ZYMO RESEARCH

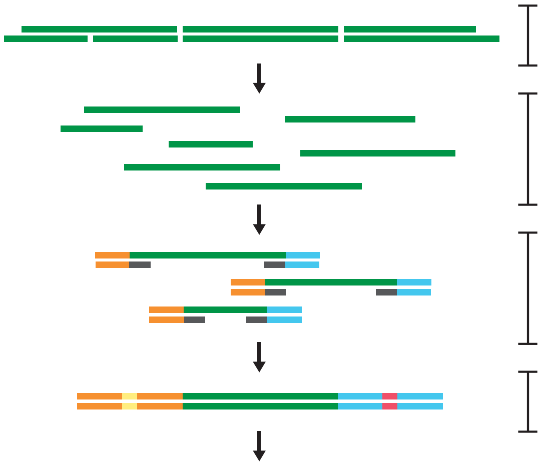
The Beauty of Science is to Make Things Simple®

Decode the Genetics and Epigenetics in a Single Step

Zymo-Seq™ Trio WGBS Library Kit

- **Co-Detection of Genetic and Epigenetic Information:** Seamlessly analyze both genomic data and DNA methylation in a single experiment, with the validated open-source bioinformatics tools and comprehensive step-by-step guides.
- **True-End Fragment Analysis:** Designed for optimal performance with small or degraded DNA fragments, including cell-free DNA (cfDNA) and FFPE-derived DNA, to capture the fragment's true end.
- **Accurate Methylation Detection:** Achieve precise methylation calling with a direct ligation-based protocol that preserves native termini, ensuring accuracy in each DNA fragment analysis

Lightning Bisulfite Conversion with Single-Stranded Library Preparation



Pre-Fragmented Input
- Compatible with sonicated genomic DNA, sonicated FFPE DNA, cfDNA, etc.

Lightning Bisulfite Conversion
- EZ DNA Methylation-Lightning's unique chemistry gently converts all DNA > 99.5 % with minimal sample loss

Adapter Ligation
- Splinted adapters are directly ligated onto ssDNA simultaneously

Index PCR Amplification
- Indexing PCR adds full length adapters with Unique Dual Indexes (UDIs)

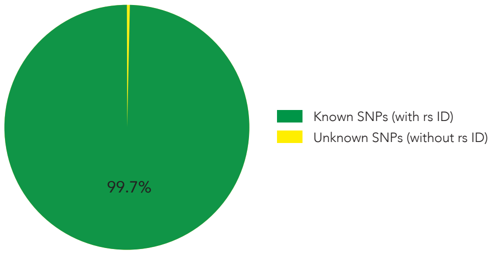
Trio WGBS librarey is ready!

Overview of the Zymo-Seq™ Trio WGBS Library Kit Workflow. The unique single-stranded library preparation begins with the EZ DNA Methylation-Lightning bisulfite conversion of the input DNA. Then the simultaneous ligation of adapters onto either end of the converted DNA fragment is performed for the capture of native methylation information of the native termini. The adapterized samples are then indexed and amplified via PCR, allowing for sequence-ready WGBS libraries in as little as 6 hours.

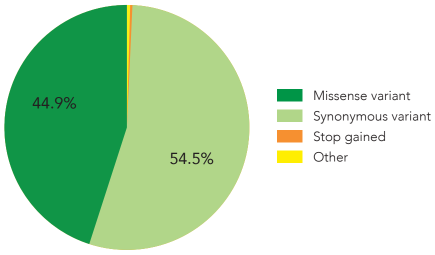
Scan QR code for Step-by-Step bioinformatic support.

Functional genomic variance detected aside DNA methylation

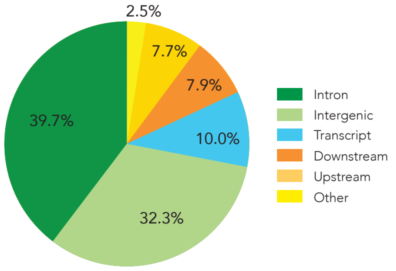
Distribution of SNPs



Variants by Effect Types



Variants by Genomic Region



Genetic information was extracted from Zymo-Seq Trio WGBS libraries using the 'step-by-step' bioinformatics guide. Variant annotations were generated using the SNP Effect (SNPEff) tool, which predicts the functional impact of genetic variants.

