

Figure S1. Sample sequencing depth distribution. a: JD; b: JZ; c: SD; d: SZ.

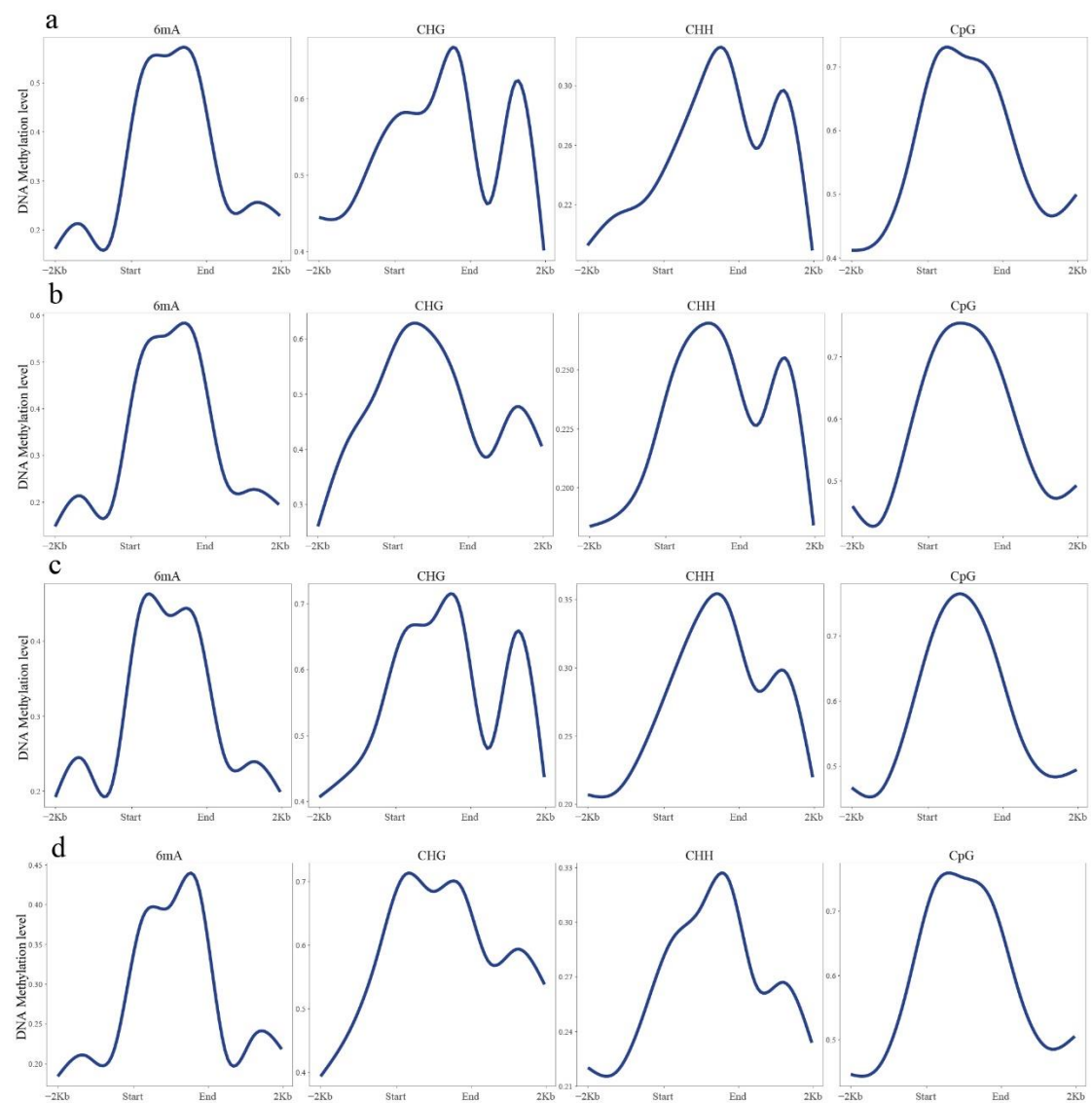


Figure S2. Repeat region methylation levels for each sample. a: JD; b: JZ; c: SD; d: SZ.

