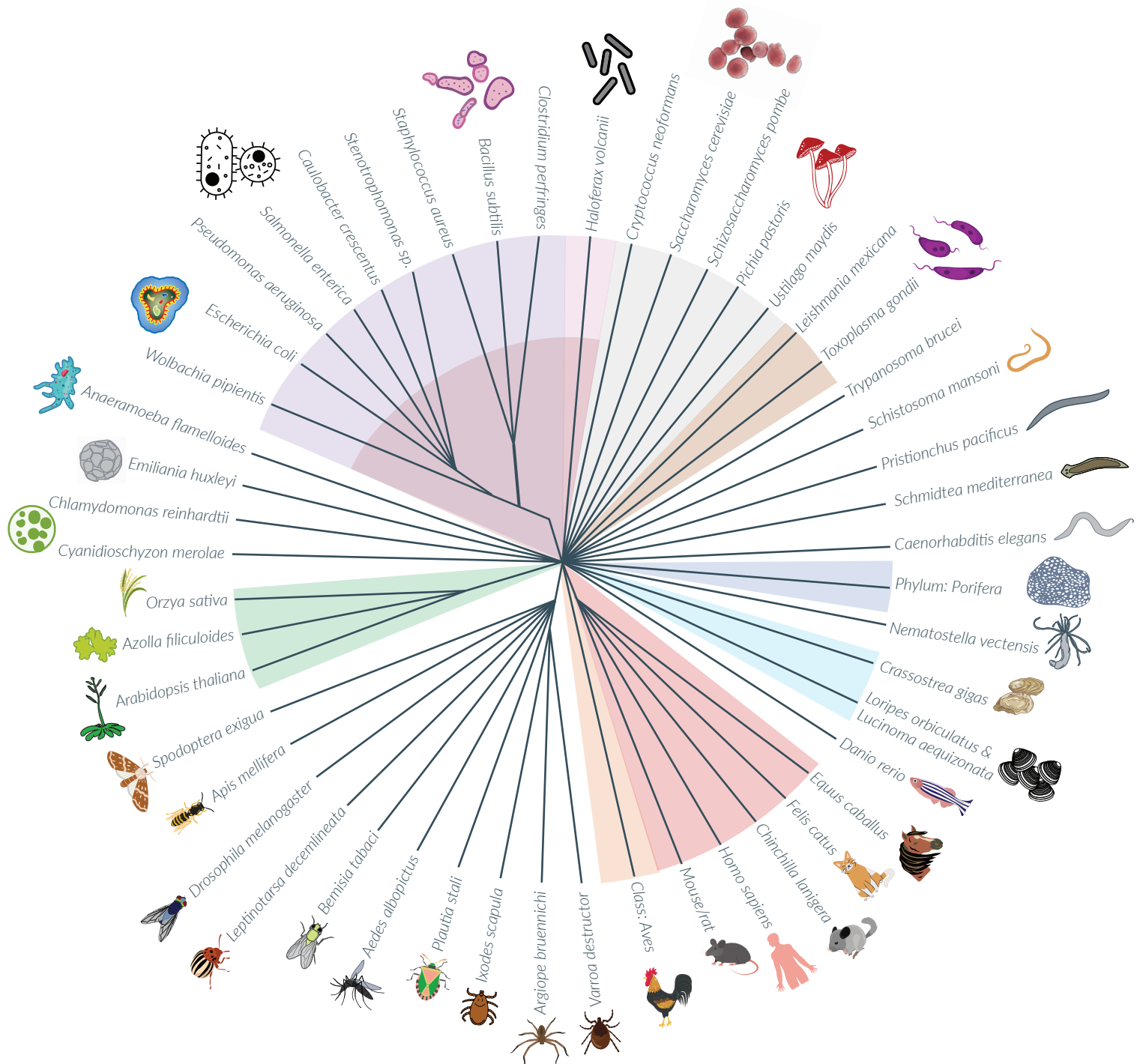












# Improve your NGS workflow with **riboPOOLS** ribosomal RNA depletion kits for any species



## Pan-riboPOOLS

- |  |  |
|--|--|
|  Pan-Plant  |  Pan-Bacteria   |
|  Pan-Bird   |  Pan-Archaea    |
|  Pan-Mammal |  Pan-Prokaryote |
|  Pan-Sponge |  Pan-Fungi      |
|  Pan-Mussel |  Blood Parasite |

## Special riboPOOLS

### riboPOOLS Mix

Seawater (standard RNA-Seq)

### riboPOOLS for abundant RNAs

Human Globin mRNA (standard RNA-Seq)

Poly A (Poly-Adenylated RNAs)

SARS-CoV-2 RNA (standard RNA-Seq)

# riboPOOLS species diversity

## rRNA depletion for any species

Check-out our **riboPOOL phylogenetic tree**, if your species is not listed we can design a species-specific or custom riboPOOL .

### Why riboPOOLS?

ribosomal RNA (rRNA) accounts for 80-90% of the transcriptome, limiting detection efficiency of desired RNAs (e.g. mRNAs) by RNA-Sequencing (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.

### Single-species riboPOOLS

Single-species riboPOOLS are available for both well-studied, as well as lesser-known species. Single-species riboPOOLS are specifically designed based on the species' rRNA to target both conserved and non-conserved regions. Moreover, single species riboPOOLS are used on high to medium quality RNA and result in high rRNA depletion efficiency.

### Pan-riboPOOLS

The Pan-riboPOOLS are a versatile rRNA depletion solution that allows for simple mono- and multitranscriptomic studies using a single-step rRNA depletion for a phylogenetic group (e.g., bacteria, fungi, or mammals). The option to combine riboPOOLS facilitates single-step rRNA depletion in mixed samples such as environmental, blood, or infected tissue (e.g., SARS-CoV-2) samples. The so-called combination riboPOOLS enable simple metatranscriptomics studies by combining 2-4 riboPOOLS of non-related species.

### Abundant RNA

Some tissues express very high levels of certain RNAs. In blood, for instance, globin mRNA makes up 30-80% of total RNA. We offer riboPOOLS for abundant transcripts which can be combined with standard riboPOOLS for an efficient, one-step depletion of all abundant RNAs.

### Special applications riboPOOLS

#### Ribosome profiling (Ribo-Seq)

Ribo-Seq riboPOOLS cover the entire rRNA sequence with tiled oligos plus the overrepresented rRNA contaminants that are unique to ribosome profiling.

#### FFPE samples & degraded samples

For optimal rRNA depletion, FFPE riboPOOLS cover the entire rRNA sequence with tiled oligos.

### Available Formats:

#### riboPOOLS kits with cleanUP module

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

#### Probes alone

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

*(includes buffers, streptavidin-magnetic beads, reaction tubes, ethanol precipitation reagents and RNA clean-up beads)*