

Figure S1 Heatmaps of P -values and rejection regions (those with P -values ≤ 0.05 ; shaded in black): (a) Storer–Kim (SK); (b) Fisher’s exact (FE); and (c) chi-squared (CS) tests. The results are for a pair of p ’s fixed at $p_1 = 0.6$ and $p_2 = 0.4$. For each method, the rejection region is the combination of (n_1, n_2) (in the range of 1-100) for which the DMC is declared. Note that the jagged line in (b) is due to the discrete nature of the FE test.

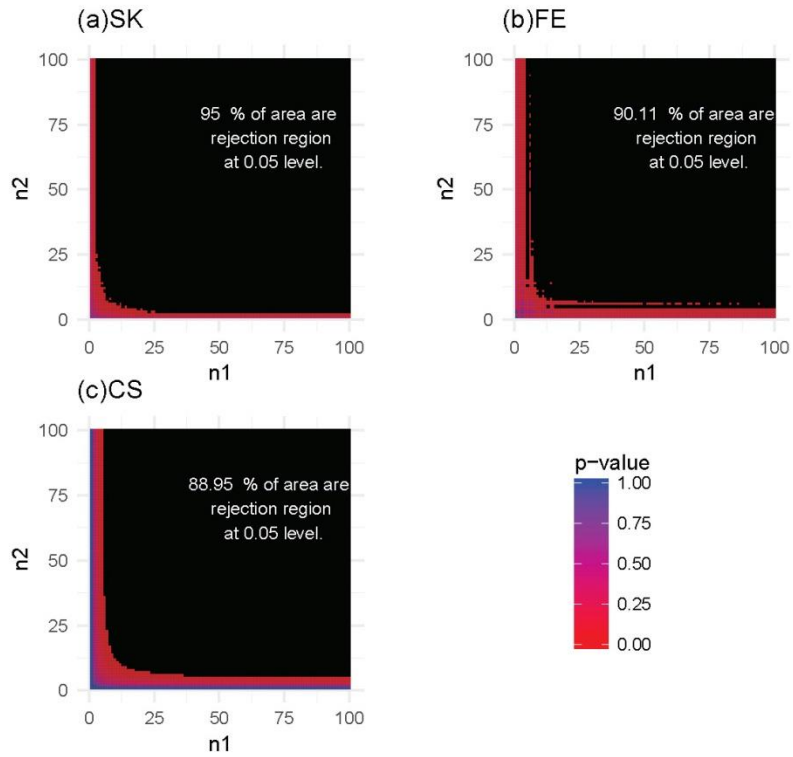


Figure S2 Heatmaps of P -values and rejection regions (those with P -values ≤ 0.05 ; shaded in black): (a) Storer–Kim (SK); (b) Fisher’s exact (FE); and (c) chi-squared (CS) tests. The results are for a pair of p ’s fixed at $p_1 = 0.75$ and $p_2 = 0.25$. For each method, the rejection region is the combination of (n_1, n_2) (in the range of 1–100) for which the DMC is declared. Note that the jagged line in (b) is due to the discrete nature of the FE test.

