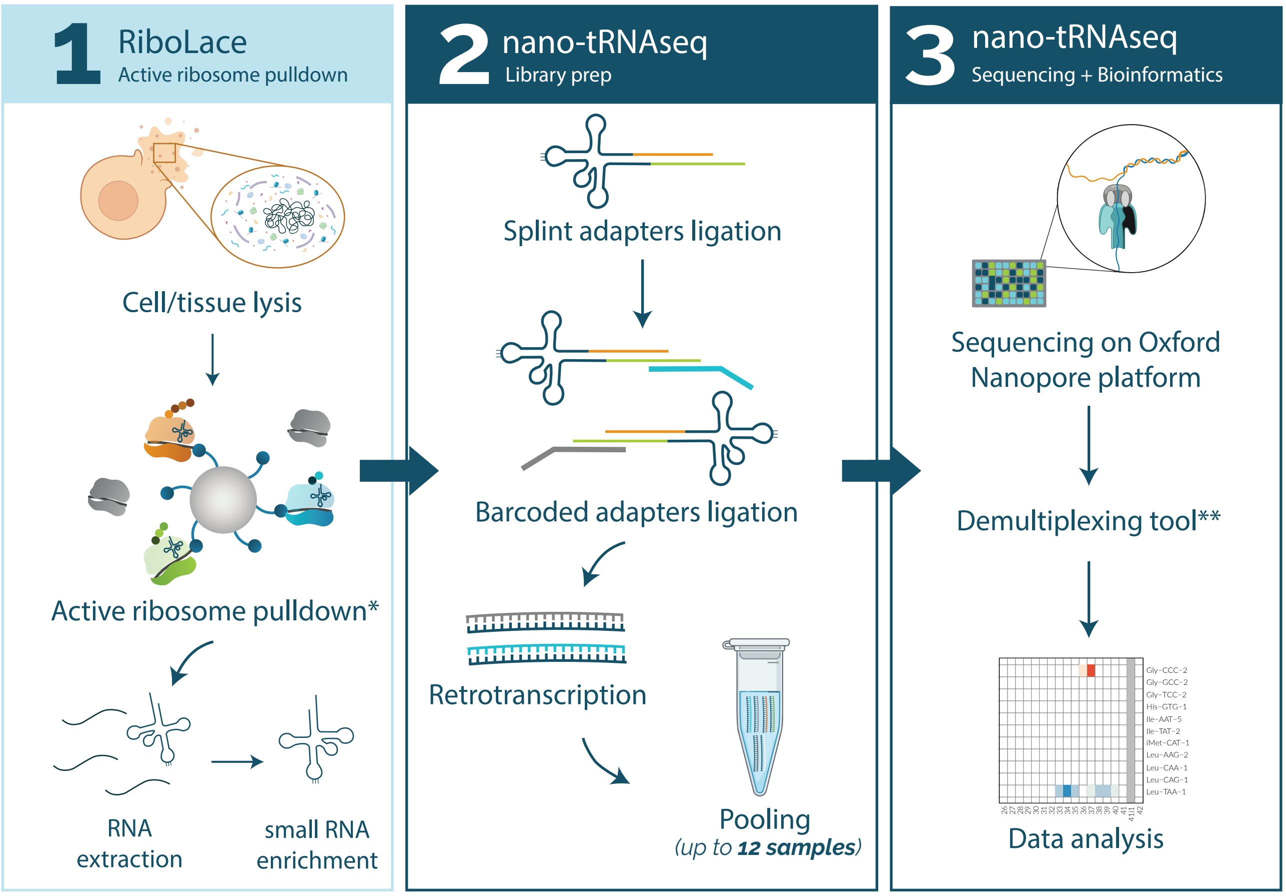
Ribo-tRNAseq PRO kit

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.



