eRibo Pro: All-Inclusive Ribosome Profiling Service

Professional End-to-End Service

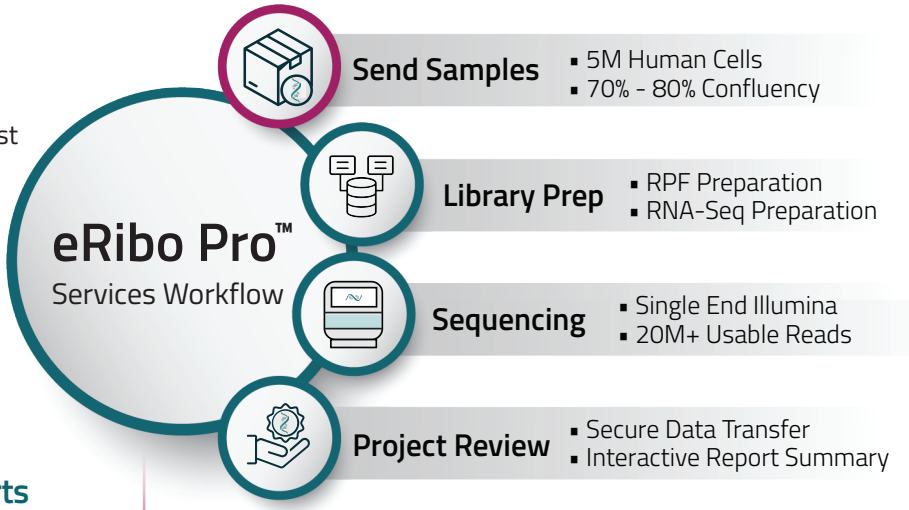
Send your samples and let Eclipsebio's fast and efficient RNA experts handle the rest

Expedited Ribosomal Insights

Comprehensive translational results without the need for training, specialized equipment, and reagent sourcing

Interactive Data Summary Reports

Transcriptome-wide data analysis with ribosome footprints mapping, differential gene expression, and ribosome occupancy



eRibo Pro Service Introduction

Widespread application of RNA-Seq has provided substantial insight into the role of gene expression, however it fails to capture regulation at the level of translation. Furthermore, while many people utilize RNA-Seq data to estimate the cellular proteome, characterization of ribosome-associated RNAs serves as a closer proxy to estimate a sample's protein levels. eRibo Pro is an exclusively licensed method for profiling ribosome-associated RNAs and the transcriptome. The eRibo Pro service is an end-to-end solution that streamlines the ribosomal profiling process, from sample processing to sequencing and data analysis. The comprehensive service includes mapping of ribosome protected fragments (RPFs) and identification of differentially transcribed and translated genes with interactive reports that allow researchers to make data driven insights. The ability to quantify ribosome occupancy transcriptome-wide using eRibo Pro will enable translatome studies to be applied more broadly in the context of research and in the development of therapeutics.

Start your eRibo Pro Experiment Today

Ready to start your all-inclusive eRibo Pro service project? Contact us using the information below and your local Eclipsebio sales representative will follow-up within 2 days to schedule your free consultation.

Visit us online at **eclipsebio.com** or
Contact us at **info@eclipsebio.com**

eRibo Pro Analysis Deliverables

Comprehensive Data Package

Interactive Summary Reports — HTML

Report includes QC metrics, visualization of gene ontology enrichment, and differential genes.

Differential Expression & Ribosome Occupancy — DESeq2

Per gene statistics table for the ribosome associated fragments (RPF) and RNA-Seq libraries

Genome Browser Track Files — BigWig

For transcriptome-wide visualization of the data in a genome viewer like IGV

Raw Sequencing Data & Processed Aligment Files — FASTQ, BAM

Raw reads from sequencer and unique sequence alignments to the reference genome

Detect changes in ribosome occupancy

eRibo Pro quantifies translation changes in response to drug treatments that would be missed by RNA-Seq alone.

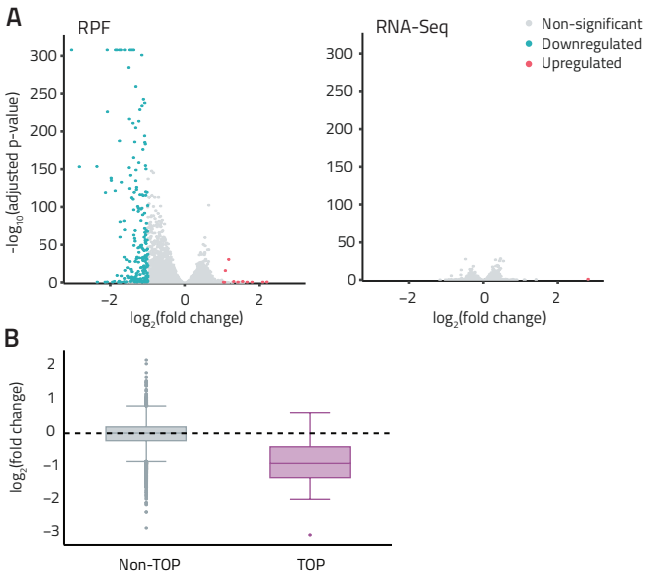


Figure 1. Torin 1, a well-characterized translation inhibitor, causes reduced ribosome occupancy on TOP- and TOP-like motif containing genes in response to acute treatment. (A) Volcano plots represent changes in gene expression as measured by changes in translational (left) as well as changes in RNA-Seq (right). (B) Box plot showing gene expression changes in RPF libraries between non-TOP (gray) versus TOP-motif containing genes (purple).

