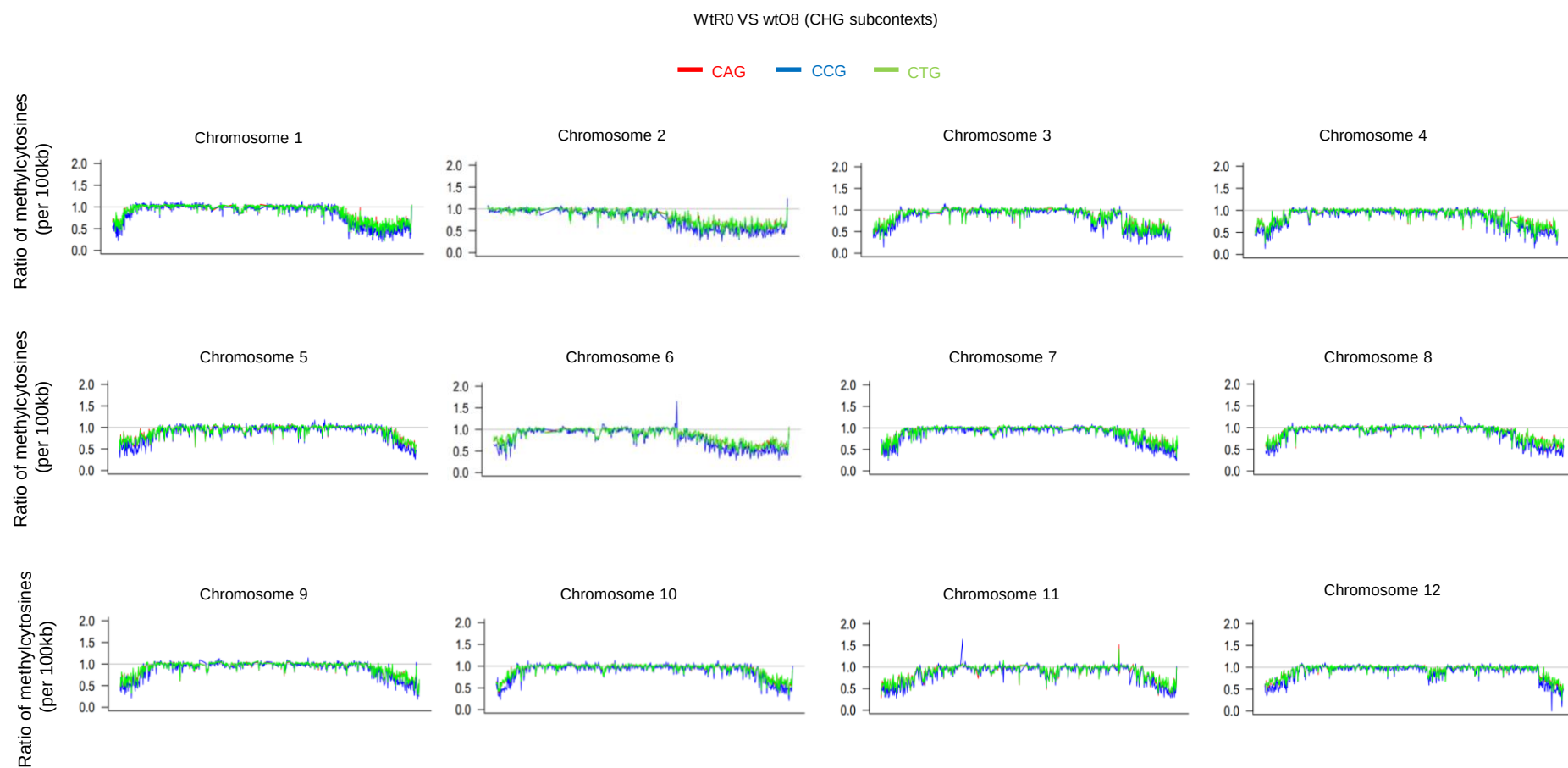


Figure S13. Comparison of methyl cytosine levels of CHG subcontexts in wtR0 versus wtO8

Methyl cytosines were counted per 100kb in all the 12 chromosomes. The horizontal axis indicates chromosomal positions, and the plotted line represents the ratios of methyl cytosine numbers in *wtR0* versus that in *wtO8*. Red indicates CAG, blue indicates CCG, and green indicates CTG.