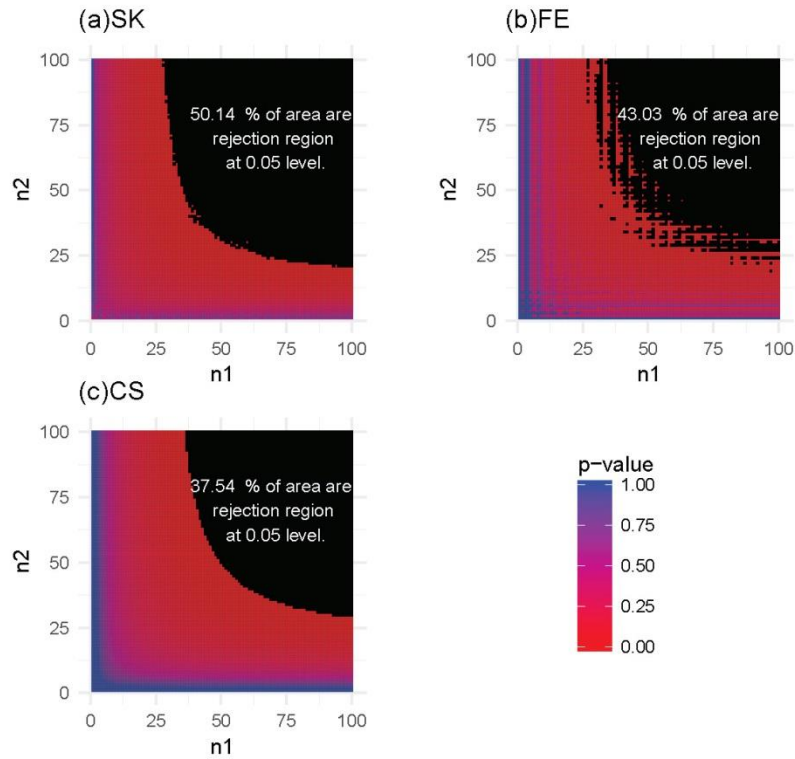


Figure S3 Heatmaps of P -values and rejection regions (those with P -values ≤ 0.05 ; shaded in black): (a) Storer–Kim (SK); (b) Fisher’s exact (FE); and (c) chi-squared (CS) tests. The results are for a pair of p ’s fixed at $p_1 = 0.8$ and $p_2 = 0.6$. For each method, the rejection region is the combinations of (n_1, n_2) (in the range of 1-100) for which DMC is declared. Note that the jagged line in (b) is due to the discrete nature of the FE test.

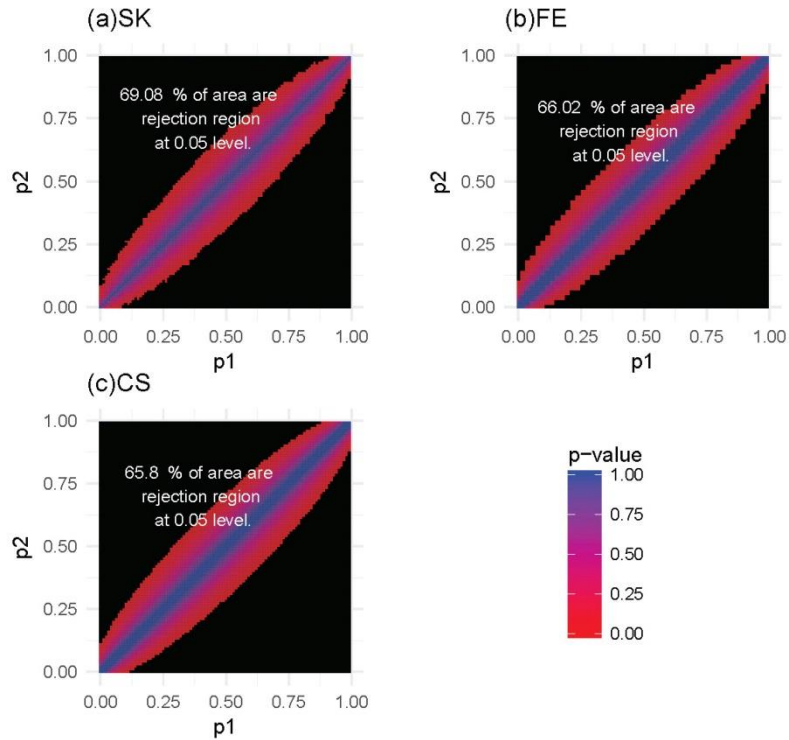


Figure S4 Heatmaps of P -values and rejection regions (those with P -values ≤ 0.05 ; shaded in black): (a) Storer–Kim (SK); (b) Fisher’s exact (FE); and (c) chi-squared (CS) tests. The results are for a scenario in which the total number of reads is 50 in both samples. For each method, the rejection region is the combination of (p_1, p_2) (in the range of 0-1) for which the DMC is declared. Note that the jagged line in (b) is due to the discrete nature of the FE test.

