CONTEXTE

PREP LIB RNASEQ (ANCHOR)

(CHRISTIAN DAVIAUD)

ILLUMINA STRANDED MRNA AND TOTAL RNA WORKFLOWS

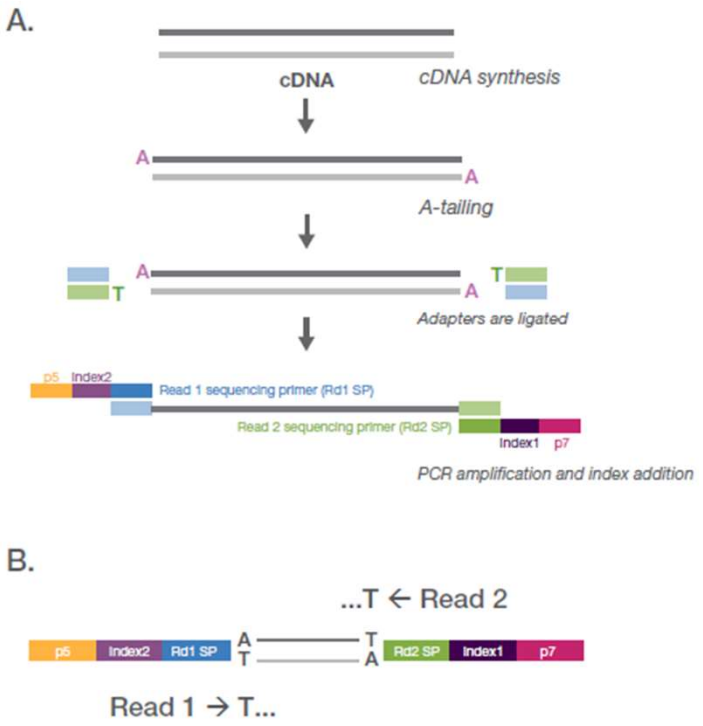


Figure 1: Illumina Stranded RNA library preparation—(A) After cDNA synthesis is complete, ligation of adapters and PCR amplification produces high-quality libraries. (B) The use of T-overhangs in sequencing adapters to facilitate rapid ligation results in all reads starting with a "T" in the first cycle.

- **Illumina Stranded mRNA Prep, Ligation** provides a cost-efficient option for coding RNA-focused analyses.
- **Illumina Stranded Total RNA Prep, Ligation with Ribo-Zero™ Plus** enables whole-transcriptome analysis, capturing coding and multiple forms of noncoding RNA.
- **Illumina RNA Prep with Enrichment** brings bead-linked transposome (BLT) technology to RNA enrichment.

Prepare Library | Sequence | **Analyze Data**

illumina

Best practices for read trimming for Illumina Stranded mRNA and Total RNA workflows

Explore the impact of the T-overhang on sequence read quality and options for read trimming.

Prepare Library | Sequence | **Analyze Data**

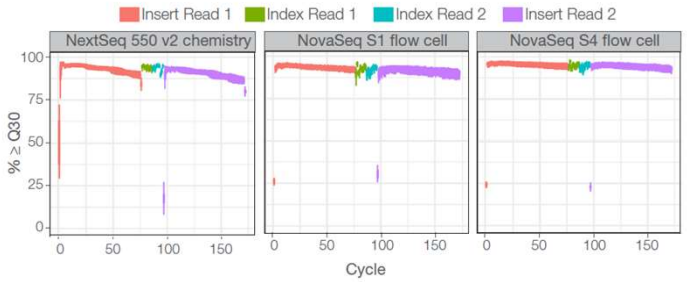
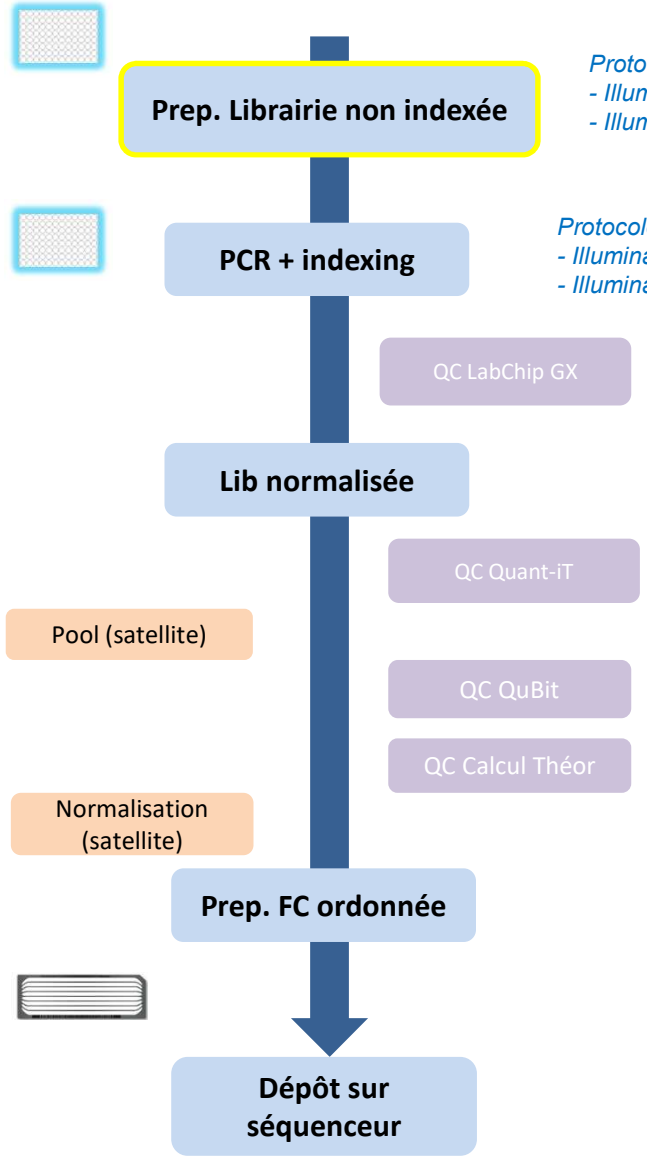


Figure 2: Impact of T-overhang on first cycle read quality—Including the T-overhang resulted in low read quality in the first cycle for Insert Read 1 and Insert Read 2 on the NextSeq 550 and NovaSeq 6000 Systems.

illumina-stranded-rna-t-overhang-tech-note-470-2020-010.pdf

Processus : Prep. Lib. pour séquençage Illumina > Prep Lib RNAseq (Anchor)



Protocole
- Illumina Anchor strand totRNAseq RiboZ+
- Illumina Anchor strand mRNAseq

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Propriétés processus :
Type processus banque
- RK - ssmRNASeq-IllAnchor
- RL - sstRNASeq-IllAnchorRiboZ+

Plaques index (UDP0001-UDP0384)
IDT for Illumina Anchor DNA Unique Dual Indexes Set A
IDT for Illumina Anchor DNA Unique Dual Indexes Set B
IDT for Illumina Anchor DNA Unique Dual Indexes Set C
IDT for Illumina Anchor DNA Unique Dual Indexes Set D

Process miniaturisé – volumes 2-3 µL