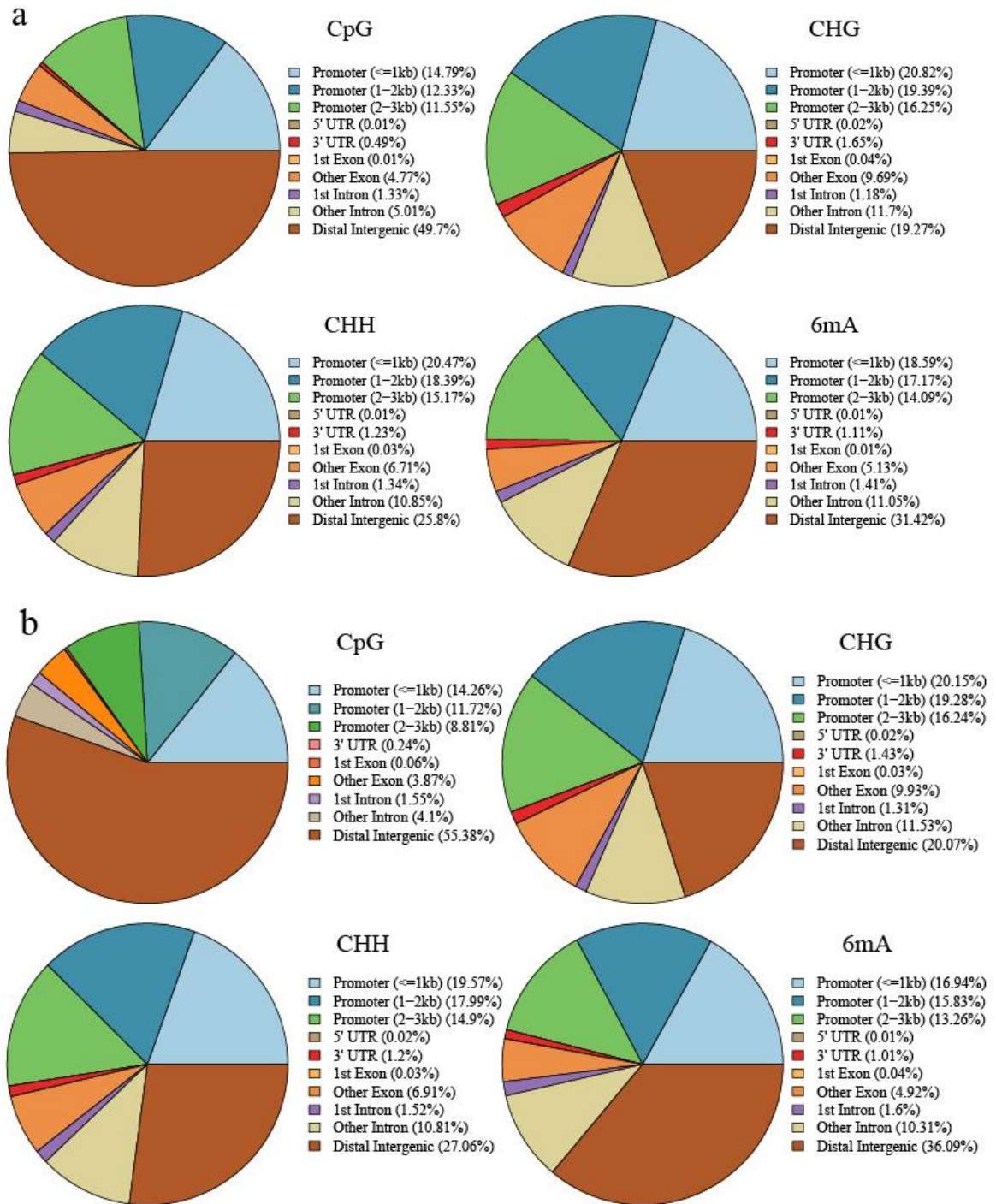


Figure S3 (A). DML gene region annotation classification. a: JZ_vs_JD; b: SZ_vs_SD.

