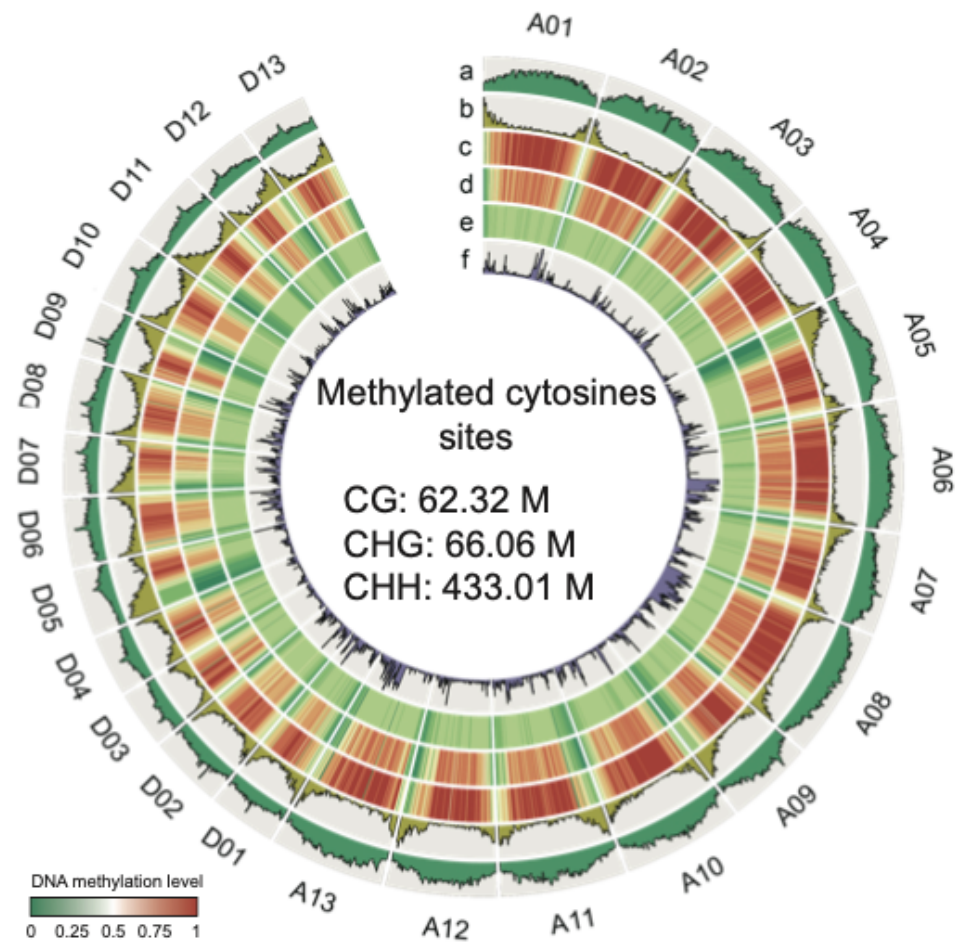




Supplementary information, Fig. S2. Circos plot showing single methylation polymorphisms in our cotton population. The outer track represents the 26 chromosomes in the *G. hirsutum* genome (A01-A13 of the A subgenome and D01-D13 of the D subgenome). Circles from a to f respectively represent (a) TE content; (b) number of protein coding genes (PCGs). (c) weighted DNA methylation levels at CG, (d) CHG, and (e) CHH sites; and the (f) distribution of SNPs. Data for each chromosome were analyzed in 1-Mb windows. Weighted methylation levels using running medians in 1-Mb windows are shown from low (0, green) to high (1, blue).