SWIFT RAPID RNA LIBRARY KIT

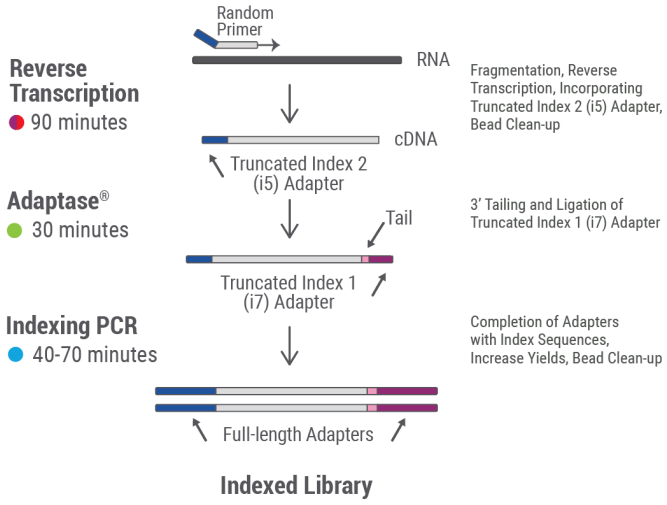
Accelerate Your RNA-Seq Discovery

Introduction

The Swift Rapid RNA Library Kit offers the fastest and lowest cost NGS transcriptomics workflow for Illumina® sequencing platforms. This kit leverages patented Adaptase® technology, enabling stranded RNA library construction directly from 1st strand cDNA without the cumbersome requirement for 2nd strand cDNA synthesis.
The kit is compatible with many upstream and downstream modules and is easily automatable.

Highlights

- **Save time and reduce costs**
- **Go from RNA to high-quality libraries in 3.5 hours**
- **Supports many workflows, compatible with a variety of indexing options and Normalase**



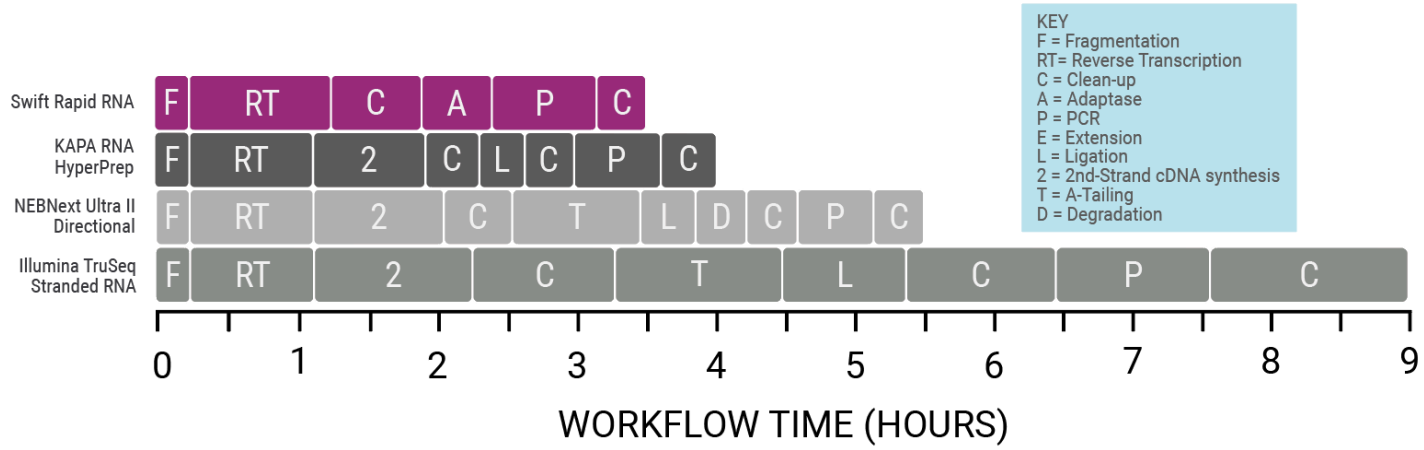
Specifications

Feature	Specification
Input Quantity	100 ng – 1 µg total RNA into upstream module • 5 ng – 100 ng purified/enriched RNA
RNA Types Supported	Poly(A)-enriched mRNA • Ribodepleted RNA • Total RNA
Time	3.5 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

