

High-resolution methylation sequencing

with targeted NGS kits and laboratory services



Why myBaits® hybridization capture for targeted sequencing?



Efficient methylation profiling: Achieve robust, high target coverage across a full range of relevant genomic contexts such as CpG islands, CpG shores, enhancers, promoters, intergenic regions, and more.



Sensitive, versatile, and reliable: With myBaits hybrid capture, you can analyze a wide range of methylation states, including from complex and rare targets like cell-free and circulating tumor DNA. Other methods, such as amplicons, often face challenges with primer design and may not effectively work with short target molecules like cfDNA.



High-end service without the premium price tag: Every myBaits design and myReads NGS service project is backed by comprehensive support from PhD-level scientists, ensuring your project's success and efficiency.

Featured myBaits studies:

Epigenetic sequencing in birds

This study demonstrates the effectiveness of the myBaits Custom Kit panel in capturing genes of interest across various methylation states in a starling species using enzymatic methylation sequencing.

Rubenstein DR, Solomon J (2023). Target-enriched enzymatic methyl sequencing: Flexible, scalable and inexpensive hybridization capture for quantifying DNA methylation. *PLoS ONE* 18(3): e0282672. <https://doi.org/10.1371/journal.pone.0282672>

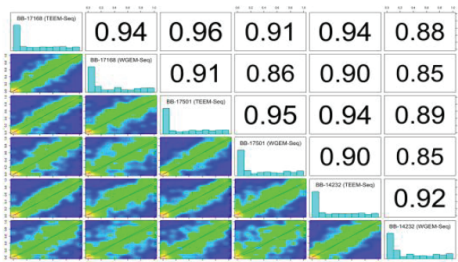


Fig 1. % methylation histograms and scatterplots comparing enriched and whole genome methyl-seq libraries from starling individuals. (Fig 3 from Rubenstein & Solomon 2023, reproduced under CC BY 4.0 creativecommons.org/licenses/by/4.0/)

Circulating tumor DNA profiling in humans

Using myBaits Custom Methyl-Seq kits on control and plasma samples, this study shows the accuracy, scalability, and reproducibility of targeted methylation sequencing of cell-free ctDNA for liquid biopsy cancer research.

Buckley, D.N., et al. (2022). Targeted DNA methylation from cell-free DNA using hybridization probe capture. *NAR Genomics and Bioinformatics*, 4(2) lqac099. <https://doi.org/10.1093/nargab/lqac099>

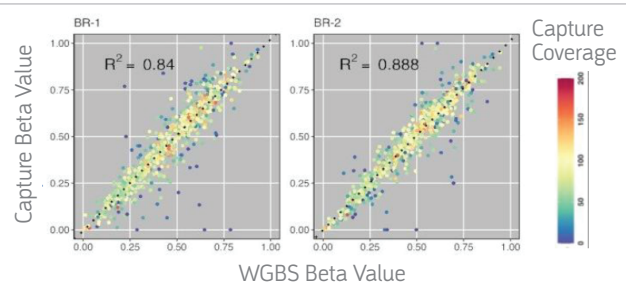


Fig 2. Scatterplots comparing beta values between non-enriched (x-axis) and enriched (y-axis) libraries from 2 samples. (Modified from Fig 5, Buckley et al. 2022, reproduced under CC BY 4.0 creativecommons.org/licenses/by/4.0/)

Daicel Arbor Biosciences provides flexible, cost-effective targeted and whole genome sequencing solutions for any species

Scan the QR code to explore solutions for complex genome methylation



Web: www.arborbiosci.com
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