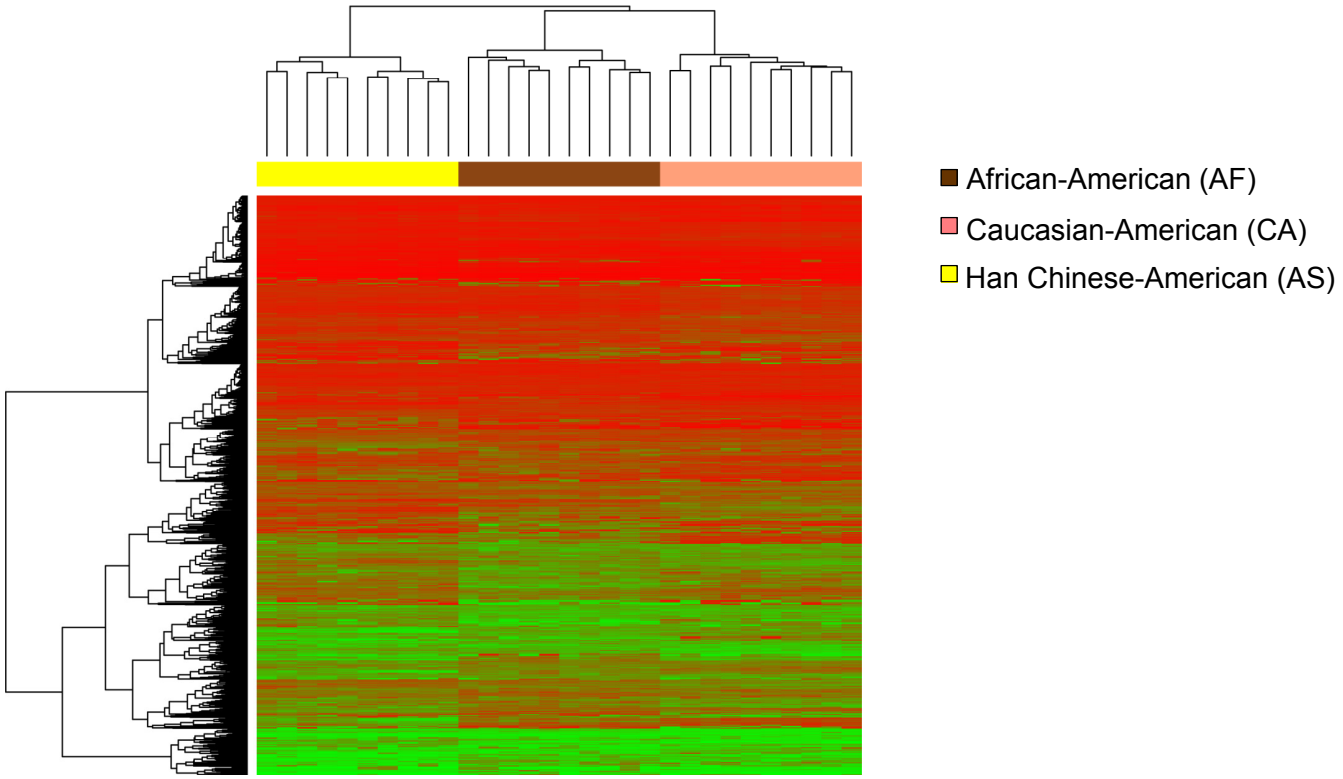
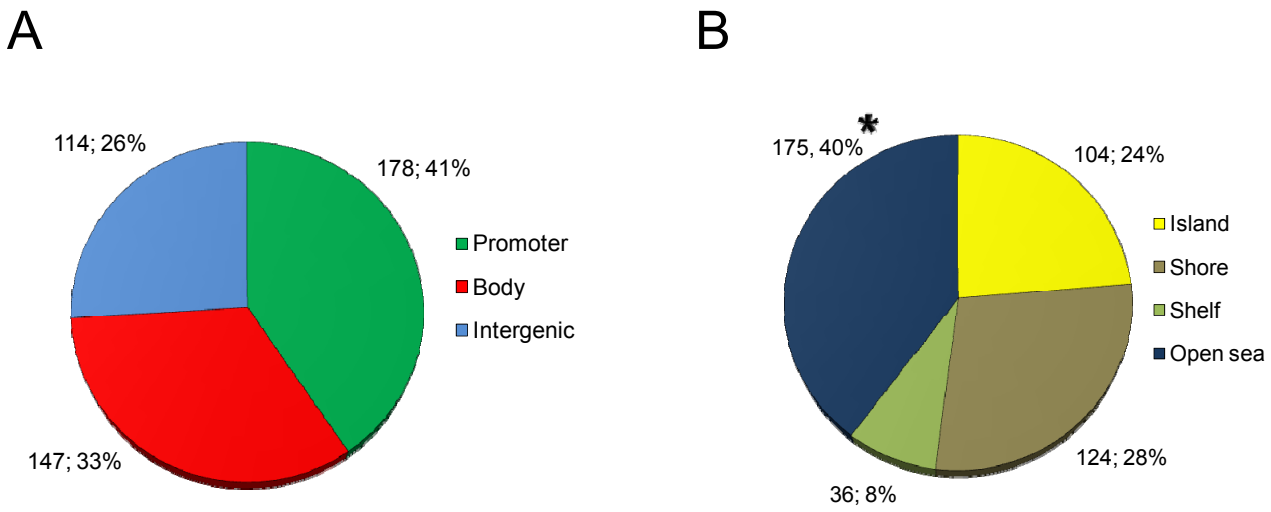
Figure S1

