DAICEL arbor biosciences

myBaits®
EXPERT PANEL

16S-Hyb

Targeted Sequencing of the Total 16S rRNA Gene

OVERVIEW

Sequencing of the 16S rRNA locus is frequently used to profile bacterial communities. Utilizing the power of in-solution hybridization capture, the **myBaits® Expert 16S-Hyb Panel** enriches the entire gene, rather than just one or two hypervariable regions, leading to better taxonomic resolution and less bias than 16S amplicon sequencing. The panel can also efficiently identify rare taxa that may be contributing to novel phenotypes in conjunction with metagenomic studies, requiring less sequence depth for individual samples. Achieve improved characterization of microbial populations in metagenomic samples in a more cost-effective manner compared to shotgun sequencing alone, and more accurately than 16S amplicon sequencing, by combining 16S-Hyb rRNA gene enrichment with low-coverage shotgun sequencing.

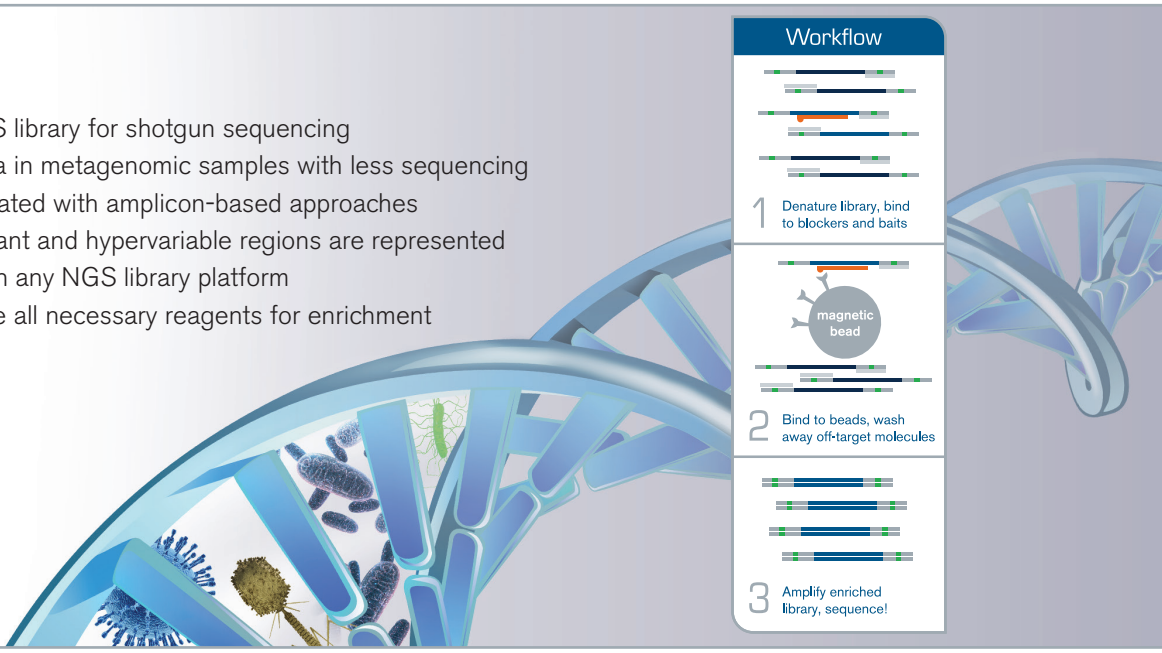
The 16S-Hyb panel is provided as a complete solution kit, including buffers, blockers, and baits, along with an easy-to-use protocol. Alternatively, the myReads® NGS service team at Arbor Biosciences is available to perform library preparation, target capture, and sequencing for your entire project.

FEATURES & BENEFITS

Convenient – Use the same NGS library for shotgun sequencing
Cost Effective – Identify rare taxa in metagenomic samples with less sequencing
Less Bias – Avoids issues associated with amplicon-based approaches
Excellent Resolution – All constant and hypervariable regions are represented
Open Platform – Compatible with any NGS library platform
Complete Solution – Kits include all necessary reagents for enrichment

APPLICATIONS

- Metagenomics
- Environmental Sampling
- Microbiome Analysis



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16S-Hyb Improves Accuracy Compared to Amplicon Approach

The myBaits 16S panel was compared to 16S amplicon and shotgun metagenomic sequencing for samples obtained from a mock community, mouse feces, and rat colon. The unenriched metagenomic sequences contained ~0.1-0.2% 16S reads; enrichment led to a 350-fold enrichment for the mock communities and 450-fold enrichment for the mouse feces and rat colon, with 60-70% of reads on target. Overall, the profile of the enriched samples using either MiSeq or HiSeq sequencing much more closely resembled the mock and shotgun profiles versus the amplicon data in all experiments.

