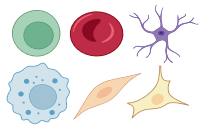
HT Ribo-Seq

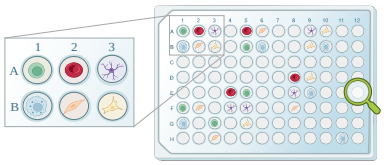
High-throughput ribosome profiling in a 96-well plate

Ribosome profiling (Ribo-Seq) enables genome-wide mapping of translating ribosomes at nucleotide resolution, yet conventional workflows remain constrained by high input requirements and limited throughput. Immagina's **HT Ribo-Seq** brings the technique to screening scale: up to **96 samples per plate** from as few as ~10,000 cells per well, while preserving footprint quality, mapping accuracy, and translational resolution.

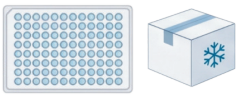
1 Sample prep

Cells





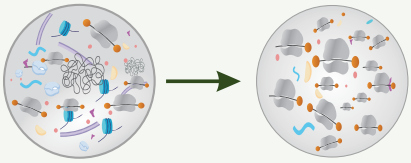
In-plate cell lysis (optional)



Ready-to-ship plate

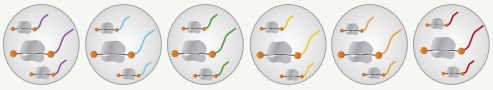
2 Experiment execution

RiboBoost™



Nuclease digestion & ribosomal fraction enrichment

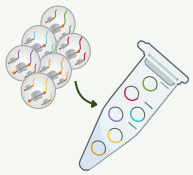
RiboTag™



Barcoding within intact ribosomes

3 Sequencing

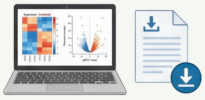
LaceSeq



Multiplexed library prep

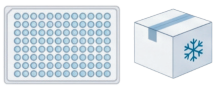


NGS & data analysis



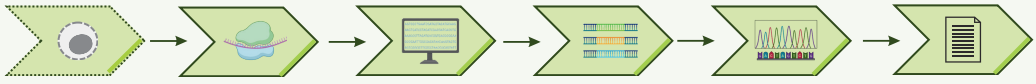
Delivery of processed data and reports

Client



Sample prep & shipment

Immagina



Specifications

Input type	Eukaryotic cells	**Turnaround time**	96 samples in 2–4 days
Input amount	10-50k cells/well	**Sequencing depth**	20M reads/sample*

*Suggested minimum

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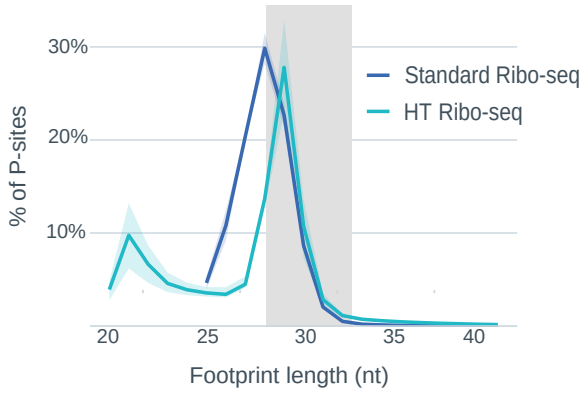
The ribosome company

For more info

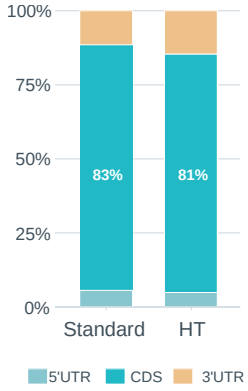
Results

HT Ribo-Seq preserves footprint quality and codon-level resolution

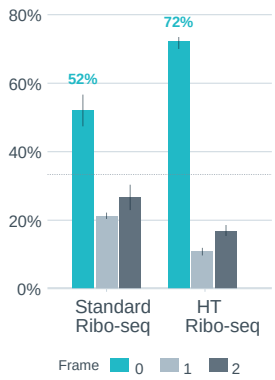
(A) Footprint length
Shaded band = 28–33 nt RPF window



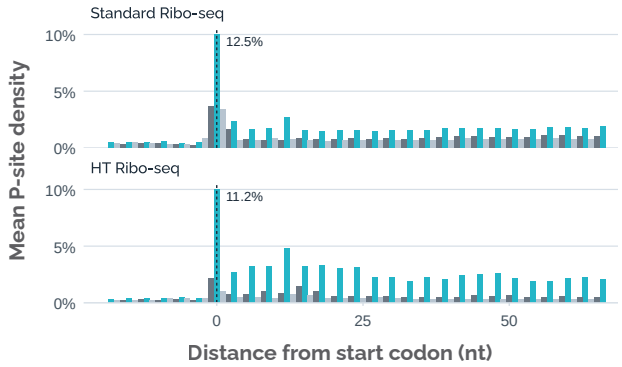
(B) Read region assignment
Mean across libraries



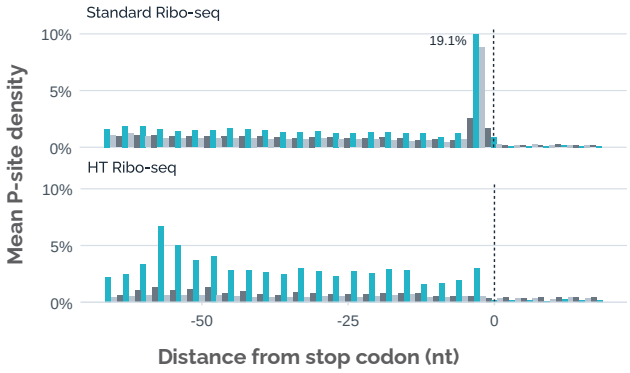
(C) Reading frame on CDS
Dotted line = no periodicity (33%)



(D) Metagene: initiation site



(E) Metagene: termination site



Benchmarking HT Ribo-Seq against Standard Ribo-Seq (conventional workflow) in HEK293T cells.
(A) Footprint length distribution; the shaded band marks the 28–33 nt ribosome-protected fragment window. **(B)** Assignment of P-sites to 5′UTR, CDS and 3′UTR. **(C)** Reading-frame distribution on the CDS; the dotted line marks the 33% expected in the absence of periodicity. **(D)** Metagene P-site density around the start codon and **(E)** around the stop codon, with in-frame positions in teal. In **(D)** and **(E)**, all profiles share a y-axis capped at 10%; bars above the cap are truncated and labeled with their value. Standard Ribo-Seq n = 2 (32.7 M P-sites), HT Ribo-Seq: n = 10 (11.9 M).

Learn more in our dedicated Application Note at immaginabiotech.com.

Highlights

High-throughput ribosome profiling

Low input requirements

Simplified library preparation

Drug screening applications

Imagine what you can discover. Immagina.