

myBaits® Expert 16S-Hyb Kit

High-resolution microbiome characterization with targeted full-length 16S rRNA gene sequencing

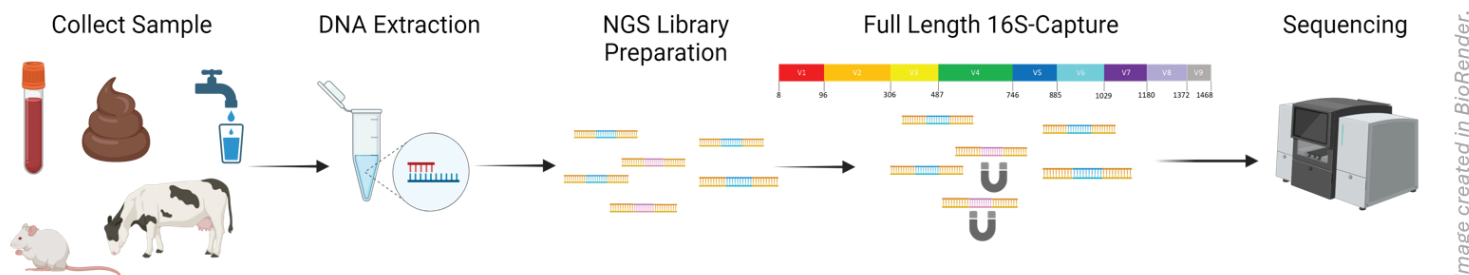


Image created in BioRender.

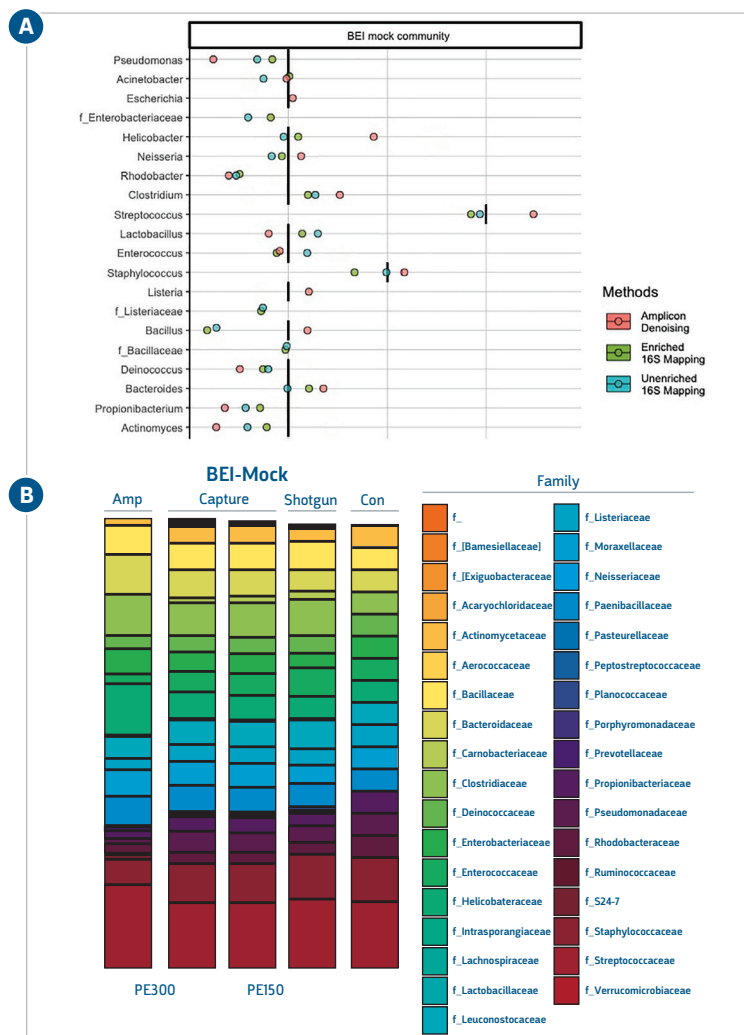
- ✓ Increased *accuracy* on identifying microbial community composition
- ✓ Better *resolution* of abundance estimates
- ✓ Can enable *species level* identification
- ✓ Allows for *full length* gene characterization on benchtop sequencers
- ✓ Avoids *bias* of focusing on individual variable regions

Higher accuracy and resolution than 16S amplicon sequencing

Sequencing of the 16S rRNA locus by targeting one or more variable regions with 'universal' primer sets is often used to metagenomically profile bacterial communities. In comparison to 16S amplicon sequencing, myBaits 16S capture identifies more genera and **achieves more accurate community abundance estimates** (figures 1, right).

