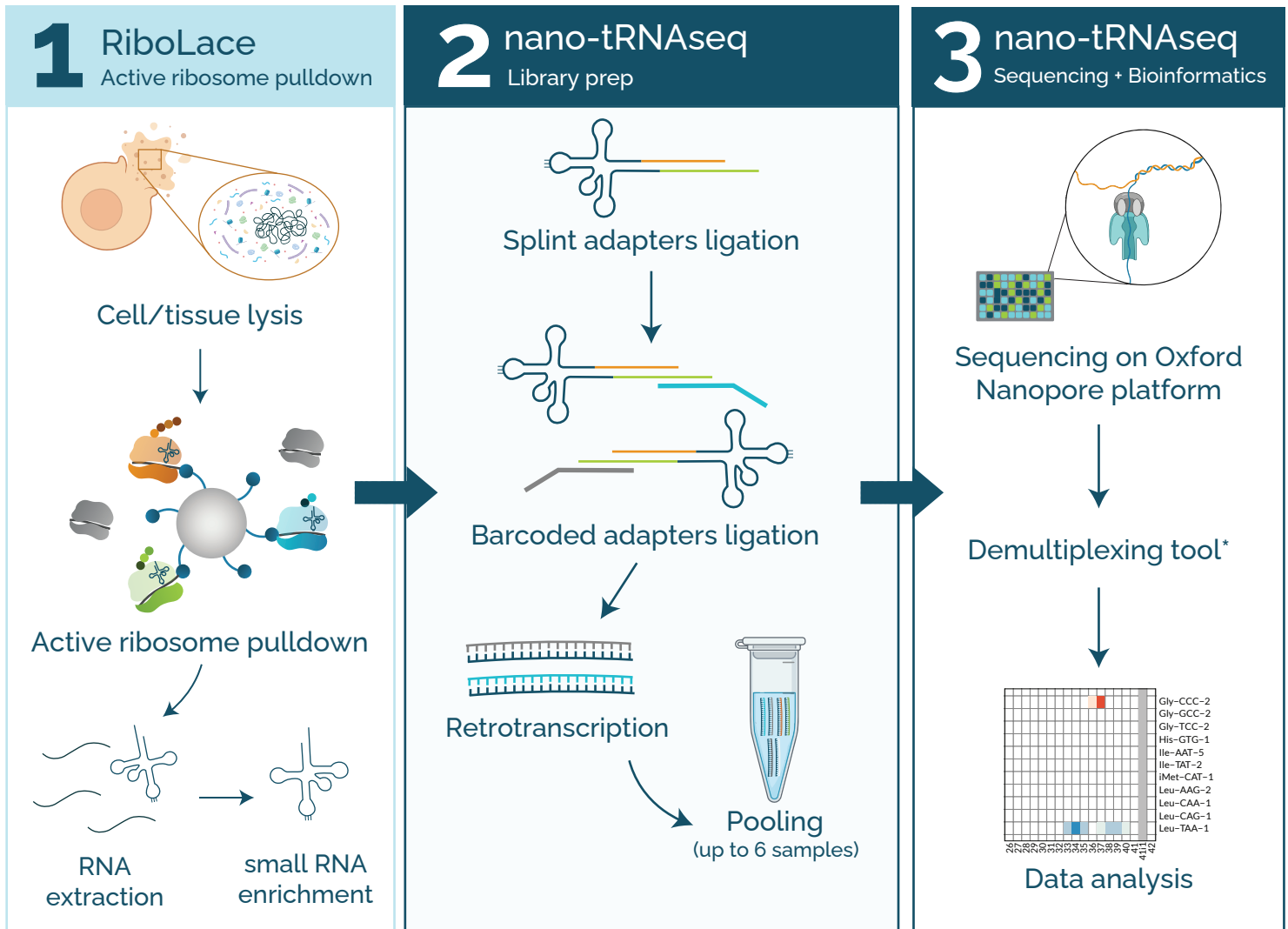


Ribo-tRNAseq kit

tRNAs used by ribosomes
once inaccessible, now on your bench

The days in which ribo-embedded tRNAs were deemed impossible to study are behind us. Introducing **ribo-tRNAseq**, our unique workflow that allows for **isolation of tRNAs actively used by ribosomes**. Leveraging our **active ribosome pulldown**, RiboLace™, with our cutting-edge **tRNA sequencing** technology, you can easily go from cell lysate to comprehensive data in a matter of days.



