High Input riboPOOLS

rRNA depletion from **up to 30µg** total RNA
for RNA sequencing of **any species**

www.sitoolsbiotech.com
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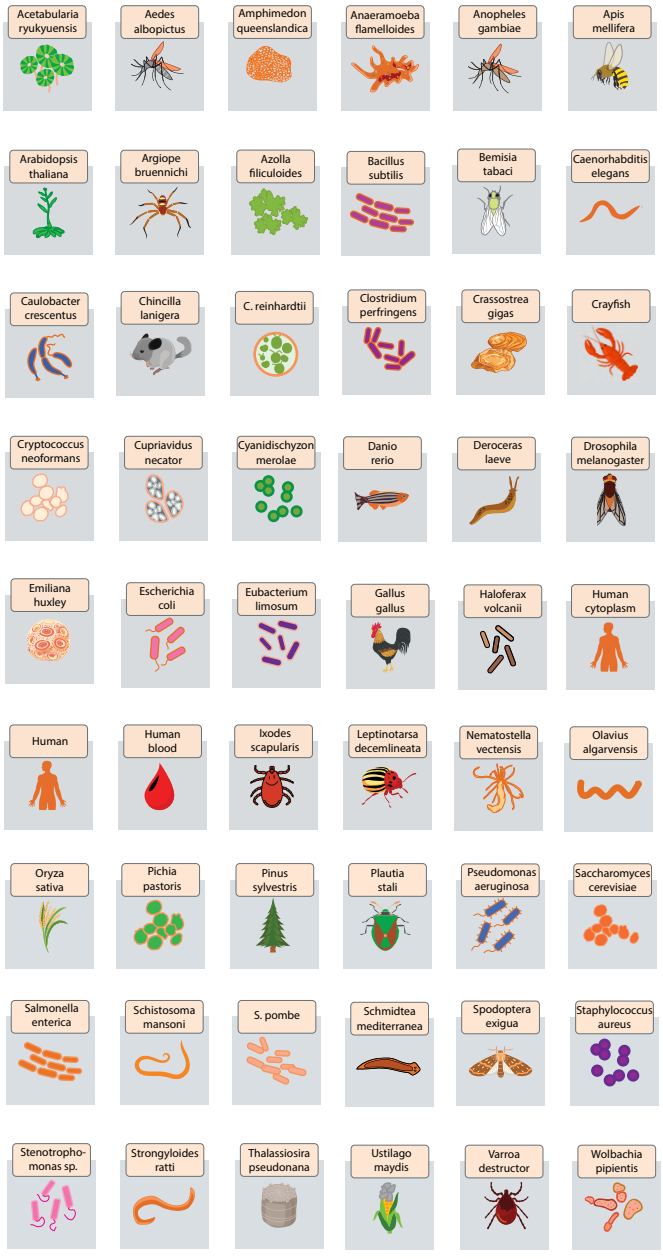
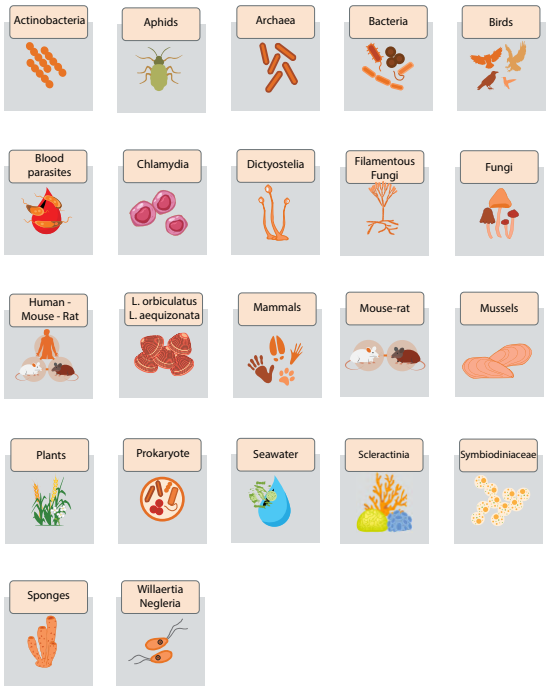
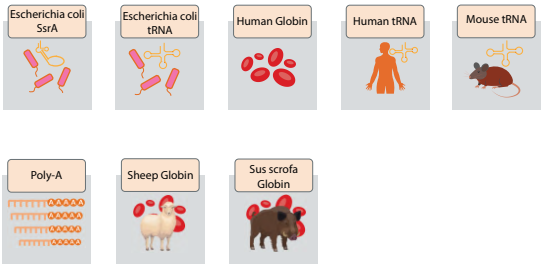
Single Species riboPOOLs



