myBaits® Custom Methyl-Seq

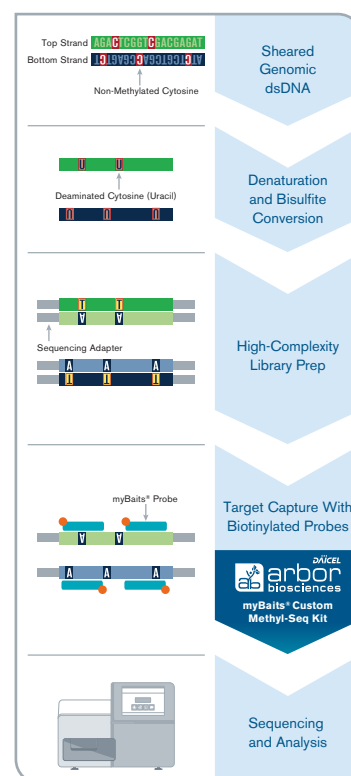## Customized NGS Target Capture Kits for Methylation Sequencing

OVERVIEW

myBaits Custom Methyl-Seq hybridization capture probes and reagents provide rapid, selective enrichment of target regions of interest from next-generation sequencing (NGS) libraries built from either bisulfite- or enzymatic-converted DNA samples. Methylation sequencing is a powerful technique for directly assessing epigenetic modifications in the genome, but it is often costly to directly sequence samples to depths needed to fully resolve methylation patterns at a given locus of interest. With myBaits Custom Methyl-Seq hybridization capture kits from Daicel Arbor Biosciences, customized in-solution probes for your genes of interest "enrich" those targets from your methyl-seq libraries without distorting original methylation patterns, while reducing per-sample sequencing costs by orders of magnitude compared to WGBS. With complimentary project development assistance and probe design from our scientific experts, myBaits Custom Methyl-Seq is the right solution for your next targeted NGS project.

FEATURES & BENEFITS

- Accurate methylation signal maintained using proprietary probe design algorithm
- Orders of magnitude target enrichment enables high coverage at low cost
- High sensitivity allows detection of rare states in cfDNA/liquid biopsy
- Simple, user-friendly protocol and chemistry are compatible with virtually all library preps

NGS SERVICES INFORMATION

myBaits kits can reduce your sequencing costs and enhance the efficiency of any NGS research project. If a complete solution is needed, from sample preparation to data delivery, our myReads® services team is available to handle projects of any size. Contact our experts today regarding your next project and join a growing community of researchers using one of the most versatile and efficient technologies in genetics research.

