Figure S7  mQTLs are highly enriched within 100 kb of the target CpG sites. The proportions of significant mQTLs (detected in the 1 mb regions) for the 36,597 differential CpG sites are shown. X-axis represents the distance between mQTLs and the target CpG sites. At 5% FDR, a total of 23,924 modification-SNP associations (1,354 CpGs) were detected in the CEU samples. 17,643 modification-SNP associations (1,918 CpGs) were detected in the YRI samples.