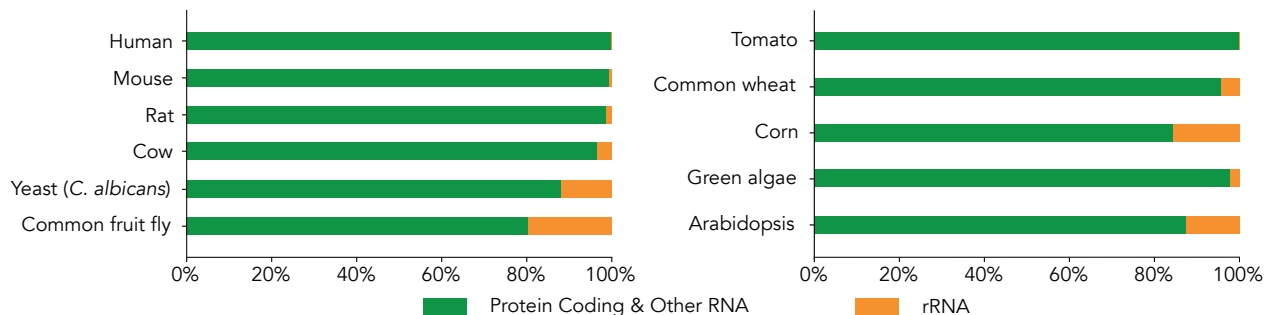# Zymo-Seq RiboFree® Total RNA Library Kit

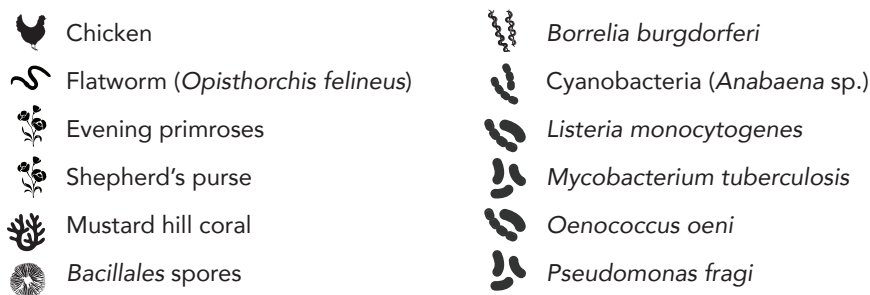*One for All. Universal rRNA Depletion for Any Organism.*

- **Universal Depletion:** Novel probe-free technology depletes rRNA from any organism.
- **Simplest Library Prep:** Simultaneous ligation of both adapters reduces hands-on processing.
- **Automation Friendly:** Streamlined protocol for increased scalability.

The Only Universal rRNA Depletion
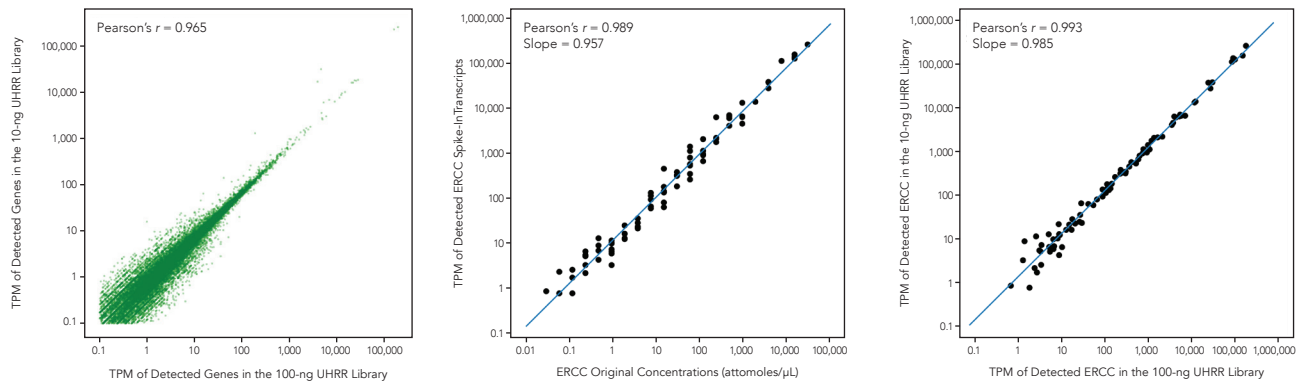### Use One Library Kit For Any Organism

Zymo-Seq RiboFree® Total RNA Library Kit produces dense coverage of protein coding and other transcripts, with rRNA efficiently depleted across different organisms. 100 ng of total RNA from each species were used as input to prepare libraries following the standard protocol with 1 hour of depletion reaction time and amplified with 11 cycles of PCR. Classification of the STAR-aligned reads was based on Ensembl annotations and RepeatMasker rRNA tracks from UCSC genome browser when applicable.

