Active ribosome profiling in one day.

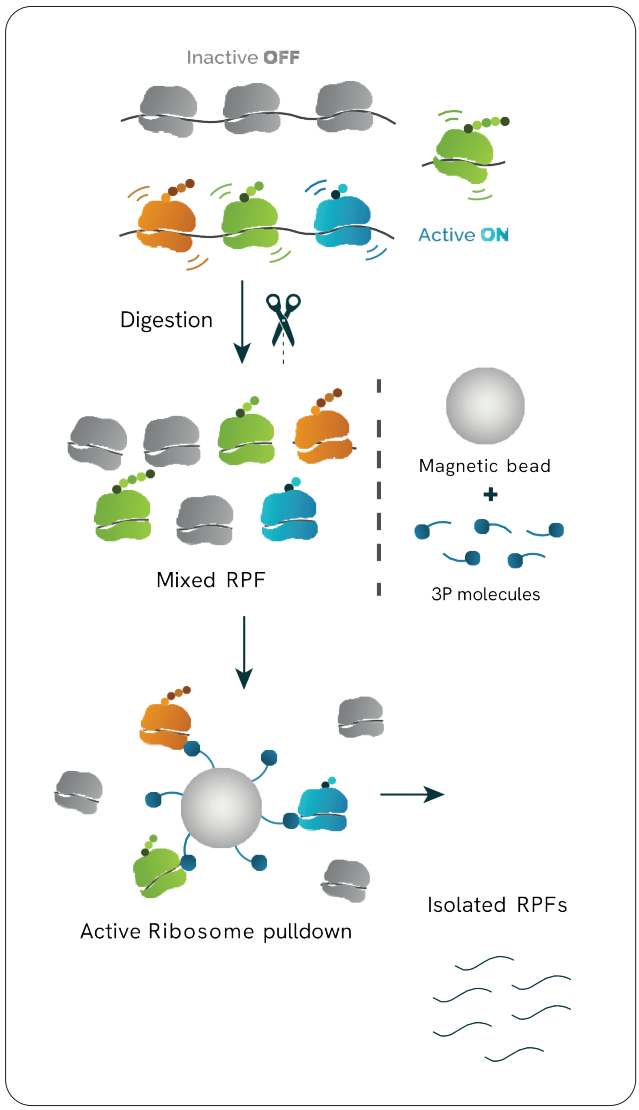
Magnetic capture of actively translating ribosomes

Classical ribosome profiling (Ribo-Seq) is technically demanding. Moreover, classical Ribo-Seq approaches do not distinguish between fragments derived from actively translating ribosomes and those derived from stalled, inactive, or non-productively bound ribosomes, confounding accurate quantification of translational activity[1].

RiboLace™ Pro provides an innovative solution to simplify Ribo-Seq without compromising data quality (Figure 1). A puromycin-derived molecule (3P) selectively binds active ribosomes, which are then captured on magnetic beads for purification of ribosome-protected fragments (RPFs). No need for gradients or ultracentrifugation. Suitable starting material includes lysates from flash-frozen tissues or immortalized/primary cell cultures.

Highlights

- Short and simple workflow
- Magnetic pull-down of active ribosomes
- No gradients. No ultracentrifugation
- Up to 30x less input required
- Antibody- and tag-free
- Nucleotide-resolution positional data
- Measure translational activity and predict protein levels accurately



1. Clamer, M. *et al.* Active ribosome profiling with Ribolace. 2018; *Cell Reports* 25(4):1097-1108.e5.

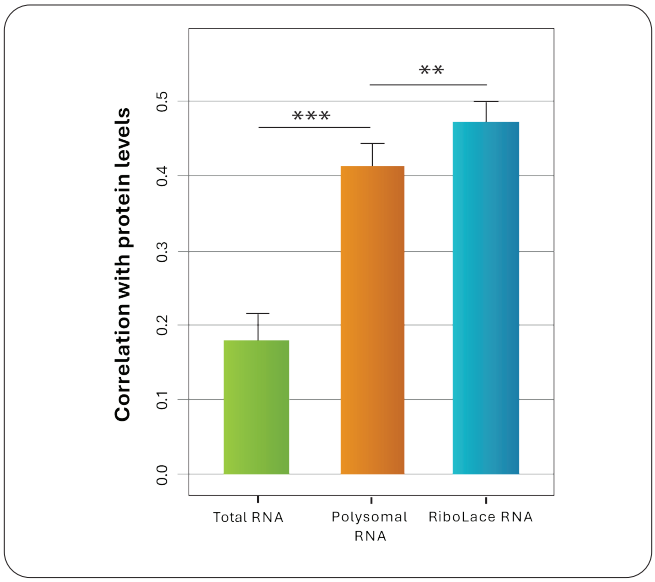


Figure 1: Experimental design to compare the cellular proteome with the global RNA repertoire of RNAs associated with total RNA, polysomal RNA, and RiboLace RNA sequencing. Correlation analysis determined by mass spectrometry and deep sequencing.

