Required Third Party Reagents:

- SuperScript III™ Reverse Transcriptase
- OneTaq® 2X Master Mix with Standard Buffer
- SPRIselect or equivalent DNA/RNA Purification Beads (also known as SPRI beads)
- Optional: RNaseH
- Optional: RNaseOUT™ Recombinant Ribonuclease Inhibitor

Recommended Input Materials

- >100 ng of purified RNA
- Concentration = 10 ng/µl or greater
- A260/A280 = 1.9 - 2.2
- Provided in nuclease-free water (must be free of residual ethanol)
- No RNA fragmentation required
- RIN>6.0

Order from: www.baseclick.eu

baseclick
DNA & RNA EXPERTS

baseclick GmbH
Floriansbogen 2-4
82061 Neuried, Germany

FAST DELIVERY WORLD WIDE

24H ORDERING ONLINE

baseclick
DNA & RNA EXPERTS

ClickSeq™

A fragmentation-free approach for RNAseq

Simple and Affordable

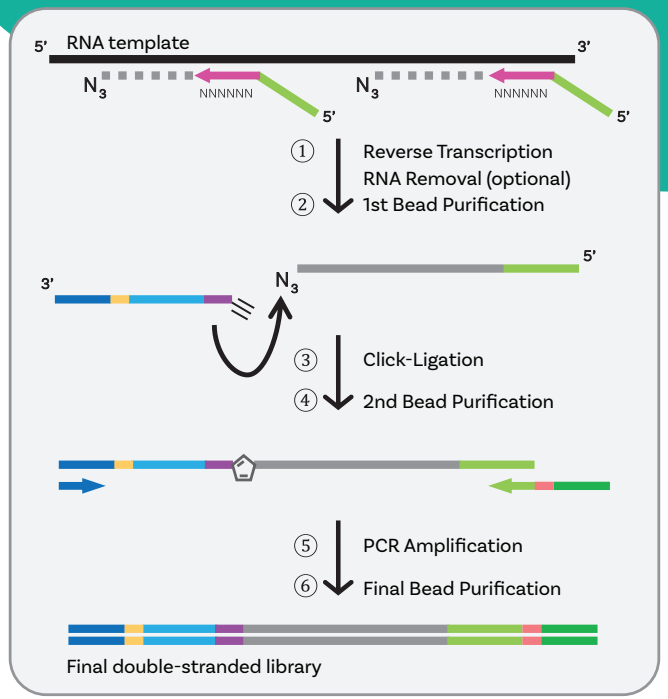
Next-Generation Sequencing, powered by Click-Chemistry

ClickSeq TECHNOLOGIES

A partnership with baseclick GmbH and ClickSeq Technologies LLC

www.baseclick.eu

www.clickseqtechnologies.com



Total Turnaround Time

2 - 3 hrs Wait Time | <2 hrs Hands On

30 - 60 min | 35-40 min

15 min | 30 min

80 - 100 min | 40 min

ClickSeq Library Prep Kit Overview

1. RNA is reverse transcribed using a 6N-primer containing a partial Illumina p7 sequencing adapter. Reverse transcription is performed in the presence of azido-nucleotides that stochastically terminate cDNA synthesis.
2. cDNA is purified using SPRI magnetic beads.
3. Click-chemistry is used to chemically ligate the Illumina p5 sequencing adapter.
4. Click-ligated cDNA is purified using SPRI beads.
5. PCR fills the remainder of the i7 indexing adapter and amplifies the amount of dsDNA library.
6. A final bead purification and size selection yields sequencing-ready libraries.

Applications

- Random-primed RNAseq approach
- mRNA sequencing
- Gene expression analysis
- Splice variant, isoform analysis, and gene fusion discovery
- RNA virus genomics and recombination analysis

Benefits

- No fragmentation steps required
- No enzymatic ligation steps, reduces artifactual recombination
- Highly degraded and/or fragmented RNA can be processed
- Stranded technique: Provides strand-of-origin information
- Excellent for the detection of rare recombination events
- Reduced sample input, as little as 10ng purified RNA required.
- Libraries generated in ~6 hours
- Unique Molecular Identifiers (UMIs) available

Compatible with Illumina platforms