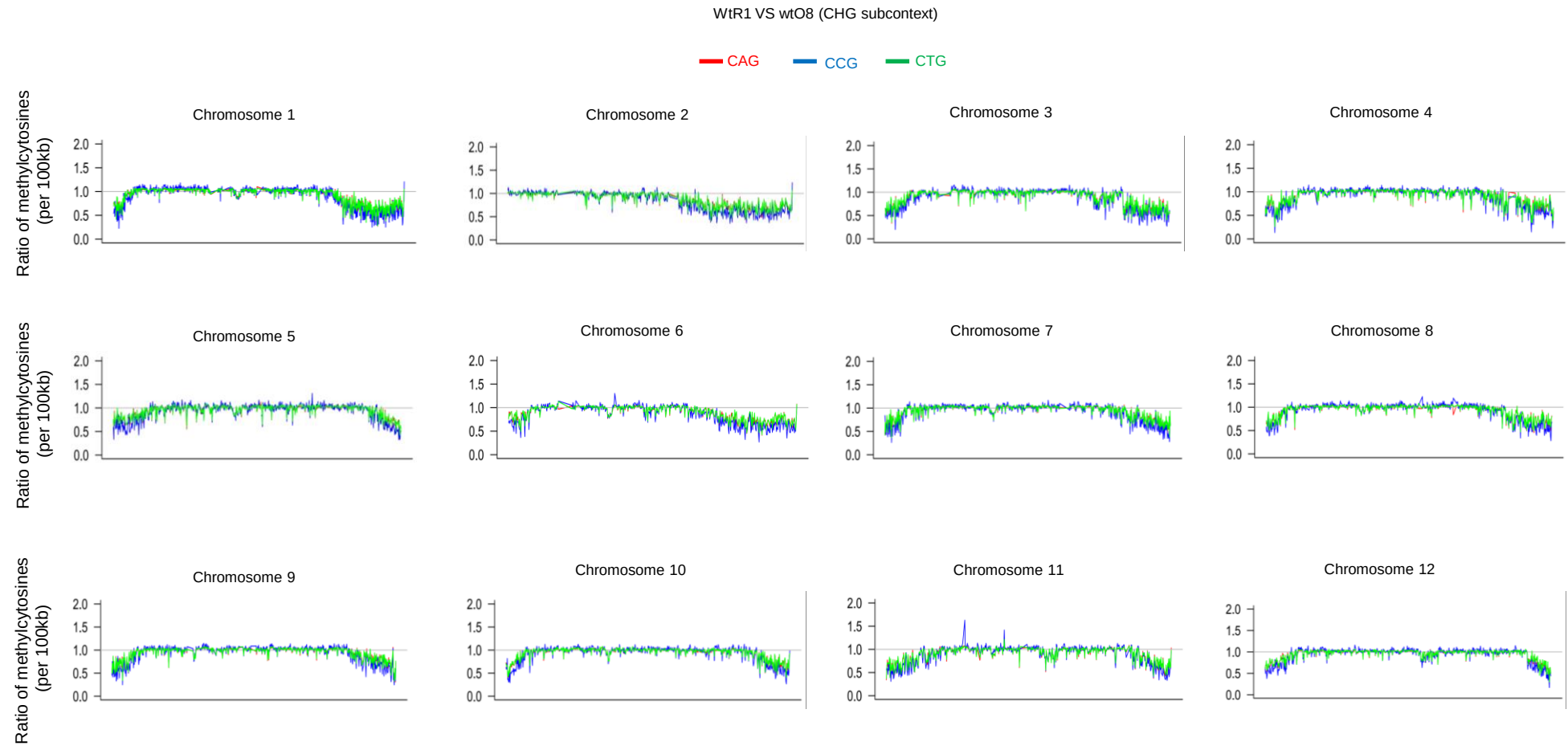


Figure S14. Comparison of methyl cytosine levels of CHG subcontexts in wtR1 versus wtO8

Methyl cytosines were counted per 100kb in all the 12 chromosomes. The horizontal axis indicates chromosomal positions, and the plotted line represents the ratios of methyl cytosine numbers in *wtR1* versus that in *wtO8*.