Efficiently Detect Complex Methylation Patterns With Custom Target Capture Kits

myBaits Custom Methyl-Seq kits provide focused NGS hybridization capture for any project size. Curated probes in customer-selected loci allow for specific, yet flexible hybridization to complementary target molecules. This dramatically increases the NGS read coverage on regions of interest. Not only does this significantly reduce the sequencing cost by orders of magnitude compared to WGBS, it is more versatile and efficient than amplicon sequencing. Daicel Arbor's innovative probe design starts with different simulated methylation states on both converted genome strands. Subsequent probes are filtered for target specificity to minimize off-target reads. The myBaits Custom Methyl-Seq system employs optimized target enrichment parameters and chemistry to achieve a high reads on-target rate with minimal locus dropout.
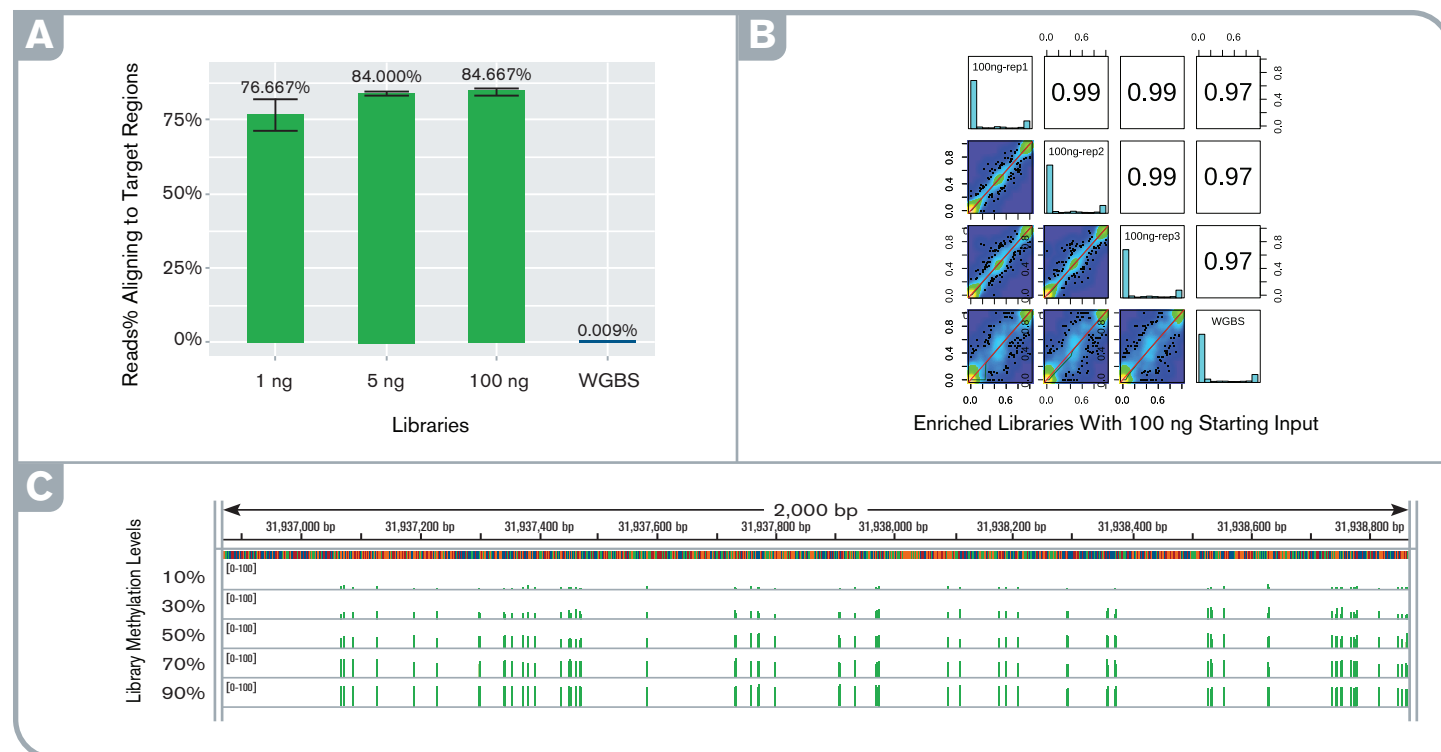
Enrichment of methyl-seq libraries with myBaits is sensitive, efficient, reproducible, and accurate. (A) Targeted regions comprise the vast majority of sequenced reads, for orders of magnitude cost-savings compared to WGBS. (B) CpG methylation levels measured with WGBS are accurately reproduced and show high consistency between replicates. (C) IGV screenshot showing the uniform distribution of methylation levels along the gene STK12 promoter locus observed with the capture libraries at various methylation levels.

PRODUCT TABLE *(additional options available at arborbiosci.com)*

Cat. No.	Description	Reactions	Samples*
300116M.v5	Designs With 1-20K Probes	16	128
300196M.v5	Designs With 1-20K Probes	96	768
300516M.v5	Designs With 80-100K Probes	16	128
300596M.v5	Designs With 80-100K Probes	96	768

* Assuming typical experimental setup with high-quality DNA samples and short-read sequencing. Please see the myBaits Methyl-Seq v1.5 manual for recommended configurations for alternative applications.

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