

Supplementary Figures

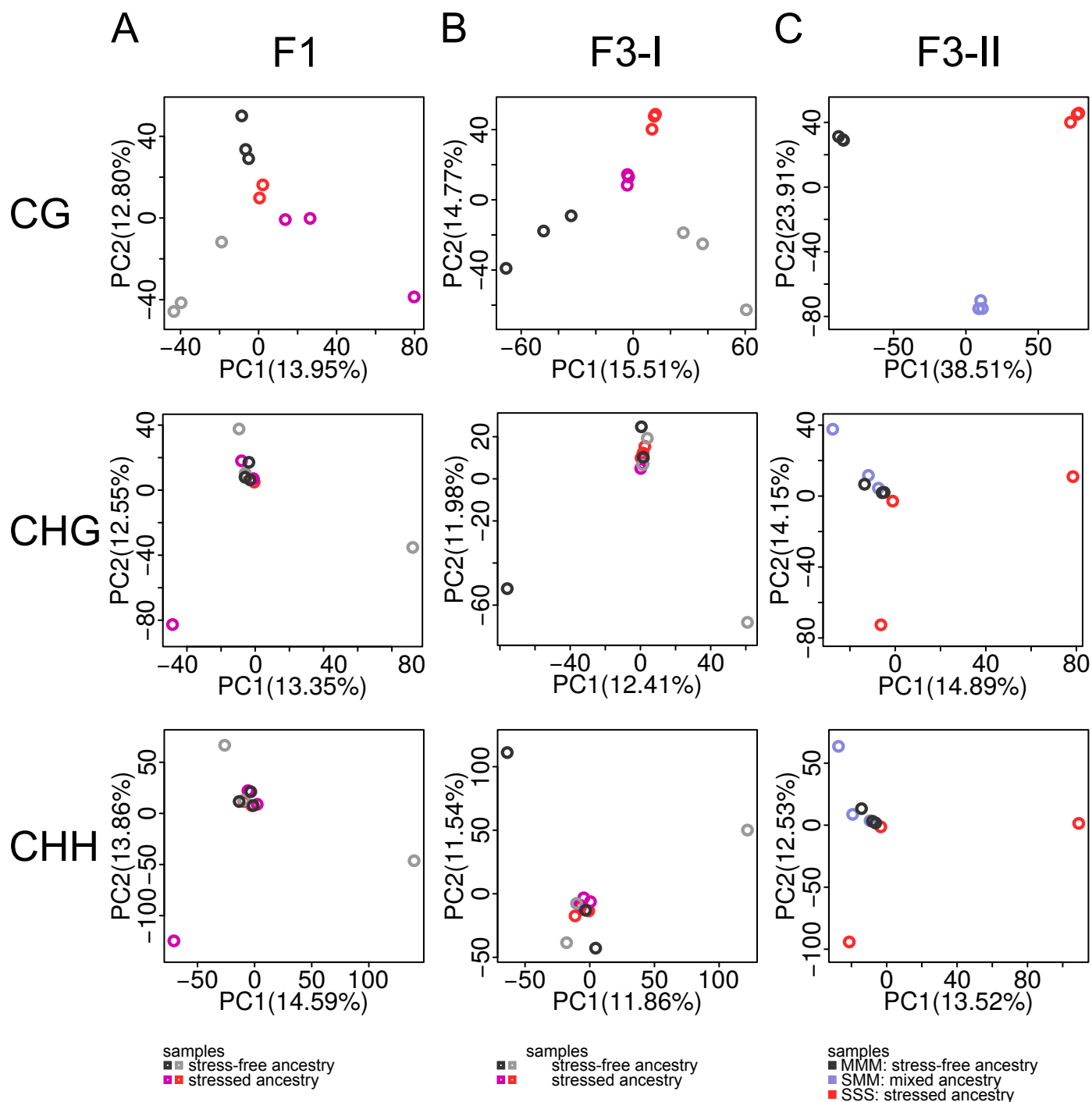
The relationship between transgenerational acquired resistance and global DNA methylation in Arabidopsis