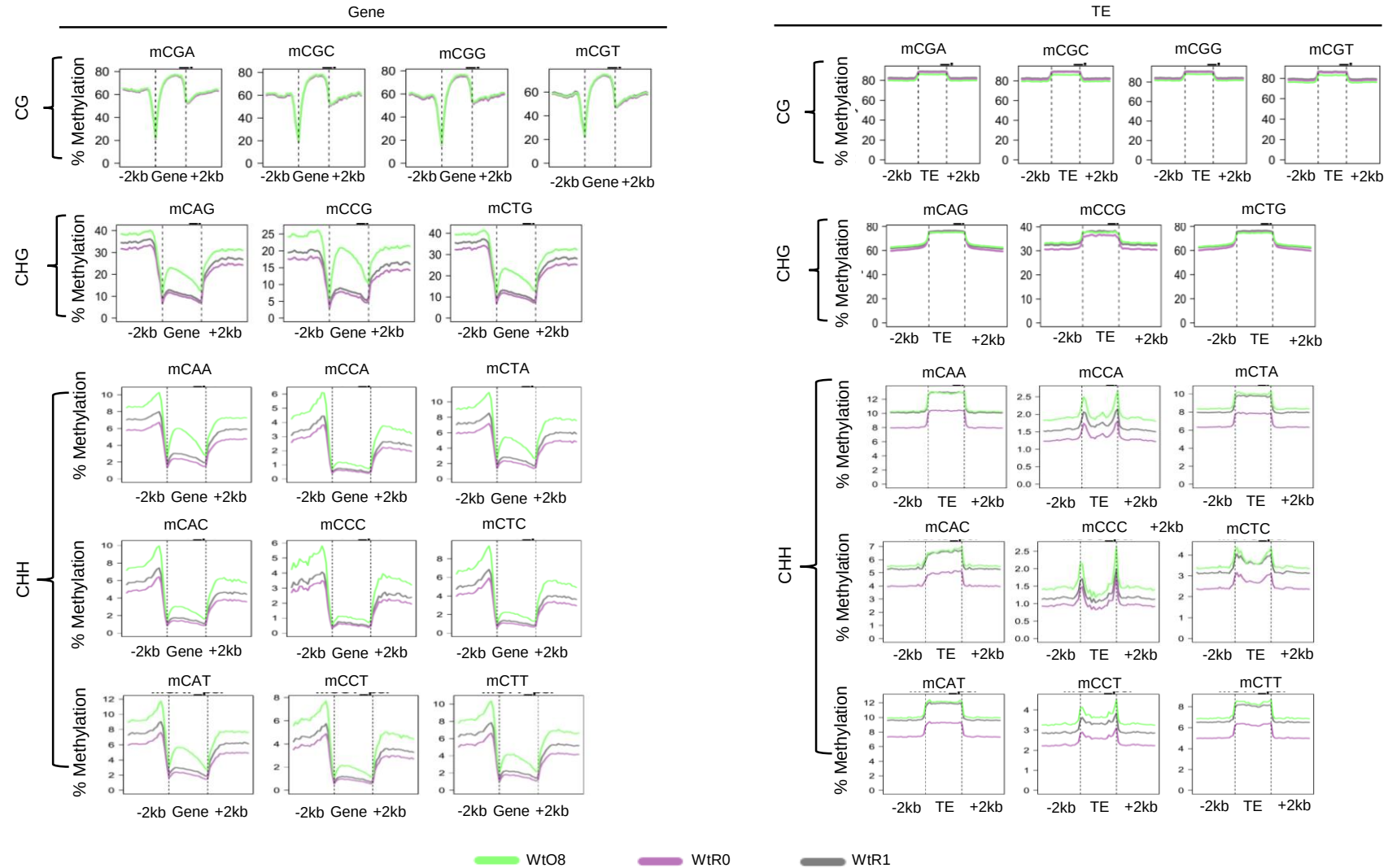


Figure S15. Genome-wide average methylation levels of subcontexts of CG, CHG, CHH and total C in gene regions and TE regions, each with their contiguous 2kb upstream and downstream flank regions in wtO8, wtR0 and wtR1

Data of wtO8, wtR0, and wtR1 are presented in green, purple, and gray colors, respectively.

