

RiboCop rRNA Depletion Kits

- Superior depletion of rRNA from human/mouse/rat, or bacterial samples
- **NEW!** Combined rRNA and globin mRNA depletion for human/mouse/rat
- **NEW!** Innovative probe design minimizing off-target effects
- Broadest input range from 1 ng to 1 µg
- Compatible with high- and low-quality RNA, including FFPE samples

Introduction

Total RNA is comprised of large amounts of undesired transcripts, such as ribosomal RNA (rRNA), which account for ~80-98 % of the total RNA sample, and globin mRNA, accounting for ~35-80 % of mRNA in blood samples. Lexogen's RiboCop rRNA Depletion Kits efficiently remove rRNA and globin mRNA from intact as well as degraded total RNA samples. The resulting depleted RNA can be directly used for Next Generation Sequencing (NGS) as well as other demanding RNA applications. RiboCop-treated RNA is compatible with all standard RNA-Seq library preparation protocols.

Benefits

- **Robust:** New, sophisticated probe design delivering robust rRNA depletion without off-target effects.
- **Reliable:** Enzyme-free protocol preserves full-length RNA and allows processing of low quality RNA samples.
- **Scalable:** Flexible input of 1 ng - 1 µg total RNA and automation-friendly.
- **Complete Workflow Solution:** Fragmentation-free RNA-Seq workflow in combination with CORALL Total RNA-Seq.
- **Universal:** Compatible with all standard RNA-Seq Library Prep Kits. Available for human/mouse/rat, including blood samples, and for bacteria.

Principle

RiboCop's rRNA depletion methodology is based on the removal of rRNA via hybridization to specifically designed oligos and subsequent affinity purification of the rRNA-oligo hybrids with magnetic beads. Lexogen has developed a sophisticated algorithm to design specific Probe Mixes for maximum rRNA removal while keeping unwanted off-target effects at a minimum. The entire protocol is automation-friendly by utilizing magnetic beads for depletion and purification, and enables convenient and fast depletion in only 1.5 hours (Fig. 1).

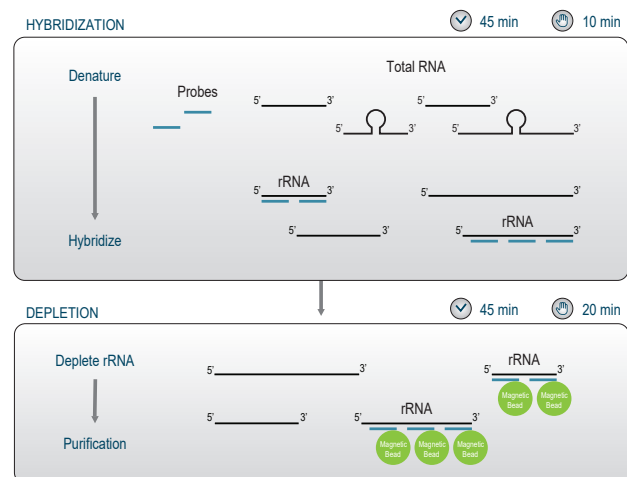


Figure 1 | Schematic overview of the RiboCop workflow.

Ordering Information

Product Name	Cat. No.	Sample Type	Depleted RNA Species
RiboCop rRNA Depletion Kit for Human/Mouse/Rat (HMR) V2	144	Human/Mouse/Rat	28S, 18S, 5.8S, 45S, 5S, mt16S, and mt12S rRNA
RiboCop rRNA Depletion Kit for Human/Mouse/Rat plus Globin (HMR+Globin)	145	Human/Mouse/Rat blood	28S, 18S, 5.8S, 45S, 5S, mt16S, and mt12S rRNA and globin mRNA
RiboCop rRNA Depletion Kit for Mixed Bacterial Samples (META)*	125	Gram positive and gram negative mixed bacterial samples and monocultures	23S, 16S, and 5S rRNA
RiboCop rRNA Depletion for Gram Negative Bacteria (G-)*	126	Gram negative bacterial monocultures	23S, 16S, and 5S rRNA
RiboCop rRNA Depletion for Gram Positive Bacteria (G+)*	127	Gram positive bacterial monocultures	23S, 16S, and 5S rRNA

*If you are uncertain which kit to choose, the [RiboCop for Bacteria Selection Tool](#) can help you find the best-suited kit for your species of interest.



For more information and additional resources on RiboCop visit our [website](#).

**RiBO
COP™**
Select and Deplete

Complete Total RNA-Seq Workflow with RiboCop

Complete RNA-Seq Workflow Including RiboCop rRNA Depletion

RiboCop efficiently removes undesired RNA from total RNA samples, and the resulting depleted RNA is directly suitable for demanding downstream applications such as NGS. RiboCop can be seamlessly integrated into Lexogen's complete workflow solutions covering all steps from RNA extraction to data analysis (Fig. 2).

