

Better RNA-Seq for all species with **riboPOOLS** rRNA depletion kits

Improve and economize your RNA-Seq experiments by removing rRNAs

Why riboPOOLS?

ribosomal RNA (rRNA) accounts for 80-90% of the transcriptome limiting detection efficiency of desired RNAs (e.g. mRNAs) by RNA-Seq. The removal of rRNAs greatly improves and economizes RNA-Seq. **riboPOOLS** are highly complex pools of biotinylated DNA oligos, offering a flexible & efficient solution for selective and bias-free rRNA depletion in any RNA sample.

Any Species or 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. riboPOOLS can be custom designed for any species and any abundant transcript. Furthermore, all riboPOOLS can be freely combined for any type of complex RNA sample.

Reproducible & Efficient rRNA Removal

riboPOOLS show high rRNA depletion efficacy across species, reaching up to 99%. For strongly degraded RNA samples we offer optimized riboPOOLS to achieve even & efficient rRNA removal of up to 95%. To meet the special requirements of ribosome profiling (Ribo-Seq) we develop dedicated **Ribo-Seq riboPOOLS** for a growing number of species. On top of excellent efficiency, in-house and customer data suggest excellent reproducibility between biological replicates.

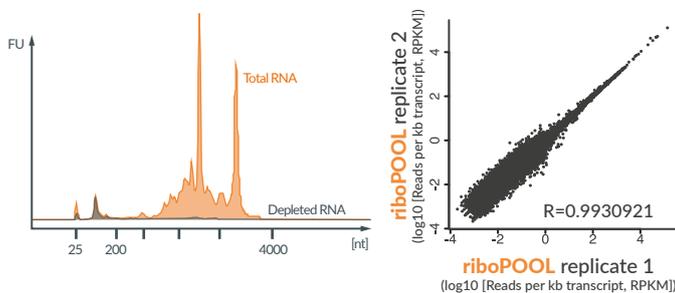


Figure 1: **Highly reproducible & efficient rRNA depletion with riboPOOLS.** Left: Agilent Bioanalyzer data demonstrating rRNA depletion with Pan-Archaea riboPOOL on *H. volcanii* total RNA. Sequencing revealed 97% depletion efficiency. Right: High reproducibility between biological replicates with human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

- ✓ Efficient & Reproducible RNA-Seq
- ✓ rRNA Depletion For Any Species Or RNA
- ✓ Easy & Fast rRNA Depletion Workflow

Simple & Fast Workflow

riboPOOLS' hybridization-based workflow allows fast & easy rRNA removal. The workflow follows four main steps:

1. Preparation of siBeads & riboPOOL
2. Hybridization of riboPOOL to target RNA
3. rRNA depletion
4. RNA clean up

The workflow can be completed within 70 minutes and allows a wide RNA input range of 10 ng - 3 µg. The riboPOOL workflow can be scaled up to 10 µg and is automation-friendly for high throughput rRNA removal. After the rRNA removal, the resulting RNA can be processed by any library preparation kit.

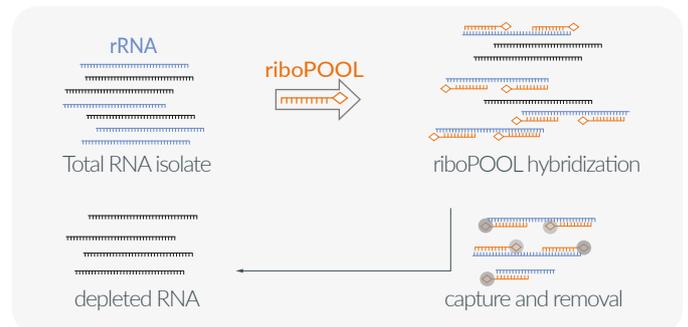


Figure 2: **Schematic riboPOOL Workflow** 1. Preparation of siBeads & riboPOOL 2. Hybridization of riboPOOL to target RNA 3. rRNA depletion 4. RNA clean up

Available Formats:

