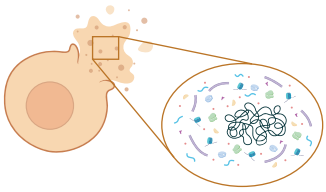
ALL-IN-ONE RiboLace Multiplexing

For a fast and reliable multiplexed RiboSeq library

Introducing ALL-IN-ONE RiboLace Multiplexing™, our newest **RiboLace™ + LaceSeq™ library preparation kit** that requires **minimal input** when compared to non-multiplexing alternatives. Process up to **36 samples in a flexible 6x6 multiplexing library** scheme with a fast, simple, and robust workflow. Ideal for cell lines (immortalized and primary), tissues and complex samples with low translation activity, this kit eliminates the need for gel purification or bulky equipment.

1 RiboLace
Active ribosome pulldown



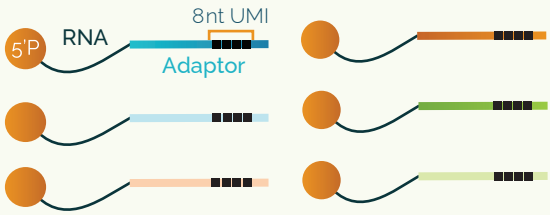
Cell/tissue lysis

Active ribosome pulldown

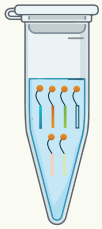
RNA extraction

2 Multiplexing technology

6 barcoded adaptors



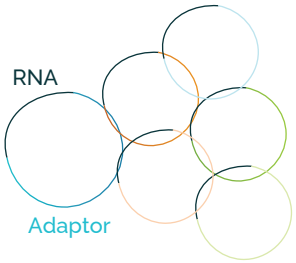
Adaptor ligation



Pooling

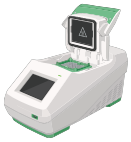
- ✓ Cost-effective
- ✓ Handle 1 instead of 6

3 LaceSeq
Library prep technology



Circularization

Retrotranscription



cDNA amplification

Input material

Minimum Cell input for RiboSeq

✓ Versatile

	Multiplexing	Gel Free	Traditional approaches
Immortalized cell lines	35k	>0.3M	>3M[1]
Primary cell lines (indicative, dependent on primary cells type)	300k	>1M	>3M[2-3]

1 - DOI: 10.1126/science.1168978 2 - DOI: 10.1016/j.celrep.2016.08.088 3 - DOI: 10.1016/j.molcel.2022.06.023

IMMAGINA BioTECHNOLOGY

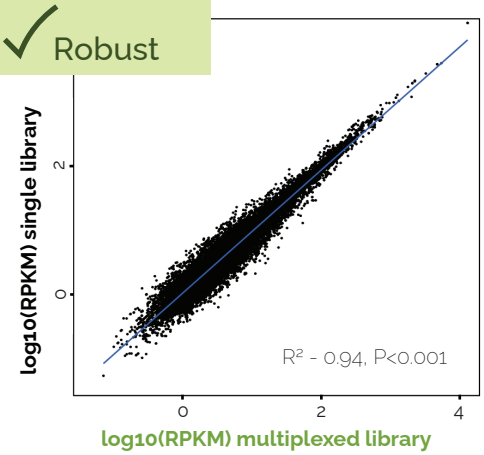
The ribosome company

For product details

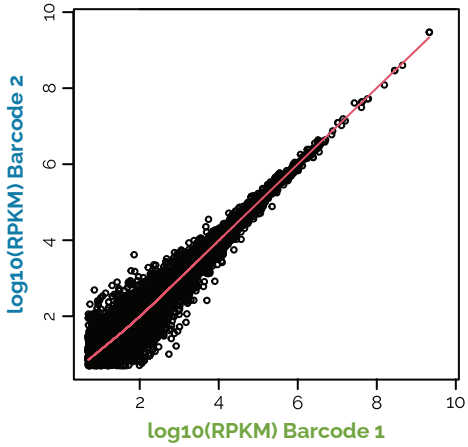
Proof-of-concept studies

(A) Multiplexing leads to no loss of information

✓ Robust



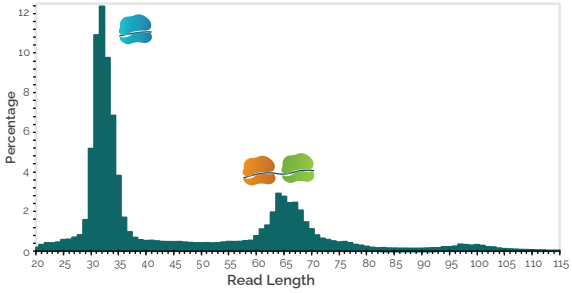
(B) Multiplexing with different barcodes leads to unbiased transcript detection



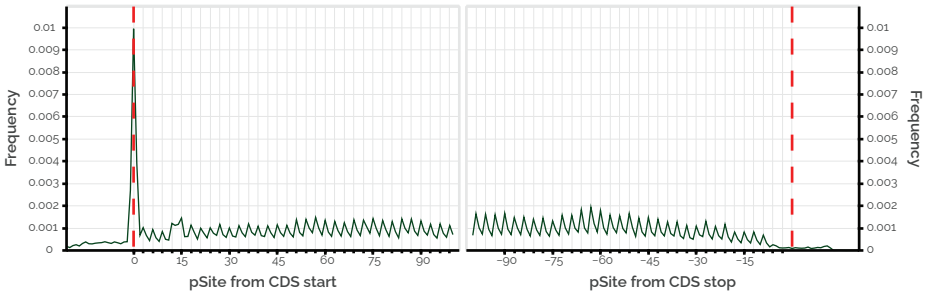
✓ Highly reproducible

ALL-IN-ONE RiboLace Multiplexing kit ensures data robustness and reproducibility. Scatter plot **(A)** shows good correlation (R2 = 0.94, p< 0.001) in transcripts detected in non-multiplexed library, starting from 1 µg of mouse lung tissue vs one multiplexed library from 50 ng. Analysis was performed on transcripts with > 5 counts. N=4. Scatterplot **(B)** shows detected transcripts in common between multiplexed libraries with different barcodes starting from 50ng of mouse lung tissue. The majority of transcripts are in common between libraries, proving the absence of barcode-related biases in transcript detection. N=4.

(C) Length Distribution



(D) Metaprofile



Bioinformatic outputs obtained using ALL-IN-ONE RiboLace Multiplexing. The input was 800k primary mouse neurons. **(C)** Representative read length distribuition graph from one multiplexed sample showing clear monosomes (30-40 nt) and disomes (60-80 nt) peaks. **(D)** Representative metagene profile of one multiplexed sample showing P-site frequencies around start (0-50 nt) and stop (-50-0 nt) positions of transcripts. Clear 3nt periodicity and low noise are observed. N=6.

Highlights

Flexible
Lower input, multiple samples

Robust
High reproducibility, avoid processing biases

Cost-effective
Reduced cost per sample

Versatile
Diverse cell types including low-translating cells

Imagine what you can discover. Immagina.