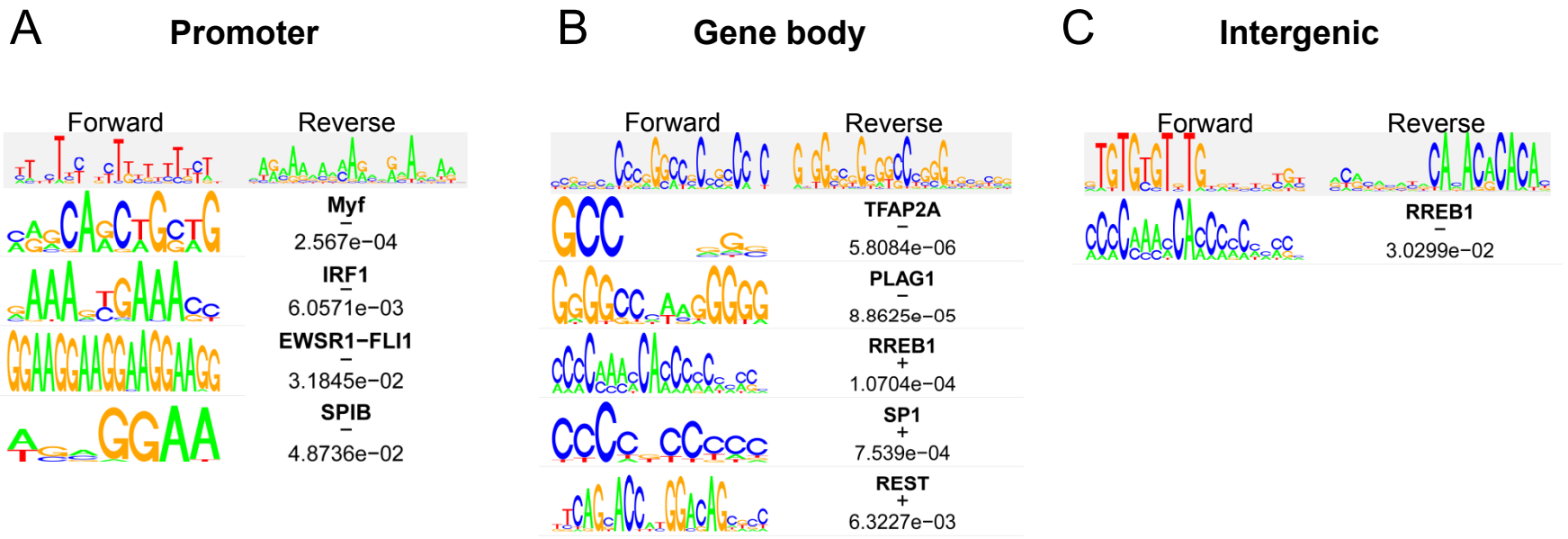


Supplemental Figure 1. Hierarchical cluster of naive blood samples (n=30) using DNA methylation levels of 1373 pop-CpG sites differentially methylated (delta mean β-values ≥ 0.12; ANOVA, FDR < 0.01) between African (AF, brown), Asian (AS, yellow) and Caucasian (CA, pink) populations in LCLs. Displayed are absolute DNA methylation levels (low: green; high: red) and samples were clustered using the complete agglomeration method for Manhattan distances.