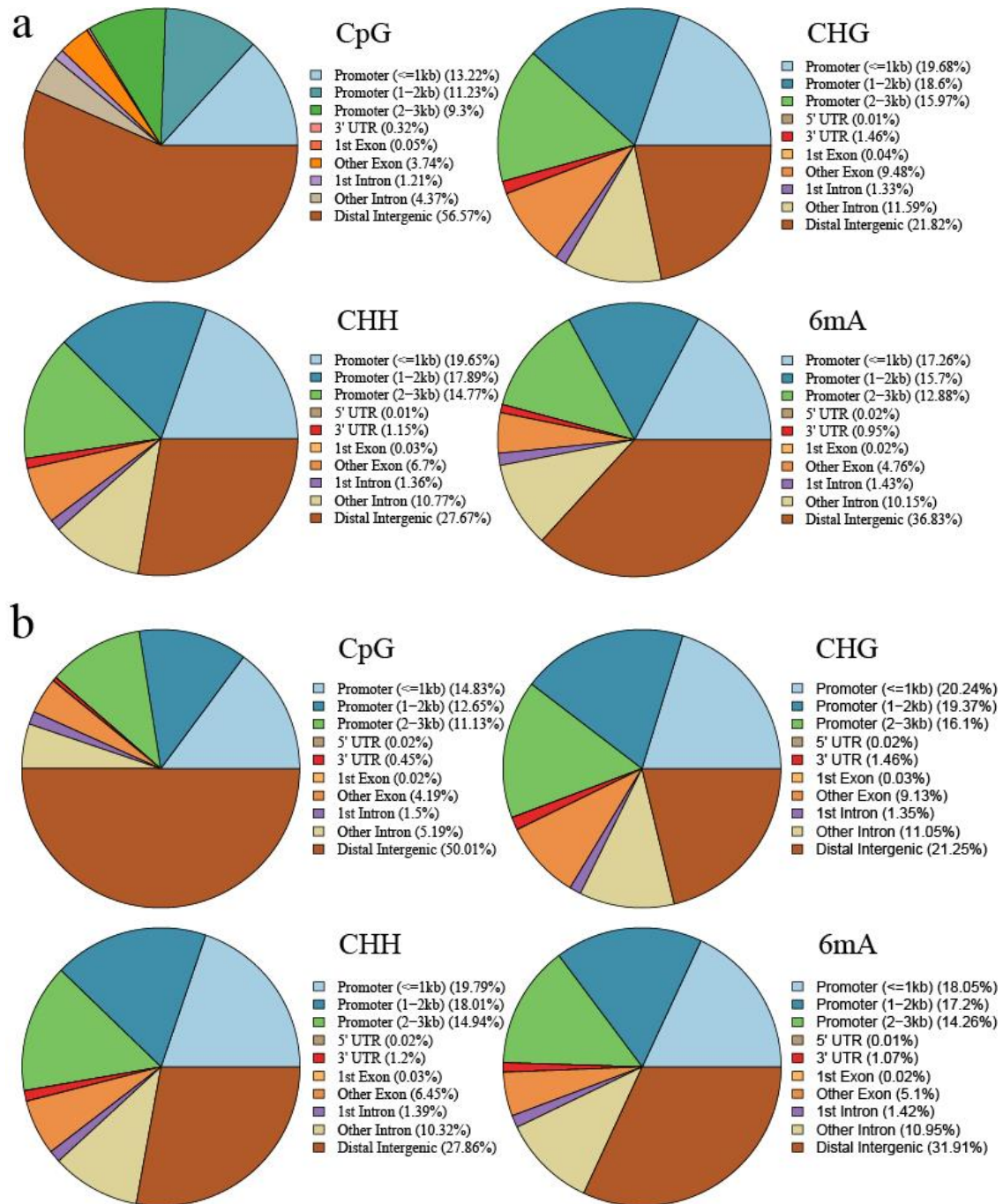


Figure S3 (B). DML gene region annotation classification. a: JD_vs_SD; b: JZ_vs_SZ.