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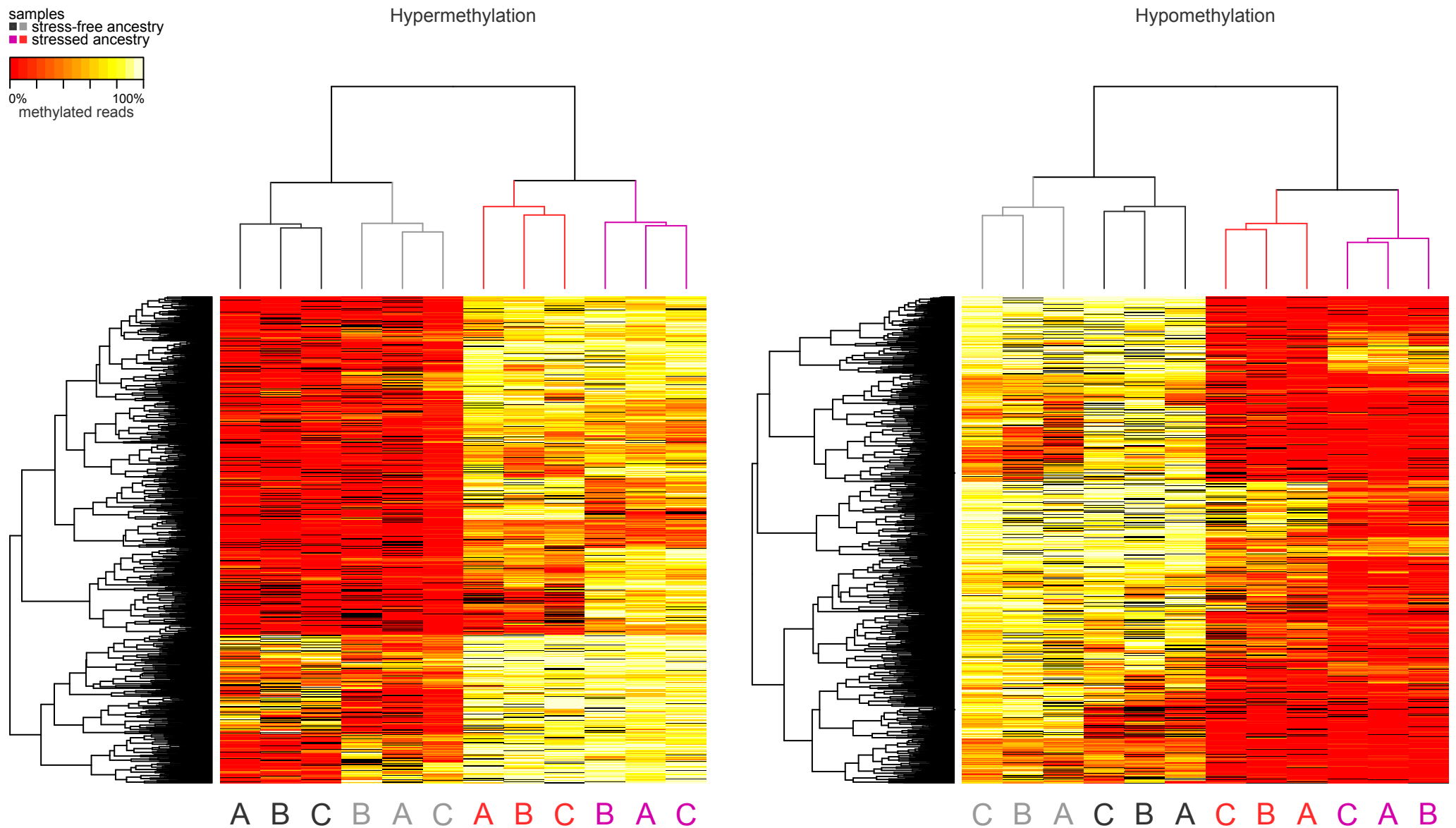
¹ Equal contribution