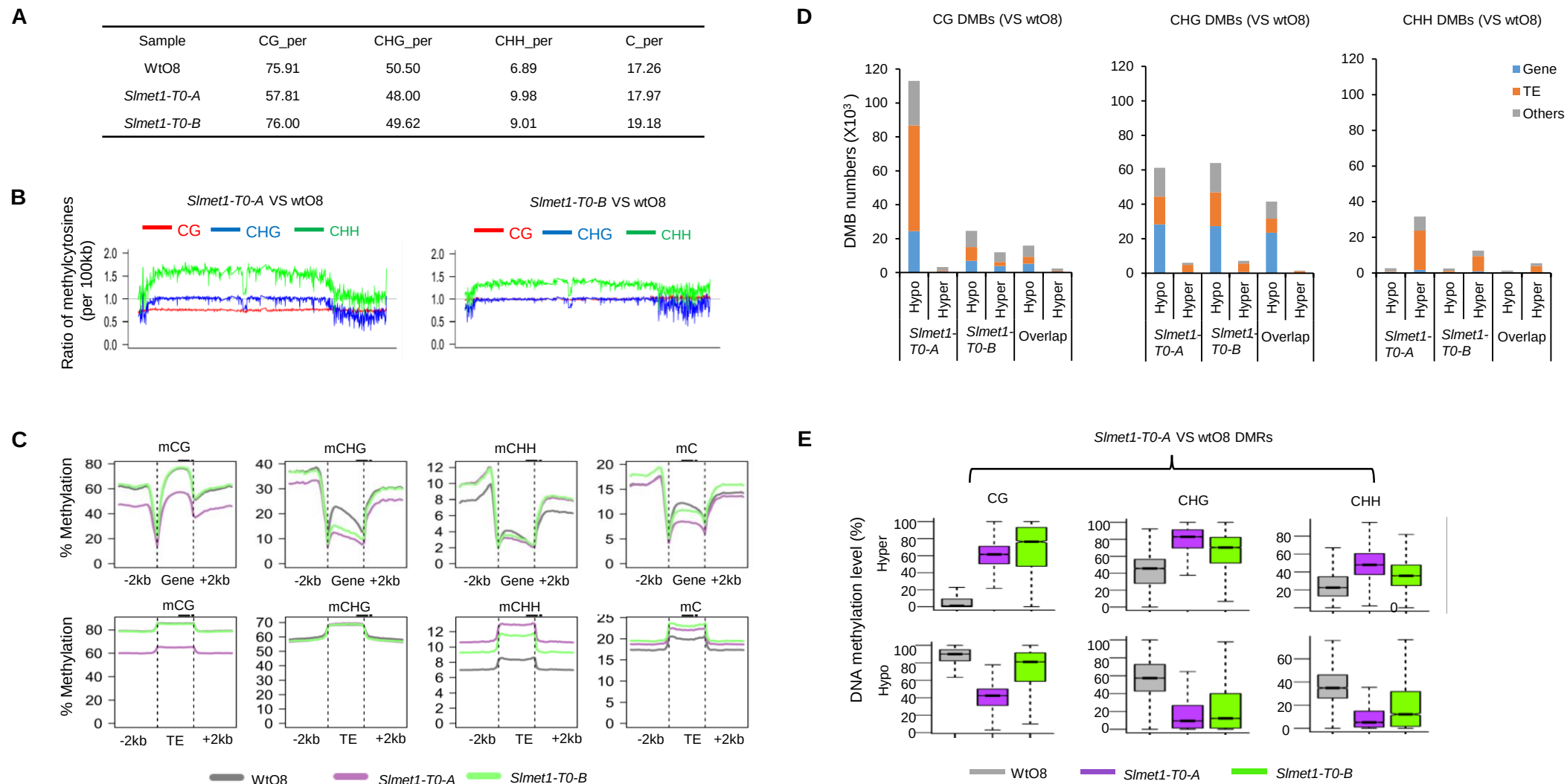


Figure S16. Genome-wide DNA methylation changes in *slmet1* mutants compared to wtO8

(A) Cytosine (C) methylation levels of CG, CHG, CHH, and total C in wtO8 and *slmet1* T0 mutants. **(B)** Ratios of the methylated cytosines in *slmet1* T0 mutants versus wtO8. Methylated cytosines were counted per 100kb of chromosome 1. **(C)** Genome-wide average methylation levels of CG, CHG, CHH and total C in gene regions and TE regions, each with their contiguous 2kb upstream and downstream flank regions. **(D)** Numbers and composition of *slmet1-T0-A* and *slmet1-T0-B* DMBs, as well as their overlapped DMBs compared with wtO8 in CG, CHG and CHH contexts. **(E)** Overall DNA methylation levels in CG, CHG and CHH contexts at hyper and hypo DMBs identified in *slmet1-T0-A* compared to wtO8.

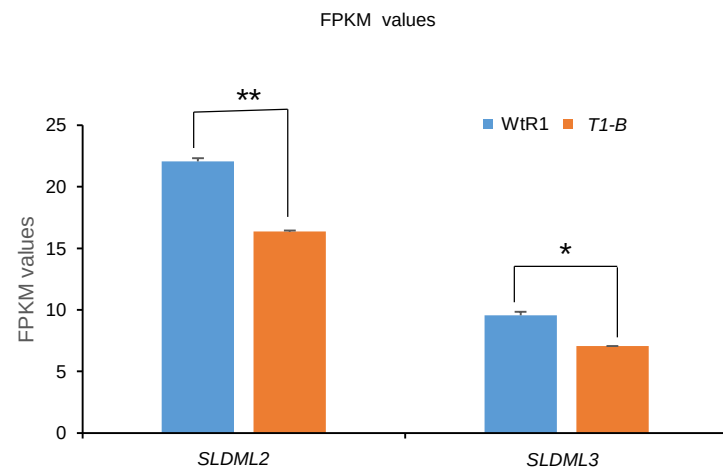


Figure S17. *DML2* and *DML3* showed significant decrease in *T1-B* compared to wtR1

FPKM values of wtR1 and *T1-B* from RNA seq data are shown. Values are mean $\pm$ SD, n=2. Asterisks indicate significant difference between wtR1 and *T1-B*: * $P < 0.05$; ** $P < 0.01$.

