



Next Generation Epigenetics – Innovative Research Tools for the Accurate Analysis of DNA Modifications

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Abstract

DNA methylation (5mC) is central to early development, stem cell dynamics, ageing and has been implicated in the control of a wide range of diseases including cancer and neurodegenerative disorders. Although several studies have shown that 5-hydroxymethylcytosine (5hmC), a TET-oxidized derivative of 5mC, is functionally distinct, traditional epigenetic research tools cannot accurately distinguish between these modifications, confounding analysis.

Cambridge Epigenetix (CEGX) has developed TrueMethyl® oxidative bisulfite (oxBS) technology to quantitatively measure 5mC and 5hmC at single base resolution. Compatible with conventional array and enrichment techniques such as the 450K and EPIC array, amplicon sequencing and pyrosequencing, TrueMethyl® can also be coupled with NGS for targeted sequencing or whole genome analysis.

To take Whole Genome Bisulfite Sequencing (WGBS) from niche to mainstream, CEGX has developed TrueMethyl® Whole Genome (TMWG). This innovative, all-in-one workflow brings together TrueMethyl® oxBS technology with a single-stranded, template independent, post-conversion library construction technology and a ready-to-use bioinformatics pipeline for data analysis, revolutionizing the quality and simplicity of conducting WGBS experiments.

TrueMethyl® Whole Genome libraries overcome existing limitations of traditional pre-BS and random-priming PBAT library construction methods, and offer high yield, high diversity and low duplicate libraries at low DNA input burden, for outstanding data quality and cost-efficient WGBS sequencing.