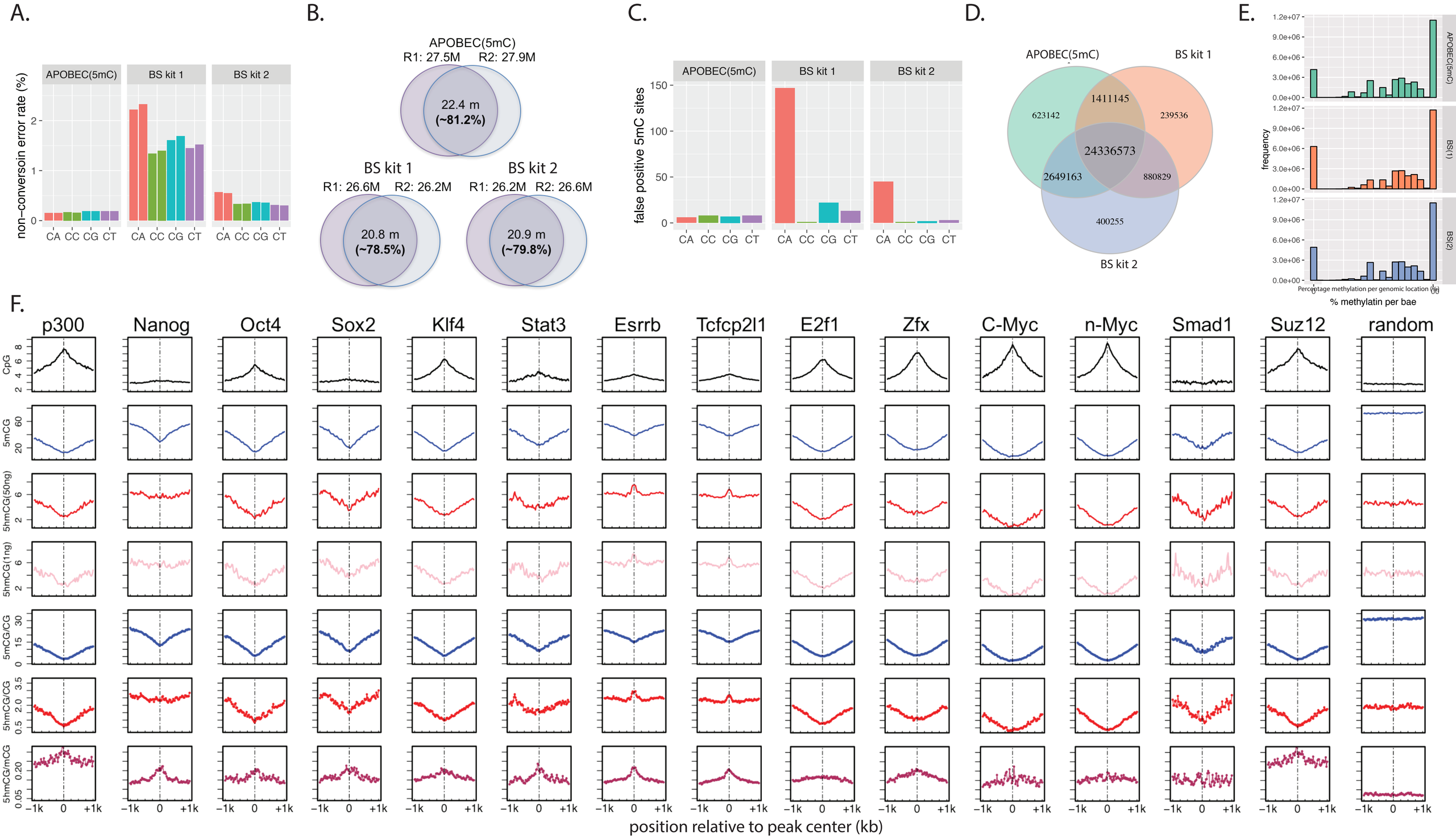

Supplemental Figure 1

(A) False positive methylation call rate (non-conversion error rate) at each dinucleotides context (CpA, CpC, CpG and CpT) estimated from the unmethylated lambda genome. Two technical replicates were performed for each of the three methylation sequencing methods performed in this study: Illumina libraries of APOBEC(5mC); WGBS from kit 1 and WGBS from kit 2. **(B)** Overlap of 5mCG sites identified between the two technical replicates of the 3 protocols: APOBEC(5mC), BS kit 1 and BS kit 2. **(C)** Numbers of false positive 5mC sites in the unmethylated Lambda control at each dinucleotide context after binomial correction using library specific average non-conversion error rates. Both of WGBS libraries had significantly more false positive 5mC sites in the CpA context compared to other contexts. **(D)** Comparison of CpG methylation identified by the enzymatic deamination method APOBEC(5mC) and the two WGBS methods. 95.8% and 95.5% of the total identified 5mCpG sites from the BS Kit 1 and BS Kit 2 WGBS libraries respectively are also identified by the APOBEC(5mC) method. Three font sizes are used as indicators for the relative magnitude of the numbers. The large font size is used for numbers greater than 10 million; the middle front size is used for numbers whose values are between 1 million and 10 million; and the small font size is used for numbers smaller than 1 million. **(E)** Histograms represent genome-wide CpG methylation levels from 0% to 100% across 20 bins of 5% intervals for EM-seq and two WGBS libraries. (C) **(F)** Distribution patterns of 5mCG (blue), 5hmCG (red: 50 ng library; pink: 1ng library) and their normalized levels to the background CpG density at ESC-related transcription factor binding sites in the mouse ES cells.