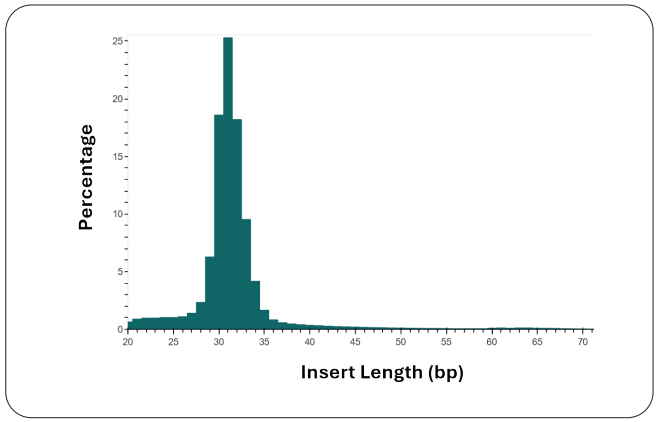


Figure 2: Plot showing the insert length of RPF prepared with NEXTFLEX Small RNA-seq kit v4. Lengths correspond to the typical footprint size of eukaryotic ribosomes.

Downstream processing of the purified RPFs with **NEXTFLEX™ Small RNA-seq kit v4** produces high-quality Ribo-Seq libraries that display expected footprint length distributions (Figure 2), strong coding sequence enrichment and clear three-nucleotide frame periodicity (Figure 3).

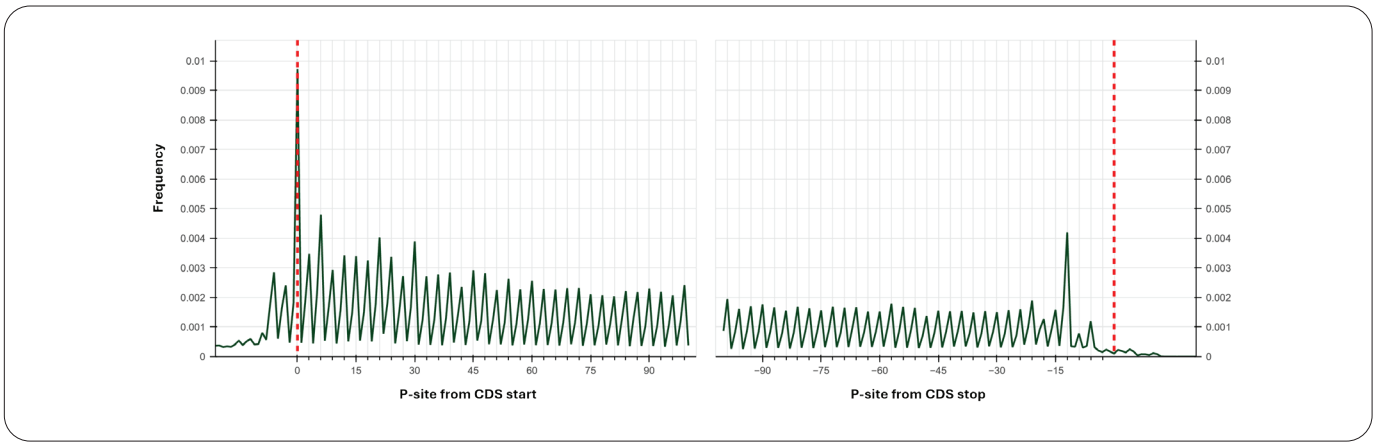


Figure 3: Metagene profile showing P-site positions for all transcripts around translation initiation sites (from 0 to 100 nt) and translation termination sites (from 0 to -100 nt) highlighted with a red line.

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Get started

Contact our team to learn how **RiboLace™ Pro** and **NEXTFLEX™ Small RNA-seq kit v4** can simplify your ribosome profiling workflow. Start generating robust, high-confidence translational data today.

Learn more

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