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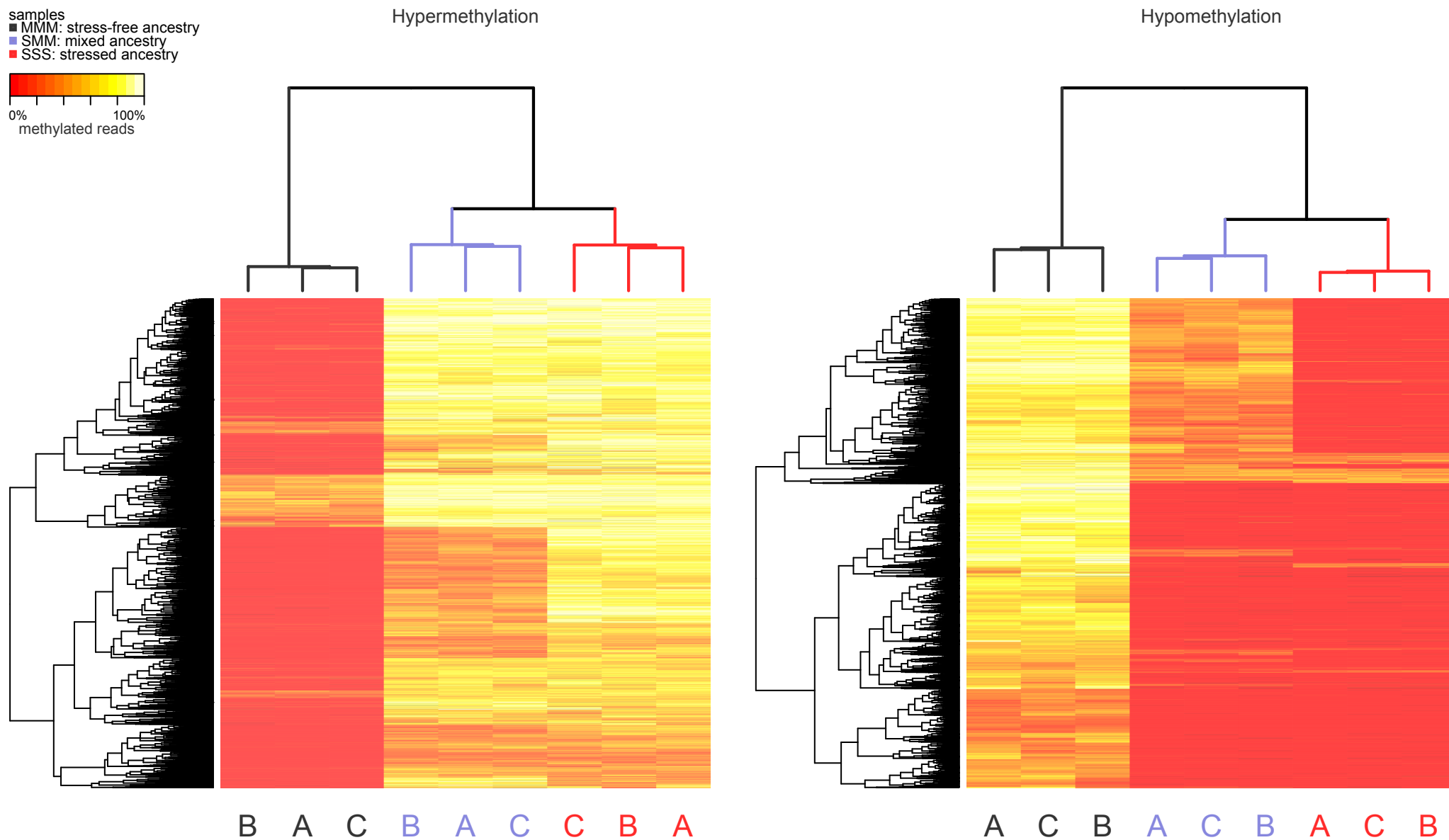
Supplementary Figure 1: Principle component analysis (PCA) of CG, CHG and CHH methylation patterns in all each experiment.

Colours indicate different lines, corresponding to the colour codes shown in the main figures.

