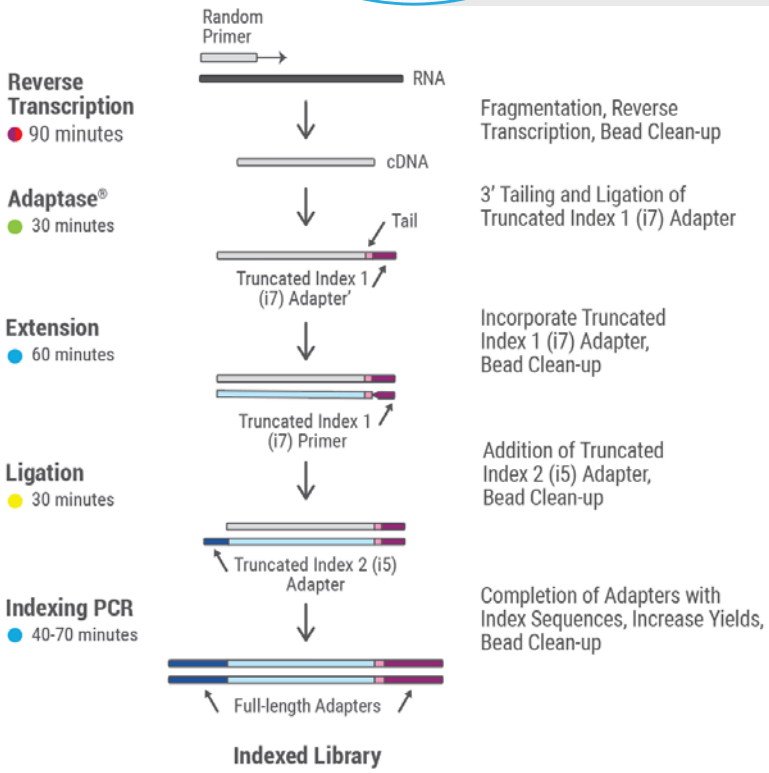
SWIFT RNA LIBRARY KIT

Deepen Your RNA-Seq Discovery

Introduction

The Swift RNA Library Kit offers a robust NGS transcriptomics workflow that provides optimal coverage and NGS data quality on Illumina® sequencing platforms. This kit leverages patented Adaptase® technology, enabling stranded RNA library construction directly from 1st strand cDNA without the cumbersome requirement for conventional 2nd strand cDNA synthesis. The kit is compatible with many upstream and downstream modules and is easily automatable.



Highlights

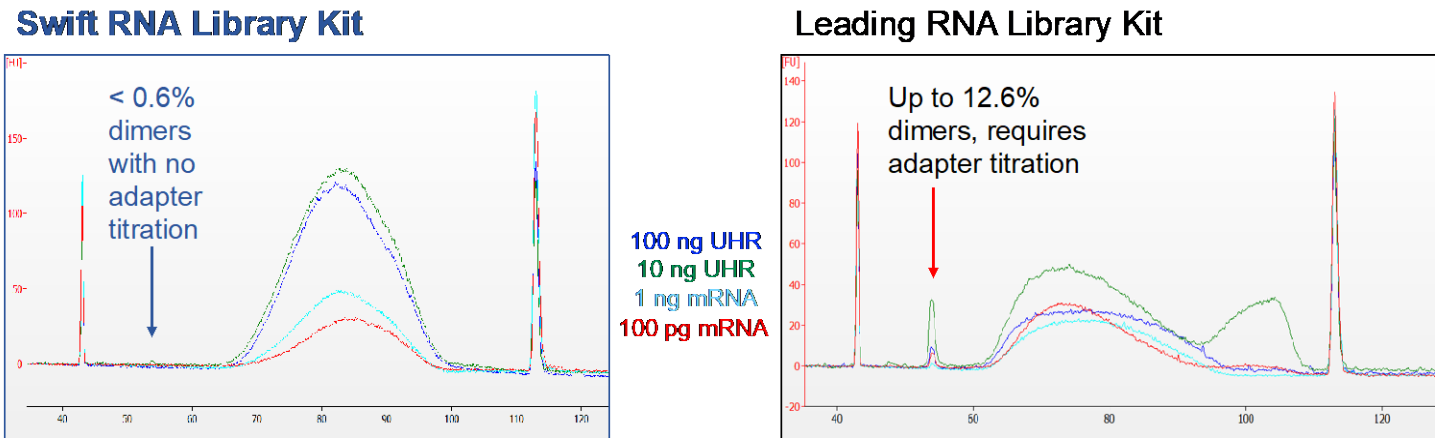
- **Quickly and reproducibly generate libraries with low dimers and no adapter titration**
- **Consolidate your workflows with a single kit that supports a broad range of RNA inputs**
- **Maximize mapping rates, genes detected, and transcript coverage**