1 RiboLace
Active ribosome pulldown

Cell/tissue lysis

Active ribosome pulldown*

RNA extraction

small RNA enrichment

2 nano-tRNAseq
Library prep

Splint adapters ligation

Barcoded adapters ligation

Retrotranscription

Pooling
*(up to **12 samples**)*

3 nano-tRNAseq
Sequencing + Bioinformatics

Sequencing on Oxford Nanopore platform

Demultiplexing tool**

Data analysis

*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

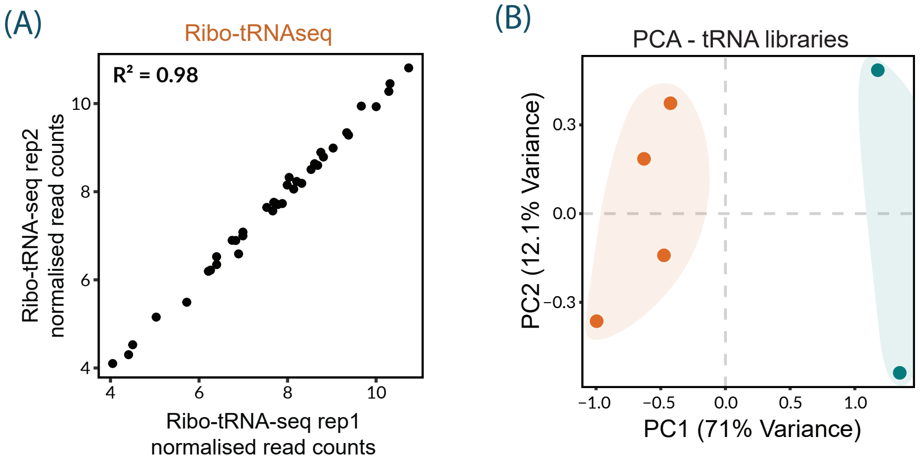


Figure 1: The Ribo-tRNAseq kit ensures data reproducibility and distinguishes actively translating tRNAs from total tRNA. **(A)** Scatter plot shows that most detected tRNAs are shared between ribo-tRNAseq replicates in HEK293T cells, indicating high reproducibility of the method.
(B) Principal component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

Case study: Perturbation in translation

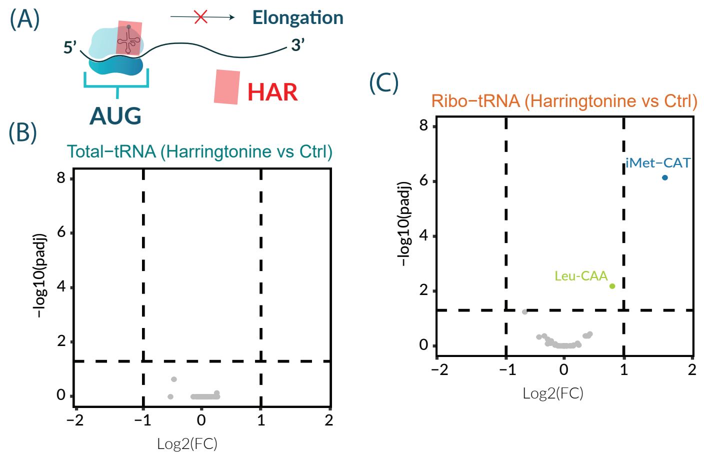


Figure 2: (A) MCF-7 cells were treated with harringtonine (HAR), a translational inhibitor that arrests elongation immediately after initiation. **(B-C)** Total tRNA-seq and Ribo-tRNAseq were performed on control and treated samples. While total tRNA levels remained largely stable across conditions **(B)**,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

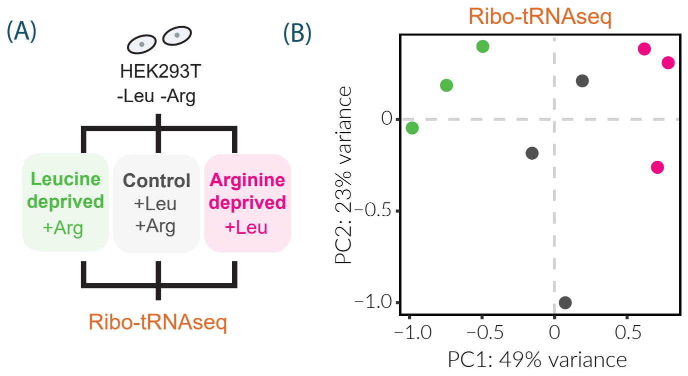


Figure 3: Leucine and arginine both play important roles in translation, impacting translation initiation and elongation, respectively. **(A)** HEK293T cells were exposed to 3 hours of selective leucine or arginine deprivation, with fully supplemented medium used as control. **(B)** PCA of ribosome-associated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