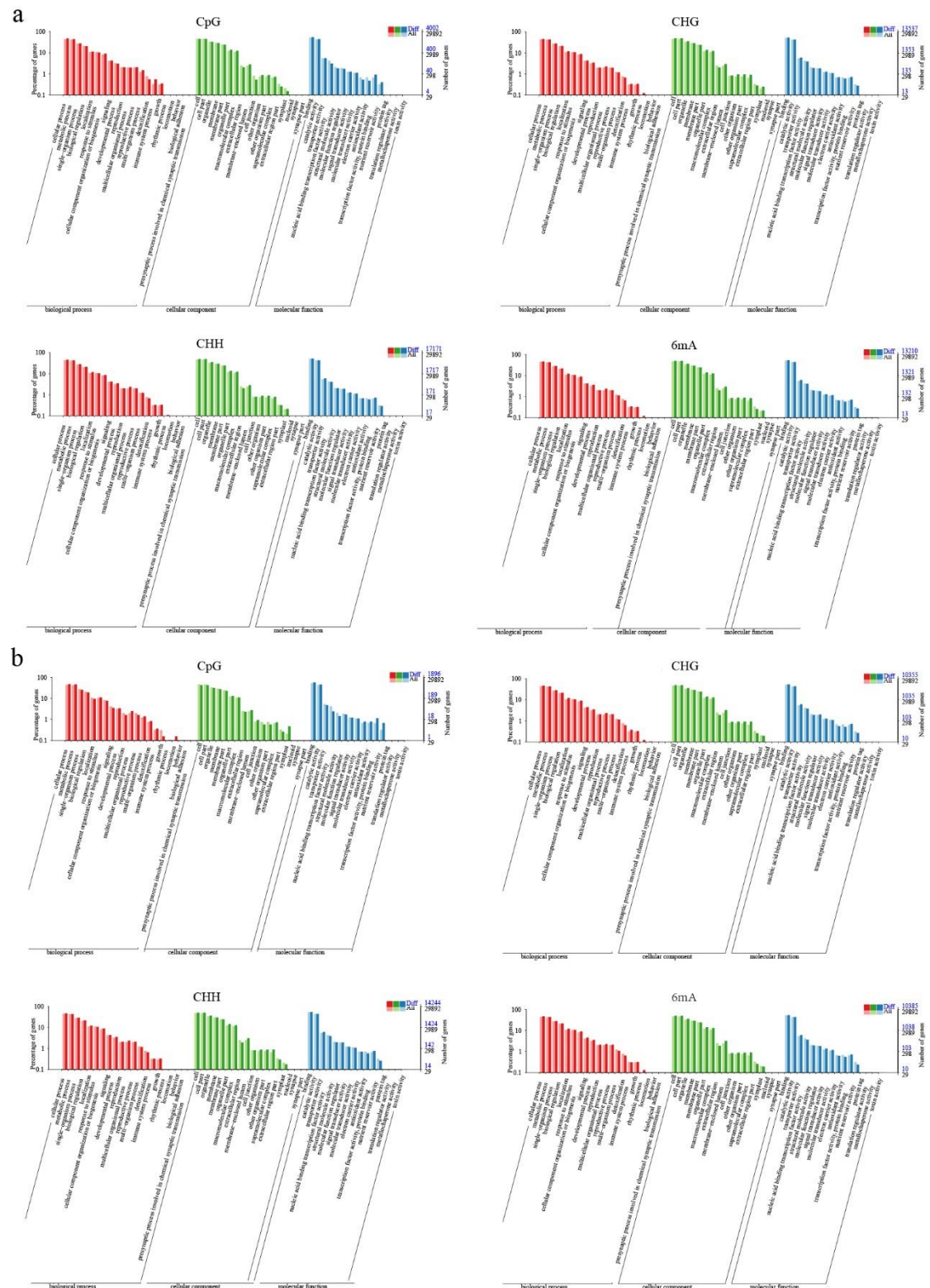


Figure S4. GO enrichment map of DMR-associated genes. a: JZ_vs_JD; b: SZ_vs_SD.