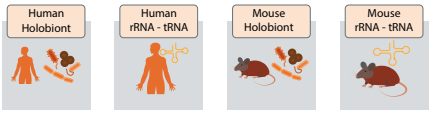
Multiple Species riboPOOLs



Additional Depletion Modules



Combination riboPOOLs



Applications

- **Direct RNA sequencing** (Oxford Nanopore)
  - Requires high RNA input due to absence of PCR amplification
  - Supports RNA modification analysis (epitranscriptomics)
- **Detection of rare transcripts**
  - rRNA depletion enriches biologically relevant transcripts
  - Improves detection of rare and low-abundance RNAs
- **Long-read sequencing workflows**
  - Compatible with Oxford Nanopore Technologies and PacBio
  - Improves transcript and splice variant characterization

You don't see what you are looking for?

Contact us at info@sitools.de to enquire about:

- **Custom combinations:** combine up to 4 of any probe set.
- **Custom riboPOOLs:** design of novel depletion probes for your species of interest.

riboPOOL Depletion Workflow

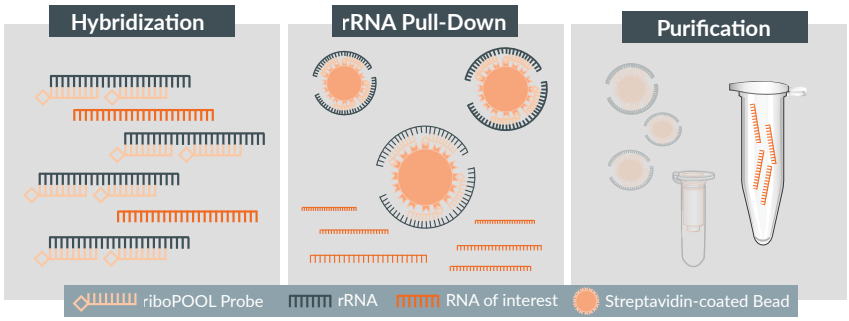


Fig. 1 Schematic overview of the riboPOOL rRNA depletion workflow.

- ✓ Fast (< 90 minutes)
- ✓ Enzyme-free
- ✓ Any Species
- ✓ up to 30 µg input
- ✓ selective recovery of
  - all RNA (> 17 nt) or
  - large RNAs (> 200 nt)

High input riboPOOL Performance (Direct RNA Sequencing)

