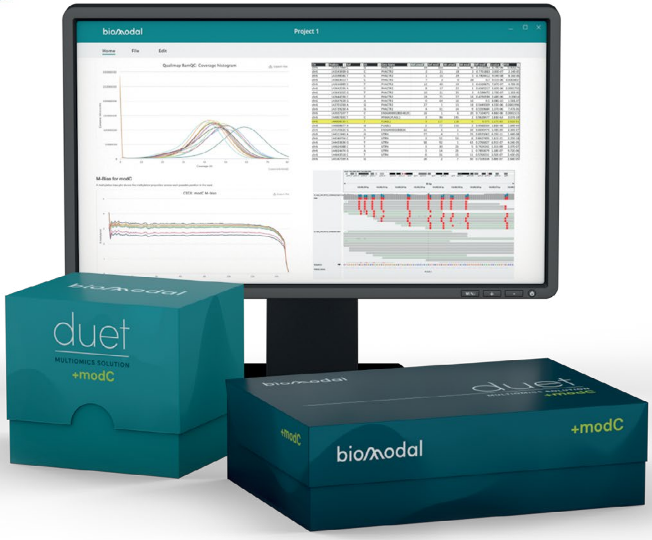
Product Sheet

biomodal

duet multiomics solution +modC



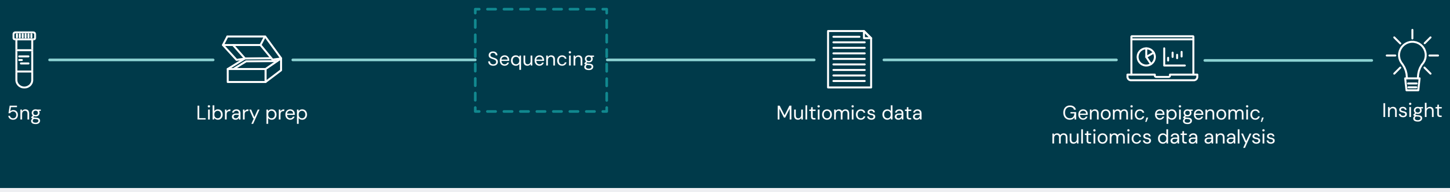
Simultaneously Sequence Genetics & Epigenetics in a Single Workflow

Complete genetic and modified cytosine (modC) information from a single low volume DNA sample. The duet multiomics solution is a streamlined workflow providing standard genomic calls plus modC without errors and biases associated with other enzymatic or bisulfite treatment. Investigate the whole genome using your existing next generation sequencer and with phased results in a single read.