Specifications

Feature	Specification
Input Quantity	10 ng – 1 μg total RNA into upstream module • 100 pg – 100 ng purified/enriched RNA
RNA Types Supported	Poly(A)-enriched mRNA • Ribodepleted RNA • Total RNA
Time	4.5 hours
Kit Reaction Sizes	24 • 96
Components Provided	Fragmentation module • RT module • Library Prep • Polymerase
Indexing Options	Single • Combinatorial Dual • Unique Dual • Normalase
Multiplexing Capability	Up to 768 libraries
Compatible Platforms	Illumina sequencing instruments
Automation	Compatible with Liquid Handlers • Reagent Overfill • Custom Packaging • FAS Support

Robust Library Outputs with Minimal Dimers and No Adapter Titration

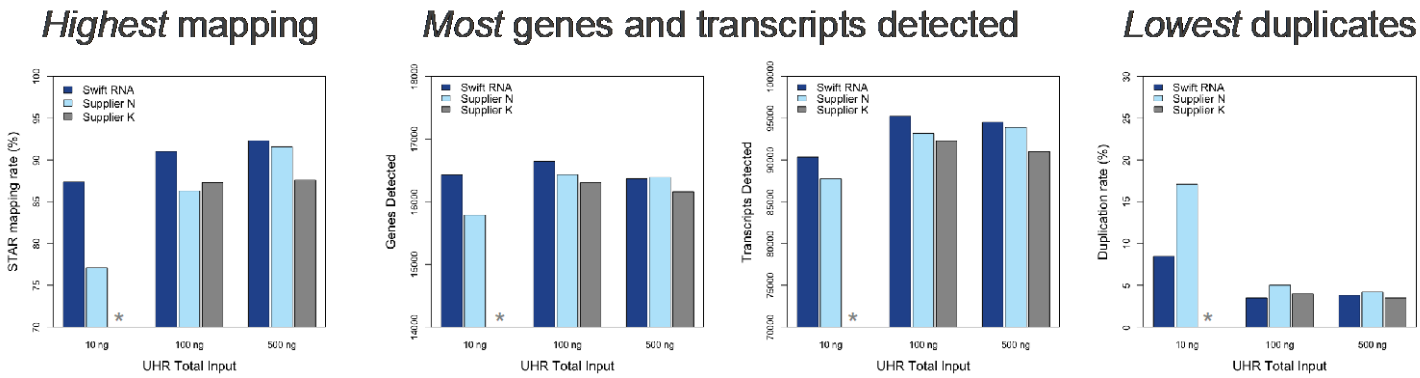
The Swift RNA Library Kit leverages patented Adaptase® technology to convert 1st strand cDNA into consistent, high-quality libraries with low adapter dimers from a broad range of RNA input amounts. Compared to kits supporting the same input ranges, Swift RNA libraries show superior data and more consistent performance.



Libraries were prepared using the same quantity of input material and subjected to the same number of PCR cycles for library amplification. Representative Agilent Bioanalyzer traces illustrate typical libraries generated from the same input series of poly(A)-enriched Universal Human Reference (UHR) RNA or human brain mRNA when processed by either the Swift RNA Library Kit (left panel) or a leading RNA library kit (right panel). The arrows indicate adapter dimer peaks that were generated during library preparation; numbers reported indicate the percentage of adapter dimers detected in the sequenced reads (Miniseq 2 x 75).

Highest Mapping and Transcript Detection with Low Duplication Rates

The Swift RNA Library Kit provides the most reproducible and optimal library sequencing metrics. These metrics include higher mapping rates, more genes and transcripts detected, and lower duplication rates. The Swift RNA Library Kit has a dramatic advantage at lower inputs (10 ng total RNA), allowing you to deepen your RNA-Seq research at your most challenging inputs.

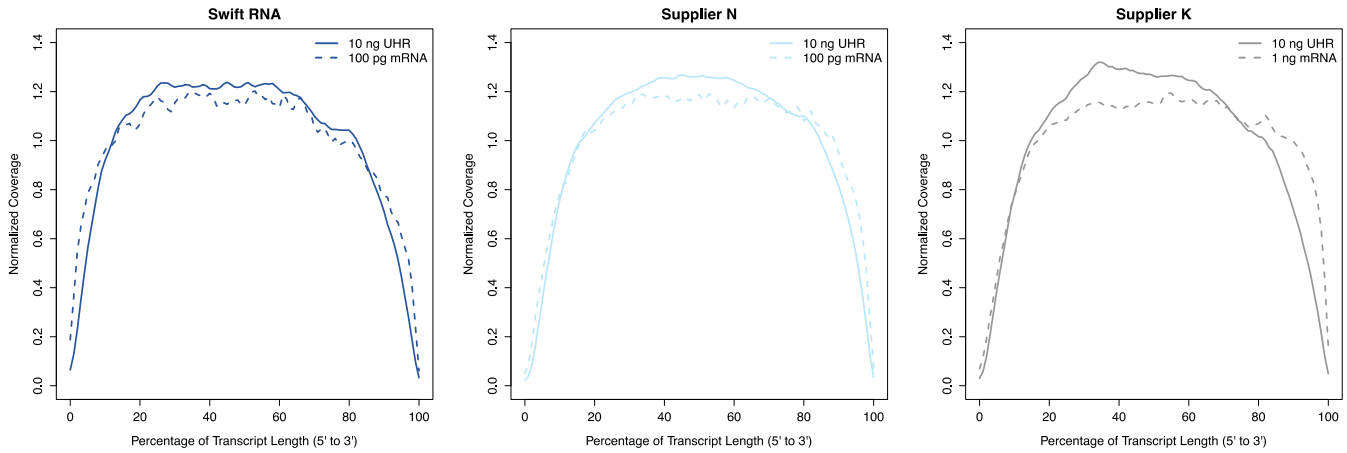


10 ng Universal Human Reference Total RNA (Agilent 740000) was poly(A) enriched using the NEBNext poly(A) mRNA Magnetic Isolation Module (NEB E7490) before being processed through the Swift RNA Library Kit or processed following the supplier recommendations. Libraries were sequenced on a MiniSeq with 2 x 75 paired-end reads. Fastq files were downsampled to 2.2 million reads before analysis using STAR (mapping rate) or rnaseqc (genes/transcripts detected, duplication rate).

Even Coverage of Transcripts - Even at Low Inputs

Swift RNA Library Kit provides even coverage of transcripts across all supported inputs, elevating your effective transcriptome annotation. This evenness is maintained even at low inputs (10 ng total RNA, 100 pg mRNA).