*License provided with kit

Specifications

Cell input		Kit size	12 rxns	Catalogue number
Eukaryotic cell lines	>0.5M	Workflow time	3 days	#RLNTR-12
Tissues*	>10 mg			

*with annotated genome



Proof-of-concept studies

Ribo-tRNAseq accurately distinguishes tRNAs used in translation

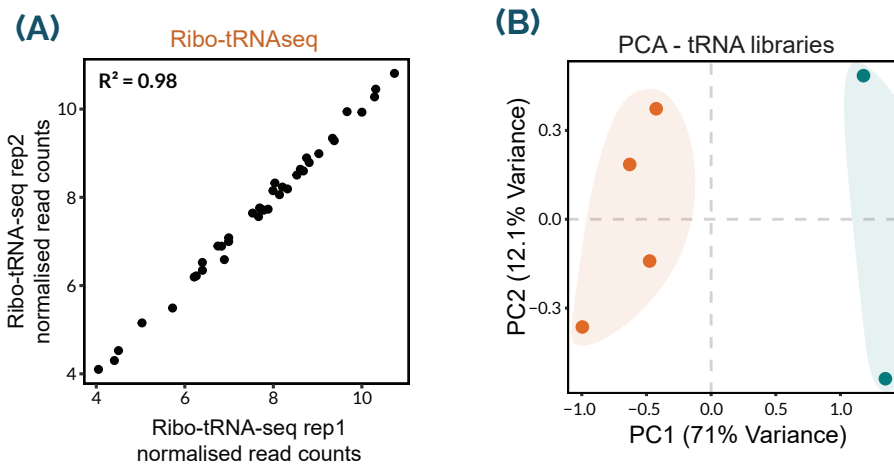


Figure 1: The Ribo-tRNAseq kit ensures data reproducibility and distinguishes tRNA in active use from total tRNA. Scatterplot (A) shows that the majority of detected tRNAs are in common between ribo-tRNAseq replicates of HEK293T cells, proving high reproducibility of the method. Principal component analysis (B) shows clear clustering between ribo-tRNA (orange) and total tRNA libraries (blue).

Case study: Perturbation in translation

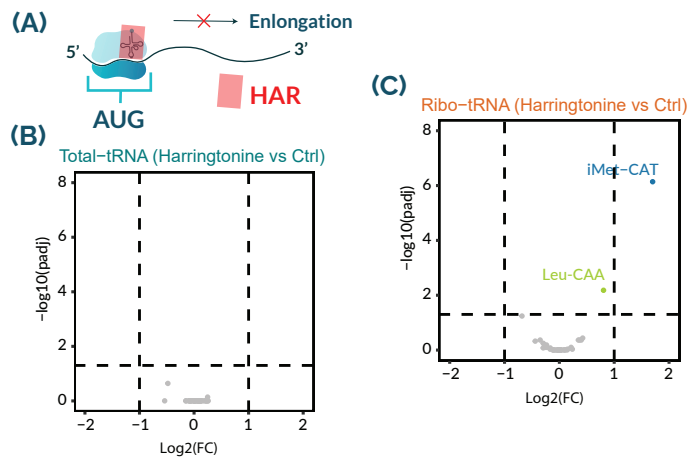


Figure 2: MCF-7 cells were treated with harringtonine (HAR), a translational inhibitor that arrests elongation immediately after initiation (A). Total tRNAseq and Ribo-tRNAseq were performed on control and treated samples. While total tRNA levels remained largely stable across conditions (B), Ribo-tRNAseq (C) revealed significant changes in ribosome-associated methionine (iMet), compliant with HAR role in inhibiting elongation.

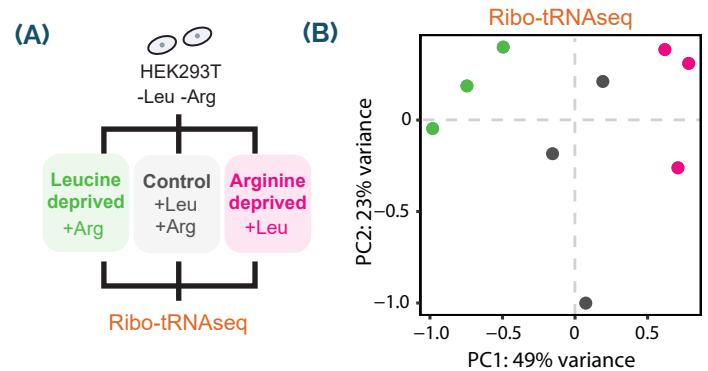
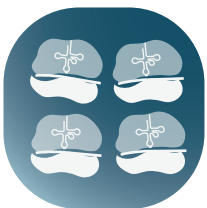


Figure 3: HEK293T cells were exposed to 3 hours of selective leucine or arginine deprivation, with fully supplemented media being used as control (A). Leucine and arginine both play important roles in translation, impacting translation initiation and elongation, respectively. PCA of ribosome-associated tRNA profiles (B) revealed a clear separation of conditions, indicating the sensitivity of the method to detect dynamic tRNA usage.

Highlights



Uncover abundance and modifications of active tRNAs



Explore role of actively used tRNAs in diseases



Reveal dynamic tRNA usage during translational shifts



Gel-free multiplexing fast workflow