Specifications

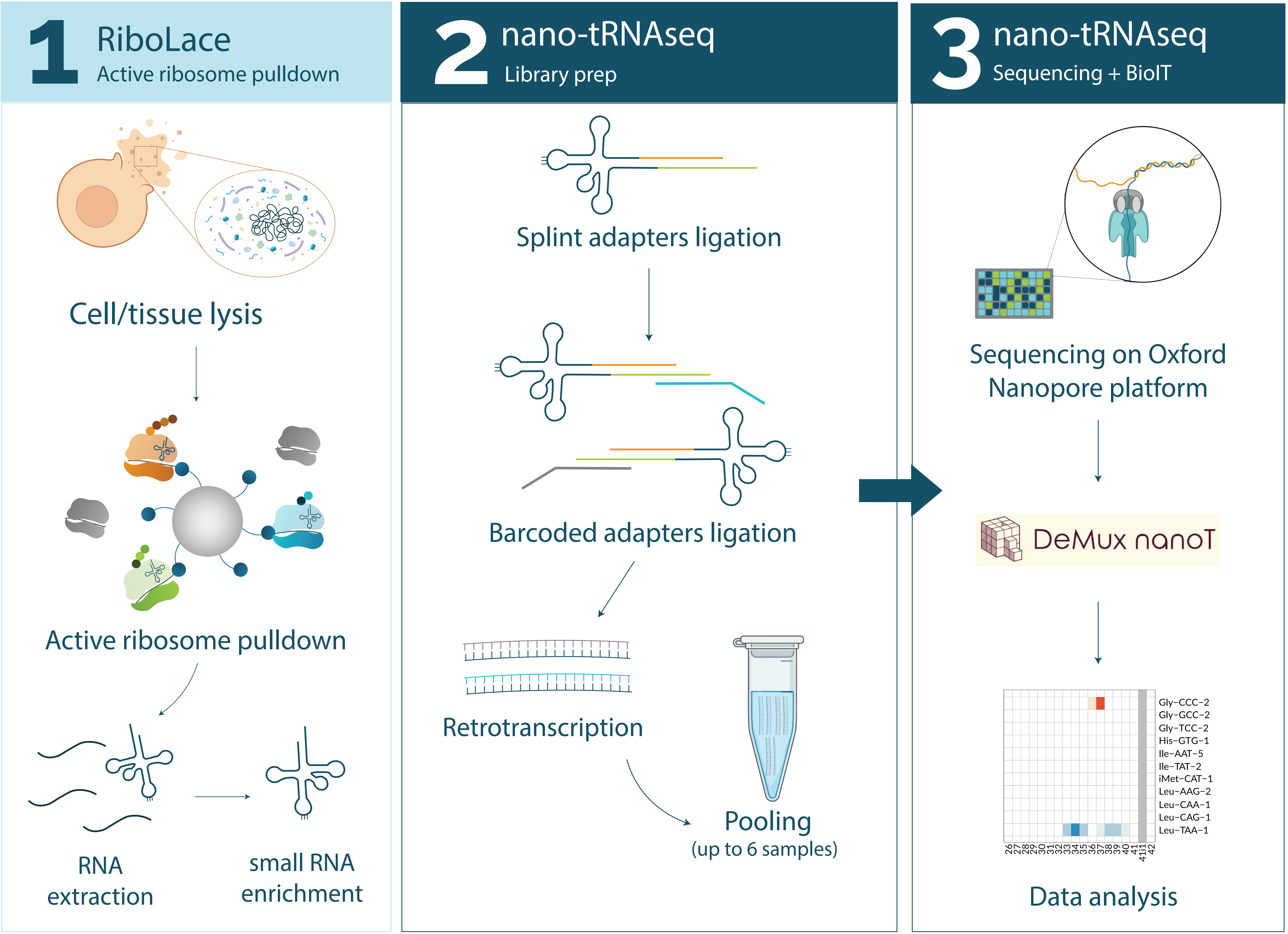
Minimum suggested input	
Cells†	3-10 M
Tissues†	50-100 mg

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.