Figure S2

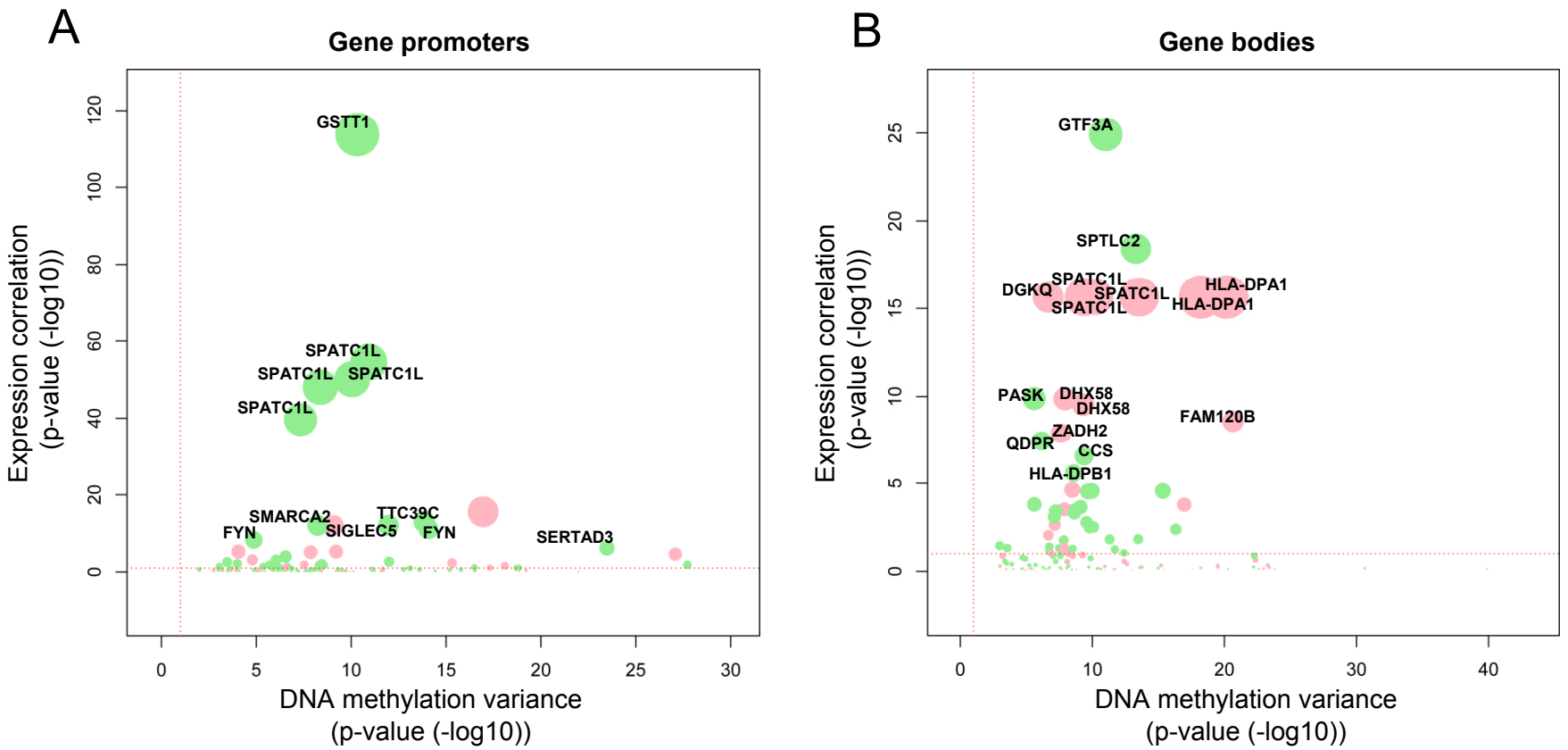


Supplemental Figure 2. Genomic distribution of the 439 pop-CpG sites. CpG sites were mapped to the human genome and assigned to different genetic features (A) and regional CpG density properties (B). Significant enriched features in regard to their representation on the DNA methylation array platform are indicated (*; Fisher's test; $p < 0.05$).