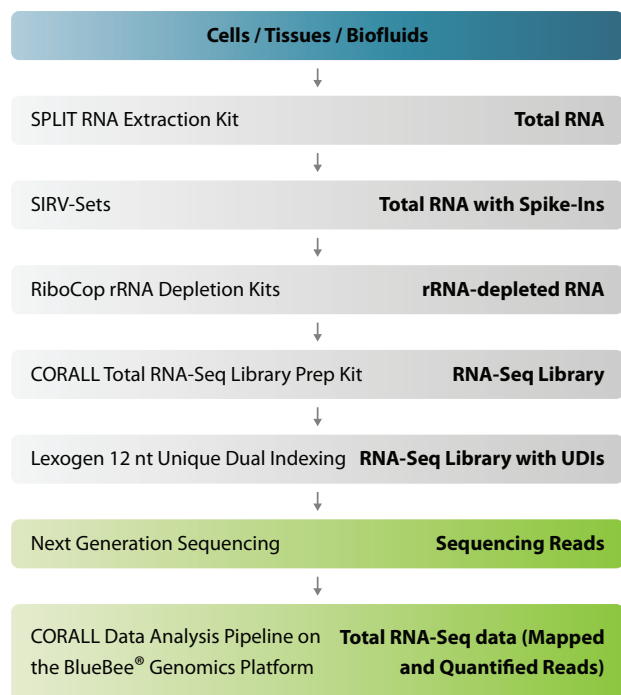


Figure 2 | Complete total RNA-Seq workflow based on Lexogen kit solutions.

SPLIT RNA Extraction Kits enable extraction of high quality, high purity RNA from cells, tissues, or biofluids. Universal Spike-In RNA Variants (SIRVs) mimic transcriptome complexity enabling validation of complete RNA-Seq workflows and control of experiments within a series and across sites. RiboCop rRNA Depletion Kits remove undesired rRNA to focus sequencing reads on RNAs of interest. RiboCop-treated RNA is suitable for all total RNA-Seq library preps, such as CORALL Total RNA-Seq. In combination with Lexogen's UDI 12 nt Unique Dual Indexing Sets the output of sequencing experiments can be maximized by superior error correction capacity for rescue of mis-assigned reads. The CORALL Data Analysis Pipeline available on BlueBee® Genomics enables fast and easy data analysis even without bioinformatics experience.

Ordering Information

Product Name	Cat. No.	Specification
SPLIT RNA Extraction Kit	008	RNA Extraction kit
SIRV-Set 1, Set 2, Set 3, Set 4	025, 050, 051, 141	Different SIRV-Sets for all experimental needs
CORALL Total RNA-Seq Library Prep Kit	095	Stand-alone kit for full flexibility
CORALL Total RNA-Seq Library Prep Kit with RiboCop (HMR)	146	RiboCop (HMR) and CORALL bundle
CORALL Total RNA-Seq Library Prep Kit with RiboCop (HMR+Globin)	147	RiboCop (HMR+Globin) and CORALL bundle
CORALL Total RNA-Seq Library Prep Kit with UDI 12 nt Set A1 to A4, or B1	117, 132-134, 119, or 118	CORALL and UDI bundles
Lexogen UDI 12 nt Unique Dual Indexing Add-on Kits, Set A1 to A4, or B1	107-110, or 111	Optional: UDI Add-on kits

Benefits for Lexogen's Innovative Workflow Solutions

SPLIT RNA Extraction

- Total RNA from various sample types in 30 minutes.
- Option of splitting your sample to obtain large and small RNA fractions.
- High RNA integrity and purity, free of genomic DNA*.
- Excellent extraction efficiency.
- **OPTIONAL:** SPLIT for Blood combines red blood cell lysis and RNA extraction for removal of globin mRNA from blood samples.

*for most sample types

Spike-In RNA Variants (SIRVs)

- SIRVs are universal controls for RNA-Seq experiments with all organisms and for all platforms.
- Evaluate only 1% of your data to draw valid conclusions on the whole data set and compare results across data sets.
- SIRVs allow validation of complete RNA-Seq workflows. SIRVs mimic the isoform, abundance, and length complexity of natural transcriptomes and indicate deviations, biases, and blind spots in RNA-Seq workflows.

CORALL Total RNA-Seq

- Elevated transcript start and end site coverage.
- Ready-to-sequence libraries within 4.5 hours.
- Unique Molecular Identifiers (UMIs) seamlessly included.
- Excellent protocol-inherent strandedness (>99 %).
- 1 ng to 1 µg of total RNA input.
- Fragmentation-free, easy-to-handle, all-in-one protocol.
- Compatible with optimized 12 nt unique dual indexing (UDI).
- Data analysis pipeline available on BlueBee® Genomics as easy-to-use non-expert solution.

12 nt Unique Dual Indexing Sets (UDIs)

- 384 Unique Dual Indices cover all barcoding needs.
- Optimized distances translate into superior index error correction.
- Rescue of mis-assigned reads through index error correction maximizes data output and saves sequencing costs.
- Adjustable index read-out length accommodates each experiment scale.

Find out more about RiboCop at www.lexogen.com

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