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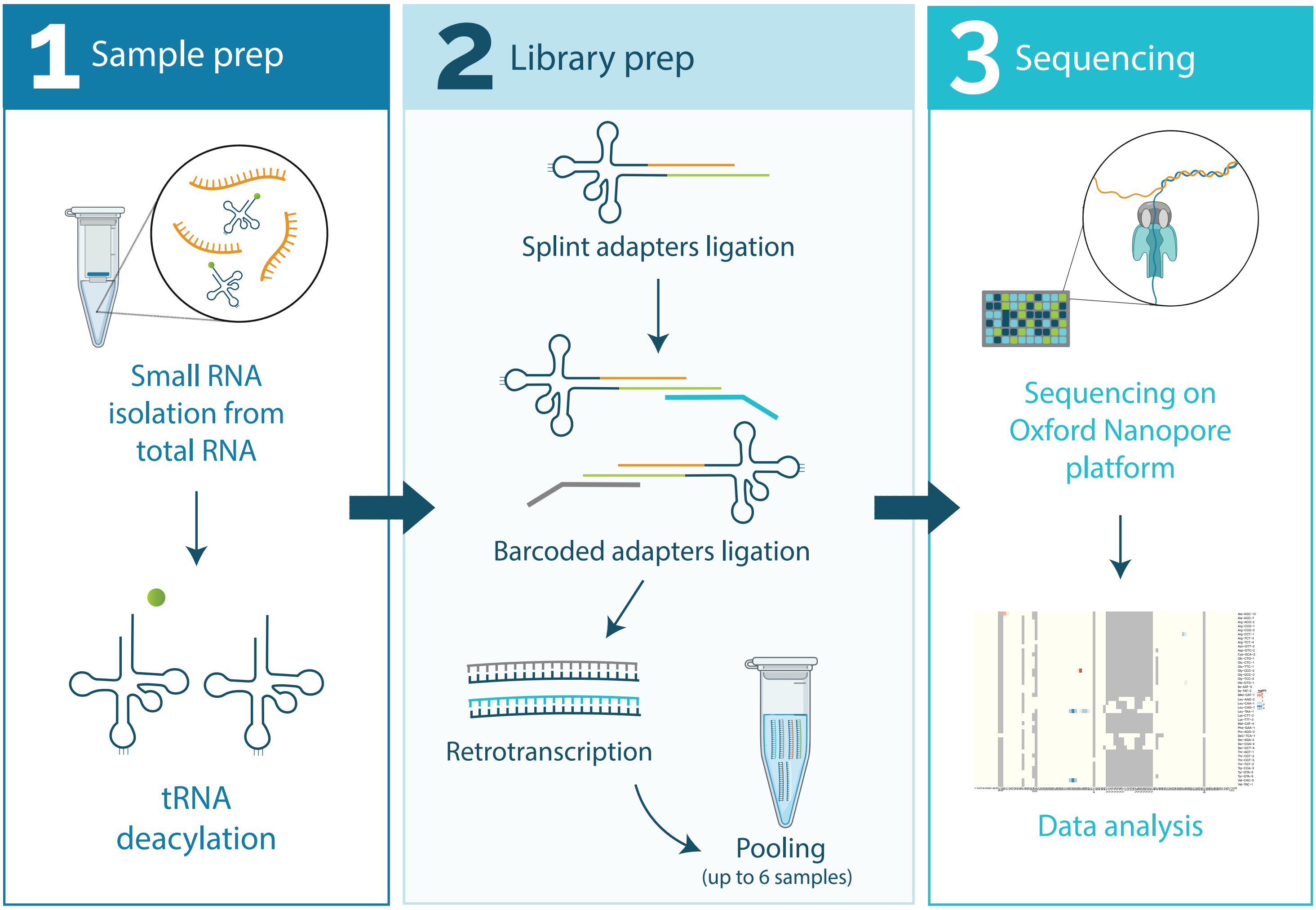
DeMux nanoT

Data analysis

nano-tRNAseq kit

Unlock the secrets of tRNA on your bench

Introducing nano-tRNAseq: the only kit that allows for full-length, sequencing of native tRNA molecules. Simply starting from total RNA, you can now quantify tRNA abundances and detect chemical modifications. With 12 reactions included, we make sure you have everything you need to unlock the secrets of tRNA... for all species*!



