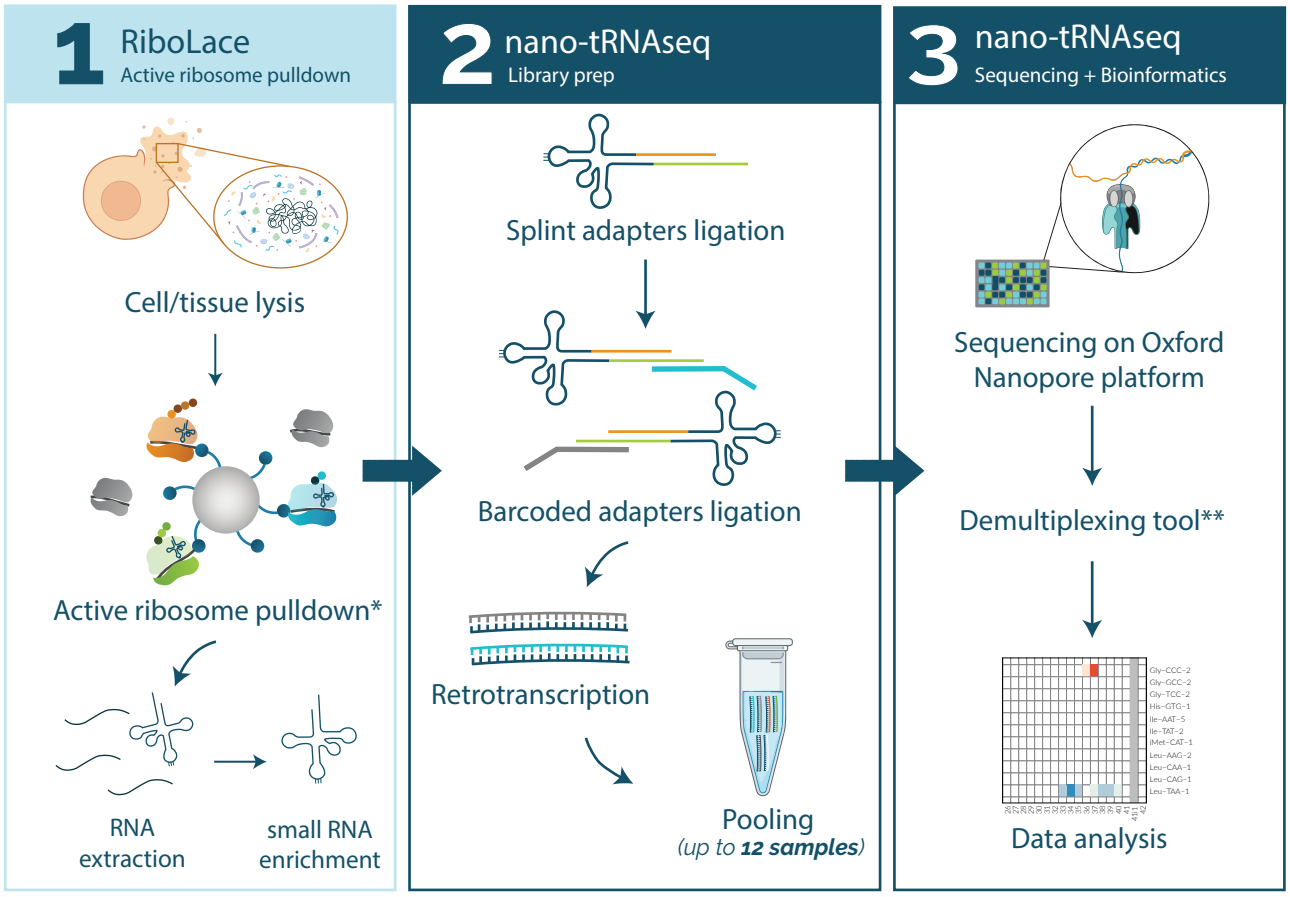
Ribo-tRNAseq PRO kit

Unlocking ribosome-bound tRNAs

Introducing **ribo-tRNAseq PRO (12 samples-12 barcodes)**, our integrated solution for profiling tRNAs engaged in **active translation**. By combining **RiboLace™**, which selectively enriches actively translating ribosomes, with **nano-tRNAseq**, for full-length sequencing and chemical modification detection, the kit provides an end-to-end workflow for ribosome-associated tRNA analysis directly from cell lysates. Supporting multiplexing of **up to 12 samples per run**, it enables flexible sample pooling while reducing sequencing costs and batch-to-batch variability. Compatible with MinION and PromethION nanopore sequencing platforms.