Save Time with Direct Conversion of 1st Strand cDNA

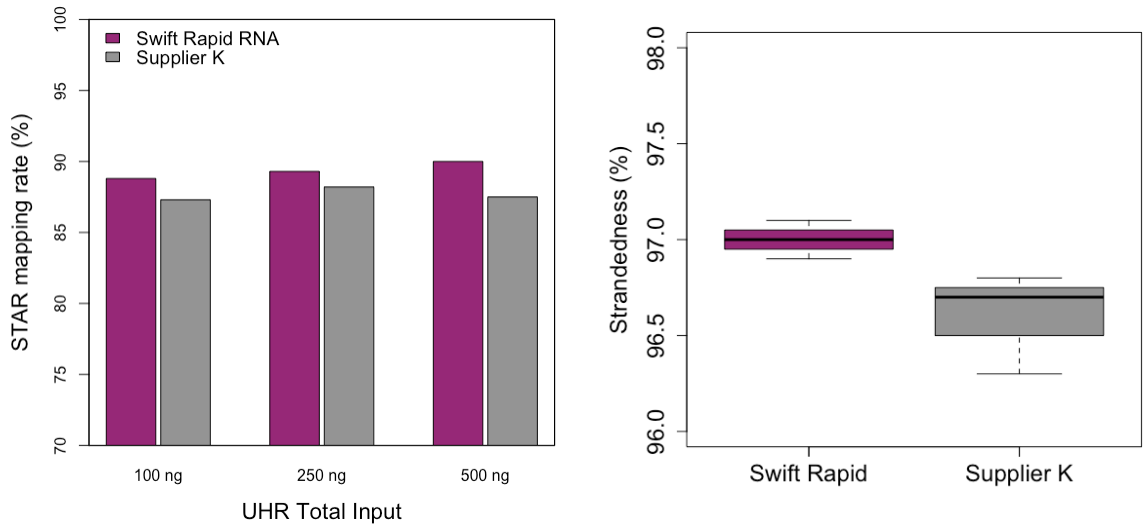
The Swift Rapid RNA Library Kit leverages patented Adaptase® technology to add adapters directly to 1st strand cDNA in an efficient and expedited workflow that does not require adapter titration. Compared to kits supporting the same input ranges, Swift libraries are more economical for both time and cost. Further accelerate your RNA-Seq workflows through automation with our instrument-specific resources and recommendations.

Swift Rapid RNA – the fastest RNA library kit, completed in 3.5 hours



Robust Mapping and Strand Specificity

The Swift Rapid RNA Library Kit provides competitive metrics compared to other RNA library preps for routine transcriptomics, including high mapping rates and maintenance of strand specificity.