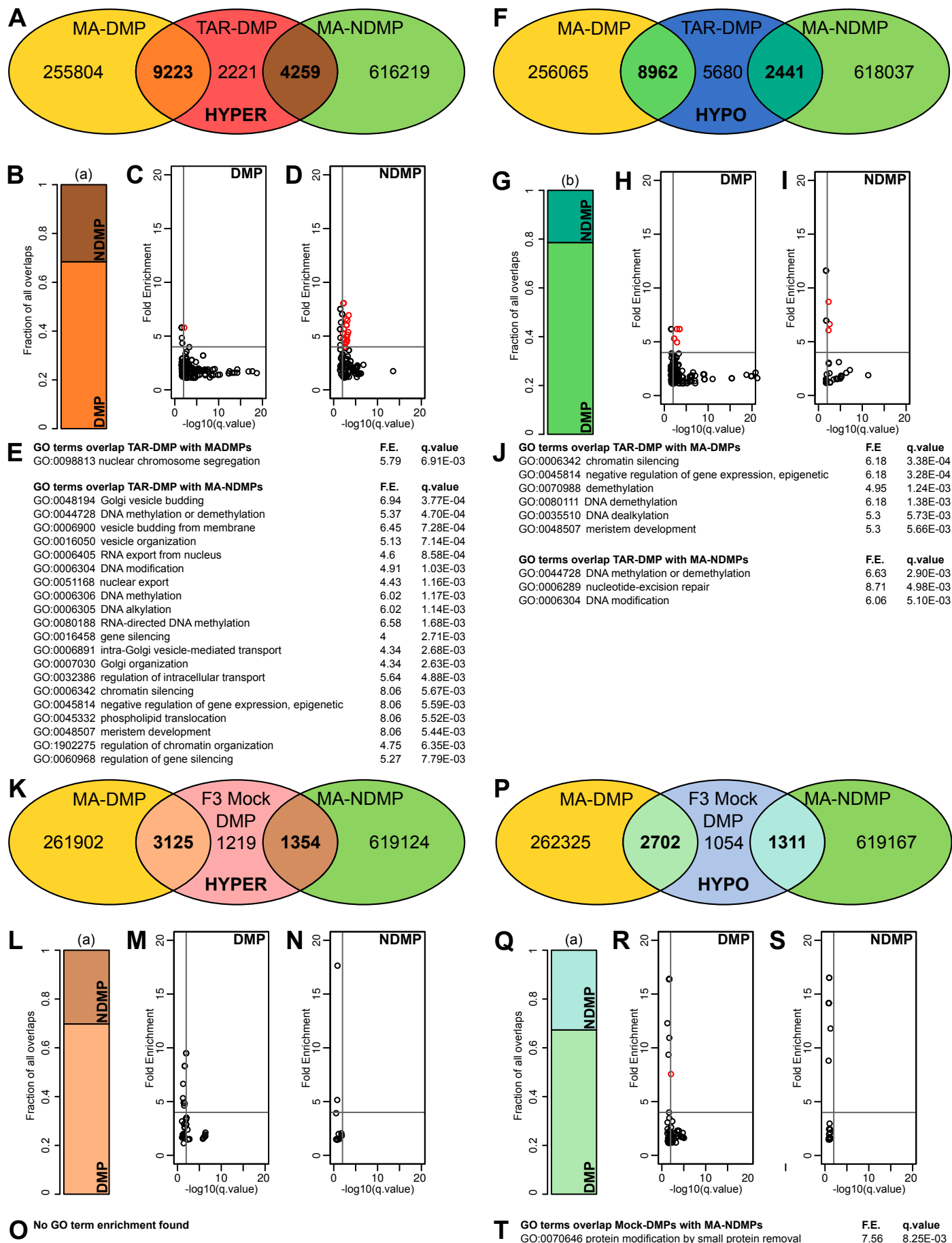


Supplementary Figure 2: Methylation levels at differentially methylated CG positions between *Pst*- and mock-treated F3 progenies (first F3 experiment).

Heatmap values represent percentages of methylated reads at 2,941 CG positions that are differentially methylated in *Pst*-exposed lines relative to mock-treated control lines of the first F3 experiment (1,509 hyper-methylated, 1,432 hypo-methylated). Values were clustered by DMP and sample (Pearson correlation, Ward). Letters at the bottom indicate replicate population samples within lines, whose colours match the progeny annotations in Fig. 2A.