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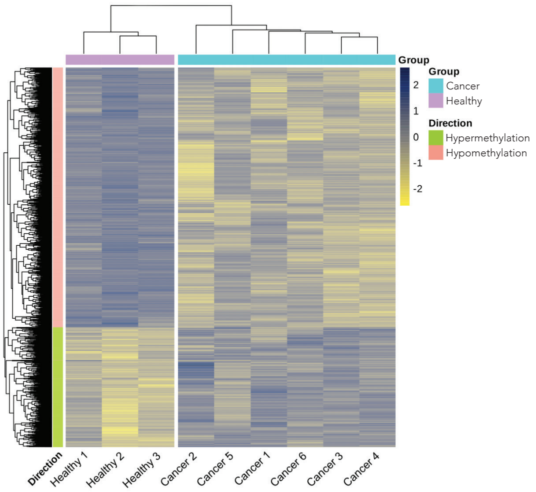
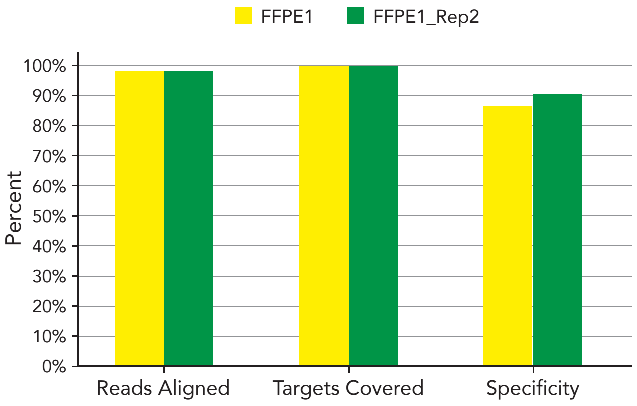
Exceptional Performance for Small or Degraded DNA Fragments

Distinct DMRs in cfDNA Samples



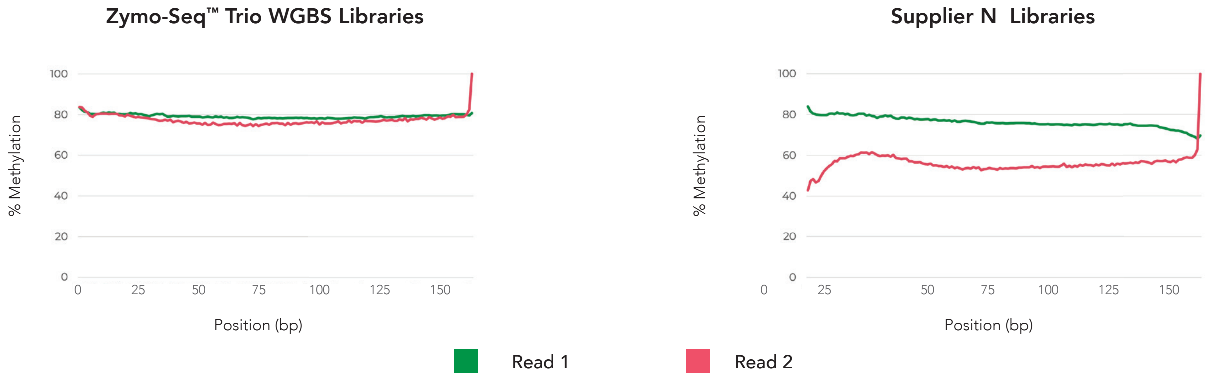
Zymo-Seq™ Trio WGBS libraries show clear distinction of CpG methylation levels between lung cancer and healthy cfDNA samples. Libraries were prepared from 5 ng of cfDNA derived from donors with lung cancer or no disease. Differentially methylated regions (DMRs) were determined by the publicly available package DSS (v2.24.0, adjusted p-value < 0.05). The direction of methylation level difference was relative to the healthy control group.

Robust and Reliable Targeted Bisulfite Sequencing for FFPE



High-quality libraries generated by Zymo-Seq™ Trio WGBS are well-suited for targeted enrichment and direct whole genome bisulfite sequencing. DNA was extracted from human FFPE tissue samples using Zymo *Quick*-DNA FFPE Miniprep (D3067) .50 ng extracted FFPE DNA were processed for targeted methyl-seq using Zymo-Seq™ Trio WGBS kit protocol followed by commercially available targeted capture panel (Twist Bioscience). All three FFPE targeted libraries showed outstanding alignment rates and capture uniformity, as well as high median target coverage.

Accurate Methylation Calling Across the Entire Read


Zymo-Seq™ Trio WGBS Libraries

Supplier N Libraries

Zymo-Seq™ Trio WGBS libraries minimize library preparation bias commonly found in conventional methods. Unbiased libraries will have consistent methylation levels across the entire read length. Other commercial protocols that include an end-repair step incorporate artificial nucleotides to blunt damaged DNA termini, resulting in significant methylation bias on the 3' end of the DNA fragments. The Zymo-Seq™ Trio WGBS Library Kit directly ligates the adapters, eliminating the need for end-repair and thus preserving the integrity of native methylation present on the fragment termini. The Zymo-Seq™ Trio WGBS libraries (left) shows consistent CpG methylation across both Read 1 and Read 2 whereas the Supplier N libraried (right) shows significant bias. The M-Bias plots shown above were generated by plotting the average CpG methylation levels across each position of the mapped read.

Product	Cat. No.	Size
Zymo-Seq™ Trio WGBS Library Kit	D5462 D5463	24 preps 96 preps

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