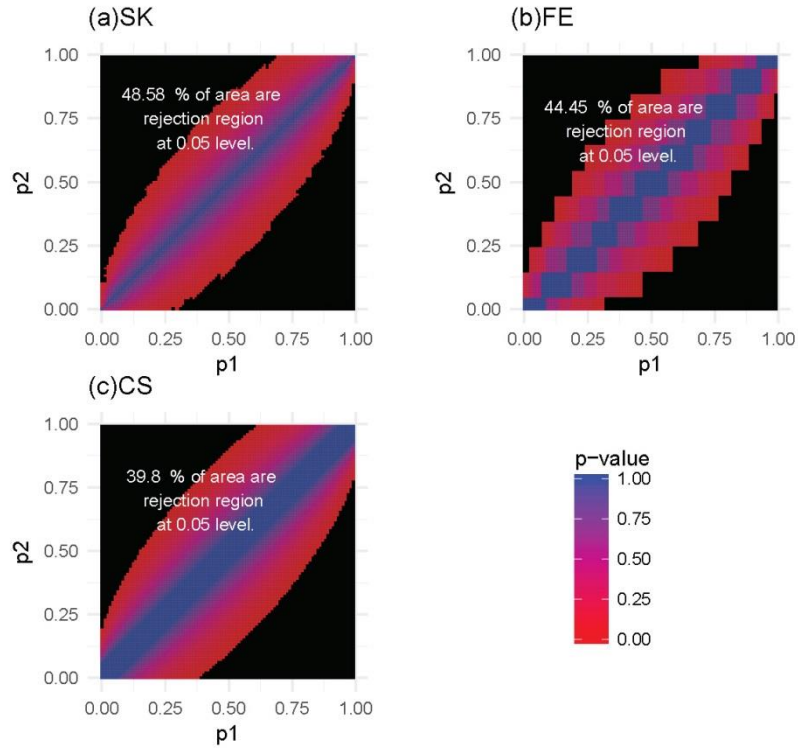


Figure S5 Heatmaps of P -values and rejection regions (those with P -values ≤ 0.05 ; shaded in black): (a) Storer–Kim (SK); (b) Fisher’s exact (FE); and (c) chi-squared (CS) tests. The results are for a scenario in which the total numbers of reads are 40 and 10 in the two samples. For each method, the rejection region is the combination of (p_1, p_2) (in the range of 0-1) for which the DMC is declared. Note that the jagged line in (b) is due to the discrete nature of the FE test.

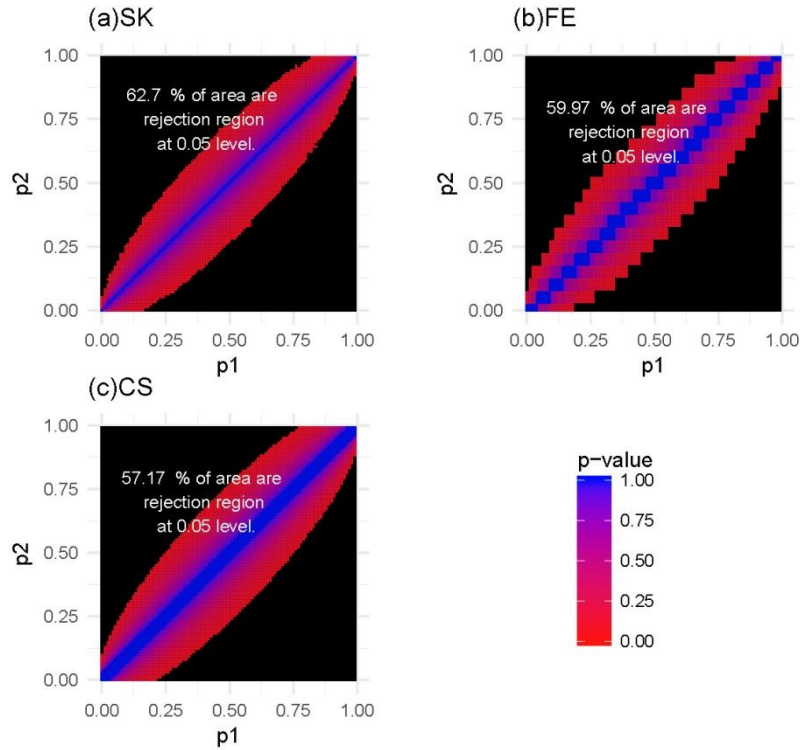


Figure S6 Heatmaps of P -values and rejection regions (those with P -values ≤ 0.05 ; shaded in black): (a) Storer–Kim (SK); (b) Fisher’s exact (FE); and (c) chi-squared (CS) tests. The results are for a scenario in which the total numbers of reads are 80 and 20 in the two samples. For each method, the rejection region is the combination of (p_1, p_2) (in the range of 0-1) for which the DMC is declared. Note that the jagged line in (b) is due to the discrete nature of the FE test.

