

SENSE Total RNA-Seq Library Prep Kit for Illumina

- 3 hours from RNA to ready-to-sequence libraries
- simple no fragmentation step
- strand-specificity of >99.9%

Introduction

SENSE Total RNA-Seq Kit is a library preparation protocol which takes just 3 hours, maintains strand-specificity (>99.9 %), and thus allows the mapping of reads to their corresponding strand on the genome, enabling the discovery and quantification of antisense transcripts and overlapping genes.

Library insert size can be varied during the purification step, meaning that size selection with additional kits is not required. Optional multiplexing of libraries can be carried out using up to 96 external barcodes included in the kit. Libraries are compatible with both single-end and paired-end sequencing reagents. The typical input amount of poly(A) or rRNA-depleted RNA is 1 ng - 500 ng.

Workflow

The SENSE Total RNA-Seq Kit is based on Lexogen's proprietary strand displacement stop/ligation technology.

Library generation starts with the random hybridization of the starter/stopper heterodimer mix to the poly(A) selected or rRNA-depleted RNA. A single-tube reverse transcription and ligation reaction extends the starter to the next hybridized heterodimer, where the newly synthesized cDNA insert is ligated to the stopper. RNA or cDNA fragmentation is not required as the insert size is dictated by the distance between starter/stopper binding sites. During second strand synthesis the RNA is hydrolyzed and the library is converted to double-stranded DNA. The double-stranded library is purified using magnetic beads to adjust the library length and get rid of second strand synthesis reaction components. The library amplification is performed to add the complete adaptor sequences required for cluster generation and to produce sufficient material for quality control and sequencing.

External barcodes can be added during this step in order to be able to multiplex the samples for the sequencing run. The finished library is purified from PCR components which can interfere with quantification. Library quantification can be performed with standard protocols, e.g. microcapillary electrophoresis or qPCR.

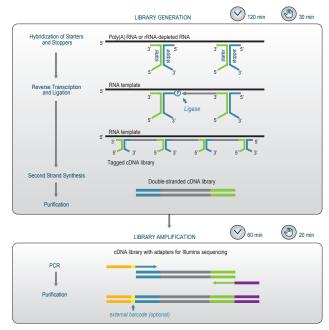


Figure. Schematic overview of the SENSE Total RNA-Seq Library Prep workflow.

Ordering Information

Catalog Numbers:

009.08 (SENSE Total RNA-Seq Library Prep Kit for Illumina, including Barcode Set 1,8 preps)

009.24 (SENSE Total RNA-Seg Library Prep Kit for Illumina, including Barcode Set 1–3, 24 preps)

009.96 (SENSE Total RNA-Seq Library Prep Kit for Illumina, including Barcode Set 1–12, 96 preps)