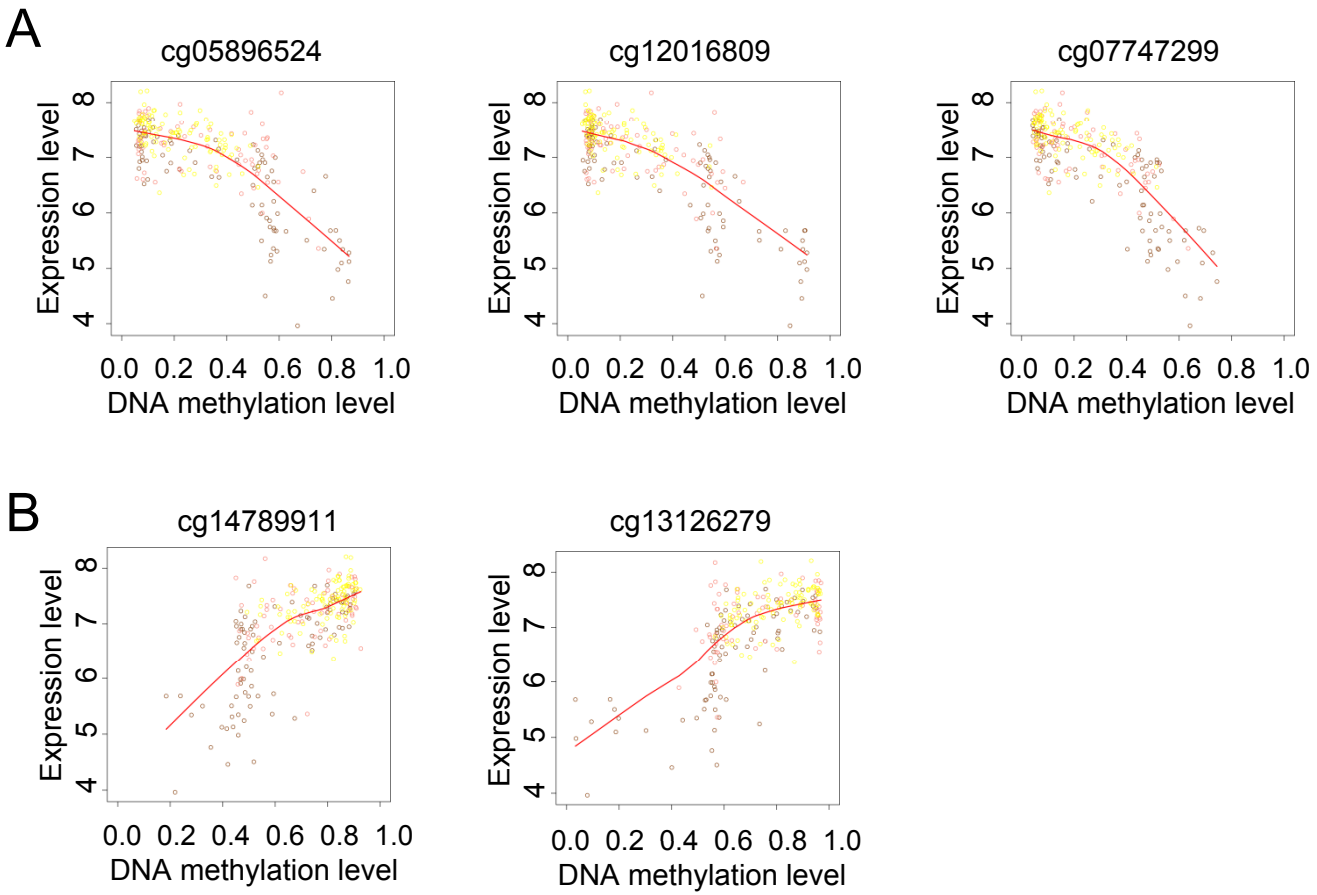
Supplemental Figure 3. Sequence motif enrichment analysis for pop-CpG sites in promoters (A), gene bodies (B) and intergenic loci (C*). De novo* sequence motifs (grey highlighted, e-value < 0.05) were identified using GADEM (Li, 2009). Associated transcription factor binding motifs were assigned using JASPAR. The consensus motif confidence is represented by letter size of the nucleotide bases (A,T,C,G). The strand (+/-) of the transcription factor motif in respect to the *de novo* motif is indicated.