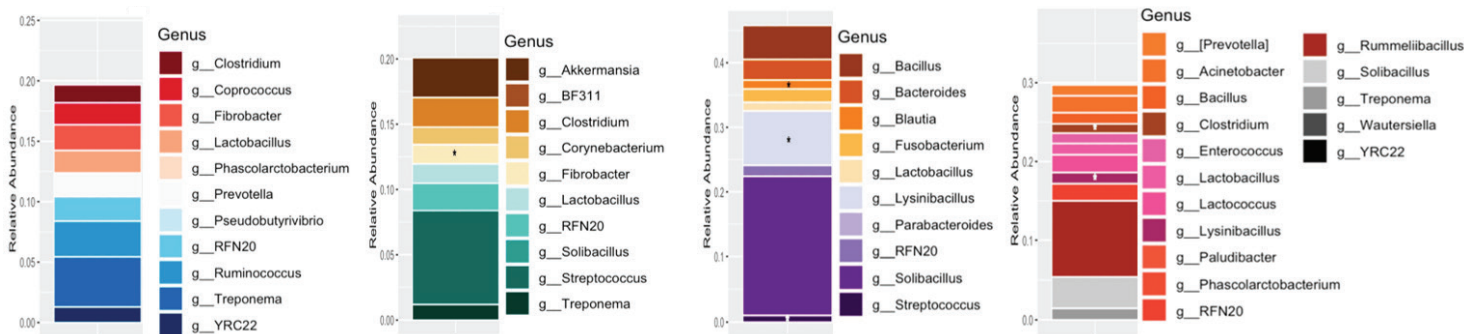
And for even greater data resolution, myBaits 16S capture can be combined with shallow shotgun sequencing from the same NGS library, **enabling comprehensive microbiome profiling** for a fraction of the cost and analysis time of deep sequencing experiments.

Figure 1. (a) A lollipop chart reflecting known content (black lines) with colored dots signifying measured relative abundance from their respective approach. Redrawn from fig 3, Beaudry et al. 2021, Frontiers in Microbiology, reproduced under CC BY 4.0. (b) Stacked bar charts representing relative abundance of a mock community at the family level. Each bar plot represents a different condition.



Compatible with a wide range of samples and DNA qualities

myBaits 16S capture has been used on a wide range of sample types, including microbial communities, animal samples, and environmental samples. In the data shown below, four different horse fecal samples were analyzed with the myBaits 16S-Hyb kit, depicting a wide range of bacterial community compositions that can be retrieved with the same enrichment workflow (images from Álvarez Narváez et al. 2024 figure 4, DOI 10.3390/ani14030445, license CC BY 4.0).



References

- Beaudry, M.S. et al. (2021). Improved Microbial Community Characterization of 16S rRNA via Metagenome Hybridization Capture Enrichment. *Frontiers in Microbiology*. DOI 10.3389/fmicb.2021.644662
- Álvarez Narváez, Sonsiray, et al. (2024). Improved Equine Fecal Microbiome Characterization Using Target Enrichment by Hybridization Capture. *Animals*. DOI 10.3390/ani14030445

Applications

- Targeted sequencing for DNA samples for bacterial community composition and abundance
 - Human, plant, animal, fungus, virus, or bacteria samples
 - Degraded, museum, herbarium, or historical samples

Ordering information

Catalog #	Description
308608.v5	myBaits Expert 16S-Hyb, 8 reactions
308616.v5	myBaits Expert 16S-Hyb, 16 reactions
308648.v5	myBaits Expert 16S-Hyb, 48 reactions
308696.v5	myBaits Expert 16S-Hyb, 96 reactions

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