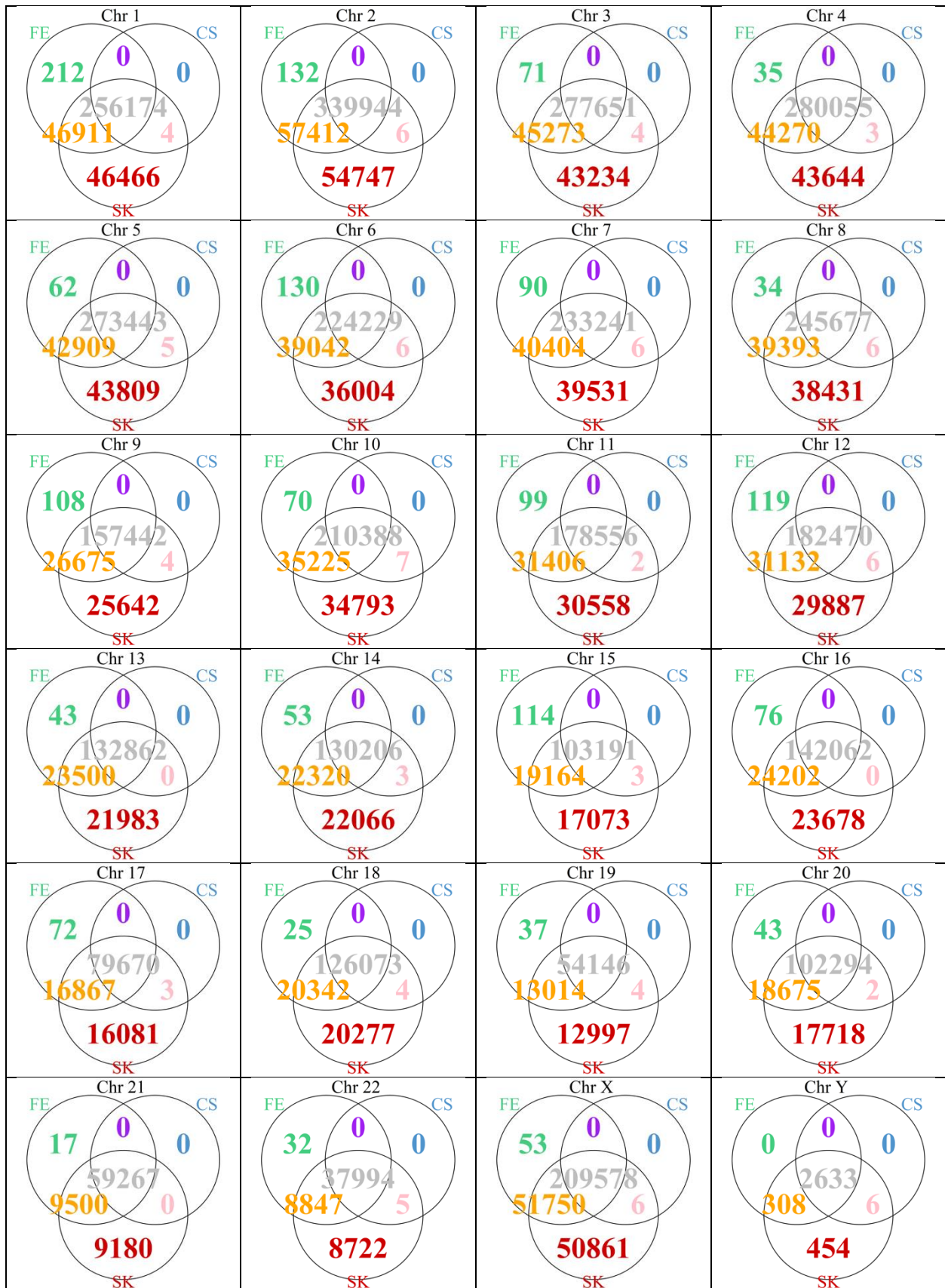


Figure S7 Venn diagrams of numbers of DMCs detected by three methods chromosome-by-chromosome. Note that a site is designated a DMC if the chromosome-wise FDR ≤ 0.05 .

