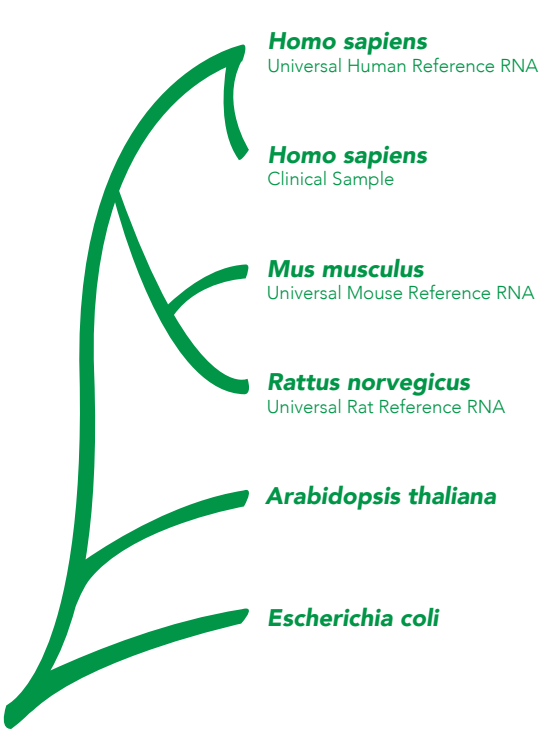
ZYMO RESEARCH
The Beauty of Science is to Make Things Simple®

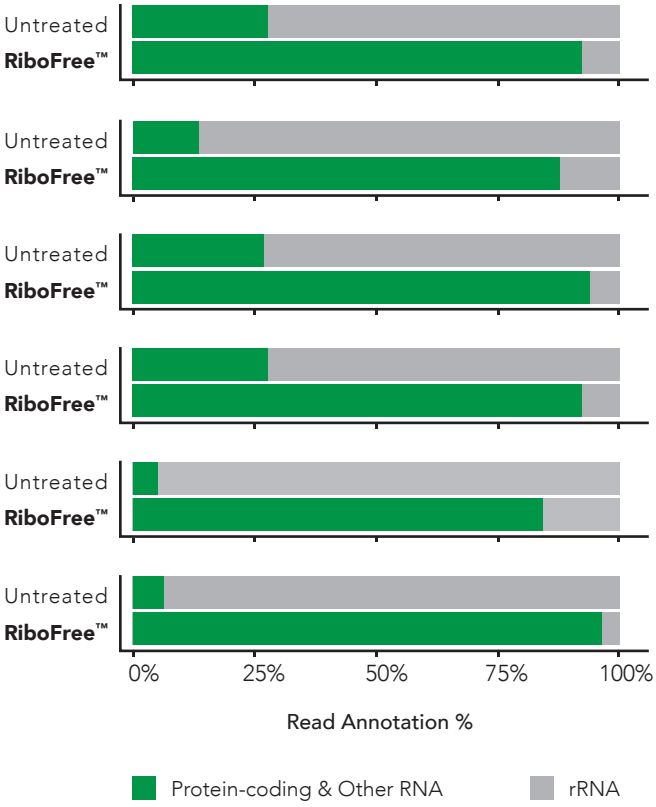
Zymo-Seq RiboFree™ Universal cDNA Kit

- **The Easiest Kit:** Prepare RiboFree™ cDNA from total RNA in as little as 5 pipetting steps.
- **Compatible With Any Organism:** Novel probe-free technology depletes rRNA & globin from any RNA source.
- **The Most Accurate:** Eliminate bias from rRNA depletion.

The Only Universal rRNA Depletion

Use One Kit For Any Sample Type





RNA From Any Sample Type or Organism

Reverse Transcription
30 mins

RiboFree™ Universal Depletion
0.5-1 hour

First-strand cDNA is ready for any downstream application

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.

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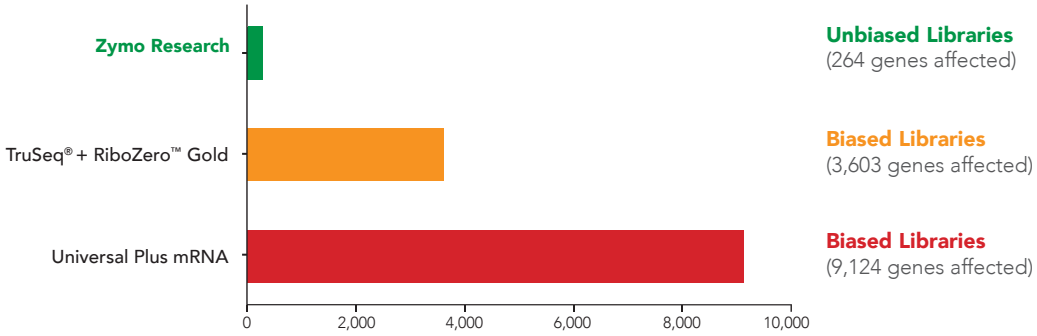
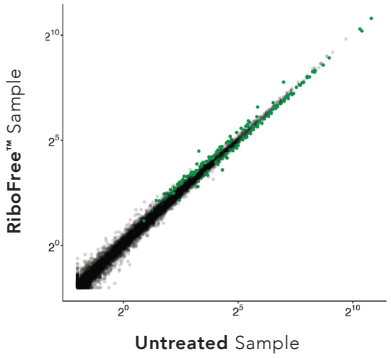
Probe-Free Technology Eliminates Bias

35x Less Biased Expression Profiles

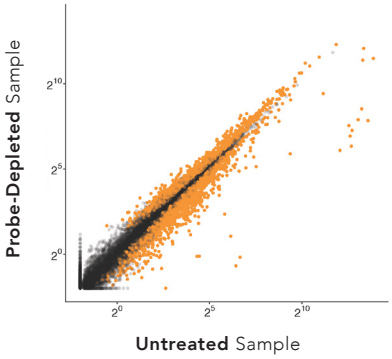


Genes Significantly Affected (p.adj<0.05)
Quantification of colored points in scatterplots below

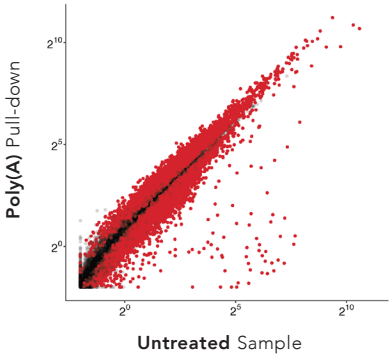
Zymo Research
Unbiased Libraries
(264 genes affected)



TruSeq® + Ribo-Zero™ Gold
Biased Libraries
(3,603 genes affected)



Universal Plus mRNA
Biased Libraries
(9,124 genes affected)



RiboFree™ Universal Depletion maintains native expression profiles unlike TruSeq® Total RNA [probe-based Ribo-Zero™ Gold] and Univeral 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™ Universal cDNA Kit	R3001	12 preps

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