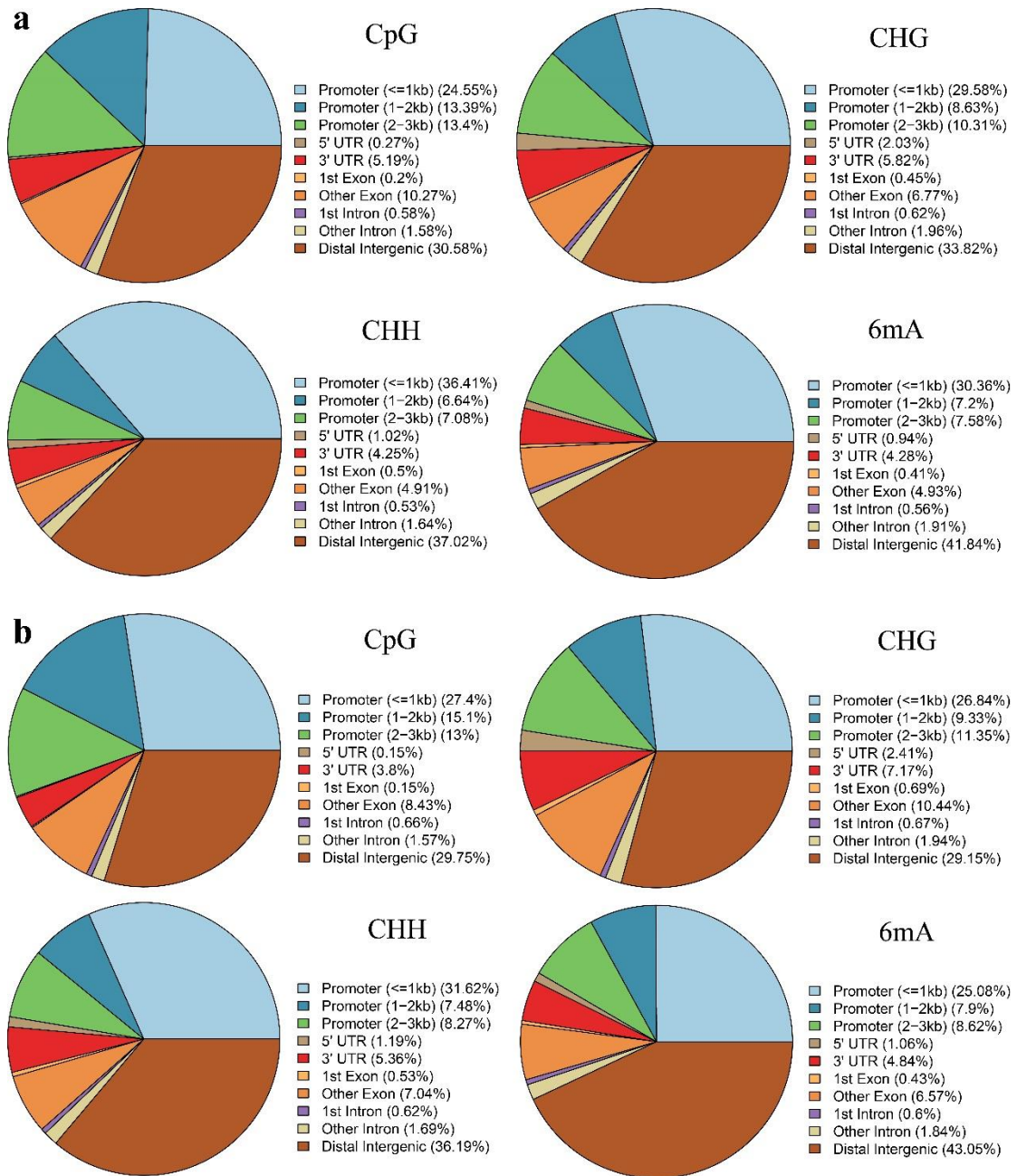


Figure S5 (A). DMR gene region annotation classification. a: JZ_vs_JD; b: SZ_vs_SD.

