CLARETBIO

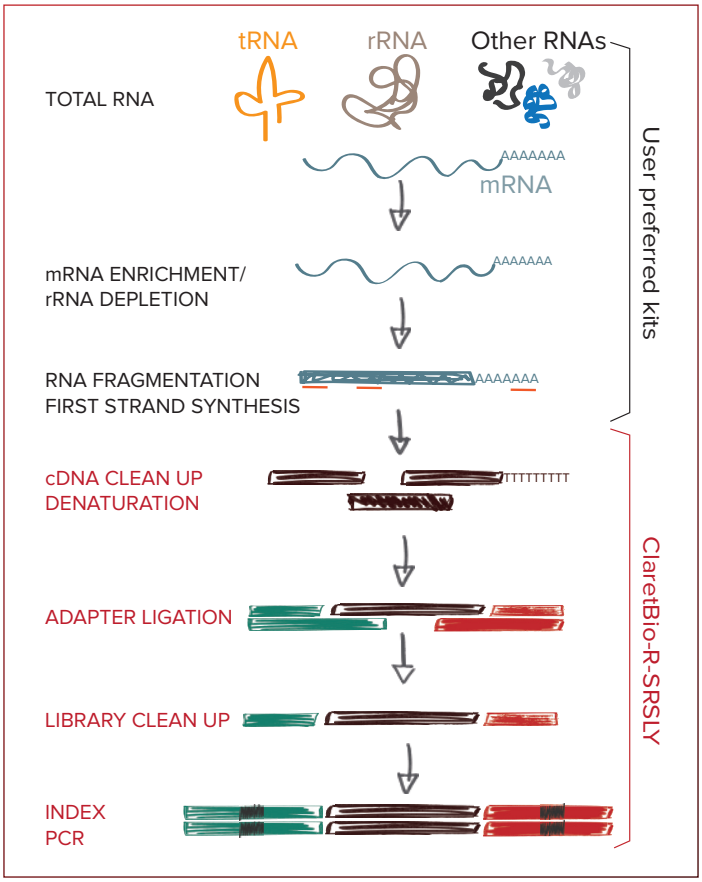
R-SRSLY™

EFFICIENT SINGLE-STRANDED LIBRARY METHOD FOR RNA-SEQ WORKFLOWS

RNA-Seq is a next-generation sequencing (NGS) workflow routinely used for gene expression profiling and whole transcriptome analyses, key to characterizing biological states in all organisms.

R-SRSLY is a directional RNA-Seq library preparation method that uses unique NGS adapters to generate libraries directly from the first strand cDNA, eliminating second strand synthesis and DNA end-polishing. The result is improved library quality with significant reductions in cost and time.

R-SRSLY WORKFLOW



PRODUCT SPECIFICATIONS

- Goes directly from mRNA to Illumina® sequence-ready library in ~4 hours
- Contains reagents for adapter ligation to cDNA, indexing PCR and magnetics beads for purification.
- Is compatible with commercially available first strand cDNA synthesis protocols
- Optimized for 1-10ng of mRNA
- Produces sequence-ready libraries in minimal time
- Requires fewer PCR cycles – reduces sequence biases

APPLICATION

- Gene expression profiling
- Isoform analysis
- Splice variant detection

SAMPLE TYPES

- Total RNA from cell-culture
- RNA from fresh frozen and FFPE tissues
- Single cell RNA and cfRNA (in development)

WHAT ARE THE BENEFITS OF USING A SINGLE-STRANDED APPROACH TO RNA-SEQ?

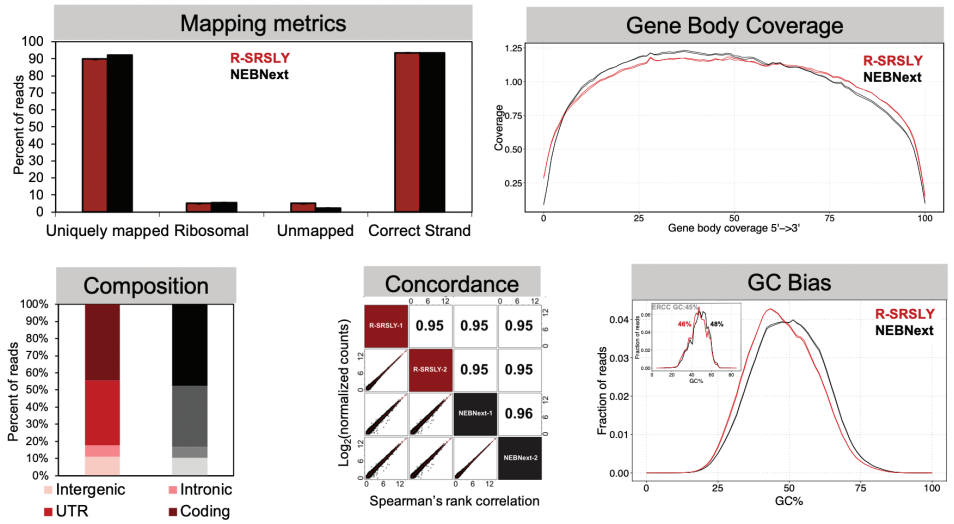
Methods that require second-strand synthesis must degrade or label one strand in order to maintain transcript directionality. Single-stranded approaches instead offer a truly directional library.

R-SRSLY libraries have high concordance between replicates, retain library strandedness, and capture true mRNA GC composition, while saving hours of time and costly reagents.

R-SRSLY PROTOCOL TIME COMPARISON

Directional RNA-Seq Kits	Method Type	Protocol time (hours)	PCR cycles for 10ng input
ClaretBio R-SRSLY	Single-stranded	~4	9
NEBNext Ultra II Directional RNA-Seq kit	Double-stranded	~7	10 to 11
NuGen Universal mRNA library kit	Double stranded	~7	>15
Truseq mRNA Stranded library kit	Double stranded	~8.5	15

R-SRSLY SEQUENCING METRICS COMPARISON



Feature	SRSLY	NEBNext
Mapping metrics	✓✓	✓✓
Strandedness	✓✓	✓✓
Uniform gene body coverage	✓✓	X
True Genomic Composition	✓	X
Protocol time	✓✓	X
Minimal PCR cycles	✓✓	✓

R-SRSLY and NEBNext Ultra II Directional libraries were generated in replicate following manufacturer's recommendations. Each library was sequenced to a depth of >10 million reads (Illumina MiSeq 2x76 bp). Mapping metrics and library concordance were calculated after reads were mapped to the human or spike-in control reference genome using STAR v 2.6.1d. Picardtools CollectRNASeqMetrics was used to obtain all other quality metrics. Overall R-SRSLY rivals or outperforms NEBNext in library performance metrics.

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