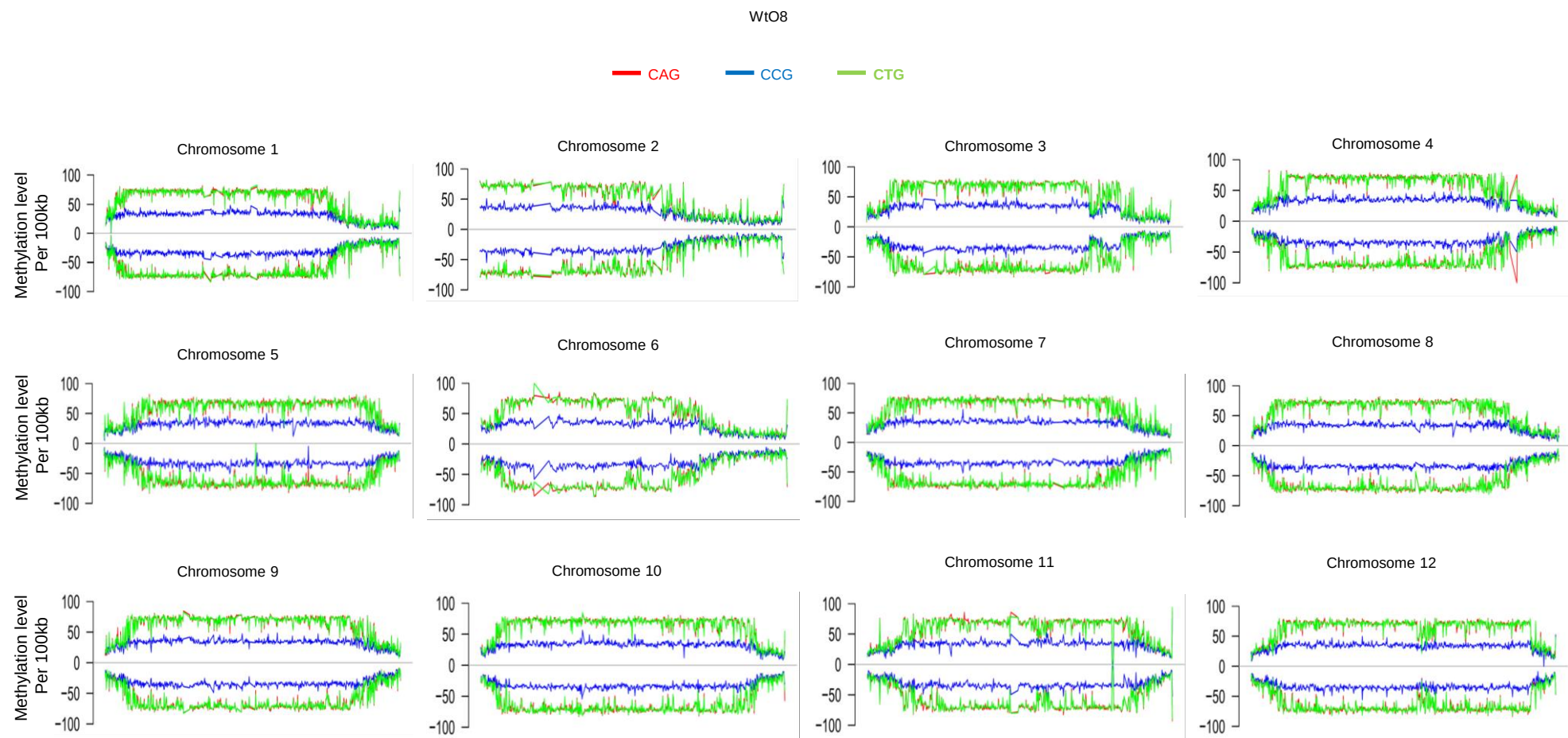


Figure S18. Chromosome distribution of methylcytosines in CHG subcontexts in wtO8

Red indicates CAG; blue indicates CCG; and green indicates CTG.