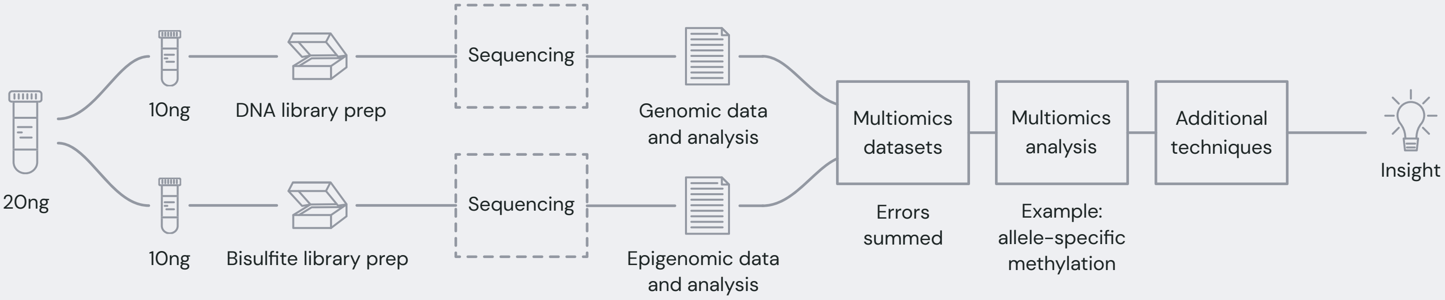
One Sample, One Workflow, One Solution

- Simultaneous whole genome sequencing results with all canonical DNA bases plus modC with improved sensitivity and specificity
- Preserve your valuable samples by using as little as 10 ng of cfDNA
- Accurately detect C>T changes, the most common type of genetic mutation in the human genome and in cancer
- Integrate a fully optimized analysis pipeline that phases SNP calling and methylation marks at read level, while suppressing PCR and sequencing errors
- Interpret allele-specific methylation calls using our proprietary analytics module for further insight into your samples

duet multiomics solution workflow



Conventional workflows



Higher Sensitivity & Specificity

Achieve higher sensitivity to uncover methylation patterns alongside genetic information while avoiding bisulfite damage and data loss.

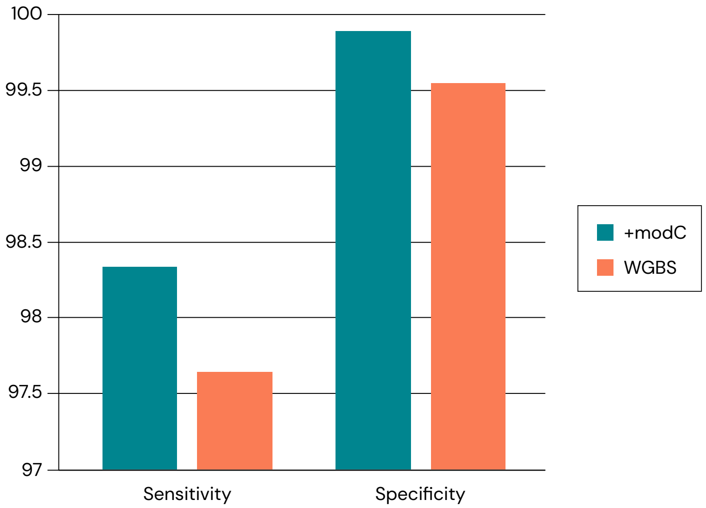


Figure 1: The duet multiomics solution +modC by biomodal achieves higher sensitivity and specificity when detecting methylated cytosine than WGBS to provide the most accurate epigenetic results.

Improved Coverage in Actionable Areas

A single comprehensive workflow provides more uniform coverage from low-input DNA samples compared to whole genome bisulfite sequencing workflows, without trade-offs for quality.

