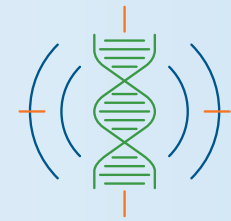


Efficient microbial sequencing

with targeted NGS kits and laboratory services

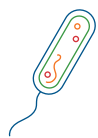
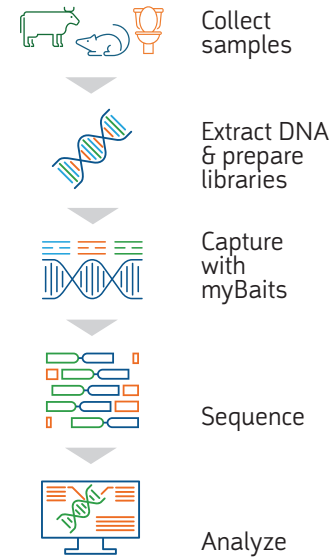


Why myBaits® hybridization capture for targeted sequencing?

Flexible and versatile: myBaits kits feature a simple design compared to other NGS methods like amplicons. Working with any genome or gene set, myBaits eliminates the need for panel optimization, and effectively handles complex regions, including rearrangements.

Perfect for complex samples: Whether working with plant or animal tissues, environmental or trace samples, fecal samples, or other challenging substrates, myBaits capture enables cost-effective profiling of important bacteria, viruses, fungi, parasites, and other microbes.

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.



Bacteria

- 16S rRNA
- Antimicrobial resistance
- *M. tuberculosis*
- Treponema
- *Y. pestis*



Viruses

- African Swine Fever Virus
- Hepatitis B
- Herpesvirus
- HIV
- Respiratory viruses



Parasites

- *Cryptosporidium*
- Malaria
- Protozoa
- *Toxoplasma*
- *Trypanosoma*



Vectors/Reservoirs

- Companion animals
- Mosquitos
- Livestock
- Ticks
- Wildlife

Infectious disease

Antibiotic resistance

Pathogen monitoring

Population genetics

Microbiome / metagenomics

Veterinary diagnostics

Public health surveillance

Vaccine development



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 Twitter: @ArborBio



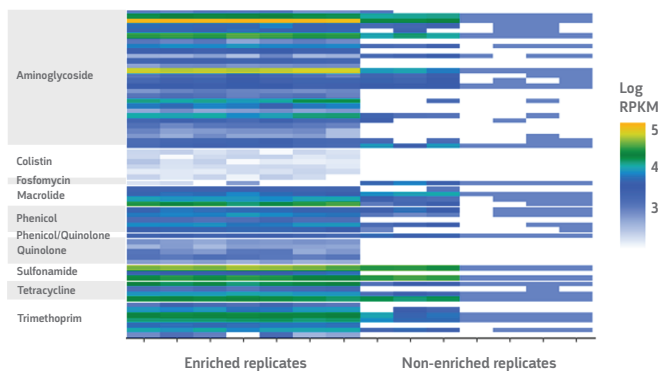
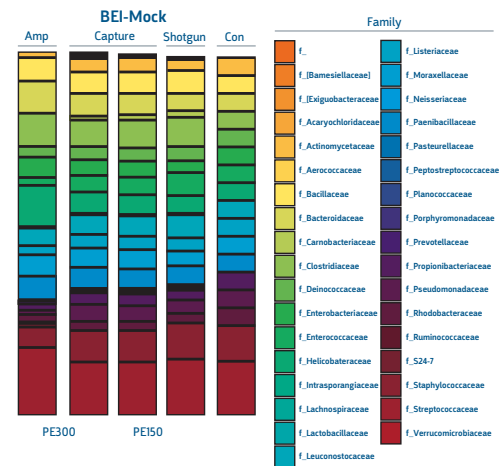


Featured myBaits products:

myBaits Expert 16S-Hyb Kit

- Higher accuracy versus traditional 16S rRNA amplicon sequencing for microbial community composition/profiling
- Better resolution of abundance estimates
- Can enable species-level identification
- Allows for full-length gene characterization
- Avoids bias of focusing on individual variable regions

Stacked bar charts representing relative abundance of a mock community at the family level. Each bar plot represents a different condition. In comparison to 16S amplicon sequencing, myBaits 16S capture identifies more genera and achieves more accurate community abundance estimates.



myBaits Community Panels for Antimicrobial Resistance

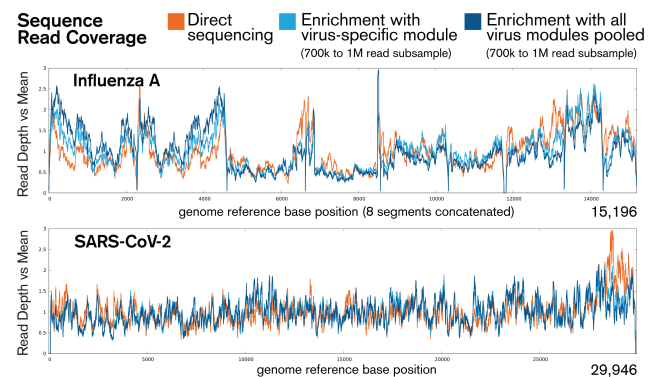
- Comprehensively profile antibiotic resistance gene (ARG) diversity, even from diverse and complex sample types such as soil and feces
- Maintain signals of relative abundance and sensitivity, without the high cost of shotgun sequencing

RPKM analysis of the non-equalized resistance mock community comparing the depth of sequencing of ARGs in enriched vs. non-enriched libraries. From data depicted in Beaudry et al. 2021, *Environ. Microbiol.*

myBaits Expert Respiratory Virus Kit

- Confirm existing variants, including co-infections
- Discover novel viral genome variation
- Characterize tens to thousands of samples on a single sequencing run
- Flexibility to enrich single or multiple viral groups, depending on research needs

Two mock samples with two different viruses (Influenza A and SARS-CoV-2) are enriched with their individual target modules as well as with the combined set of 21 modules, and compared with direct non-enriched shotgun sequencing.



Daicel Arbor Biosciences offers targeted and whole genome sequencing for bacteria, viruses, fungi, and parasites. Contact us for custom solutions!

Scan the QR code to see how to enhance your microbial sequencing



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