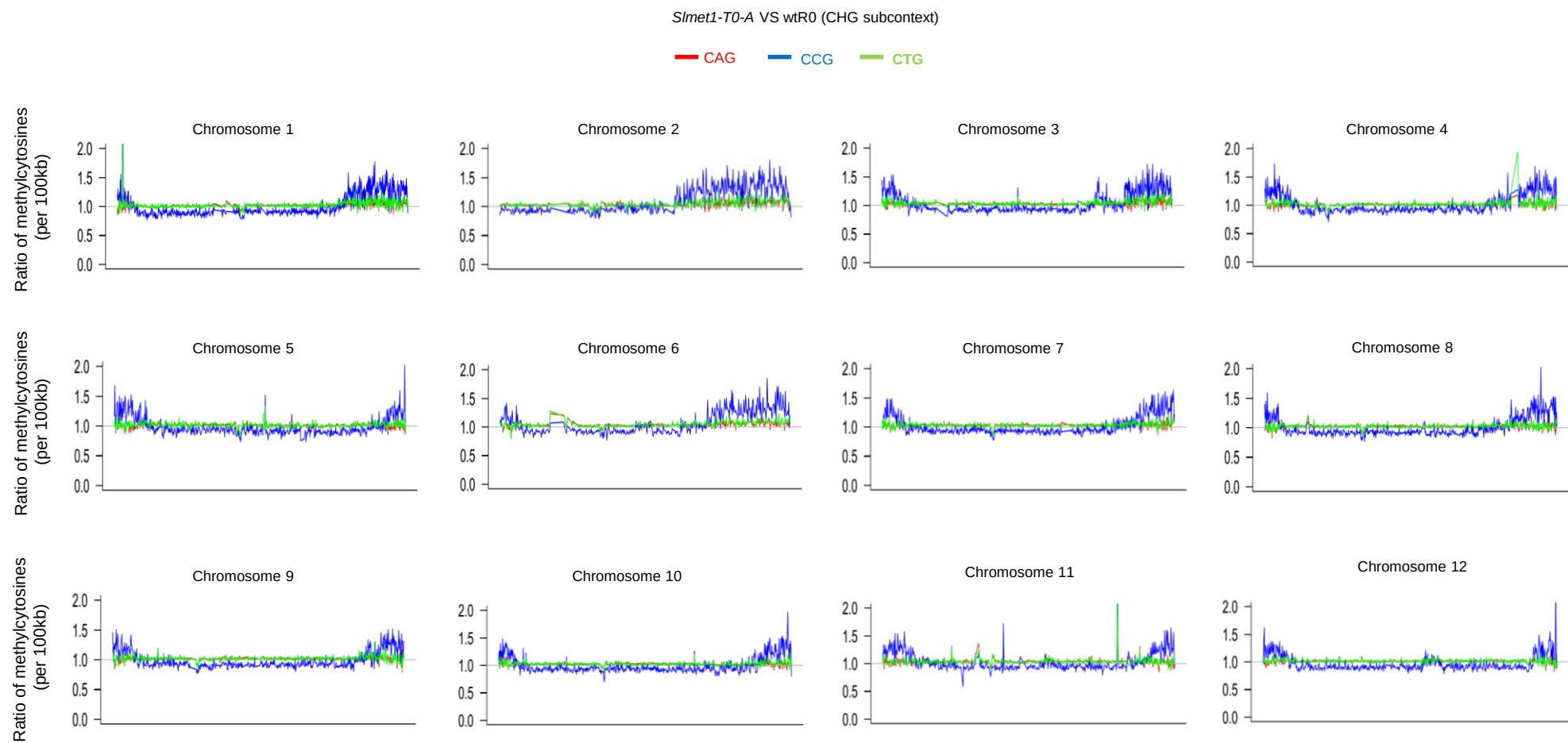


Figure S19. Comparison of methyl cytosine levels of CHG subcontexts in *slmet1-T0-A* versus wtR0

Methyl cytosines were counted per 100kb in all the 12 chromosomes. The horizontal axis indicates chromosomal positions, and the plotted line represents the ratios of methyl cytosine numbers in *slmet1-T0-A* versus wtR0.