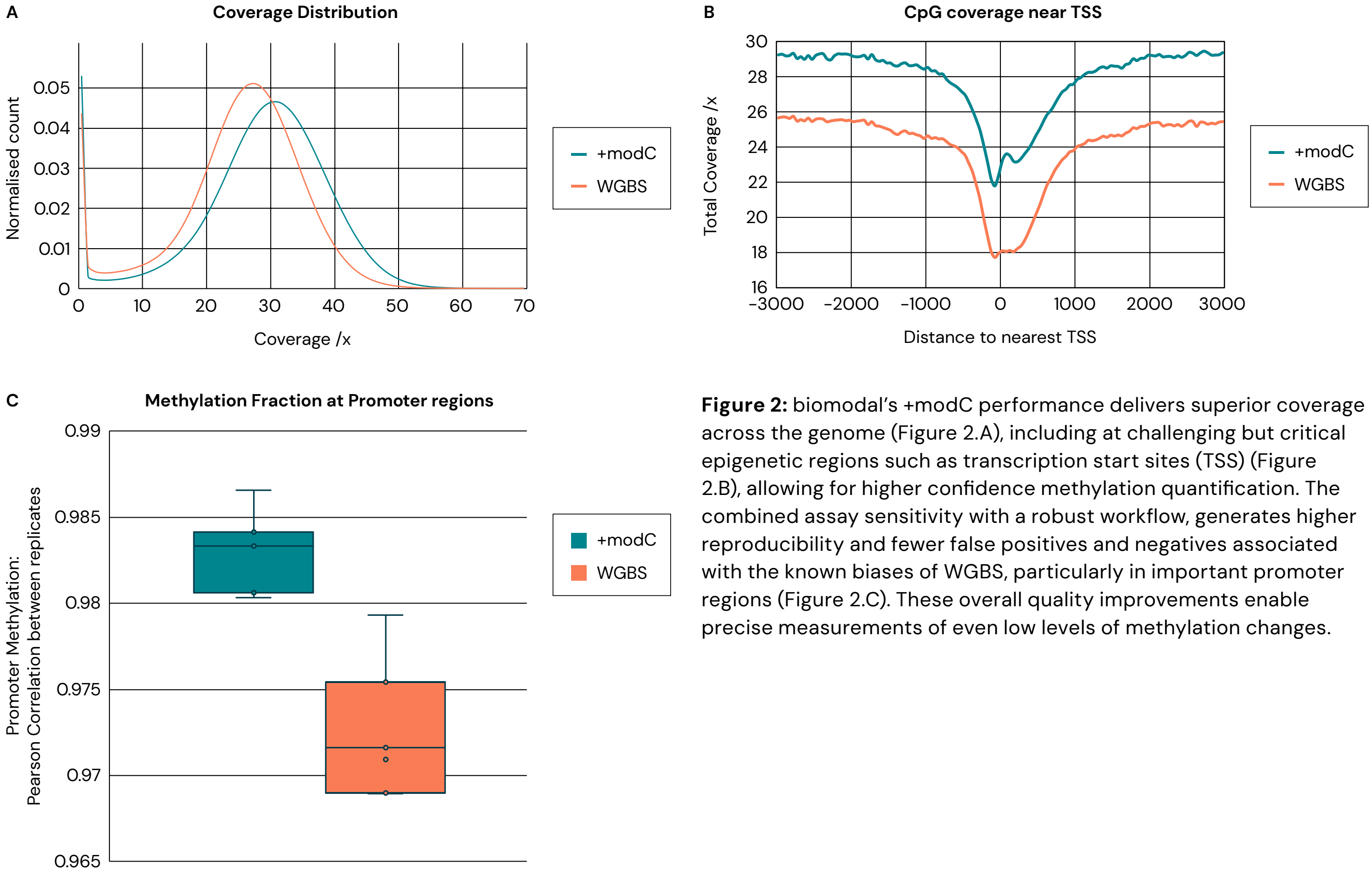


Figure 2: biomodal's +modC performance delivers superior coverage across the genome (Figure 2.A), including at challenging but critical epigenetic regions such as transcription start sites (TSS) (Figure 2.B), allowing for higher confidence methylation quantification. The combined assay sensitivity with a robust workflow, generates higher reproducibility and fewer false positives and negatives associated with the known biases of WGBS, particularly in important promoter regions (Figure 2.C). These overall quality improvements enable precise measurements of even low levels of methylation changes.

Reference-quality SNP calling without ambiguity in C-to-T Mutation calls

Precise sequence information in one run, eliminating the inaccuracy of C-to-T miss-calls or data loss from merged sequencing workflows.