Figure S4



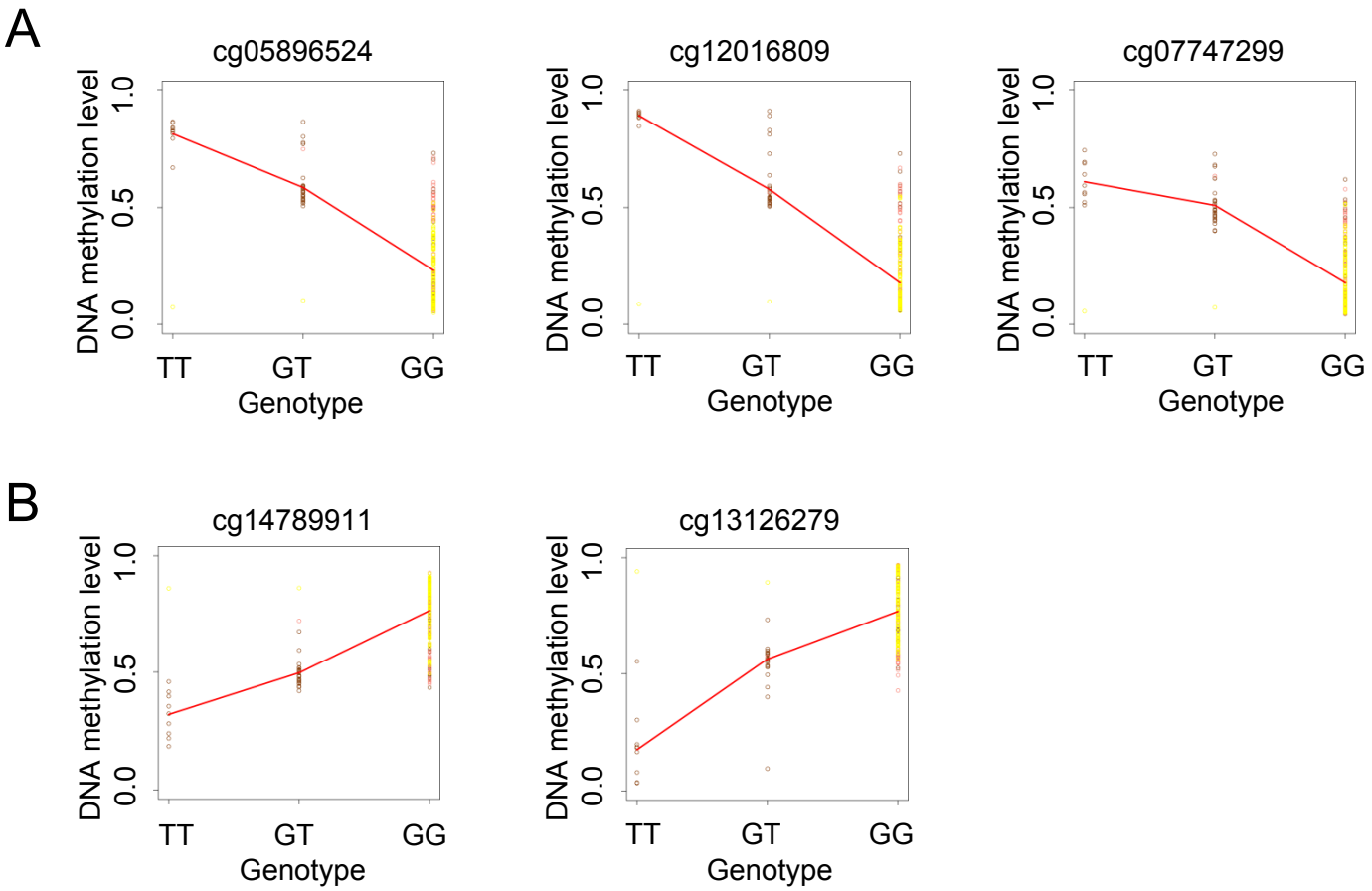
Supplemental Figure 4. Relationship between transcriptional activity and DNA methylation levels in pop-CpG related promoters (A) and gene bodies (B). Significant (red line; ANOVA test; FDR < 0.01) variation in CpG methylation (x-axis) was correlating significantly (red line; Pearson's correlation test; FDR < 0.01) to gene expression changes (y-axis). Positive (red) and negative (green) correlations are color-coded and the Pearson's coefficient (rho) is represented by circle size. Gene symbols for correlations $p < 1 \times 10^{-5}$ are indicated.

Figure S5



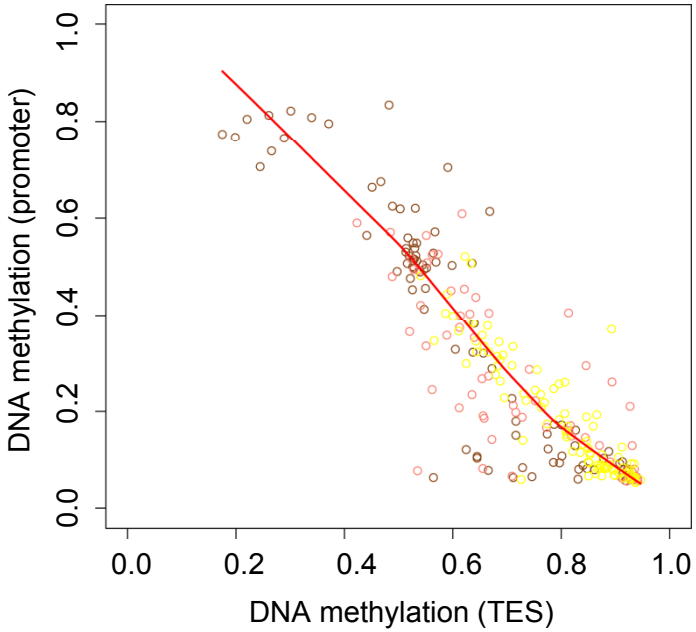
Supplemental Figure 5. DNA methylation of the *SPATC1L* promoter inversely correlates to gene expression. (A) pop-CpG sites differentially methylated in African-Americans correlate inverse with gene expression of *SPATC1L*. (B) pop-CpG sites flanking the transcription end sites reveal a positive correlation with gene expression of *SPATC1L* .

