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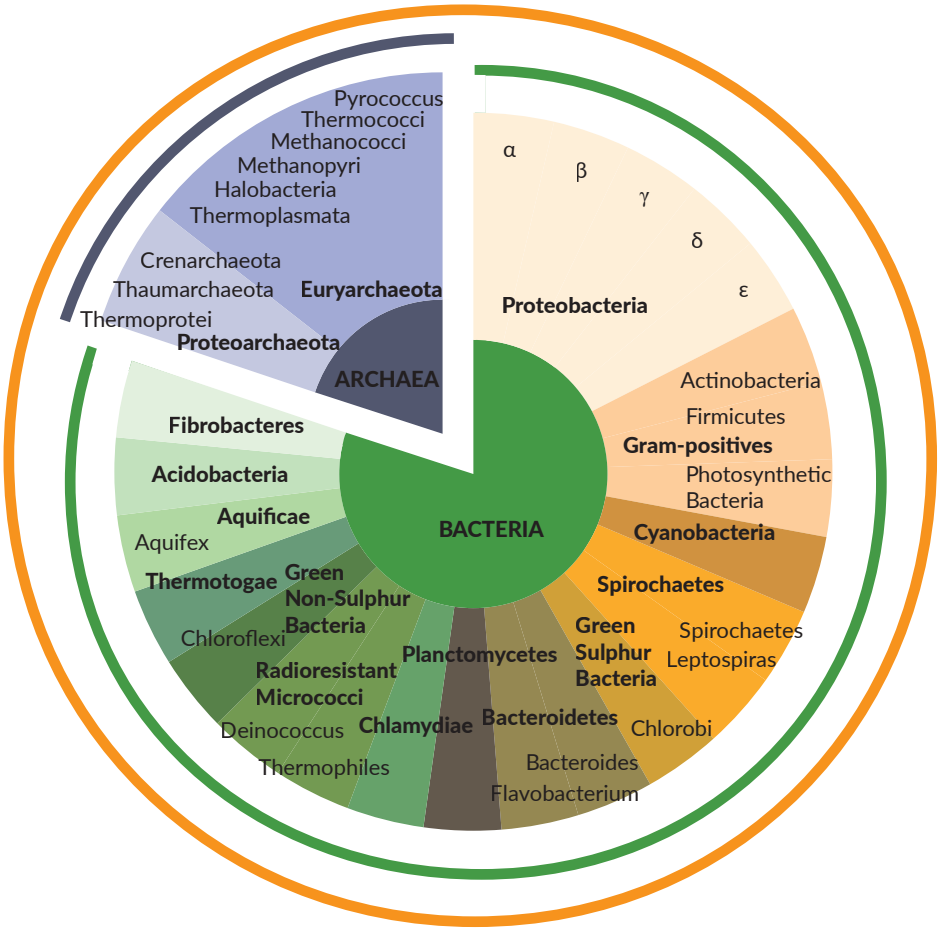
Better RNA-Seq for Microbes

Universal, Efficient rRNA Depletion with riboPOOLs

Improve and economize microbial RNA-Seq experiments

ribosomal RNA (rRNA) accounts for 80-90% of the transcriptome limiting detection efficiency of desired RNAs by RNA-Seq. The removal of rRNAs greatly improves and economizes RNA-Seq. riboPOOLs are highly complex pools of biotinylated DNA oligos, designed using our Pack-Hunter approach. riboPOOLs offer a flexible & efficient solution for selective and bias-free rRNA depletion in any RNA sample.



Benefits

- ✓ Better performance for metatranscriptomics/ microbiome sequencing
- ✓ Applicable as Combination riboPOOL for mixed human & bacteria samples
- ✓ Optimal coverage of rRNA based on our Pack Hunter targeting approach
- ✓ Easy & fast workflow
- ✓ Wide RNA input range (10 ng - 3 µg)

Pan-Prokaryote riboPOOL

Wide species coverage for prokaryotes including Bacteria & Archaea

Pan-Bacteria riboPOOL

Optimal rRNA coverage of bacteria (gram positive and negative)

Pan-Archaea riboPOOL

Optimal rRNA coverage of archaea (Proteo- and Euryarchaeota)

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Pan-Prokaryote riboPOOL, Pan-Bacteria riboPOOL and Pan-Archaea riboPOOL have been validated by RNA-Seq on many species:

Species Tested

- Acetobacterium woodii
- Acinetobacter baumannii
- Bacteroides thetaiotaomicron
- Bifidobacterium breve
- Burkholderia glumae
- Campylobacter jejuni
- Clostridioides difficile
- Clostridium saccharoperbutylacetonicum
- Escherichia coli
- Fusobacterium nucleatum
- Helicobacter pylori
- Janthinobacterium sp.
- Methanocaldococcus jannaschii
- Moorella thermoacetica
- Mycobacterium tuberculosis
- Pseudomonas aeruginosa
- Pseudomonas putida
- Pyrococcus furiosus
- Salmonella typhimurium
- Sinorhizobium fredii
- Sporomusa ovata
- Staphylococcus aureus
- Streptococcus pneumoniae
- Streptococcus pyogenes
- Streptomyces coelicolor
- Sulfolobus acidocaldarius
- Sulfolobus solfataricus
- Thermoanaerobacter kivui
- Thermotoga maritima

riboPOOLs show high rRNA depletion efficacy across tested species (i.e. *Escherichia coli*, *Staphylococcus aureus*), reaching up to 99% rRNA depletion efficiency. rRNA depletion efficiency may vary across species, sample type and experimental conditions.

On top of excellent efficiency, in-house and customer data suggest superb reproducibility between biological replicates.

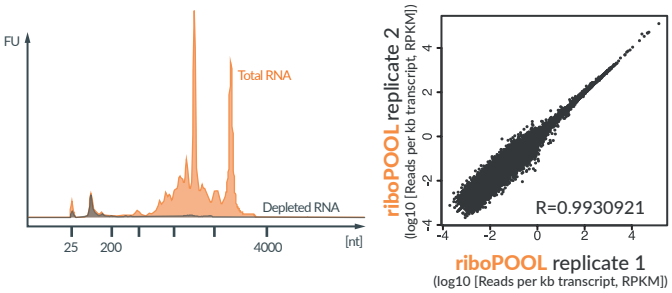

Figure 1: **Highly reproducible & efficient rRNA depletion with riboPOOLs**. Left: Agilent Bioanalyzer data demonstrating rRNA depletion with Pan-Archaea riboPOOL on H. volcanii total RNA. Sequencing revealed 97% depletion efficiency. Right: High reproducibility between biological replicates with human riboPOOL.

riboPOOL IDs:

	riboPOOL ID:
Bacteria & Archaea Pan-Prokaryote riboPOOL	003
Bacteria Pan-Bacteria riboPOOL (Gram Positive & Gram negative Bacteria)	026
Archaea Pan-Archaea riboPOOL	027

Available Formats:

1. riboPOOL kits
   (includes buffers, streptavidin-magnetic beads, reaction tubes and ethanol precipitation reagents)

6 rx Trial	*12 rx*	*24 rx*	*96 rx*
Catalog-No. dp-K006	Catalog-No. dp-K012	Catalog-No. dp-K024	Catalog-No. dp-K096

2. Probes alone with nuclease-free water

12 rx	24 rx	96 rx
Catalog-No. dp-P012	Catalog-No. dp-P024	Catalog-No. dp-P096

3. siBeads

12 rx	24 rx	96 rx
Catalog-No. dp-M012	Catalog-No. dp-M024	Catalog-No. dp-M096