Fast and efficient Post-Bisulfite-Seq Library construction with QIAseq Ultralow Input DNA Library Protocol

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Abstract

Epigenetic changes play a crucial role in the regulation of important cellular processes such as gene expression and cellular differentiation, and were also identified as key factors in many various diseases. The methylation of cytosines in the genome, an important epigenetic regulatory mechanism, reduces the transcriptional activity of adjacent genes. Whole genome bisulfite sequencing (WGBS), combining bisulfite-mediated conversion of un-methylated cytosine to uracil and next generation sequencing (NGS), allows the genome-wide detection of 5-methylcytosine residues at unprecedented single-base resolution and thus enables the connection between gene activity and the precise localization of a DNA methylation mark. However, the widely used approach to treat samples after NGS library preparation with bisulfite to convert un-methylated cytosines to uracils reveals major challenges such as significant bisulfite-induced sample loss due to DNA degradation. Therefore, the traditional library prep method for bisulfite sequencing demands very high DNA input amounts or requires a large number of PCR cycles during NGS library construction.

Here we present a fast and streamlined workflow for bisulfite treatment, double strand synthesis and NGS library construction, which overcomes these traditional challenges. The combination of highly specific bisulfite conversion reagents of the EpiTect Fast Bisulfite Conversion Kit and the ultra-efficient end-polishing and adapter ligation chemistries of the QIAseq Ultralow Input Library Kit allows fast and efficient bisulfite conversion and NGS library preparation to accurately interrogate the methylome.