LEXOGEN
The RNA Experts

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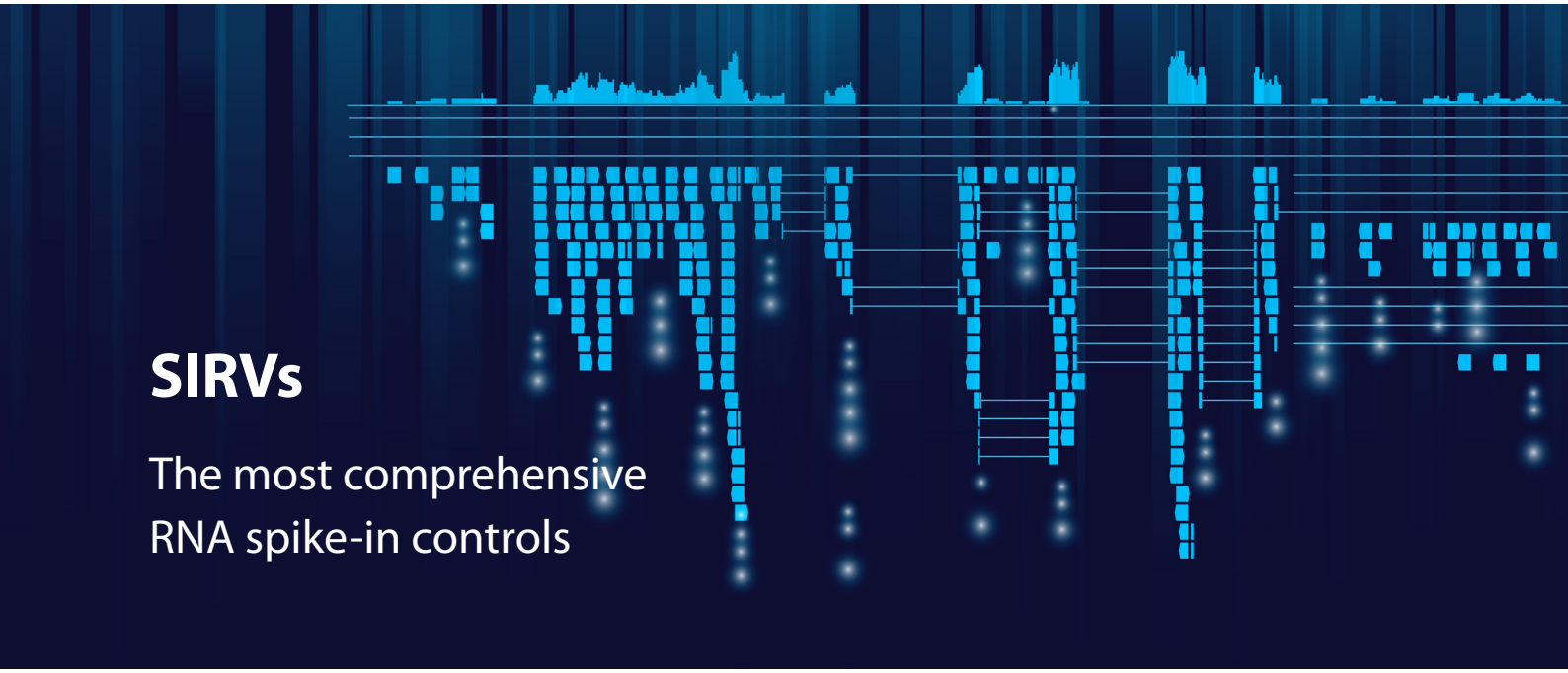

SIRVs

The most comprehensive RNA spike-in controls

Take control over your RNA-Seq experiments - use Lexogen's SIRVs!

Spike-in controls are crucial to assess the performance and the limits of RNA-Seq workflows, including data analysis. Spike-ins allow to evaluate technical variability and data quality before digging deep into the RNA-Seq data analysis. Use Lexogen's SIRVs - the most comprehensive RNA spike-ins and feel confident about your data!

Ensure consistent quality of your experiments

Set up, validate and monitor each stage of your RNA-Seq workflow. Get a grip on technical variability to ensure you are exploring meaningful biological variation.

Feel confident about your data

Understand the capacity of your RNA-Seq workflow to detect (novel) isoforms, quantify transcripts, and validate experimental and pipeline parameters.

Assess transcriptome complexity

SIRVs are designed to mimic the complexity of natural transcriptomes: covering isoform complexity, transcript concentration, and transcript length.

Any organism, any platform

SIRVs can be used with any organism and RNA input down to single-cell level. They are compatible with both short- and long-read sequencing technologies.

For more information, visit our website lexogen.com or contact us at sales@lexogen.com

SIRVs in RNA-Seq workflow

SIRVs are added to the samples before library preparation, undergo the same processing steps and sequencing. Typically, **only 1% of the total reads are allocated to SIRVs**. These can be analyzed to assess data quality before entering into elaborate data analysis (Fig. 1).