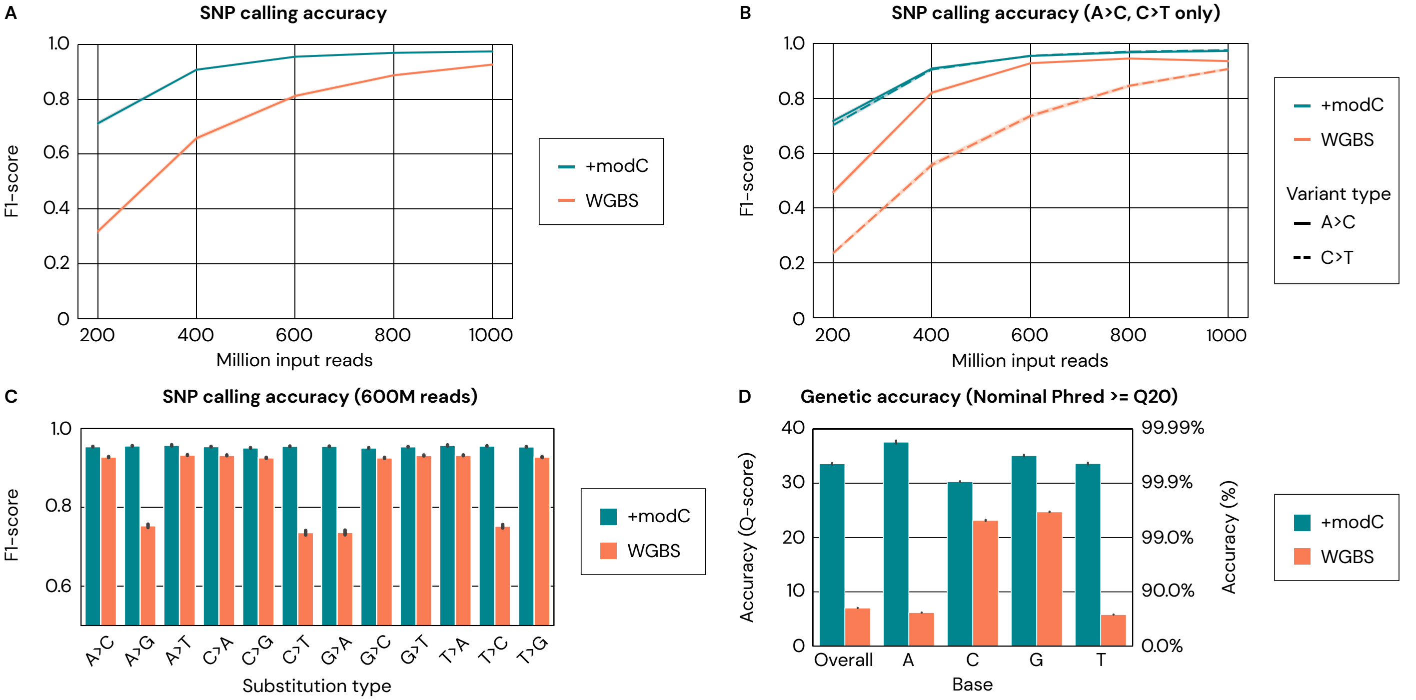


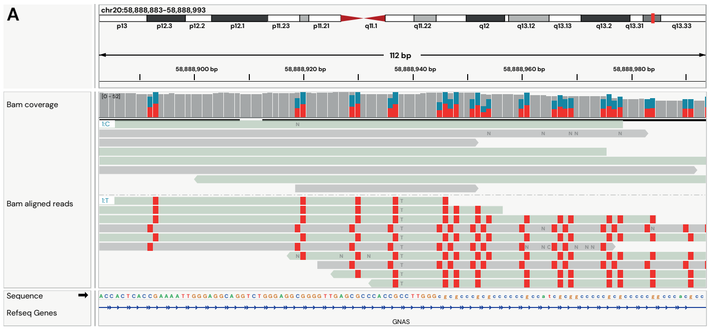
Figure 3: Accurate SNP calling at lower depth regardless of sequence. Where traditional DNA methylation methods can damage DNA, biomodal's novel chemistry retains the integrity of both the methylation state and base call with fewer reads required (Figure 3.A). C-to-T mutations, the most commonly identified SNP in the human genome, have been associated with a number of different cancers. biomodal's combined and novel pipeline allows for the most accurate phenotyping of a WGS sample without loss of C-to-T mutation visibility (Figure 3.B). Beyond the most common challenge in WGBS, the duet multiomics solution +modC retains the fidelity of the underlying genetics across all major genomic context (Figure 3.C). Retain confidence in your whole genome sequencing studies for accurate representation with all bases >Q30 (Figure 3.D).