Figure S6



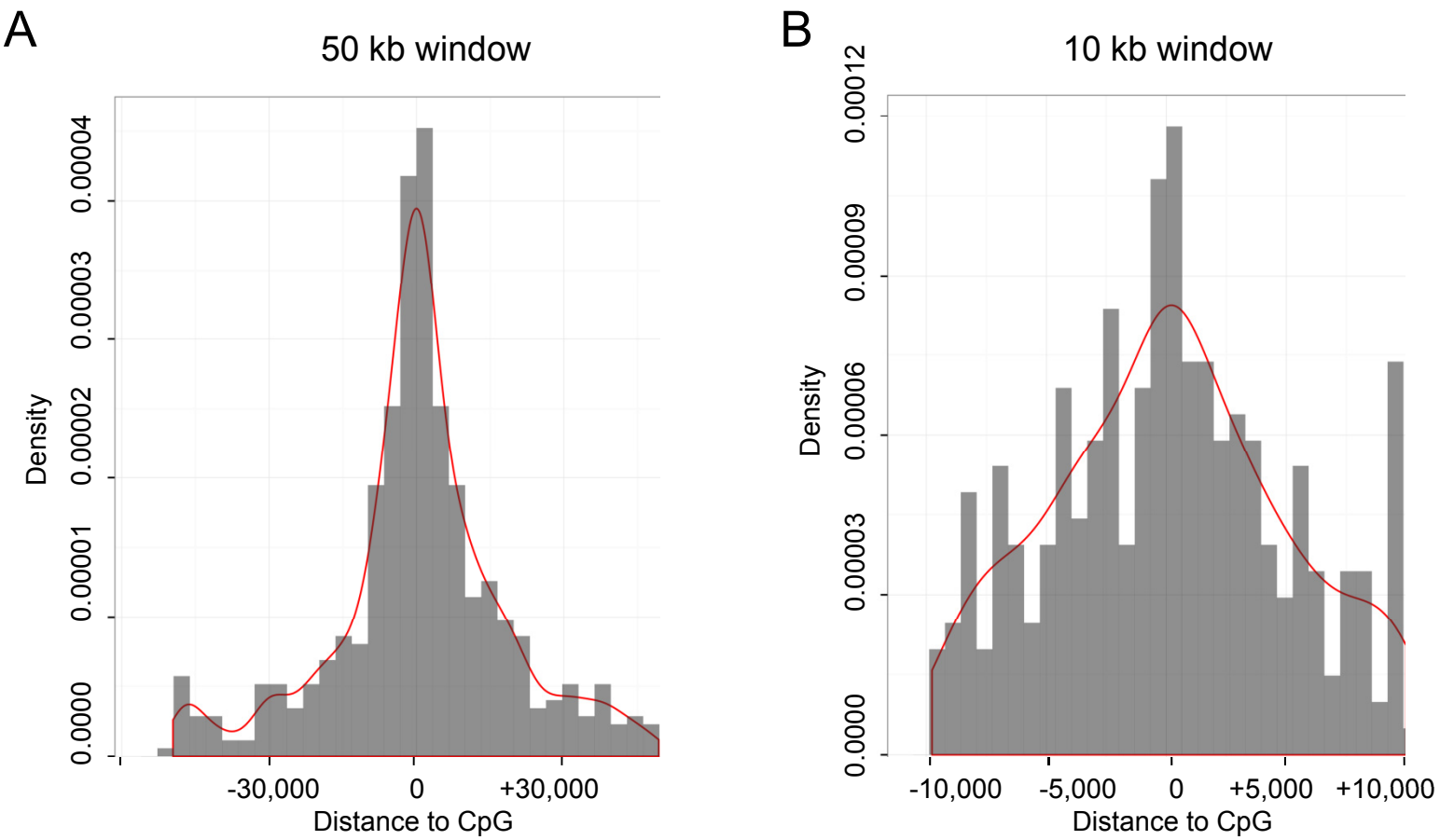
Supplemental Figure 6. DNA methylation of the *SPATC1L* promoter is directly related to the genetic background. *SPATC1L* promoter (A) and transcription end site (B) related pop-CpG sites with differential DNA methylated in African-Americans are closely associated to the genotype (rs8133082).