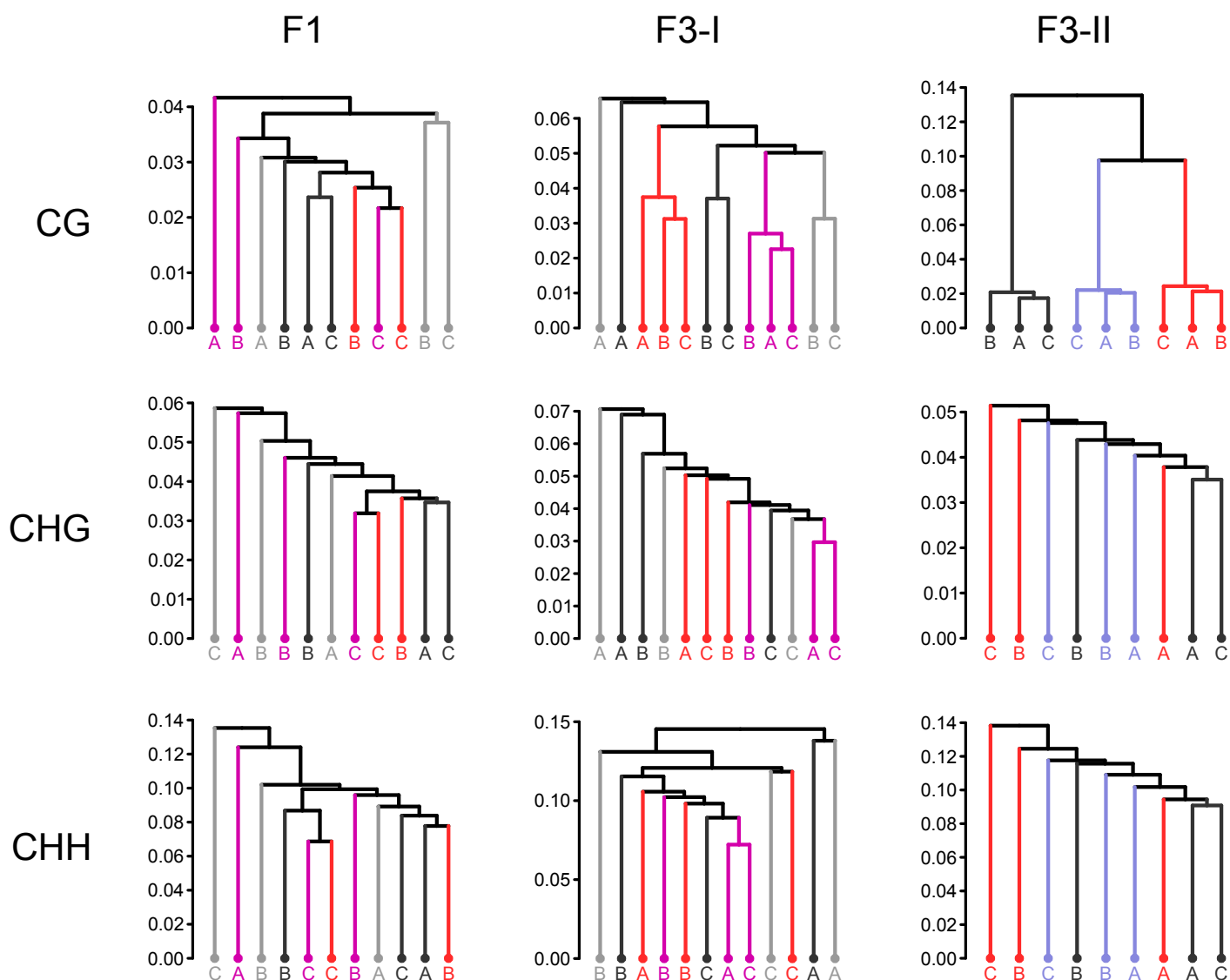


Supplementary Figure 3: Methylation levels of differentially methylated CG positions in SMM and SSS plants relative to MMM plants (second F3 experiment). Heatmap values represent percentages of methylated reads at 32,786 CG positions that are differentially methylated in both the SMM and SSS lines relative to MMM plants. Values were clustered by DMP and sample (Pearson correlation, Ward). Letters at the bottom indicate replicate population samples within lines, whose colours match the progeny annotations in Fig. 3A.



Supplementary Figure 5: Overlap between DMPs from the second F3 experiment and previously reported labile (MA-DMP) or stable (MA-NDMP) cytosine positions between mutation accumulation lines²⁹.

A-E: overlap with hyper-methylated TAR-DMPs, **F-J:** overlap with hypo-methylated TAR-DMPs, **K-O:** overlap with spontaneous hyper-methylated DMPs between mock-inoculated lines (F3 Mock-DMPs), **P-T:** overlap with spontaneous hypo-methylated DMPs between mock-inoculated lines (F3 Mock-DMPs). Venn diagrams show numbers of positions overlapping with MA-DMPs or MA-NDMPs (**A,F,K,P**). Stacked bar graphs show relative distributions of DMPs between MA-DMPs and MA-NDMPs (**B,G,L,Q**). Different letters above the stacked bars indicate statistically different distributions (χ^2 , p value < $1e-10$). **C,D,H,I,M,N,R,S:** Enrichment of gene ontology (GO) terms of genes carrying TAR- or Mock-DMPs that overlap with MA-DMP or MA-NDMPs (p value < $1e-3$). Graphs plot enrichment value against statistical significance. Terms with ≥ 4 -fold enrichment and q -value < 0.01 are shown in red and are further specified in panels **E,J,Q,T**. F.E.: fold enrichment.