Normalized Coverage of Transcripts

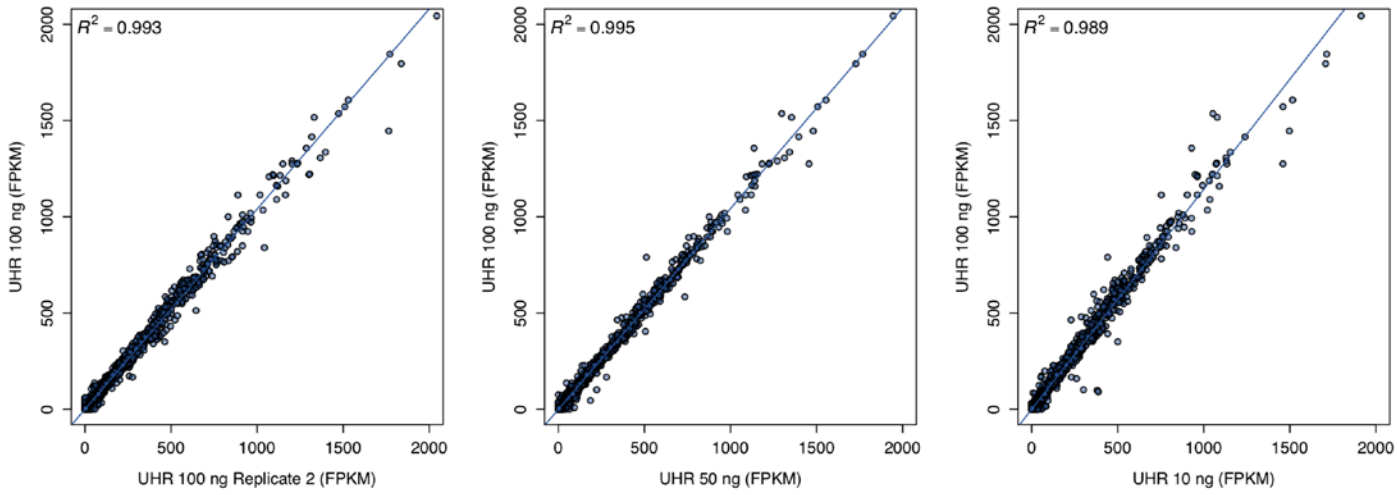


Normalized coverage of transcripts for two representative low inputs. 10 ng Universal Human Reference total RNA (Agilent 740000) was poly(A) enriched using the NEBNext poly(A) mRNA Magnetic Isolation Module (NEB E7490) before being processed through the Swift RNA Library Kit or processed following the supplier recommendations. 100 pg of human brain mRNA (Clontech 636102) was used as input directly into the Swift RNA Library Kit or alternate supplier kits. Libraries were sequenced on a MiniSeq with 2 x 75 paired-end reads. Fastq files were downsampled to ~2 million reads before analysis using STAR and picard.

Consistent Expression Profiling Across Inputs

The Swift RNA Library Kit provides consistency in transcript detection and expression across variable inputs, down to as little as 10 ng of total RNA.

FPKM for 100 ng, 50 ng, and 10 ng of Universal Human Reference RNA



Inputs of 100 ng, 50 ng, or 10 ng Universal Human Reference Total RNA (Agilent 740000) were poly(A) enriched using the NEBNext poly(A) mRNA Magnetic Isolation Module (NEB E7490) before being processed through the Swift RNA Library Kit. Libraries were sequenced on a MiniSeq with 2 x 75 paired-end reads. Fastq files were downsampled to 3.5 million reads before analysis using STAR, picard, and RSeQC. Fragments per million mapped reads per kilobase (FPKM) values are shown for all UCSC transcripts (n = 78,807).

Ordering Information

Product Name	Kit Size (rxns)	Cat. No.
Swift RNA Library Kit	24	R1024
	96	R1096

An Indexing Primer Kit is required for complete functionality. Please select from the following:

Single Indexing Primer Kit Set A (12 indices, 2 rxns ea)	24	X6024
Combinatorial Dual Indexing Primer Kit (96 combinations, 1 rxn ea)	96	X8096
Swift Set S1-S4 Combinatorial Dual Indexing Primer Kits	24 x 8 (192)	X85192 – X88192
	96 x 8 (768)	X89768
Swift Unique Dual Indexing Primer Kits (96 UDIs)	96	X9096
	384	X90384

Swift Normalase® is compatible with this kit. Please order both of the following:

Swift Normalase® Kit	96	66096
Normalase Combinatorial Dual Indexing Primer Kit (96 combinations)	96	68096

Visit **www.swiftbiosci.com** for easy ordering.

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