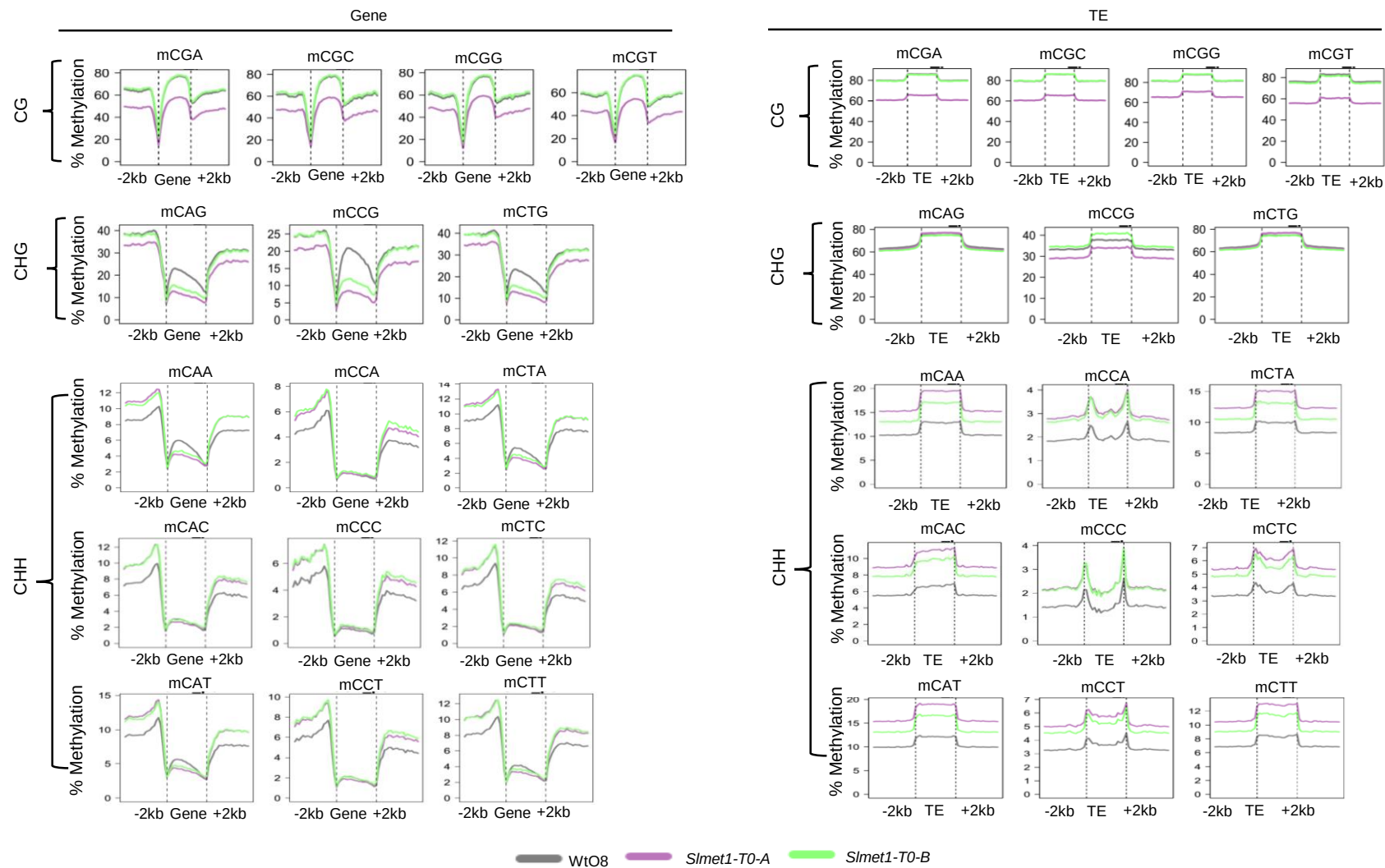


Figure S20. Genome-wide average methylation levels of subcontexts of CG, CHG, CHH and total C in gene regions and TE regions, each with their contiguous 2kb upstream and downstream flank regions in wtO8, *slmet1-T0-A* and *slmet1-T0-B*

Data of wtO8, *slmet1-T0-A*, and *slmet1-T0-B* are presented in gray, purple, and green colors, respectively.

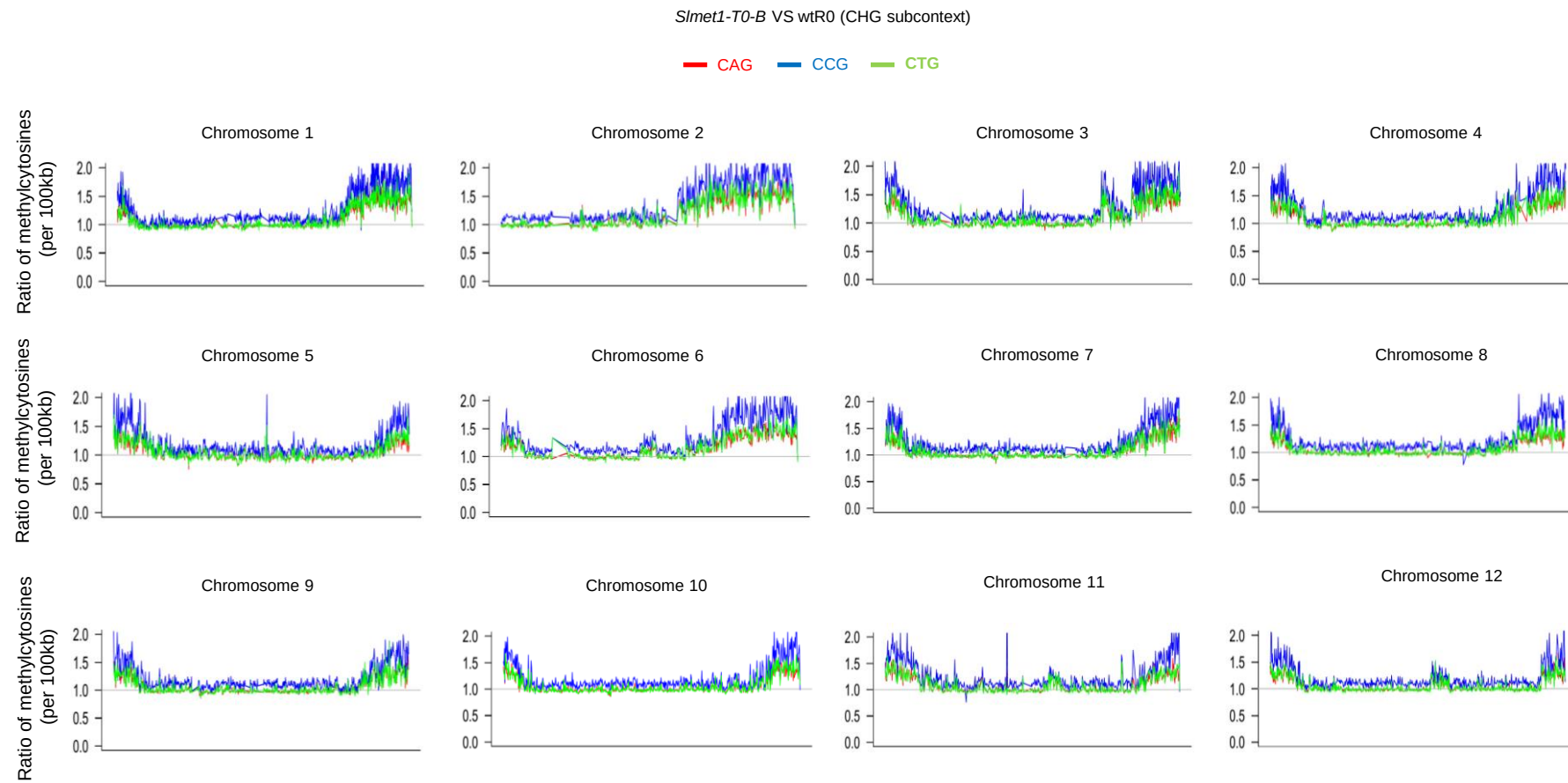


Figure S21. Comparison of methyl cytosine levels of CHG subcontexts in *slmet1-T0-B* versus wtR0

