Tagmentation-based whole genome bisulfite sequencing (TWGBS)

TBWGBS enables to determine the quantitative methylation states of all CpGs in a genome with tiny amounts of input DNA, as low as 10-30 ng. (i) The method starts with the assembly of the transposome consisting of a hyperactive Tn5 transposase and a double-stranded, partially methylated DNA adapter. (ii) Tagmentation of the genomic DNA using the transposome fragments the DNA and appends the adapter to the fragments. (iii) Combined oligo replacement and gap repair replaces an unmethylated adapter oligo and closes a gap between adapter and genomic fragment. (iv) Bisulfite treatment of fragmented DNA converts unmethylated Cs to Ts, methylated Cs remain unconverted. (v) Low cycle number PCR generates a sequencing library. (vi) The library is analysed by next generation sequencing.

References: