

Product Overview

Sampling	RNA Preparation	NGS Library Prep	NGS Data Analysis
<p>SLAMseq for High-Throughput Kinetic RNA Sequencing</p> <ul style="list-style-type: none"> » Explorer Modules » Kinetics Modules <ul style="list-style-type: none"> Analyze RNA synthesis and degradation (RNA kinetics) in a time-resolved manner. Combined with QuantSeq to gain novel insights into the control of gene expression. <p>RNA/DNA Defender Solution ^{NEW}</p> <ul style="list-style-type: none"> Stabilize RNA and DNA in fresh tissue and cell culture samples. Postpone RNA or DNA extraction to when more convenient. Various storage options: one day at 37 °C, one week at room temperature, one month at 4 °C, or up to one year at -20 °C. 	<p>TraPR Small RNA Isolation</p> <ul style="list-style-type: none"> Isolation of pure, functional sRNA. Fast and easy column-based purification. Species independent. <p>SPLIT RNA Extraction</p> <ul style="list-style-type: none"> Extraction of high-quality, high-purity RNA from a wide range of biological samples, including cell culture, animal and plant tissue, and fluid samples. 	<p>Expression Profiling</p> <ul style="list-style-type: none"> » QuantSeq 3' mRNA-Seq V2 with UDI ^{NEW} New and improved PCR system. » QuantSeq 3' mRNA-Seq FWD and REV » QuantSeq-Pool Sample-Barcoded 3' mRNA-Seq » QuantSeq-Flex Targeted RNA-Seq Cost-efficient gene expression profiling - including low-input, low-quality, and blood samples. Unique Molecular Identifiers (UMIs). Up to 384 Unique Dual Indices (UDI). Easily scalable to 36,864 samples for large screening projects. » LUTHOR 3' mRNA-Seq True single-cell expression profiling. High resolution for ultra-low input. 	<p>Demultiplexing and Index Error Correction Tool</p> <p>QuantSeq Data Analysis</p> <ul style="list-style-type: none"> Automated, in-house data analysis pipeline, including SLAMdunk for SLAMseq data analysis. User-friendly, streamlined data analysis.
	<p>RiboCop rRNA Depletion</p> <ul style="list-style-type: none"> rRNA depletion (>99 %) at lowest cost, without off-target effects. Suitable for demanding downstream applications (e.g., NGS). Available for human, mouse, rat, bacteria and yeast. ^{NEW} Simultaneous rRNA and globin mRNA depletion for human, mouse, rat. 	<p>Whole Transcriptome</p> <ul style="list-style-type: none"> » CORALL RNA-Seq V2 ^{NEW} Fragmentation-free library size adjustment. ^{NEW} Uniform transcript coverage. UMIs included. UDIs included. Fast (4.5 h) and easy protocol. » CORALL mRNA-Seq V2 ^{NEW} » CORALL Total RNA-Seq V2 ^{NEW} 	<p>CORALL Data Analysis</p> <p>Automated, in-house data analysis pipeline.</p> <ul style="list-style-type: none"> Uses Mix² for accurate transcript abundance estimation. User-friendly, streamlined data analysis.
	<p>Poly(A) RNA Selection</p> <ul style="list-style-type: none"> Highly specific poly(A) RNA enrichment. Rapid turnaround, automation-friendly, easy scaling. 	<p>Small RNA-Seq</p> <ul style="list-style-type: none"> User-friendly workflow, high level of multiplexing (up to 96 unique i7 indices included). Optimized for low RNA content samples such as plasma, serum, and urine. 	<p>Mix² RNA-Seq Data Analysis Software</p> <ul style="list-style-type: none"> Accurate estimation of isoform concentration with best quantity, quality, and accuracy measures. Fast and small memory footprint. Identification of positional biases in RNA-Seq data.
cDNA Preparation			
<p>TeloPrime Full-Length cDNA Amplification</p> <ul style="list-style-type: none"> Best 5' cap specificity for full-length cDNA generation. Preservation of short and long RNA molecules, suitable for long-read sequencing (e.g. PacBio™ and Oxford Nanopore™). 			
NGS Controls			
<p>Spike-In RNA Controls</p> <ul style="list-style-type: none"> » SIRV-Set 1 (Iso Mix E0, E1, E2) » SIRV-Set 2 (Iso Mix E0) » SIRV-Set 3 (Iso Mix E0 / ERCC) » SIRV-Set 4 (Iso Mix E0 / ERCC / long SIRVs) Comprehensive design - isoform and abundance complexity. Validate, monitor, and compare RNA-Seq experiments and pipelines. 			<p>SIRV Suite Spike-In Analysis Software</p> <ul style="list-style-type: none"> Design and evaluate your SIRV experiment, derive RNA-Seq quality measures and compare experiments.
Lexogen NGS Services			
<p>Library Preparation</p> <ul style="list-style-type: none"> Flexible options from nucleic acid extraction to data analysis. Library preparation solutions tailored to your needs. Focus on highest quality data and reproducibility using internal standard controls. Excel with low-input and low-quality samples. 	<p>Automation and Sequencing</p> <ul style="list-style-type: none"> Automated liquid handling for high-throughput projects. From tens to thousands of samples. Flexible sequencing platforms, read mode and depth options. 	<p>Data Analysis</p> <ul style="list-style-type: none"> Fully integrated data analysis pipelines. Data analysis report including standard metrics, and (differential) gene expression. Custom design data analyses available. 	