1 Sample prep

Small RNA isolation from total RNA

tRNA deacylation

2 Library prep

Splint adapters ligation

Barcoded adapters ligation

Retrotranscription

Pooling
(up to 6 samples)

3 Sequencing

Sequencing on Oxford Nanopore platform

Data analysis

Specifications

Species	All species*	Kit size	12 rxns	Catalogue number
Total RNA input	≥ 10 µg of total RNA	Workflow time	2 days	#NTRSQ-12

*all species with annotated genome

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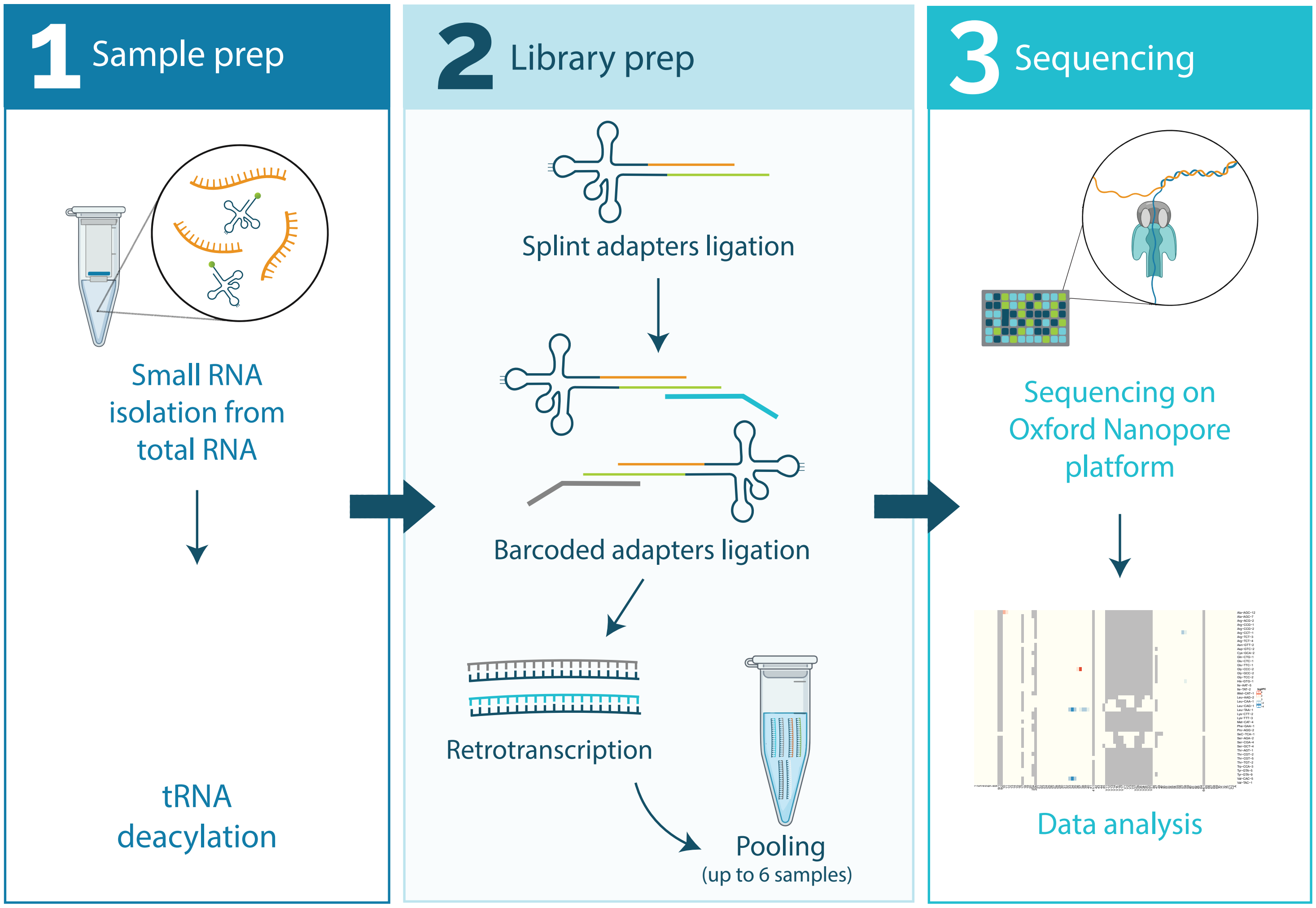
The ribosom company