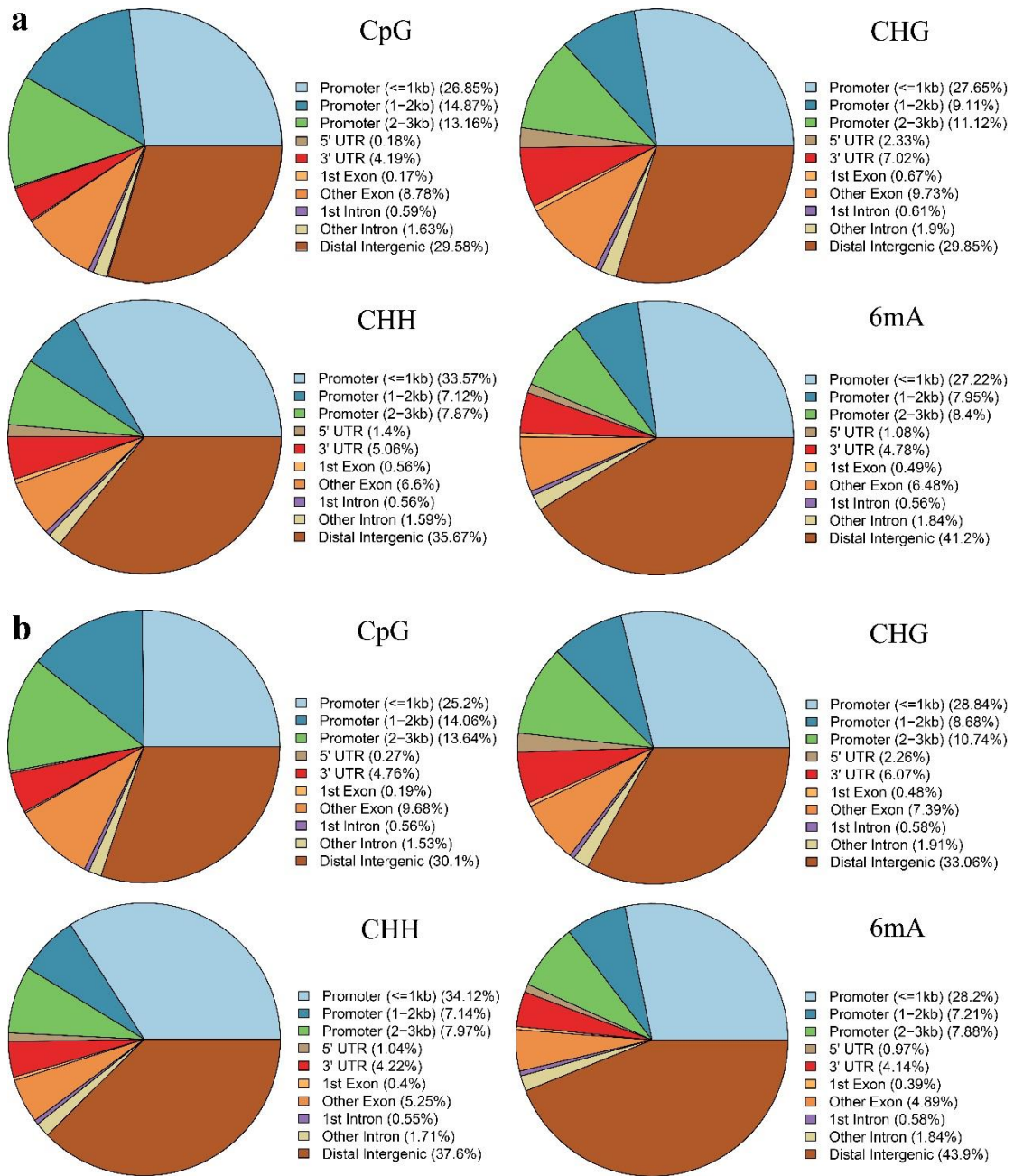


Figure S5 (B). DMR gene region annotation classification. a: JD_vs_SD; b: JZ_vs_SZ.