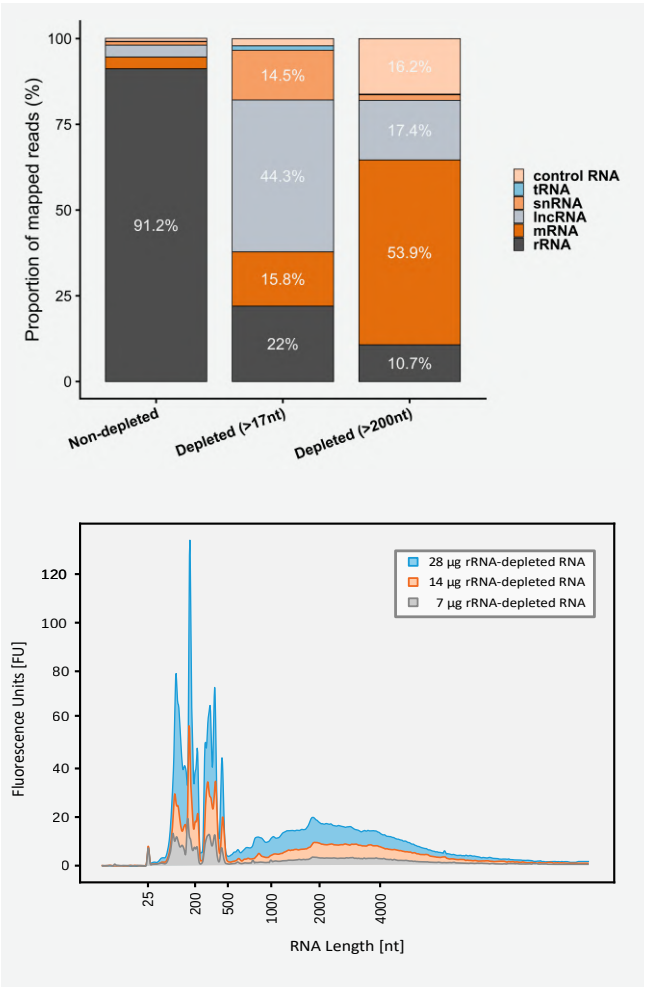


Fig. 2 Top) Proportion of sequencing reads mapping to rRNA, mRNA, lncRNA, snRNA, tRNA, and yeast spike-in control RNA in A549 cells samples before (non-depleted) and after rRNA depletion using the human high-input riboPOOL (depleted). Data were generated by direct RNA sequencing using Oxford Nanopore Technologies following in vitro polyadenylation. For depleted samples, analyses were performed either on all retained fragments >17 nt or on a size-selected fraction containing only reads >200 nt. **Bottom)** Bioanalyzer profiles after ribodepletion of 7, 14 and 28 µg of total input RNA (all fragments > 17 nt).

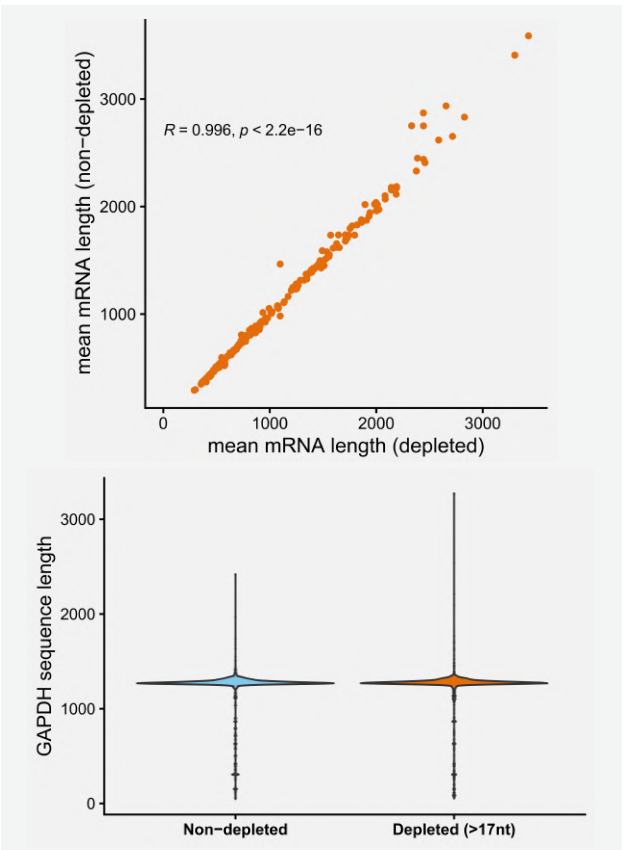


Fig. 3 Mean mRNA length **(top)** and GAPDH sequence length **(bottom)** in non-depleted and rRNA-depleted A549 cells samples. Data were generated by direct RNA sequencing using Oxford Nanopore Technologies without in vitro polyadenylation

Free coverage assessment

Would you like to have more information on how well Pan-riboPOOL probes are expected to target the rRNAs of your species of interest?

Simply contact us at info@sitools.de

Kit content

Reagent	6 reaction kit	12 reaction kit	24 reaction kit
High-Input Hybridization Buffer H-HB	1 x 1 ml	1 x 1 ml	1 x 1 ml
High-Input Depletion Buffer H-DB	1 x 8 ml	1 x 8 ml	2 x 8 ml
H_2O – Nuclease-free water	1 x 1 ml	1 x 1 ml	1 x 1 ml
Streptavidin-coated magnetic beads	1x 3.3 ml	1x 6.6 ml	1x 13.2 ml
riboPOOL - RP*	1x lyophilized powder	1x lyophilized powder	1x lyophilized powder