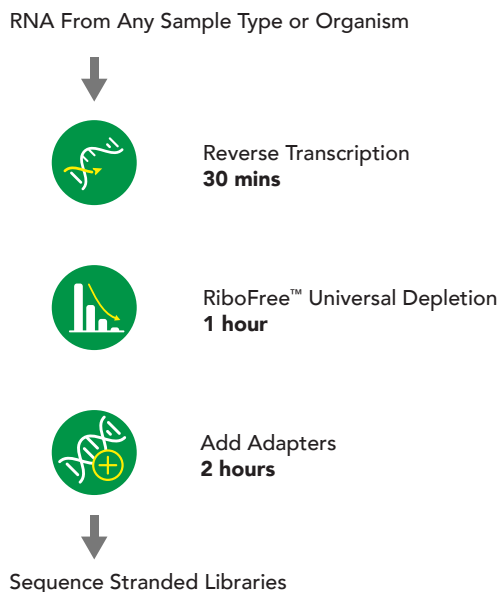


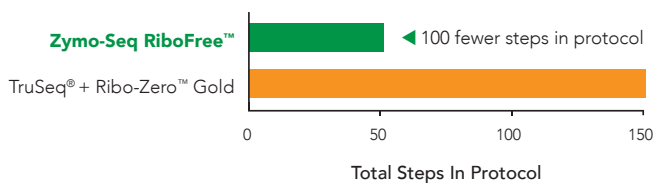
Zymo-Seq RiboFree™ Total RNA Library Kit

- **The Fastest & Easiest Kit:** Prepare stranded, RiboFree™ libraries from total RNA in 3.5 hours.
- **Compatible With Any Organism:** Novel probe-free technology depletes rRNA & globin from any RNA source.
- **The Most Accurate:** Eliminate bias from rRNA depletion.

The Fastest RNA-Seq Library Prep Kit



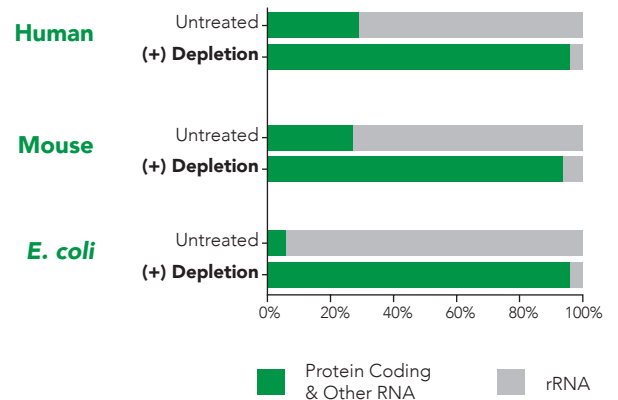
The Easiest Protocol For Library Prep



The Zymo-Seq RiboFree™ Total RNA Library Kit minimizes the number of reagents and steps needed to generate stranded rRNA-depleted total RNA libraries. 60% less pipetting significantly reduces the amount of hands-on time and saves over 6 hours compared to the TruSeq® Stranded Total RNA kit.