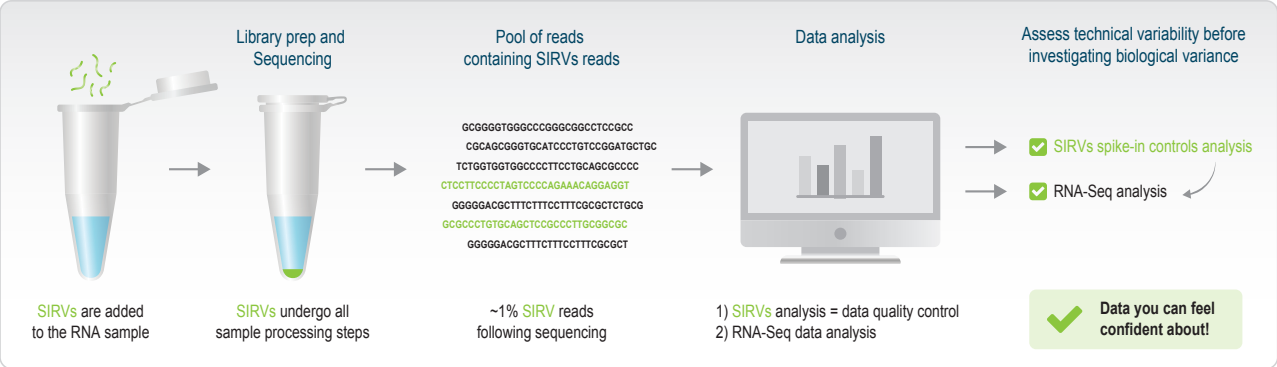

Figure 1 | SIRVs in RNA-Seq workflow. SIRVs are added to the RNA sample in minuscule amount and processed through the entire RNA-Seq workflow. SIRVs analysis allows for the data quality assessment before performing RNA-Seq data analysis.

Spike-ins need to reflect transcriptome complexity!

SIRVs are artificial, polyadenylated RNAs that were designed to mimic the natural complexity of the transcriptome: **isoforms**, **concentration**, and **transcript length** - including transcripts above average length up to 12 kb (Fig. 2). Thus, SIRVs are ideal for evaluation of long-reads sequencing protocols and technologies.

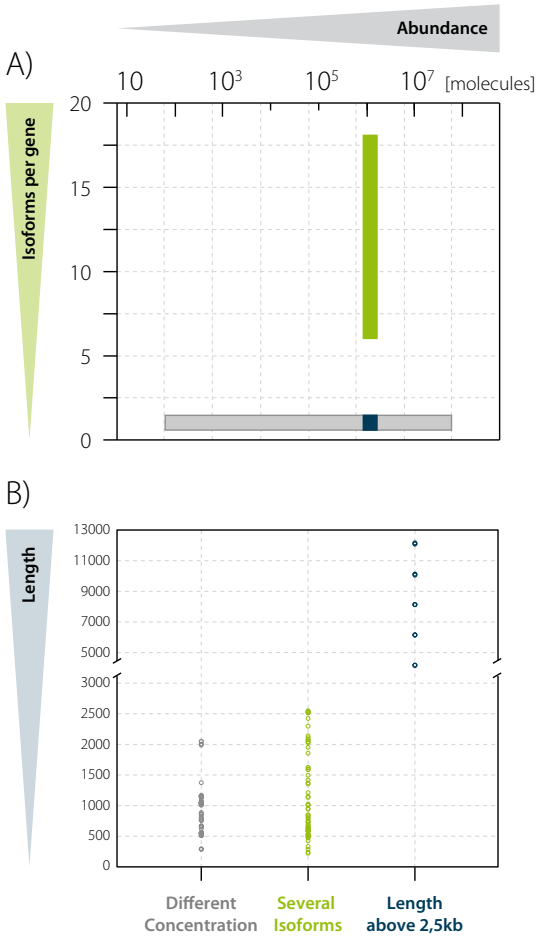

*Figure 2 | The representation of isoform complexity, transcript abundance, and length distribution of SIRVs. SIRVs contain transcripts with **several isoforms**, transcripts with **different concentration** and **long transcripts up to 12 kb**.*

Choose the right SIRV set for your experiment

Four different SIRV-Sets are available. Choose the best SIRV set for your experiment according our SIRVs selection guide table (Tab.1).

Table 1 | SIRV sets selection guide.

Application	Set 1	Set 2	Set 3	Set 4
Workflow validation	✔	-	-	-
Isoform analysis (discovery and quantification)	✔	✔	✔	✔
Transcript concentration and dynamic range	*	-	✔	✔
Length > 2.5 kb, long read sequencing	-	-	-	✔

***** *Set 1* contains 3 different mixes of SIRV isoforms with molar ratios of transcripts in mixes at magnitudes of 0, 1, and 2, respectively, thus this set is perfect for workflow validation and can be eventually used also for transcript concentration and dynamic range evaluation.

Free tool for SIRVs data evaluation

SIRVsuite is publicly available ready-to-use command line tool which allows you to evaluate the data quality of your RNA-Seq experiment using SIRVs.

SIRVs compatible products

Cat. №	Product Name
171 - 176	CORALL RNA-Seq V2 Library Prep Kit with UDIs (Set A1, A2, A3, A4, B1, or A1- A4)
177 - 182	CORALL mRNA-Seq V2 Library Prep Kit with UDIs (Set A1, A2, A3, A4, B1, or A1- A4)
183 -184	RiboCop HMR V2 and CORALL Total RNA-Seq V2 Library Prep Kit with UDIs (A1 or B1)

Ordering Information

Cat. №	Product Name	Kit sizes
025	SIRV-Set 1	3 vials
050	SIRV-Set 2	1, 3 vials
051	SIRV-Set 3	1, 3 vials
141	SIRV-Set 4	1, 3 vials

For more information and additional resources, please visit our website.