RiboFree® Universal Depletion
Also Applied in Peer-Reviewed Publications

- Chicken
- Flatworm (*Opisthorchis felineus*)
- Evening primroses
- Shepherd's purse
- Mustard hill coral
- *Bacillales* spores
- *Borrelia burgdorferi*
- Cyanobacteria (*Anabaena* sp.)
- *Listeria monocytogenes*
- *Mycobacterium tuberculosis*
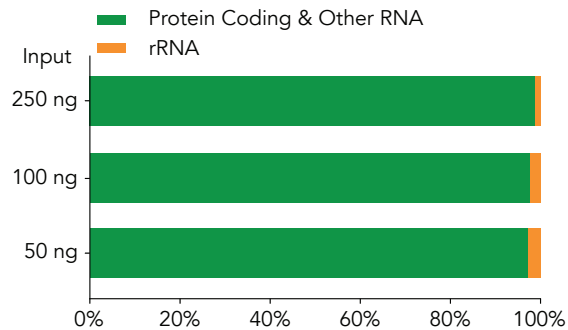- *Oenococcus oeni*
- *Pseudomonas fragi*

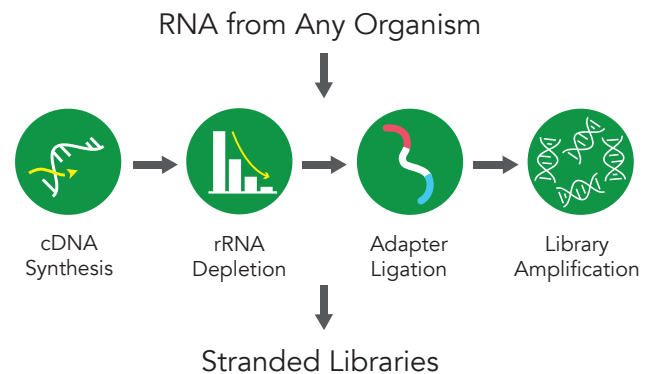And Many More!

High Consistency at Different Input Amounts

Consistent gene detection (unique Ensembl GRCh38 gene IDs, TPM > 0.1) and high correlation of ERCC counts (TPM > 0.1) between conditions showcase the robustness of the Zymo-Seq RiboFree® method. Zymo-Seq RiboFree® Total RNA libraries were prepared with 100 ng and 10 ng of Universal Human Reference RNA (UHRR, RIN > 8) containing ERCC Spike-In Controls Mix 1, respectively. Left: TPM correlation between the two libraries. Each library detected > 28,900 genes, with 26,400 genes co-detected. Middle: Correlation between TPM of the 84 detected ERCC transcripts in the 10-ng UHRR library and their original concentrations. Right: TPM correlation of the 82 co-detected ERCC transcripts between the two libraries. TPM: Transcripts Per Million. All the shown Pearson's *r* and slope values were calculated on log-transformed TPM or concentration values.

Suitable for Degraded Samples

Efficient rRNA depletion also achievable with degraded samples using the Zymo-Seq RiboFree® Total RNA Library Kit. Libraries were prepared with 250 ng, 150 ng, and 50 ng of total RNA extracted from formalin-fixed, paraffin-embedded (FFPE) human tissues (RIN = 1.6, peak < 200 nt), respectively.

Simplest Total RNA Library Prep

RNA from Any Organism

cDNA Synthesis → rRNA Depletion → Adapter Ligation → Library Amplification

Stranded Libraries

With **30-50% less hands-on time** compared to alternative kits, it's RNA-Seq Made Simple with the Zymo-Seq RiboFree® Total RNA Library Kit. The automation friendly protocol shines with pre-mixed reagents and **a single adapter ligation step** for adding both adapters in this streamlined procedure.

Product	Cat. No.	Size
Zymo-Seq RiboFree Total RNA Library Kit	R3000	12 preps
	R3003	96 preps