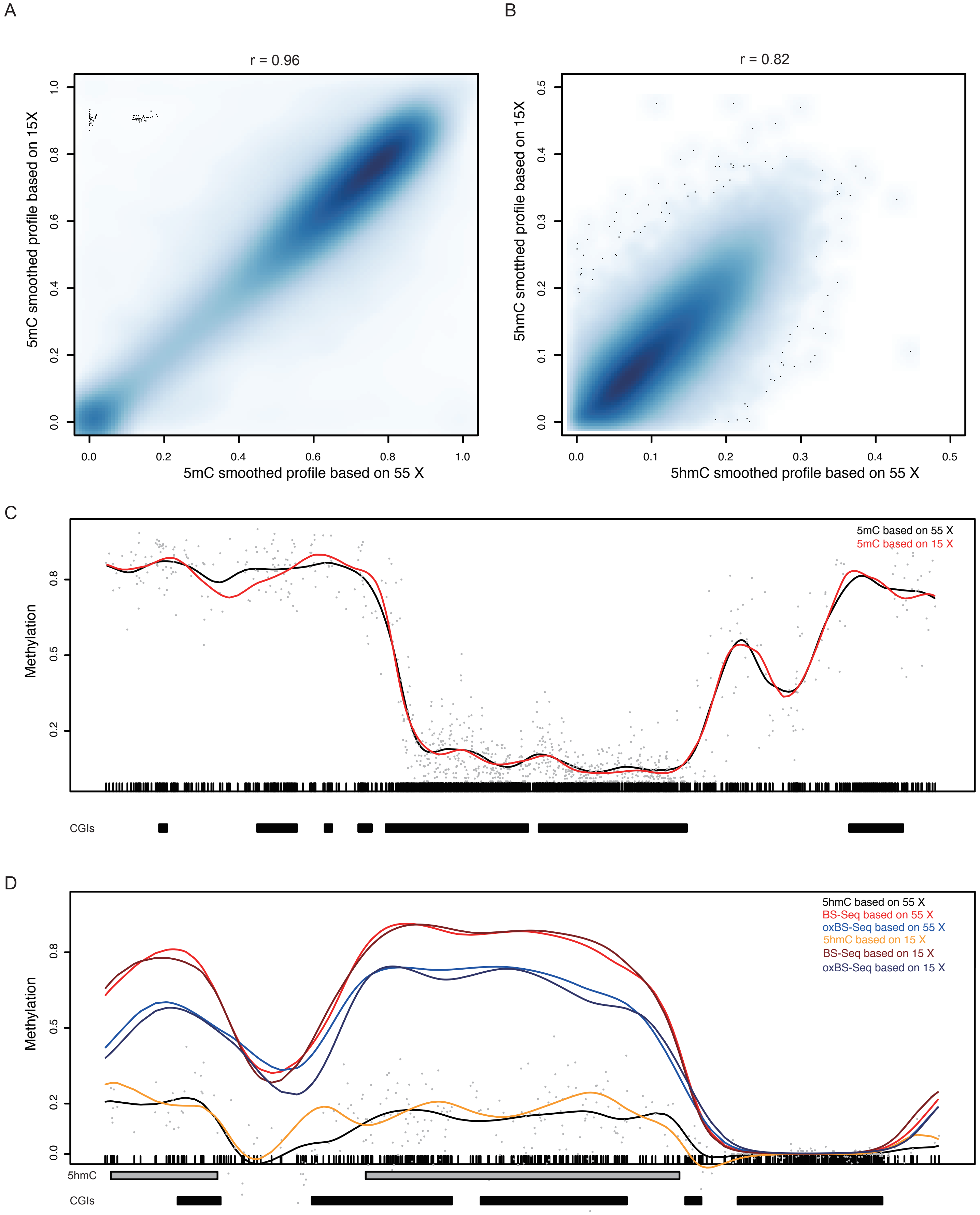

Supplemental Figure 2. Verification of BSmooth algorithm. High whole-genome Spearman correlation between low and high coverage datasets for (A) 5mC (B) 5hmC. 5hmC level of CpG sites were estimated based on smoothed value. (C) Close agreement of methylation profiles between low and high coverage data. Each grey dot represents methylation level of a CpG site estimated by 55 × dataset. Black (15 ×) and red lines (55 ×) represent methylation levels estimated based on smoothed profiles. (D) 5mC profiles of both oxBS-seq and BS-seq libraries and 5hmC profiles between low and high coverage data on an identified 5hmC region. Identified 5hmC regions were indicated as grey boxes, while CGIs were indicated as black boxes.