

Pathway-level Analysis at Scale with QuantSeq-Pool

QuantSeq-Pool Sample-Barcoded 3' mRNA-Seq Library Prep Kit The right choice for large scale, high-throughput expression studies

QuantSeq-Pool, based on the trusted QuantSeq 3' mRNA-Seq technology, represents the optimal solution for gene expression profiling for large screening projects. By combining sample barcoding, early pooling, and **batch processing of up to 96 samples in a single reaction**, QuantSeq-Pool enables a **streamlined workflow that easily scales to multiplexing up to 36,864 samples**. The convenient workflow and scalable multiplexing capacities make **QuantSeq-Pool the optimal choice for performing gene expression profiling studies with exceptional cost and time efficiency**.



Reproducible & reliable results

Reduce technical variability and consistently process large numbers of samples in parallel. Built-in UMIs remove PCR duplicates for high-precision expression profiling.



Scalable multiplexing for massive throughput

Massive multiplexing of up to 36,864 samples streamlined large-scale studies. The automation-friendly workflow ensures seamless scalability and efficiency at every step.



Gene expression screening - faster than ever

Save valuable time and accelerate your workflow with early pooling and batch processing of up to 96 samples in one reaction, enabling rapid and efficient gene expression screening.



Significant cost reduction

Cut costs for sequencing, consumables, and data analysis through cost-efficient 3' mRNA-Seq and prior sample pooling, making large-scale gene expression studies more affordable than ever.

Massive Streamlining and Upscaling Enabled by Early Sample Pooling Step with QuantSeq-Pool

Lexogen's QuantSeq-Pool combines early sample barcoding with the benefits of 3' mRNA-Seq. Total RNA of up to 96 samples is pooled into a single reaction in the initial library generation step, enabling subsequent processing of individually labeled samples in parallel (Fig. 1). Thereby, QuantSeq-Pool tremendously increases multiplexing capacities and ensures library preparation consistency. Its highly streamlined protocol reduces hands-on time as well as expenses for consumables, sequencing, and data analysis.

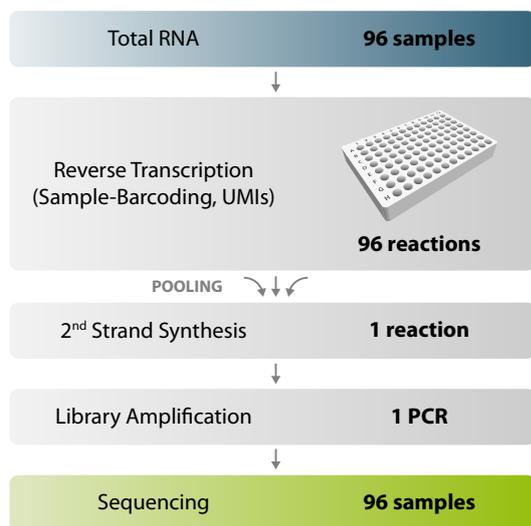


Figure 1 | Early pooling of sample-barcoded libraries allows batch processing of 96 samples in a single reaction.

Efficient and Optimized Workflow for Focused Gene Expression Screening

Lexogen's proprietary QuantSeq 3' mRNA-Seq technology, as implemented in QuantSeq-Pool, generates one fragment per transcript at the 3' end of polyadenylated mRNA, enabling straightforward gene counting for cost-efficient gene expression analysis. Batch processing with QuantSeq-Pool significantly shortens the complete RNA-to-sequencing workflow by reducing handling time and eliminating the need for quantification, quality control, and equimolar pooling of individual libraries, compared to conventional mRNA-Seq. Lower sequencing depth per sample produces reduced amount of data, simplifying analysis and reducing computational complexity, while still providing unparalleled insights into gene expression profiles at scale (Fig. 2).

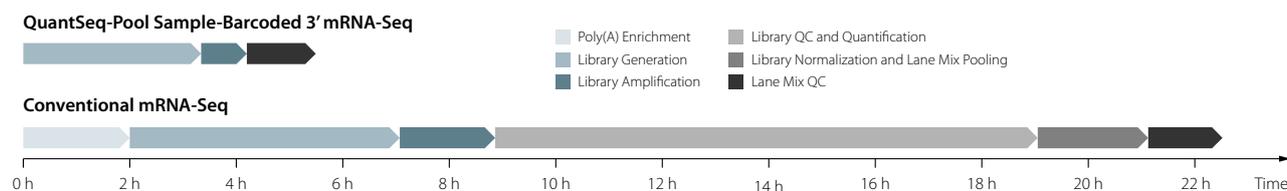


Figure 2 | QuantSeq-Pool enables completion of the RNA-to-sequencing workflow for 96 samples in ~5.5 hours.

Ordering Information

Cat. №	Product Name
139	QuantSeq-Pool Sample-Barcoded 3' mRNA-Seq Library Prep Kit, 96 preps
101-104	Lexogen UDI 12 nt Set A1-A4, 96 preps
105	Lexogen UDI 12 nt Set B, 96 preps
156	Lexogen UDI 12 nt Set A1-A4, 384 preps
208	PCR Add-on and Reamplification Kit V2 for Illumina, 96 preps

Robust Gene Detection at Low Sequencing Depth for Consistent and Reliable Data

High-throughput screening projects, such as those used for target identification and validation in drug discovery, require robust and reliable gene expression profiling, even at low read depths. QuantSeq-Pool consistently detects 7,500 to 9,000 highly expressed genes (CPM > 10) at very shallow read depths of 100 K to 1 M reads per sample (Fig. 3). Robust expression results are achieved with high consistency, even with low input amounts (10 ng total RNA).

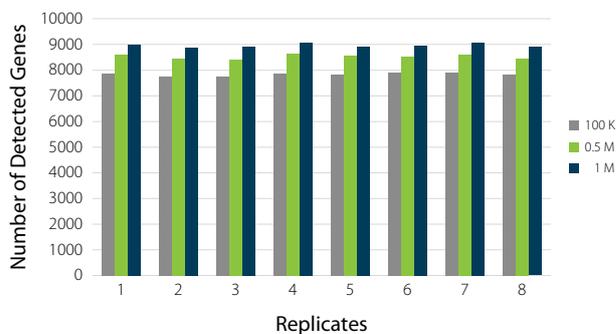


Figure 3 | QuantSeq-Pool enables robust and consistent gene detection already at low sequencing depth across 8 replicates with 10 ng input (UHRR) at different sequencing depth with gene counting threshold of CPM > 10.

Accelerate Drug Discovery with QuantSeq-Pool

QuantSeq-Pool has been validated with various cell lines and xenografts for drug discovery applications, including:

- ✓ Target identification & validation
- ✓ Pathway-level analysis
- ✓ Dose-response expression profiles
- ✓ Mode-of-action indication
- ✓ Biomarker identification

“ We have established QuantSeq-Pool on lysates in our facility and are very happy with its performance. 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

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