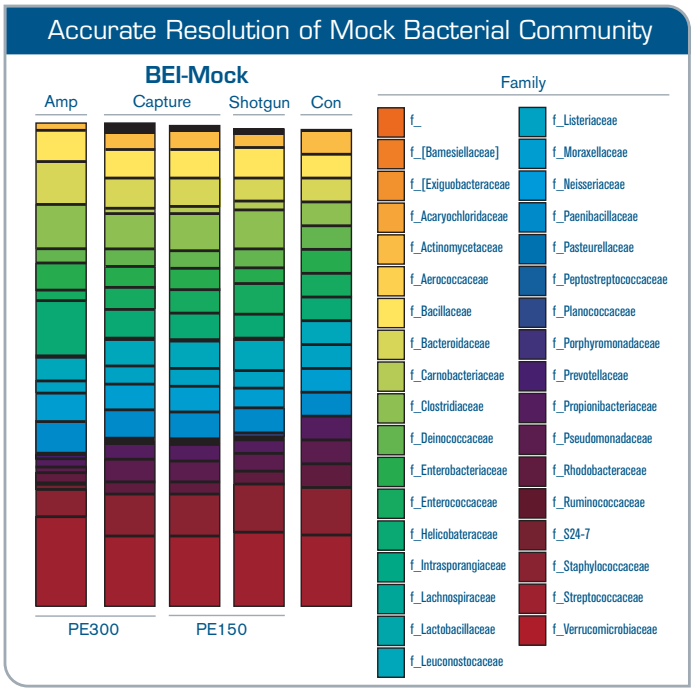

Fig 1. *The BEI Resources mock community contains a bacterial population of known content (Column 5) and was analyzed by 16S amplicon sequencing using MiSeq PE 300 (Column 1), myBaits 16S enrichment and sequencing using MiSeq PE 300 (Column 2) or HiSeq PE 150 (Column 3), and shotgun sequencing using HiSeq PE 150 (Column 4). Enriched and unenriched reads were trimmed and filtered, mapped against the GreenGenes database using bbmap, and analyzed. Amplicon reads were assessed using the Dada2 pipeline and GreenGenes database.*

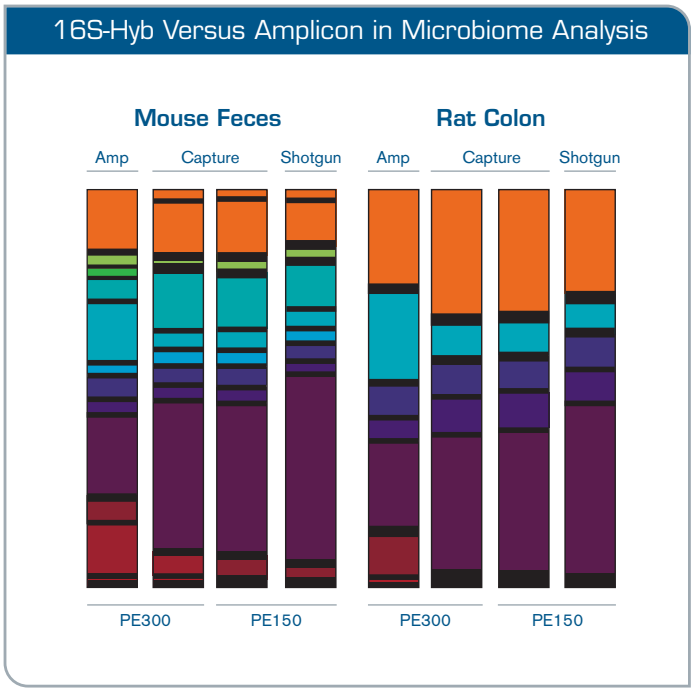

Fig 2. *DNA extracted from mouse feces and rat colon was analyzed by 16S amplicon sequencing using MiSeq PE 300 (Columns 1,5), myBaits 16S enrichment and sequencing using MiSeq PE 300 (Columns 2,6) or HiSeq PE 150 (Columns 3,7), and shotgun sequencing using HiSeq PE 150 (Columns 4,8). Enriched and unenriched reads were trimmed and filtered, mapped against the GreenGenes database using bbmap, and analyzed. Amplicon reads were assessed using the Dada2 pipeline and GreenGenes database.*

PRODUCT TABLE

Cat. No.	Description	Reactions
308616	myBaits 16S-Hyb Panel	16
308648	myBaits 16S-Hyb Panel	48
308696	myBaits 16S-Hyb Panel	96

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