Figure S7



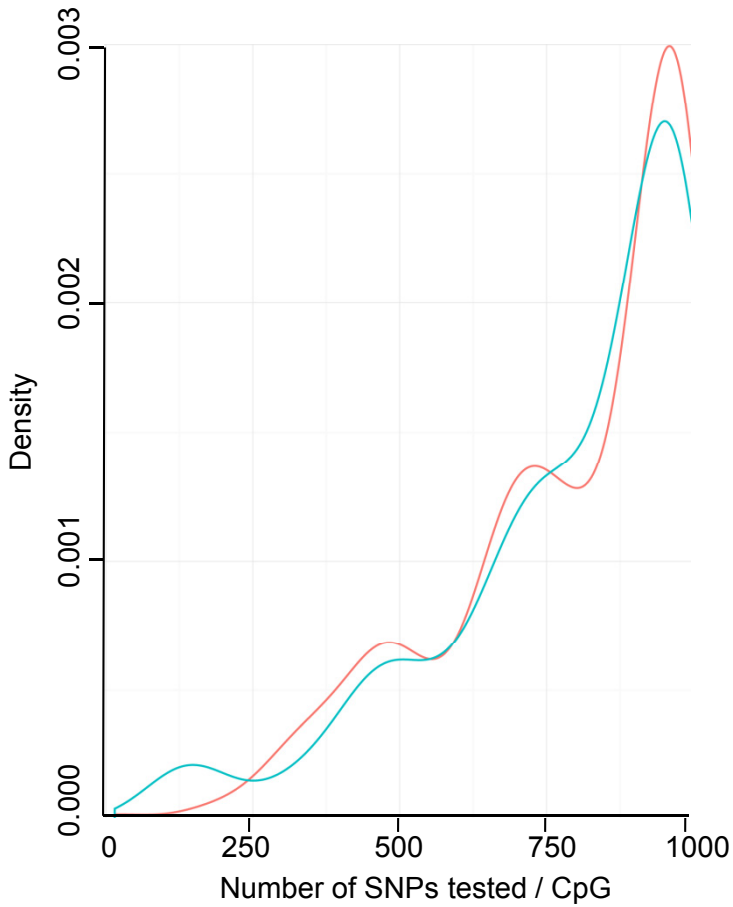
Supplemental Figure 7. DNA methylation level of pop-CpG sites at the promoter and transcription end site (TES) of *SPATC1L* are correlating inversely. Displayed are the mean DNA methylation values of the pop-CpG sites present in the promoter (n=4) or the transcription end site (TES; n=3) of African-American (brown), Han Chinese-American (yellow) and Caucasian-American (pink). Individuals with hypomethylated promoters revealed hypermethylation at the TES (Pearson's product-moment correlation, rho: 0.89).

Figure S8



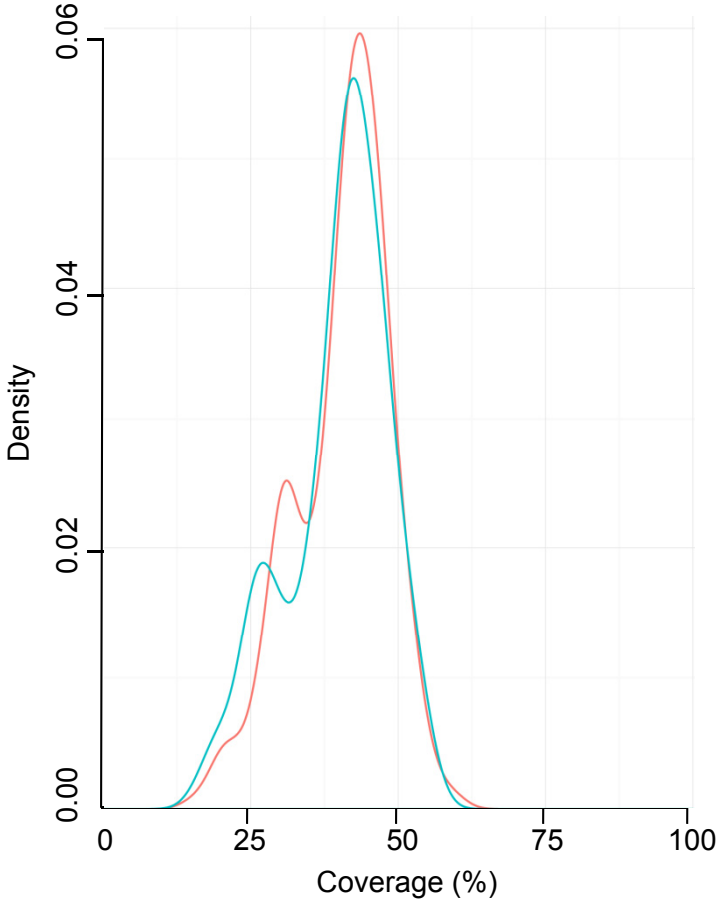
Supplemental Figure 8. Cis-acting SNPs reveal close proximity to their associated CpG sites. Distribution of SNPs relative to their associated CpG site displayed in a 50 kb (A) and a 10 kb (B) window flanking the CpG.

