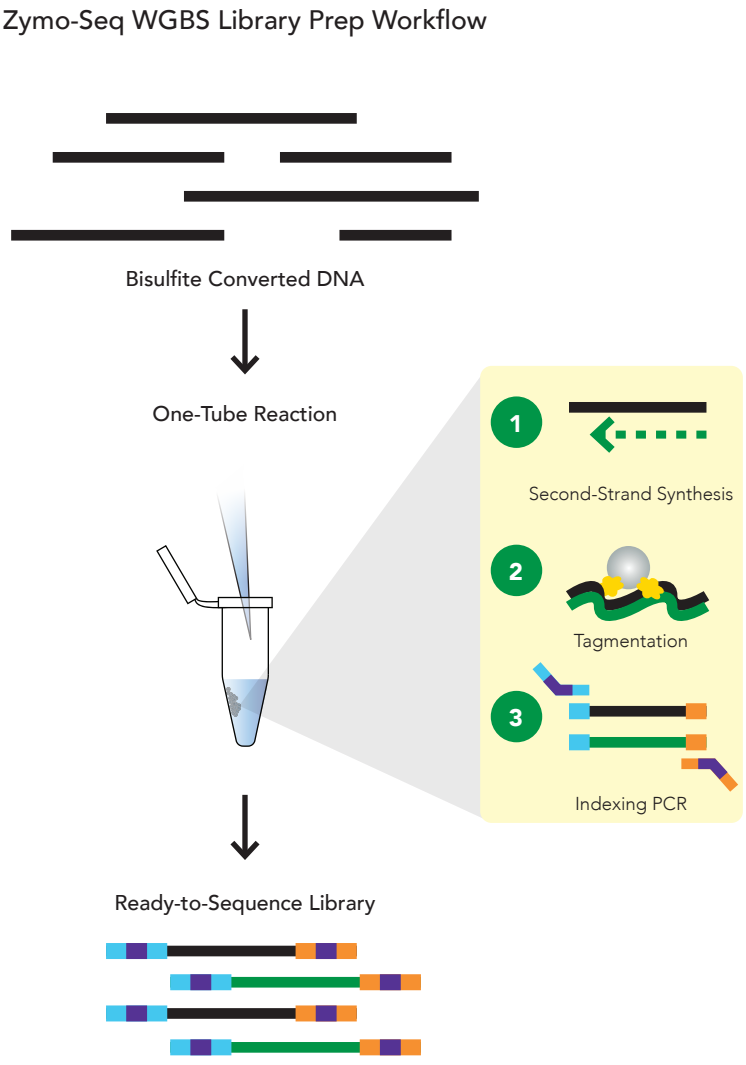
ZYMO RESEARCH
The Beauty of Science is to Make Things Simple®

Bisulfite Library Preparation in One Tube

Zymo-Seq WGBS Library Kit

- **Streamlined workflow:** From genomic DNA to ready-to-sequence library in 4 hours.
- **Consistent genome coverage:** Unbiased, single-base methylation profiling of cytosines throughout the entire genome.



Enzymatic reactions are consolidated in a single tube to minimize hands-on time. Intact genomic DNA is first bisulfite converted, which then undergoes second strand synthesis (1). Tagmentation is added directly to the reaction to tag adapters onto the double-stranded DNA (2). Indexing primers and PCR mixture are added to amplify the WGBS library (3). Purified libraries are ready for sequencing on Illumina instruments.