High quality ribosome profiling data

eRibo Pro delivers trinucleotide periodicity from translating ribosomes and captures signal from ribosomes stalled at the initation step of translation following harringtonine treatment.

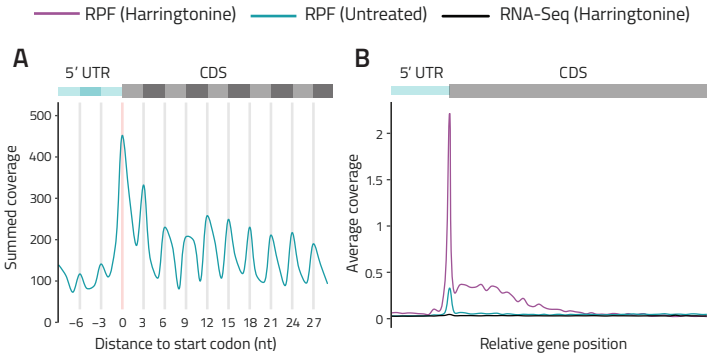


Figure 2. (A) Periodicity plot showing summed coverage across P-site corrected 5' read ends from an untreated eRibo Pro RPF library, with the listed position being relative to the annotated start codon for each gene examined. (B) Metagene plot showing the average coverage across reads mapping to the 5' UTR and upstream CDS of all genes from untreated RPF, harringtonine treated RPF, and harringtonine-treated RNA-Seq libraries.

High correlation between eRibo replicates

eRibo Pro shows high correlation between replicate libraries of RNA-Seq, ribosome protected fragments (RPF), and ribosome occupancy (RO). eRibo Pro is also highly correlated with Eclipsebio's immumoprecipitation (IP) based ribosome counting assay, eRibo Count. High replicate correlation facilitates robust and reproducible ribosome-association analysis across technologies.

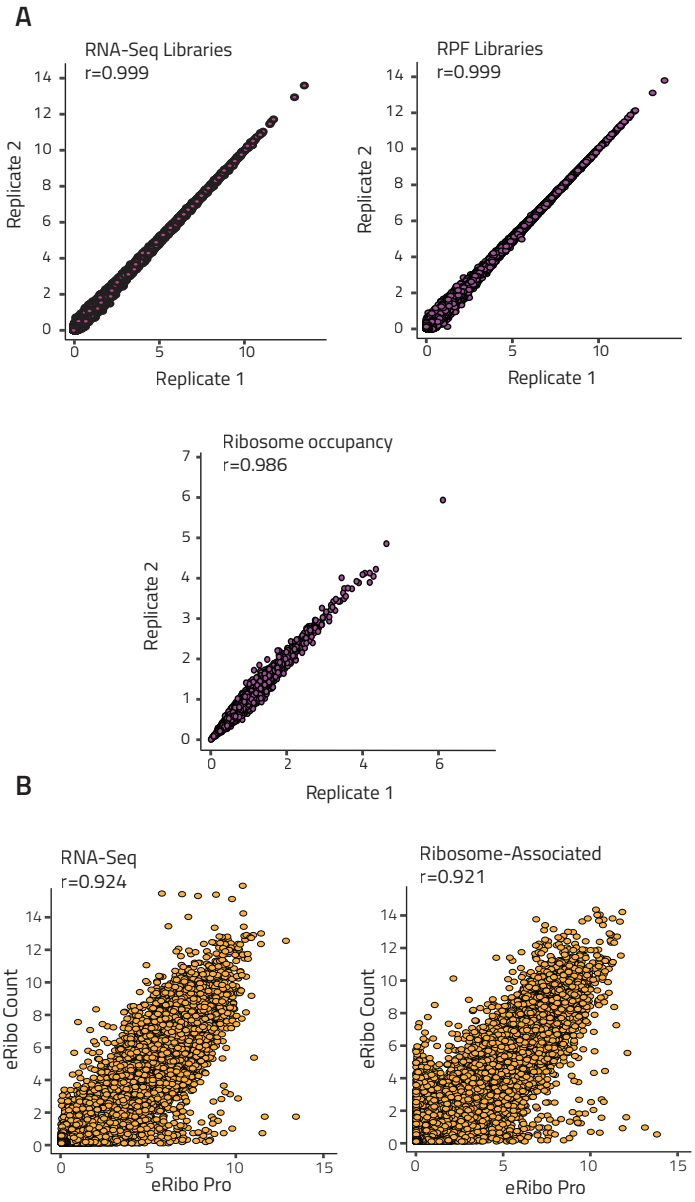


Figure 3. (A) Correlation between replicates for eRibo Pro RNA-Seq (r=0.999), RPF (r=0.999), and Ribosome Occupancy values (RO, ratio of normalized RPF levels over RNA-Seq levels, r=0.986). (B) Correlation between eRibo Pro and eRibo Count RNA-Seq (r=0.924) as well as Ribosome-Associated (r=0.921) libraries.