Figure S9



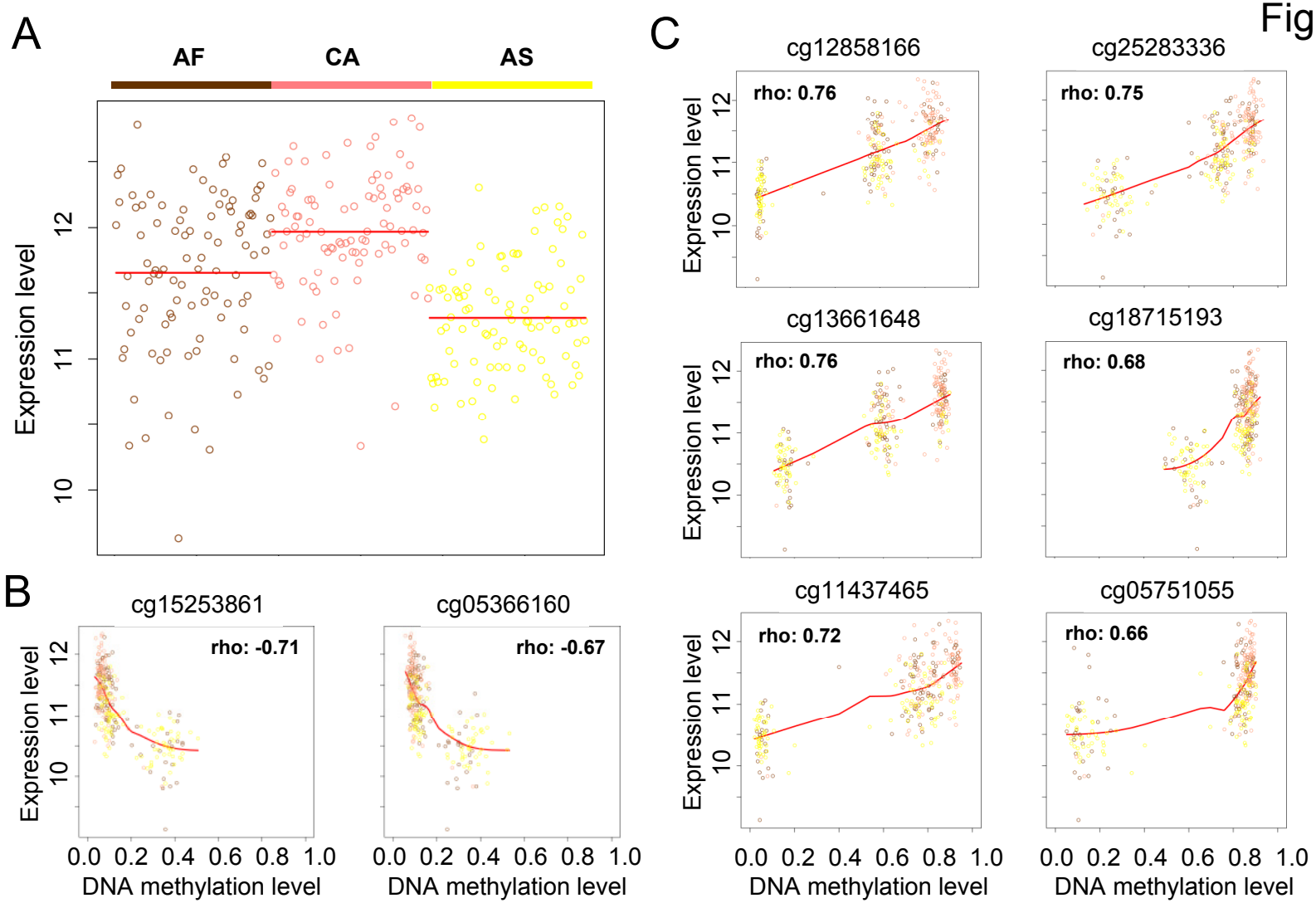
Supplemental Figure 9. Frequency of analyzed SNPs flanking pop-CpGs with (red line) or without (blue line) association to the underlying genetic background.

Figure S10



Supplemental Figure 10. Presence of repetitive elements (SINE, LINE, LTR) in the surrounding regions flanking pop-CpGs with (red line) or without (blue line) association to the underlying genetic background. Results are displayed as total coverage in 1 Mbp flanking a pop-CpG.

Figure S11



Supplemental Figure 11. *HLA-DPA1* expression is lower is populations with higher risk of HBV infection and associated to differences in DNA methylation. (A) Expression levels of *HLA-DPA1* in African-American (AF, brown), Han Chinese-American (AS, yellow) and Caucasian-American (CA, pink) individuals. Mean expression level is indicated (red bar). (B) DNA methylation of CpG sites in the gene promoter of *HLA-DPA1* that are related to SNPs previously associated to HBV risk alleles. Displayed are CpG sites with high inverse correlation to *HLA-DPA1* expression level. (C) DNA methylation of CpG sites in the gene body of *HLA-DPA1* that are related to SNPs previously associated to HBV risk alleles. Displayed are CpG sites with high correlation to *HLA-DPA1* expression level.