Methyl cytosines were counted per 100kb in all the 12 chromosomes. The horizontal axis indicates chromosomal positions, and the plotted line represents the ratios of methyl cytosine numbers in *slmet1-T0-B* versus wtR0.

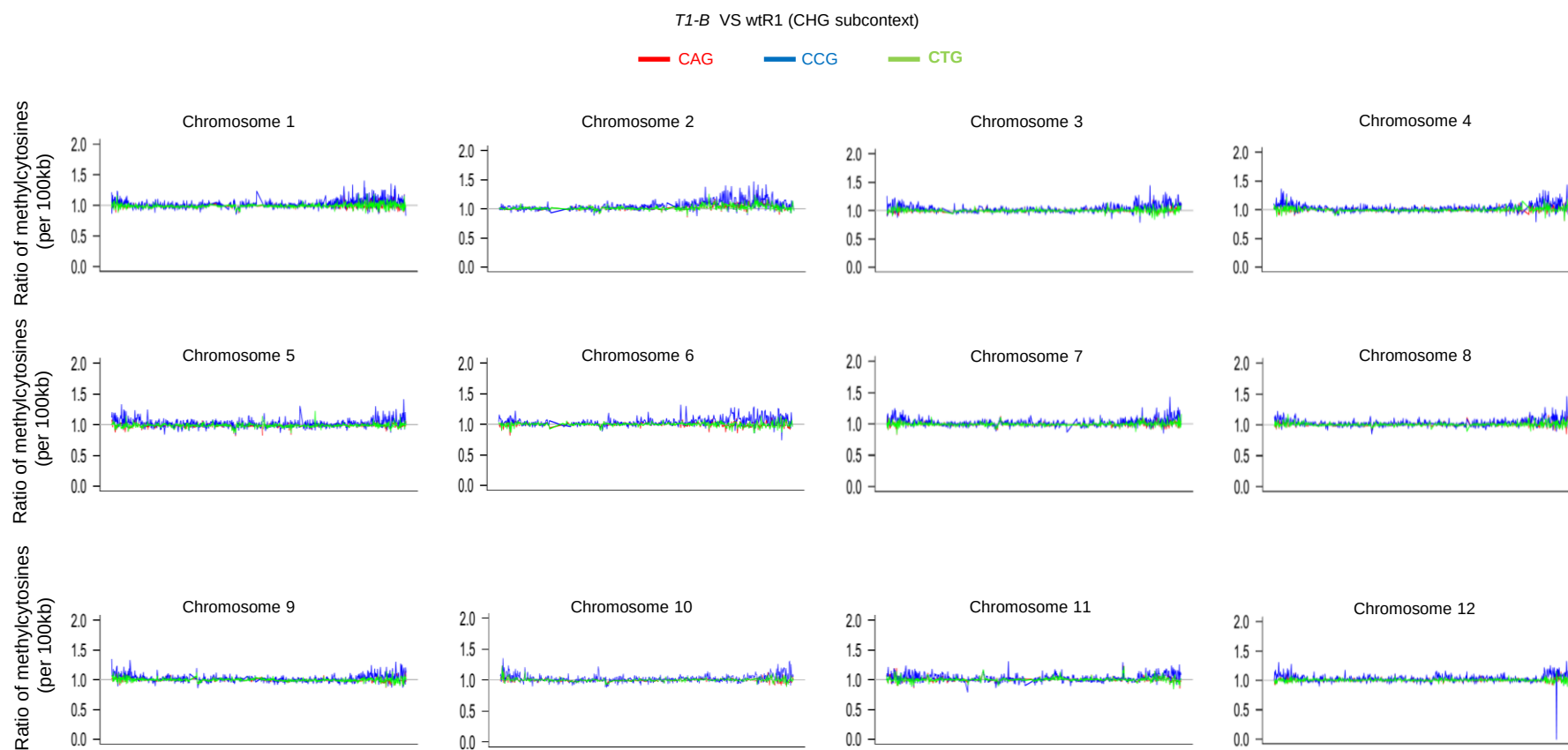


Figure S22. Comparison of methyl cytosine levels of CHG subcontexts in *T1-B* versus wtR1

Methyl cytosines were counted per 100kb in all the 12 chromosomes. The horizontal axis indicates chromosomal positions, and the plotted line represents the ratios of methyl cytosine numbers in *T1-B* versus wtR1.