Explore Epigenomics *with* NGS

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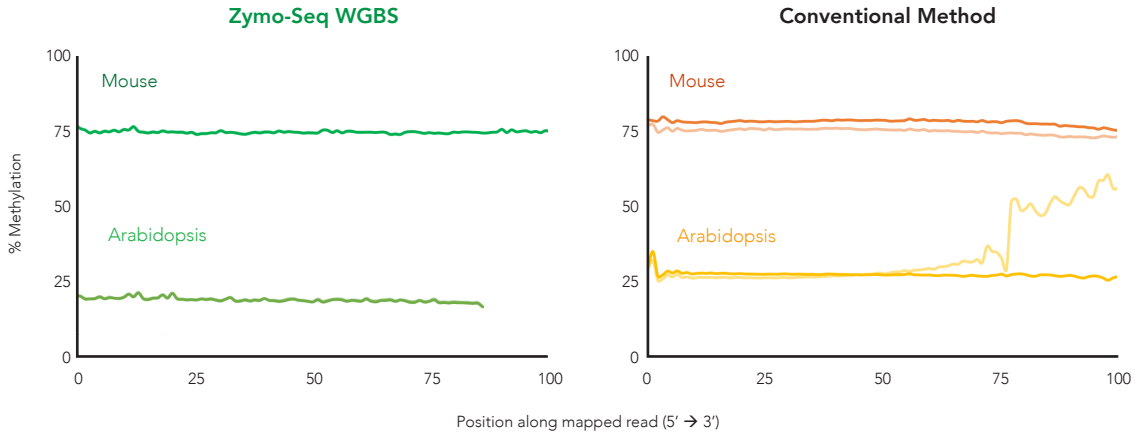
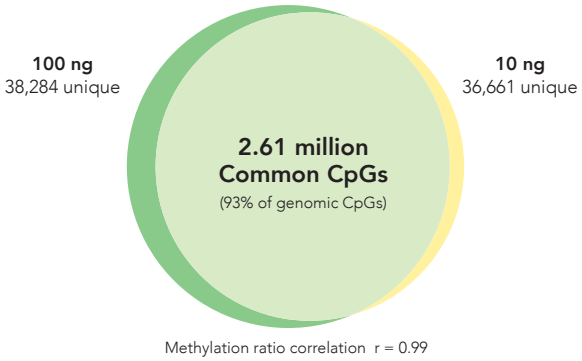
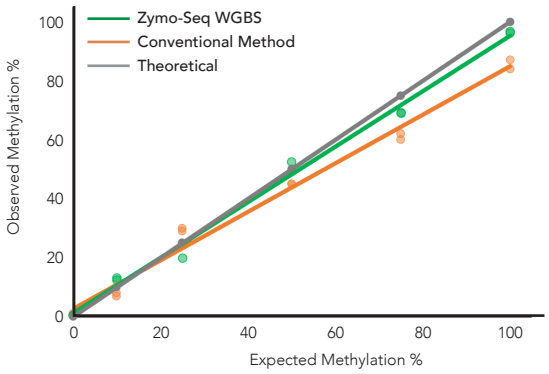
Consistent Library Preparation to Maximize Sequencing Data



Zymo-Seq libraries provide longer, useable reads by reducing library preparation bias as found in conventional libraries. Unbiased libraries will have constant methylation levels across the entire read length. Conventional methods typically require an end-repair step and artificial nucleotides incorporation, which require additional trimmings to reduce methylation bias. Mouse and Arabidopsis WGBS data were generated using the Zymo-Seq kit (left) and compared to publicly available data of WGBS libraries prepared using the conventional method (right). All sequencing reads were first trimmed and then aligned using Bismark. The M-bias plots shown above were generated by plotting the average CpG methylation level across each position of the mapped read.

Reproducible Coverage and Methylation Detection





Coverage is preserved using as little as 10ng DNA input. Over 93% of genomic CpG sites overlapped (10X depth cutoff) between Zymo-Seq libraries prepared using 100ng and 10ng of Arabidopsis genomic DNA. The two libraries had less than a 10% methylation difference in over 90% of shared CpG sites, demonstrating consistency between different inputs.

Unbiased methylation callings are produced using Zymo-Seq library preparation. Spike-ins with known methylation ratios (0%, 10%, 25%, 50%, 75%, and 100%) were added to 100ng of genomic DNA prior to processing with the Zymo-Seq WGBS Library Kit or using the conventional methodology. The observed methylation % for Zymo-Seq libraries closely matched theoretical methylation levels (R^2 = 0.997).

Product	Cat. No.	Size
Zymo-Seq WGBS Library Kit	D5465	24 preps

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