*Fully compatible with Immagina's LaceSeq™ library preparation kit

**License provided with kit

Highlights

- Uncover abundance and modifications of active tRNAs
- Reveal dynamic tRNA usage during translational shifts
- Up to 12 samples multiplexing
- Gel-free fast workflow

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For more info

See translation as it happens

Ribo-tRNAseq accurately distinguishes tRNAs used in translation

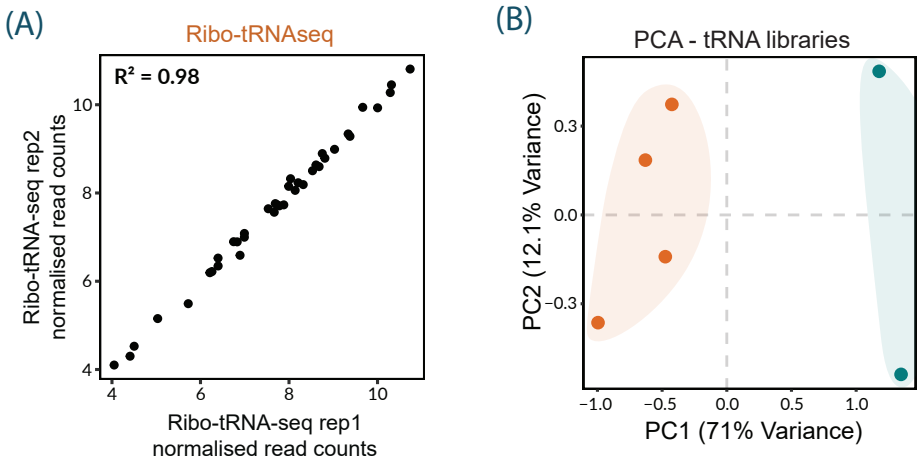


Figure 1: The Ribo-tRNAseq kit ensures data reproducibility and distinguishes actively translating tRNAs from total tRNA. **(A)** Scatter plot shows that most detected tRNAs are shared between ribo-tRNAseq replicates in HEK293T cells, indicating high reproducibility of the method.
(B) Principal component analysis shows clear separation between ribo-tRNA libraries (orange) and total tRNA libraries (blue).

Case study: Perturbation in translation

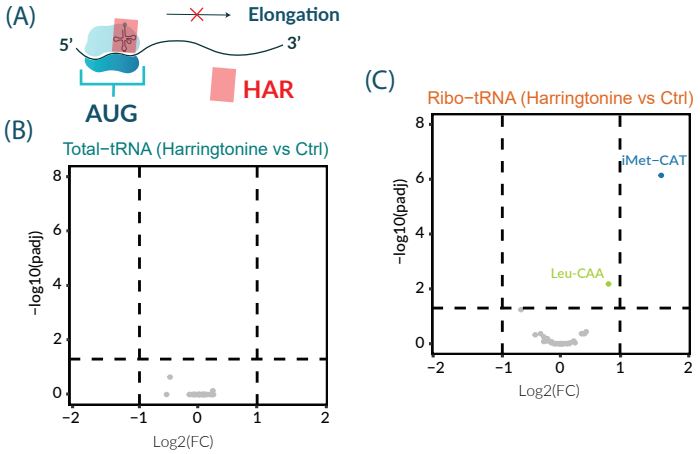


Figure 2: (A) MCF-7 cells were treated with harringtonine (HAR), a translational inhibitor that arrests elongation immediately after initiation. **(B-C)** Total tRNA-seq and Ribo-tRNAseq were performed on control and treated samples. While total tRNA levels remained largely stable across conditions **(B)**,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

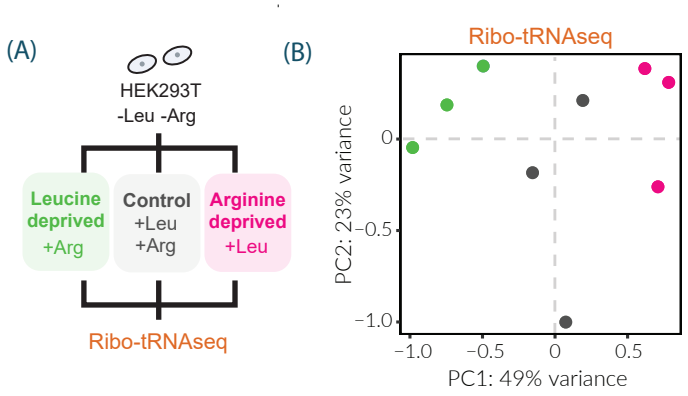


Figure 3: Leucine and arginine both play important roles in translation, impacting translation initiation and elongation, respectively. **(A)** HEK293T cells were exposed to 3 hours of selective leucine or arginine deprivation, with fully supplemented medium used as control. **(B)** PCA of ribosome-associated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

Specifications

Minimum suggested input	
Cells†	3-10 M
Tissues†	50-100 mg

Kit size	12 rxns ***(12 barcodes)***
Workflow time	3 days

†Eukaryotic samples with an annotated genome; not validated for plant samples.
Required input may vary depending on tissue/cell type.

Imagine what you can discover. Immagina.

Immagina is the exclusive license holder to IPs for research use covering key aspects of nano-tRNAseq technology developed by researchers of the Novoa Lab at the Centre for Genomic Regulation, Barcelona, Spain.