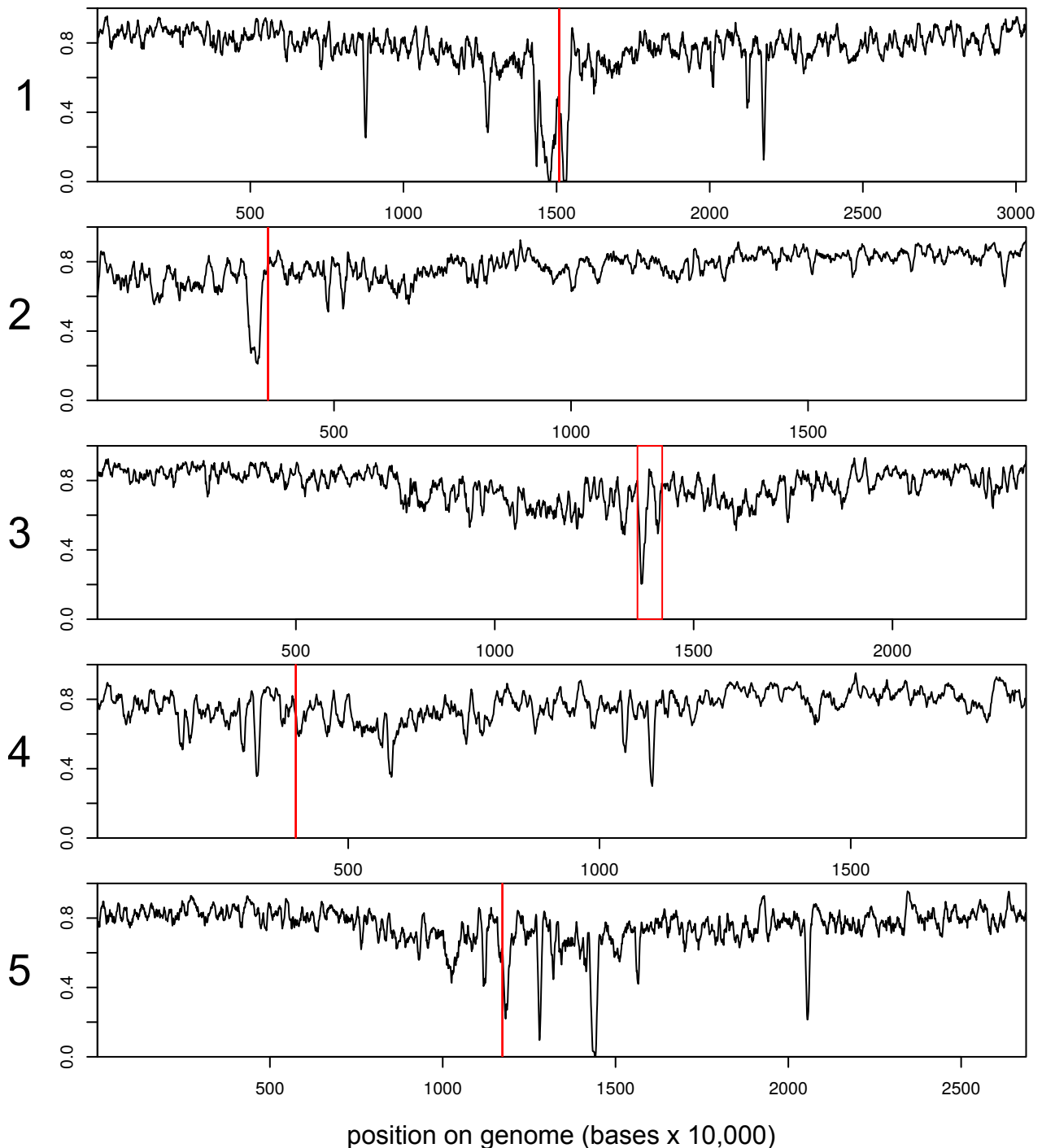


Supplementary Figure 6: Hierarchical clustering (Pearson correlation, Ward) of regional profiles of cytosine methylation.

Regional correlations were based on 100-bp-window averages (step size 50 bp) at CG, CHG and CHH sequence contexts for all lines in each of the experiments. Lines are colour-coded to match the line annotations in the corresponding pedigrees, included in the main Figures. Letters indicate replicate population samples within a line.

Fraction of bases with >Q25 coverage

per chromosome; averaged over 100,000 bp windows, 10,000 bp step size



Supplementary Figure 7: Global coverage of bisulfite-sequencing reads for all five chromosomes of Arabidopsis.

Shown are fractions of bases with greater than first quartile coverage from the first replicate sample of the MMM line (second F3 experiment). Fractions are calculated over a 100,000 base pair region, with a step size of 10,000 base pairs. Red lines/boxes indicate centromere annotations.