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The RNA Experts

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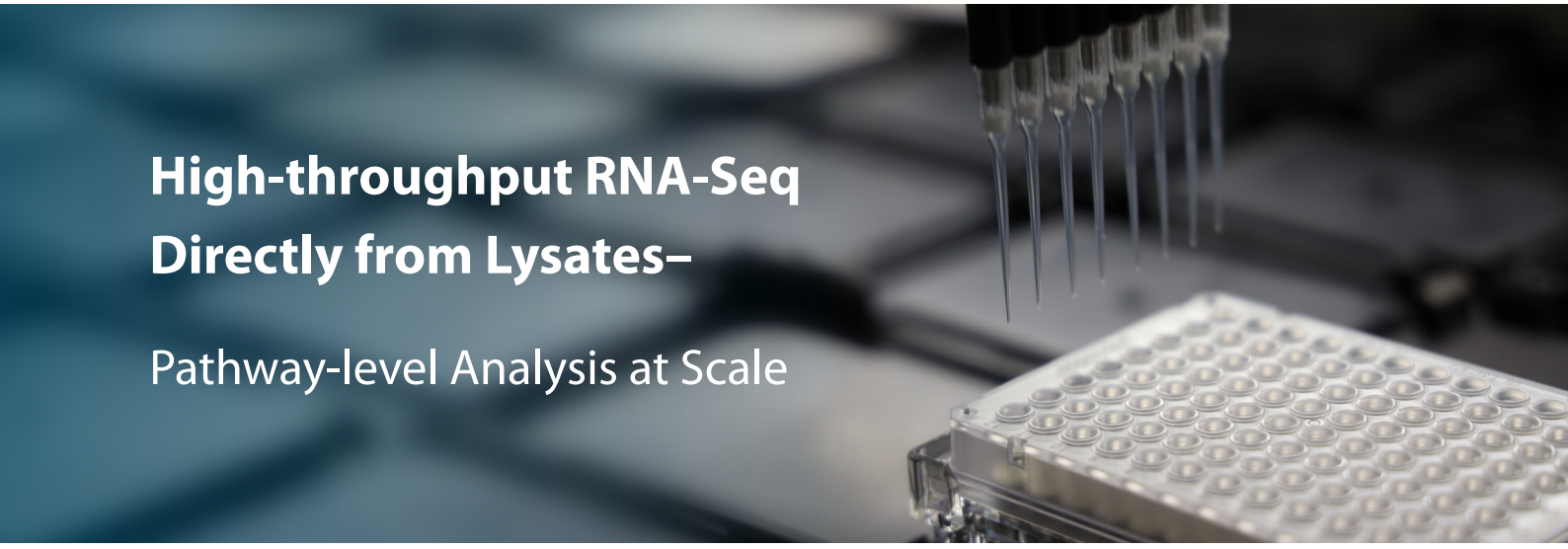

High-throughput RNA-Seq Directly from Lysates–

Pathway-level Analysis at Scale

QuantSeq-Pool and LUTHOR HD Pool: Streamlined, Cost-effective Expression Profiling to Accelerate Drug Discovery

Traditional high-throughput screening often relies on visual markers, which can be challenging to quantify and limit the scope of analysis. RNA-Seq based screening offers a comprehensive view of the transcriptome at scale; providing quantitative data for the **discovery of genes and pathways affected by active compounds** independent of visual detection. Lexogen's solutions for high-throughput screening are **lysate compatible, ultra-scalable** and applicable **for primary cells - down to single cells.**

Early Drug Discovery

Target Identification & Validation

- Reveal disease-associated pathways as potential drug targets
- Single-cell CRISPR perturbation screens for target identification

Lead Discovery

High-throughput Screening, Hit Discovery & Lead Optimization

- Pathway-level read out directly from cell lysates
- Mode of action (hits and leads)
- Dose-dependent expression profiles

Pre-Clinical Studies

Animal Models

- Comparative transcriptomics for preclinical model selection
- Treatment response monitoring
- Identification of off-target effects

Dose Range, Drug Formulation

- Efficacy studies

Precision RNA-Seq from purified RNA, cell lysates or single-cells: Drive drug discovery with an early high-definition view of your compounds mode of action!