Library Prep Kits Overview

Kit Selection Criteria	CORALL RNA-Seq			QuantSeq				LUTHOR 3' mRNA-Seq	Small RNA-Seq	Te-lo-Prime Full-Length cDNA
	+ Poly(A) (CORALL mRNA)	+ RiboCop	QuantSeq 3' FWD	QuantSeq Pool 3'	QuantSeq 3' REV	QuantSeq -Flex				
Application										
Gene Expression Profiling	✓	✓	✓	✓*	✓*	✓	✓	✓	✓	✗
Whole Transcriptome (full-transcript coverage)	✓	✓	✓	✗	✗	✗	✗	✗	✗	✓
Alternative Polyadenylation	✗	✓	✗	✓	✗	✓*	✓	✓	✗	✓
Isoform discovery & quantification	✓	✓*	✓*	✗	✗	✗	✓	✗	✗	✓
Targeted Sequencing	✗	✗	✗	✗	✗	✗	✓*	✗	✗	✓
RiboSeq (ribosomal profiling)	✗	✗	✗	✗	✗	✗	✗	✗	✓*	✗
Transcript (re)annotation	✓	✓	✓	✗	✗	✗	✉	✗	sRNA only	✓
De novo assembly	✓	✓	✓	✗	✗	✗	✗	✗	✗	✓
SLAMseq (kinetic RNA-Seq)	✓	✓	✓	✓	✓	✓	✓	✉	✓	✓
Small RNA (e.g., miRNA) analysis	✗	✗	✗	✗	✗	✗	✗	✗	✓	✗
Long non-coding RNA analysis	✓	✓ poly(A) only	✓*	✗	✗	✗	✓	✗	✗	✓ ^{pA}
RNA Input Type										
Human or animal cells, protoplasts and lysates	✗	✗	✗	✗	✗	✗	✗	✓	✗	✗
Total RNA	✓	✓*	✓*	✓*	✓*	✓	✓	✓	✓	✓
Poly(A)+ RNA (≅ mRNA)	✓*	✗	✓	✓	✓	✉	✉	✉	✗	✓
rRNA depleted RNA	✓*	✉	✗	✉	✉	✉	✉	✉	✗	✉
Small RNA	✗	✗	✗	✗	✗	✗	✗	✗	✓	✗
High quality (RIN ≥8)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
Moderate quality (RIN 5 - 8)	✓	✗	✓	✓	✓	✓	✓	✓	✓	✗
Highly degraded (RIN <5; DV ₂₀₀ <50 %)	✓	✗	✓	✓ ^M	✉	✓ ^M	✓ ^M	✗	✓	✗
Low Input <100 pg	✗	✗	✗	✗	✗	✗	✗	✓	✗	✗
Organism										
Human, mouse, rat	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
Other animals	✓	✓	✉	✓	✓	✓	✓	✓	✓	✓
Plant	✓	✓	✗	✓	✓	✓	✓	✓	✉	✓
Yeast	✓	✓	✓	✓	✓	✓	✓	✓	✉	✓
Bacteria	✓	✗	✓	✗	✗	✗	✓	✗	✓	✉
Virus	✓	✓ ^{pA}	✉	✓ ^{pA}	✓ ^{pA}	✓ ^{pA}	✓	✓ ^{pA}	✉	✓ ^{pA}
Sample Type (other sample types will also be compatible for most kits, please contact support@lexogen.com for further information)										
Tissues	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
Cells (cell lines, primary, sorted cells, etc.)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
Blood	✓	✓	✓	✓	✓	✓	✓	✓	✓	✉
Liquid biopsy (CSF, serum, plasma, urine)	✉	✗	✉	✉	✉	✉	✉	✓	✓*	✗
FFPE / Biobank samples	✓	✗	✓	✓ ^M	✉	✓ ^M	✓ ^M	✗	✓	✗
Exosomes	✉	✉	✉	✉	✉	✉	✉	✓	✓*	✗
Recommended / compatible sequencing platforms / formats										
Illumina*	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
Single-read	✓	✓	✓	✓	✗	✓	✓	✓	✓	✓
Paired-end	✓	✓	✓	✗	✓	✓	✓	✗	✗	✓
Additional Options										
Unique Dual Indexing (UDI) available	included	included	included	✓	✓	✓	✓	✓	✗	✗
Automation-compatible	✓	✓	✓	✓	✉	✓	✓	✉	✗	✗
UMIs available	included	included	included	✓	included	✗	✓	✗	✗	✉
Data Analysis pipeline available	✓	✓	✓	included	✓	included	✉	✓	✓	✓
Service available	✓	✓	✓	✓	✓	✓	✉	✓	✓	✗
Spike-In control recommendation	SIRV-Set 1/2/3			SIRV-Set 3			✗	SIRV-Set 3	✗	SIRV-Set 1/2/3/4 ✉

✓* Optimal Choice

✓ Yes

✉ For more information please contact support@lexogen.com

* Contact us at support@lexogen.com for information on compatibility with sequencing platforms

✓^{pA} Possible only if a poly(A) tail (and a 5' cap for TeloPrime) is present or with prior poly-adenylation

✓^M Protocol modifications apply

✗ Not possible or not useful