1. Probes alone with nuclease-free water

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

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

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

Pan-riboPOOLs

| | riboPOOL ID: |
|---|--------------|
| Bacteria & Archaea | |
| Pan-Prokaryote riboPOOL | 003 |
| Bacteria | |
| Pan-Bacteria riboPOOL | 026 |
| <small>(Gram Positive & Gram negative Bacteria)</small> | |
| Pan-Actionobacteria riboPOOL | 035 |
| Archaea | |
| Pan-Archaea riboPOOL | 027 |
| Plants | |
| Pan-Plant riboPOOL | 031 |
| Vertebrata | |
| Pan-Mammal riboPOOL | 041 |
| Pan-Bird riboPOOL | 032 |
| Mollusca | |
| Pan-Mussel riboPOOL | 089 |
| Fungi | |
| Pan-Fungi riboPOOL | 043 |
| Other | |
| Seawater riboPOOL | 068 |
| Blood Parasite riboPOOL | 051 |
| Pan-Sponge riboPOOL | 044 |

Special Applications riboPOOLs

FFPE & degraded RNA samples

| | riboPOOL ID: |
|--|--------------|
| Vertebrata | |
| Equus caballus | 092 |
| Felis catus | 093 |
| Homo sapiens | 057 |
| Homo sapiens / Mus musculus / Rattus Norvegicus | 056 |
| Mus musculus / Rattus Norvegicus | 058 |
| Arthropoda | |
| Drosophila melanogaster | 061 |
| Nematoda | |
| Caenorhabditis elegans | 062 |

Ribosome Profiling (Ribo-Seq)

| | riboPOOL ID: |
|--|--------------|
| Mus musculus / Rattus Norvegicus | 052 |
| Homo sapiens | 042 |
| Homo sapiens / Mus musculus / Rattus Norvegicus | 050 |
| Drosophila melanogaster | 076 |
| Caenorhabditis elegans | 067 |
| Trypanosoma brucei | 077 |
| Leishmania mexicana | 078 |
| Azolla filiculoides | 079 |
| Pristionchus pacificus | 082 |
| Toxoplasma gondii | 083 |

Single Species riboPOOLs

| | riboPOOL ID: |
|---|--------------|
| Bacteria | |
| Bacillus subtilis | 012 |
| Caulobacter crescentus | 013 |
| Clostridium perfringens | 015 |
| Escherichia coli | 004 |
| Pseudomonas aeruginosa | 018 |
| Salmonella enterica | 022 |
| Staphylococcus aureus | 021 |
| Stenotrophomonas sp. | 023 |
| Wolbachia pipientis | 086 |
| Archaea | |
| Haloferax volcanii | 016 |
| Plants & Algae | |
| Arabidopsis thaliana | 008 |
| Chlamydomonas reinhardtii | 071 |
| Cyanidioschyzon merolae | 075 |
| Emiliania huxleyi | 033 |
| Oryza sativa | 009 |
| Vertebrata | |
| Chinchilla lanigera | 014 |
| Danio rerio | 010 |
| Gallus gallus domesticus | 060 |
| Homo sapiens | 054 |
| Human blood | 094 |
| Mus musculus / Rattus Norvegicus | 055 |
| Nematoda | |
| Caenorhabditis elegans | 039 |
| Platyhelminthes | |
| Schmidtea mediterranea | 028 |
| Schistosoma mansoni | 090 |
| Sponges & Cnidarians | |
| Amphimedon queenslandica | 011 |
| Nematostella vectensis | 087 |
| Fungi | |
| Cryptococcus neoformans | 084 |
| Filamentous-Fungi | 006 |
| Pichia pastoris | 019 |
| Saccharomyces cerevisiae | 005 |
| Schizosaccharomyces pombe | 059 |
| Ustilago maydis | 024 |
| Arthropoda | |
| Aedes albopictus | 047 |
| Apis mellifera | 073 |
| Argiope bruennichi | 074 |
| Bemisia tabaci | 080 |
| Drosophila melanogaster | 007 |
| Ixodes scapularis | 030 |
| Leptinotarsa decemlineata | 072 |
| Plautia stali | 020 |
| Spodoptera exigua | 085 |
| Varroa destructor | 081 |
| Mollusca | |
| Crassostrea gigas | 063 |
| Loripes orbiculatus and Lucinoma aequizonata (Clams) | 017 |
| Other: | |
| SARS-CoV-2 RNA | 038 |
| Modules: | |
| human Globin mRNA | 025 |
| human - 7SL | 300 |
| Poly A (Poly-Adenylated RNAs) | 034 |

Custom riboPOOLs design (for the Species of your choice)

If your species is not listed above, create a Custom riboPOOL with our One-Time riboPOOL Set Up Service.



Contact us at info@siTOOLS.de or +49 (0) 89 12501 4800

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