Lysate compatible: Process samples faster with **extraction-free RNA-Seq directly from lysates. LUTHOR HD Pool** is compatible with lysates from fresh, frozen, and fixed cells and **excludes genomic DNA and rRNA** for authentic, highly sensitive gene expression data.

Highly affordable: Cost-effective solutions for large-scale drug discovery projects, **down to 2 USD per prep for LUTHOR HD Pool** with remarkable quality at low read depth.

Ultra-scalable: Use the same prep for ultra-high throughput hit discovery screens and selective assays for dose-dependent **RNA-Seq and pathway-level analysis from 8 - 36,864 samples** and down to single-cell level.

Massively multiplexed RNA-Seq with and without RNA extraction

Massively multiplexed RNA-Seq is a powerful high-throughput method that allows efficient and cost-effective expression profiling of a large number of RNA samples or cell lysates through sample barcoding (Fig.1). Sample barcodes are added in the first step allowing early pooling and batch processing for library generation (Fig. 2). Lexogen provides various workflow options tailored to your project and offers consultancy for every step as well as data analysis and pipeline development service.

Figure 1 | Massively multiplexed RNA-Seq workflow for drug discovery and development.

LUTHOR HD Pool for High-Definition RNA-Seq from Lysates and QuantSeq-Pool for purified RNA

QuantSeq-Pool uses purified RNA as input and relies on Lexogen's established 3' mRNA-Seq technology trusted by labs worldwide for more than a decade. **QuantSeq-Pool has been validated with various cell lines and xenografts for drug discovery applications,** e.g., for validation of selected small molecule hits targeting the oncogenic miRNA miR-21(Arshadi *et al.,* 2024). **LUTHOR HD Pool** is Lexogen's newest development for **extraction-free massively multiplexed expression profiling directly from cell lysates**. Validated for various cell lines, LUTHOR HD Pool enables sustainable, streamlined RNA-Seq with **pathway-level resolution for as low as 2 USD/sample** and is applicable for **cell lines, primary cells, rare cells, organoids** and **from thousands of cells down to single cells.**

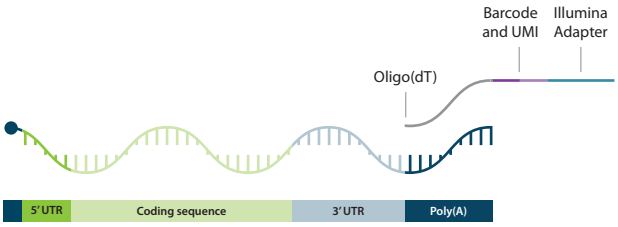

Figure 2 | Introduction of sample barcodes in the first step of RNA-Seq library generation from RNA or cell lysates tags each individual sample. Subsequently, up to 96 samples can be pooled for further processing. Indexing with unique dual barcodes enables massive scalability for processing of 8 - 36,864 samples.

Applications

Cell-based unbiased high-throughput screening in plate-format, with any type of dose-dependent perturbation, e.g.:

- ✓ Small molecules
- ✓ Oligonucleotide therapeutics and siRNAs
- ✓ CRISPR
- ✓ Antibodies

Compatible with bulk-RNA, lysates, or single cells.

QuantSeq-Pool (with RNA extraction) and LUTHOR HD Pool extraction-free RNA-Seq enable massive scaling (up to 36,864 samples per run) and significant savings in consumable cost. Shallow RNA-Seq at low read depth is sufficient for:

- Pathway-level analysis
- Dose-response expression profiles
- Mode-of-action indication
- Biomarker identification

> "In our hands, QuantSeq-Pool convinced with very low technical variability which **boosts the performance** for Differential Gene Expression analysis. QuantSeq-Pool now offers us a **robust and time-saving procedure** that we can **scale up to 1,000s of samples** for our customer projects."
>
> ***Pieter Mestdagh,*** *Principal Scientist, Biogazelle, Belgium*

Interested?

Partner with Lexogen via sales@lexogen.com or scan the code.

References

Arshadi *et al.*, 2021, *Patterns* (5): 100909, DOI: 10.1016/j.patter.2023.100909