For more info



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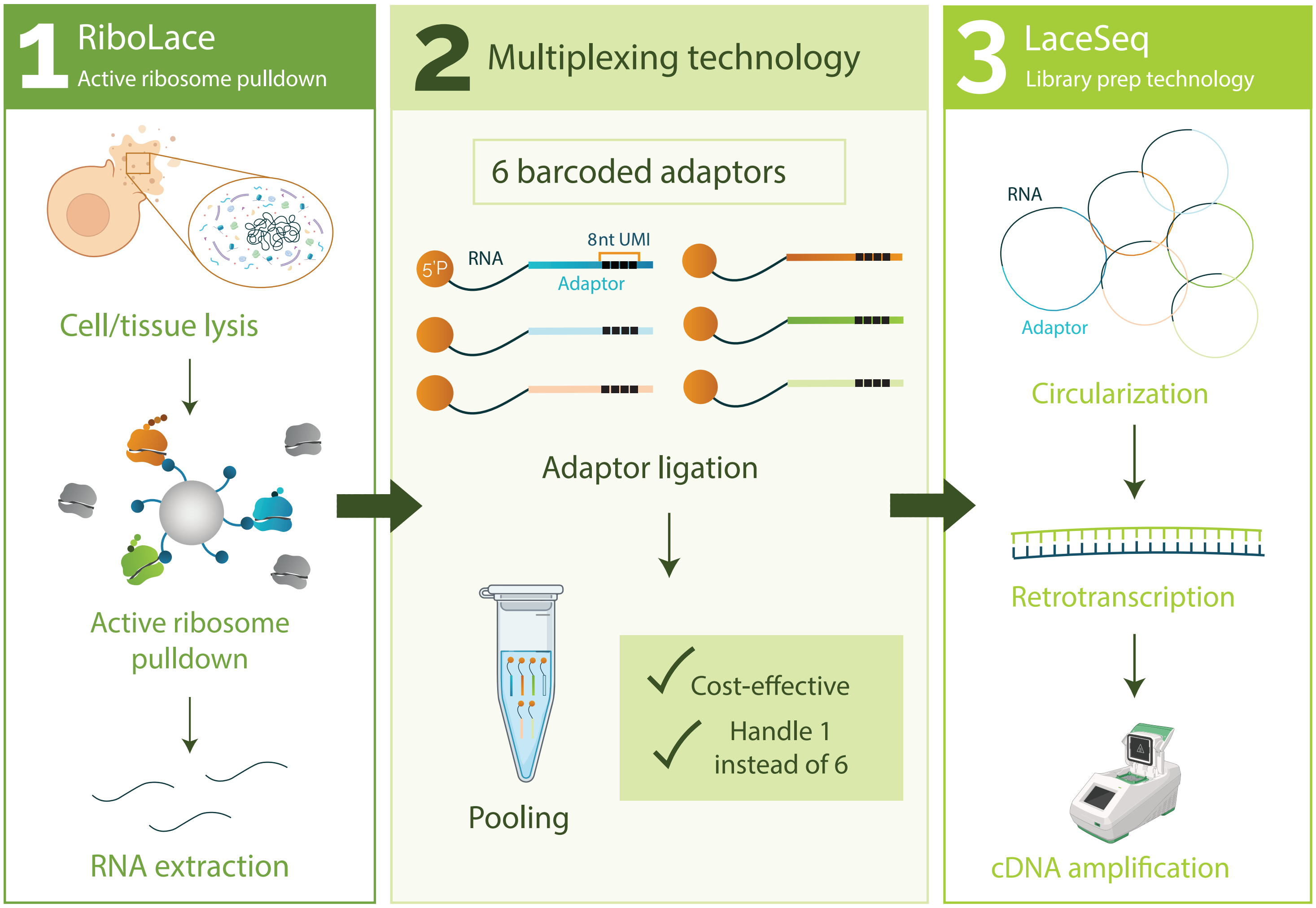

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Active ribosome pulldown

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RNA extraction

2 Multiplexing technology

6 barcoded adaptors

Adaptor ligation

Pooling

✓ Cost-effective

✓ Handle 1 instead of 6

3 LaceSeq
Library prep technology

Circularization

Retrotranscription

cDNA amplification