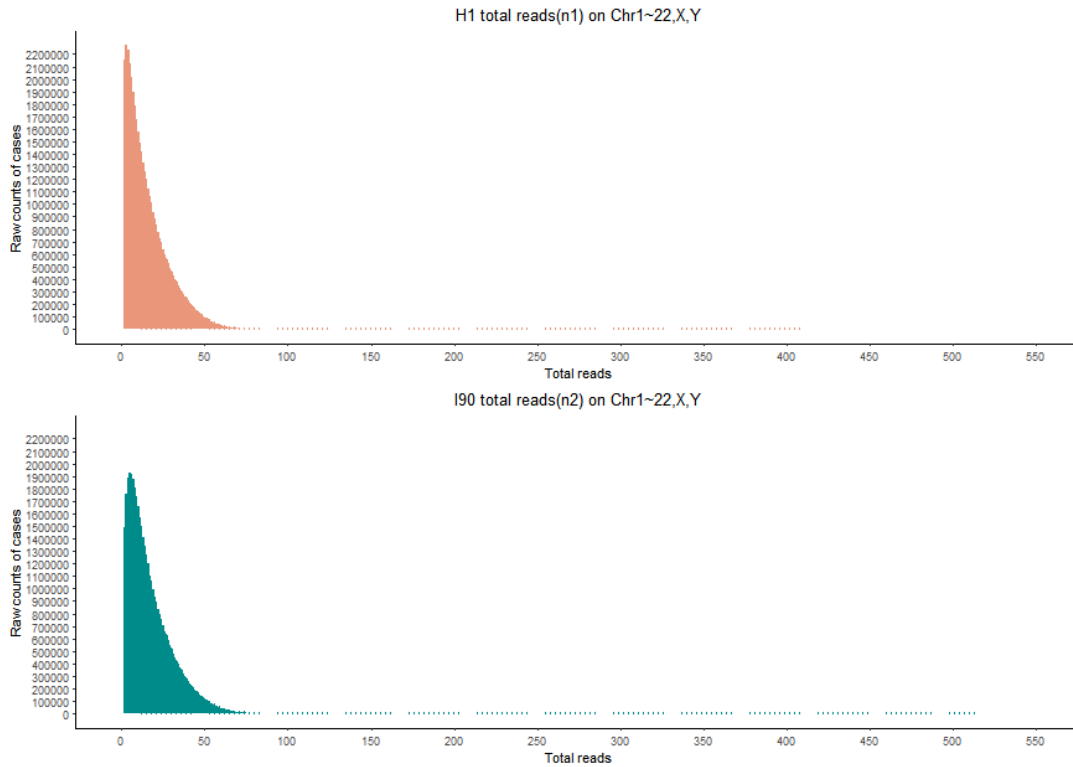


Figure S8 Histogram of the read counts for chromosomes 1–22, X, and Y from the H1 (top) and I90 (bottom) cell lines.

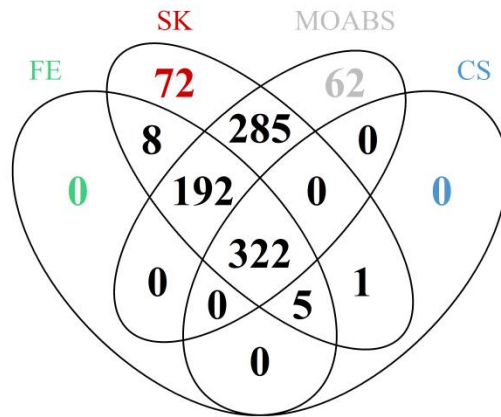


Figure S9 Venn diagram of the numbers of DMCs detected by three classical methods, FE, CS, SK, and a newer method, MOABS. For the classical methods, a site is designated a DMC if $FDR \leq 0.05$. For MOABS, a site is designated a DMC if its credible methylation difference (CDIF) is greater than 0.2, a threshold suggested in the software.