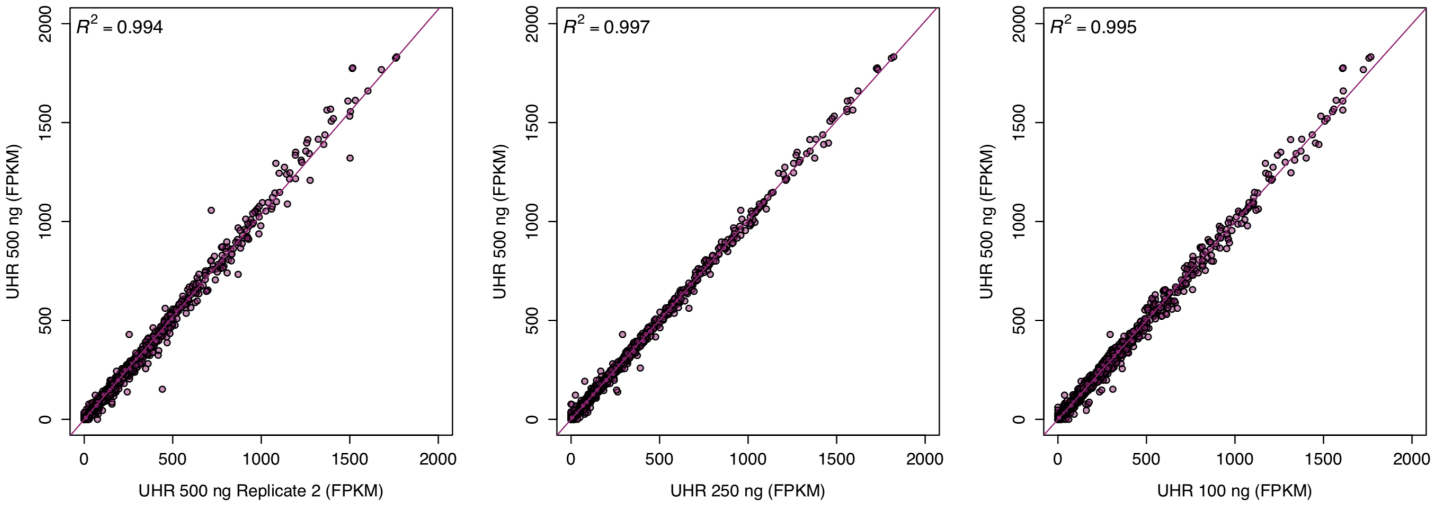


Universal Human Reference (UHR) Total RNA (Agilent 740000) was poly(A)-enriched using the NEBNext poly(A) mRNA Magnetic Isolation Module (NEB E7490) before being processed through the Swift Rapid RNA Library Kit or processed following the supplier recommendations. Libraries were sequenced on a MiniSeq with 2 x 75 paired-end reads. Fastq files were downsampled to 3.8 million reads before analysis using STAR (mapping rate) or rnaseqc (strand specificity).

Consistent Expression Profiling Across Inputs

The Swift Rapid RNA Library Kit provides consistency in transcript detection and expression across supported input ranges. Accelerate your research with a rapid workflow that provides reliable and consistent data.

FPKM for 500 ng, 250 ng, and 100 ng of Universal Human Reference RNA

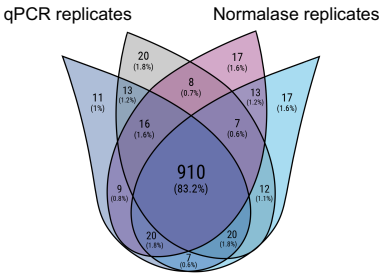


Inputs of 500 ng, 250 ng, or 100 ng Universal Human Reference Total RNA (Agilent 740000) were poly(A) enriched using the NEBNext poly(A) mRNA Magnetic Isolation Module (NEB E7490) before being processed through the Swift Rapid RNA Library Kit. Libraries were sequenced on a MiniSeq with 2 x 75 paired-end reads. Fastq files were downsampled to 4.2 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).

Swift Normalase Preserves RNA-Seq Detection of Top Transcripts

Save even more time in your RNA-to-sequencer workflow by pairing the Swift Rapid RNA Library Kit with the Swift Normalase kit, which enzymatically selects and normalizes libraries to a consistent concentration for optimal flow cell clustering.

Sample	Mean Per Base Cov.	Mean CV	No. Covered 5'	5' 200Base Norm	No. Covered 3'	3' 200 Base Norm	Num. Gaps	Cumul. Gap Length	Gap %
qPCR	273.90	0.90	860	0.27	948	0.45	669	63701	4.65
qPCR	278.39	0.90	864	0.26	954	0.45	639	62079	4.68
Normalase	277.33	0.91	859	0.26	944	0.45	661	64419	4.82
Normalase	275.19	0.91	866	0.27	944	0.45	650	61794	4.58



Four RNA-Seq libraries were generated from 50 ng human brain mRNA, amplified and indexed with either Swift Combinatorial Dual (CD) Indexing primers (n=2) or Swift Combinatorial Dual Indexing Normalase primers (CDI-N) using 9-cycles of PCR. CD libraries were pooled and normalized manually using library quants from qPCR, while CDI-N libraries were subjected to Normalase to 4nM. The two pools were combined and sequenced on a MiniSeq High Output (2x150) run. Sequencing data was downsampled to 4 million reads before analysis using STAR, picard, and RSeQC (left). Using the Top 1000 transcripts detected in each sample, Panther Gene Ontology demonstrated the similarity in functional endpoints of RNA-Seq data generated with and without Normalase (right).

Ordering Information

Product Name	Kit Size (rxns)	Cat. No.
Swift Rapid RNA Library Kit	24	R2024
	96	R2096

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

Nous contacter

Service technique
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Instrumentation : 01 30 85 92 88 - instrum@ozyme.fr