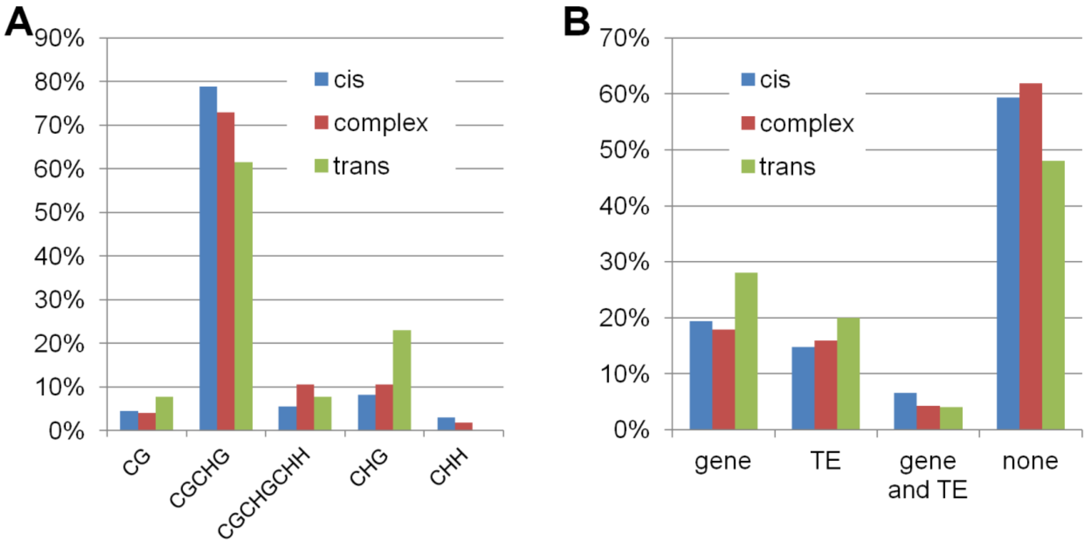

Figure S5 Association between DMR inheritance patterns and DMR types (A) or different genomic features (B). (A) Percentage of DMRs with different methylation contexts for each DMR inheritance pattern. We classified DMRs with Whole-Genome Bisulfite Sequencing data into 5 context categories: CG, CHG, CHH, CGCHG and CGCHGCHH based on the methylation difference between B73 and Mo17. For CG and CHG, we used a cutoff of 20% difference; and for CHH, we used a cutoff of 5% difference. DMRs that have methylation difference greater than the cutoff of the respective sequence context (i.e., CG, CHG, and CHH) are defined as DMRs of that sequence context. For example, CG-DMRs showed more than 20% methylation difference in CG, less than 20% in CHG and less than 5% in CHH. (B) Percentage of DMRs overlapping different genomic features for each DMR inheritance pattern. The DMR position was compared with the gene annotation (version: 5b) or transposable element (TE) annotation (version: 5a_MTEC). DMRs that don't overlap any of these annotated features were classified into the "none" group.