CD Genomics
The Genomics Services Company

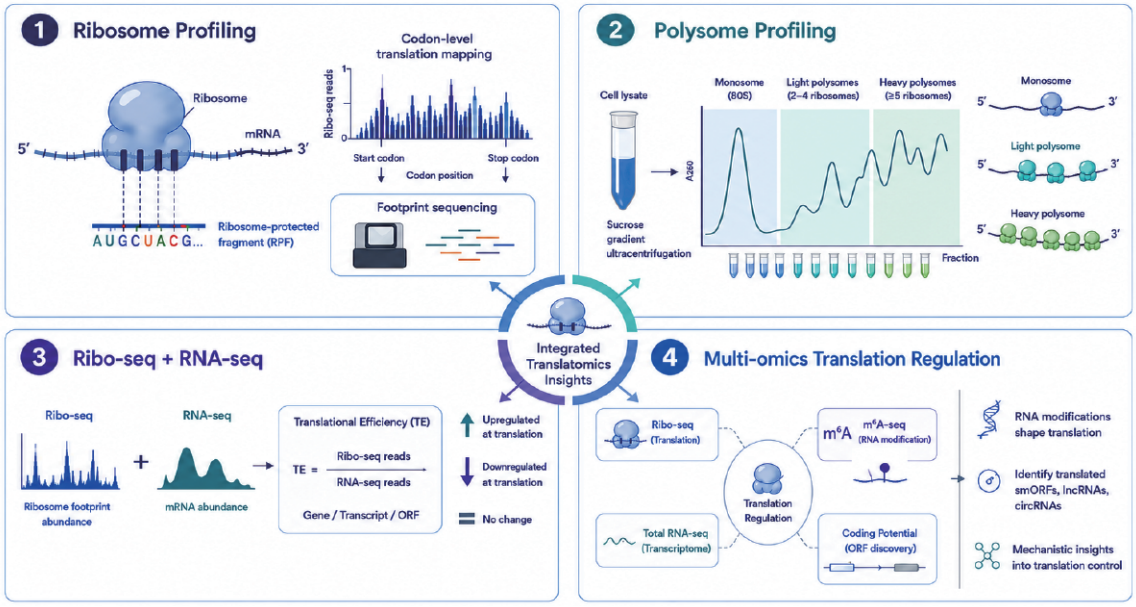
Translatomics: Ribosome Profiling & Polysome Profiling Services

CD Genomics provides translatomics services to profile active translation, ribosome occupancy, translational efficiency, and ribosome loading through Ribo-seq, Polysome profiling, and integrated RNA-seq-based analysis.

Ribo-seq | **Polysome Profiling** | **TE Analysis**

From ribosome-protected fragment mapping to polysome fraction analysis, our translatomics workflows help researchers distinguish transcriptional abundance from active translation and uncover post-transcriptional regulatory mechanisms.

Translatomics Strategy Overview



From Question to Translation Strategy

- Define active translation, ribosome loading, TE, or ORF discovery goals
- Select Ribo-seq, polysome profiling, or integrated workflows by sample and model
- Plan matched RNA-seq or multi-omics analysis for mechanism interpretation

Integrated Study Designs

- Ribo-seq + RNA-seq to calculate translational Integrated Study efficiency and separate transcriptional from translational regulation.
- Ribo-seq + m6A-seq to explore how RNA methylation affects ribosome loading and elongation.
- Ribo-seq + Total RNA-seq to evaluate coding potential in lncRNAs, circRNAs, and smORFs.

Research Outputs

- Ribosome footprint distribution, P-site mapping, and frame periodicity assessment
- Differential TE, ribosome loading, ORF-level analysis, and coding potential evaluation
- ORF/uORF/sORF discovery, pathway enrichment, figures, and structured result reports

Analysis Snapshot

Method	Best Fit	Key Strength
Standard Ribo-seq	Active translation mapping	Codon-level ribosome positioning and ORF analysis
Active Low-Input Ribo-seq	Limited or rare samples	High-resolution translation analysis with reduced input
Polysome Profiling	Ribosome loading studies	Separates monosome, light polysome, and heavy polysome fractions
Ribo-seq + RNA-seq	TE analysis	Distinguishes transcriptional and translational regulation
Ribo-seq + m6A-seq	RNA modification and translation studies	Links m6A regulation with ribosome loading and elongation

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