Automatic allele-specific methylation calls

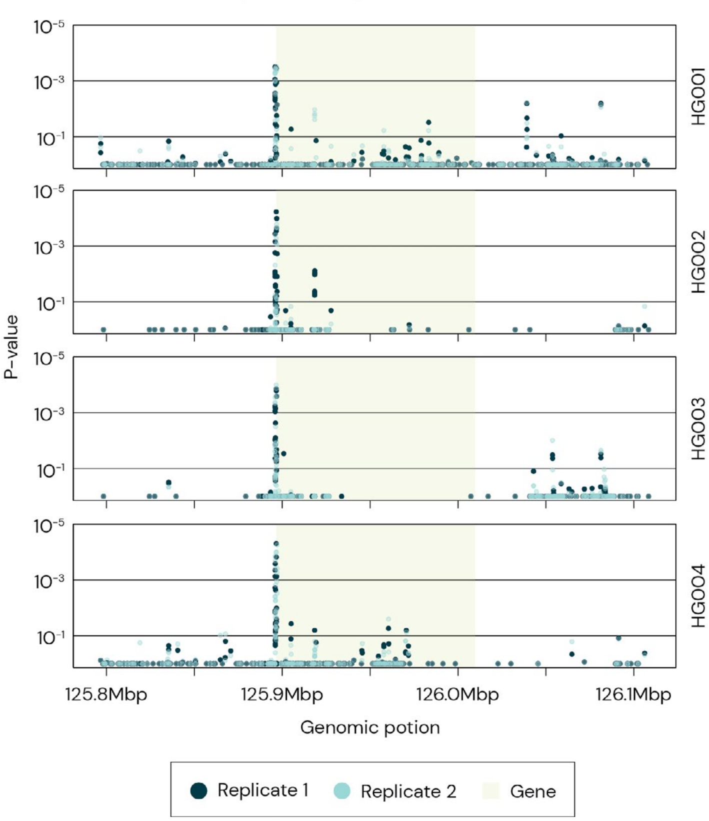
Methylation promotes or silences specific alleles causing deregulation, altered expression, or potential disease.

Figure 4: The biomodal analysis pipeline uses standard alignment and SNP calling tools with a novel method for combining both epigenetic marks and genomic results. Outputs provide automated resolved-reads for phased methylation calls ready-for-interpretation in standard visualization tools, including IGV. Here, methylated Cs (red) show significant differences across the two chromosomal copies, displaying allele-specific methylation (ASM) (Figure 4.A). +modC was used to demonstrate ASM in the FANK1 gene (Figure 4.B). Significant ASM differences are observed at the start of the gene in all four samples.

A



B



Integrated analysis software accelerates 6-base sequencing data to biological insights

Unlock the full potential of 6-base sequencing data with a versatile analysis software designed to fast-track raw multiomic datasets to meaningful biological insights, in one workflow.

modality XPLR is a powerful analysis tool designed to help visualise multiomic data, enabling researchers to extract publication-ready insights—without the bottlenecks. Consuming raw outputs from the duet pipeline, modality XPLR empowers users to explore complex datasets and uncover biological patterns. Through biological QC, users can quickly explore the biological characteristics of their data with interactive PCA, and violin plots before moving on to customisable DMR analysis and visualisations.

Specifications

Input requirements	cfDNA 5-50 ng gDNA 20-80 ng
Assay turnaround time	Less than 16 hours
Assay hands on time	Less than 8 hours
Shelf-life	Minimum 3 months

Ordering information

Catalogue number	Product name	Product description
5101	duet multiomics solution +modC; 8 reactions	Pre-sequencing workflow + post-sequencing analysis software for 8 reactions
5102	duet multiomics solution +modC; 24 reactions	Pre-sequencing workflow + post-sequencing analysis software for 24 reactions

Learn more about modality XPLR

Disclaimer

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