

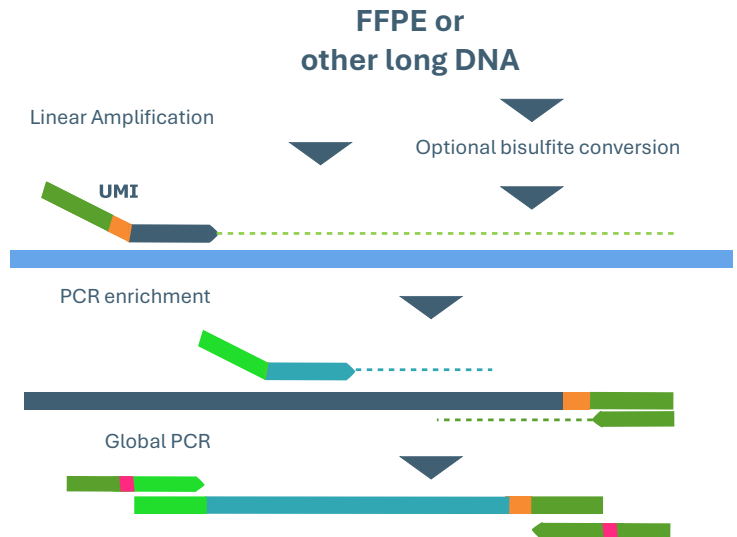
BOSON-Seq

An amplicon-based solution for strand-aware UMI sequencing of DNA

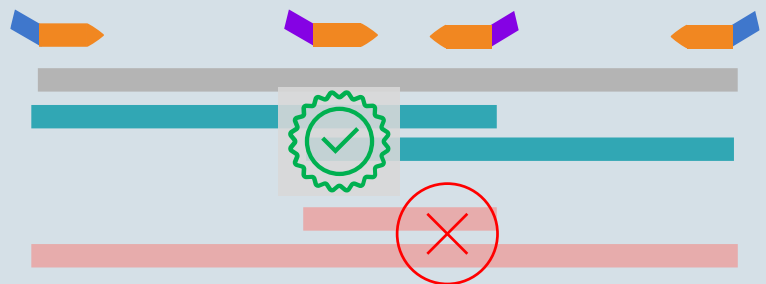
Proprietary tiled multiplex PCR-based enrichment chemistry which allows for single-tube coverage of large genomic regions from FFPE or other long DNA

Uniquely designed for simplicity and throughput

- Single-tube amplification
- Minimal hands-on time
- Extremely flexible and fully automatable
- Efficient with low input quantities
- Unique molecular identifiers for error suppression



Primer tiling across large regions blocks formation of small, unwanted PCR products



BOSON-Seq advantages

Ideal for genetic and epigenetic enrichment

Single pool of primers for all genomic sizes

Simple, rapid protocols for high-throughput

Lower DNA inputs with single-tube assay

Enrich-Seq

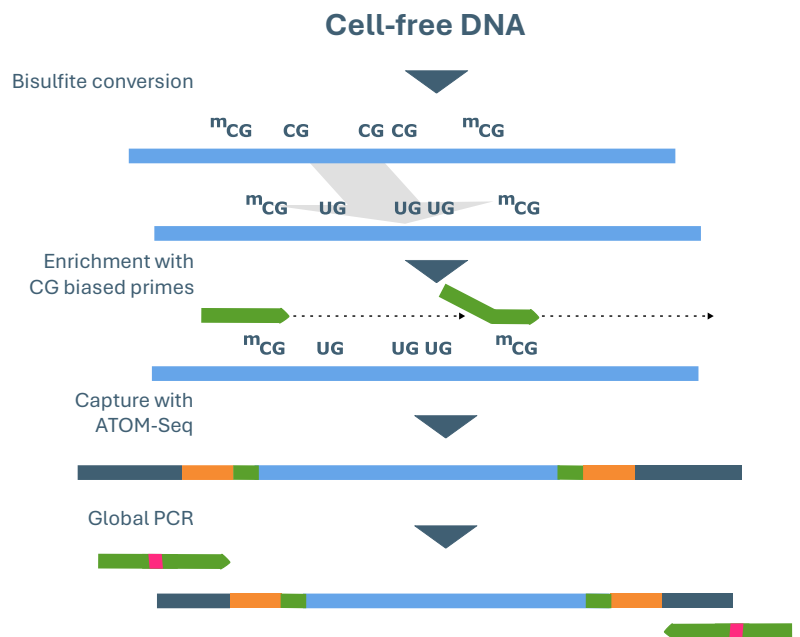
A global enrichment solution for capturing methylated DNA

Proprietary capture chemistry to non-specifically enrich methylated DNA to reduce the sequencing need for whole genome methylation workflows

High-performance alternative to whole-genome bisulfite sequencing

The Enrich-Seq provides superior enrichment of bisulfite converted single-stranded DNA based on CpG methylation.

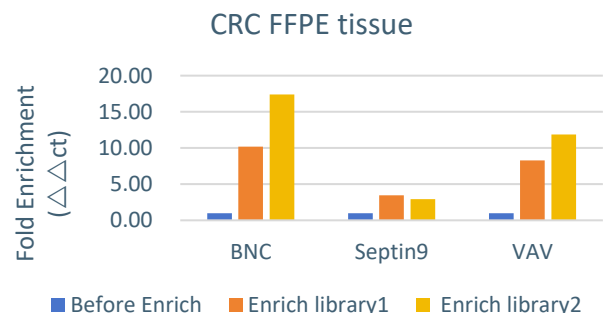
Allowing a detailed analysis of differentially methylated regions (DMRs), enabling researchers to make crucial comparisons between samples and to focus on specific methylation densities of interest, ultimately aiding in the identification of cancer signatures.



- Highly sensitive and efficient, with quantitative accuracy
- Reduce sequencing demands for whole genome methylation by enriching for methylated DNA
- Use very small amount of starting material, from as little as 5ng of cfDNA
- Very simple experimental workflows
- 3x to 17x-fold enrichment for methylated CG sites

The enrichment of 3 methylated regions was validated using Enrich-Seq and assessed by qPCR before and after the workflow.

FFPE samples were found to be between 10-17x enriched for BNC, 3-3.5x for Septin9 and 8.3-11.9x for VAV. These data demonstrate successful Enrich-Seq enrichment.



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