The Only Universal rRNA Depletion

Use One Kit For Any Sample Type



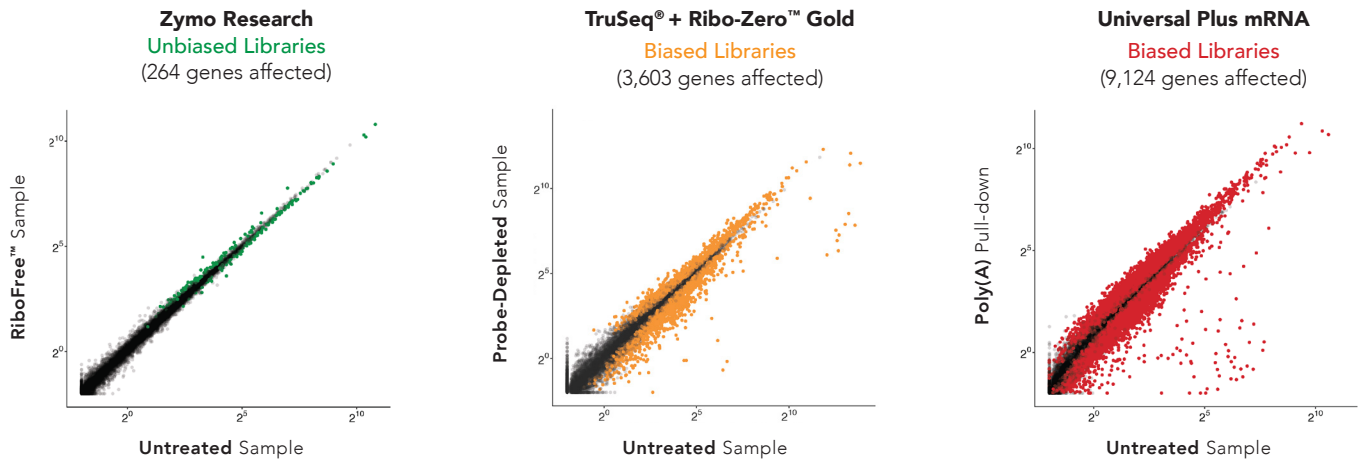
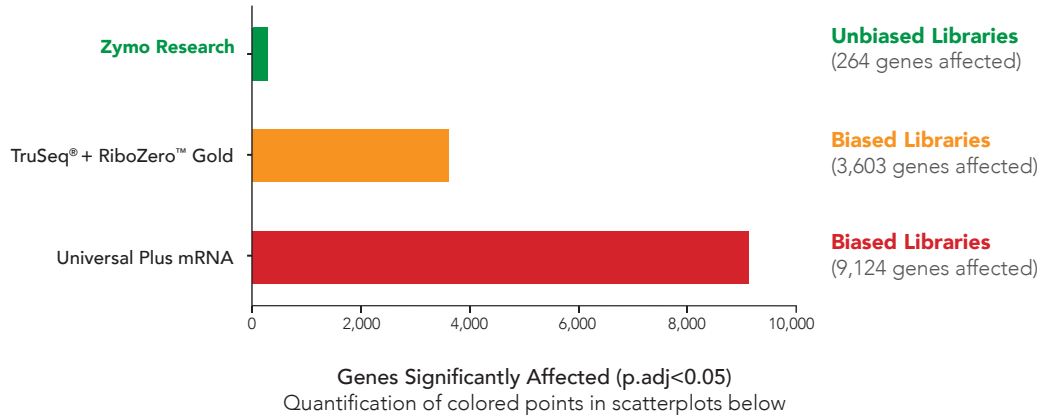
RiboFree™ Universal Depletion enzymatically removes rRNA from any sample type. Paired-end sequencing was performed on stranded total RNA-Seq libraries, both with and without RiboFree™ Universal Depletion. Read pairs were aligned to their respective genomes using the STAR aligner. Read classes were defined using a combination of Ensembl GTF gene biotypes and RepBase repeat masker annotations. Number of reads overlapping each annotation class were divided by total reads in that library to calculate percent reads of each annotation class.

RiboFree™ Universal Depletion Also Validated With:

- ✓ *Arabidopsis*
- ✓ Rat
- ✓ Whole Blood
- ✓ Peripheral Leukocytes
- ✓ FFPE
- ✓ And Many More!

Probe-Free Technology Eliminates Bias

35x Less Biased Expression Profiles



RiboFree™ Universal Depletion maintains native expression profiles unlike TruSeq® Total RNA [probe-based Ribo-Zero™ Gold] and Universal Plus mRNA-Seq [poly(A) enrichment]. Paired-end sequencing was performed on libraries prepared from Universal Human Reference RNA (Invitrogen) containing ERCC Spike-In Mix 1 (Life Technologies), both with and without rRNA removal or poly(A) enrichment. Libraries were sequenced to a depth of ~35 million reads per library, and read pairs were aligned to the hg38 human genome using the STAR aligner. Read classes were defined using Ensembl GTF gene biotypes. The DESeq2 package was used to apply the “apeglm” log-fold-change shrinkage estimator to determine which of the 20,004 protein coding genes and ERCC Spike-In transcripts were significantly affected (p.adj < 0.05) by rRNA removal. Significantly affected transcripts are represented as colored points in the scatterplots.

Product	Cat. No.	Size
Zymo-Seq RiboFree™ Total RNA Library Kit	R3000	12 preps

Kit avec 12 index UDI inclus

Index UDI disponibles séparément

ZD3096 Zymo-Seq UDI Primer Plate (Indexes 1-96) 1 plaque

Nous contacter

Service technique

Réactifs : 01 34 60 60 24 - tech@ozyme.fr

Instrumentation : 01 30 85 92 88 - instrum@ozyme.fr