LEXOGEN
The RNA Experts

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Accelerate Discoveries from FFPE Samples

Seamless FFPE RNA-Seq Workflows

Enhancing FFPE Transcriptomics

Get the best sequencing results with convenient end-to-end RNA-Seq workflows!

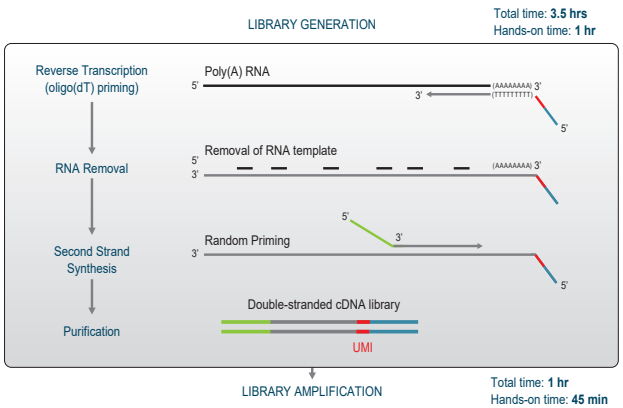

Figure 1 | QuantSeq FFPE workflow, library generation

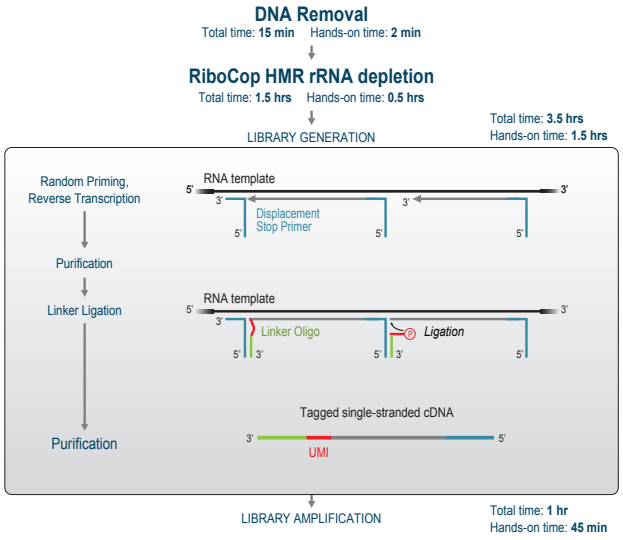

Figure 2 | CORALL FFPE workflow, library generation

FFPE RNA Extraction

The **SPLIT One-Step FFPE RNA Extraction Kit** enables fast and highly efficient RNA extraction from any FFPE tissue with **optimized decrosslinking and paraffin / detergent removal.** The obtained RNA is ideal for seamless integration into library preparation for RNA-Seq and other demanding downstream analysis.

Expression Profiling for FFPE Samples

QuantSeq FFPE focuses on the 3′ ends of all polyadenylated transcripts and is thus ideal for expression profiling from degraded and FFPE RNA. **No depletion or prior enrichment is required**, allowing the preparation of ready-to-sequence libraries in only 4.5 hours. Starting from total RNA, an oligo(dT) primer initiates reverse transcription (first strand synthesis) and random priming (second strand synthesis) completes cDNA library generation (Fig. 1). **UMIs are seamlessly introduced** in the first reaction step for highly accurate expression analysis. Lexogen's FFPE expression profiling workflow builds on the established **cost-efficient QuantSeq technology** and is now **validated for FFPE samples from various tissues and species**.

Whole Transcriptome RNA-Seq for FFPE

CORALL FFPE covers the whole length of the transcripts and uses Lexogen's proprietary displacement-stop technology to generate NGS library inserts, **without any RNA fragmentation steps** (Fig. 2). CORALL FFPE is validated on a range of FFPE tissues from different organisms. Paired with **RiboCop for enzyme-free rRNA depletion**, CORALL FFPE is ideal for any FFPE application requiring coverage uniformity, including coverage analysis, alternative splicing or fusion gene detection and analysis of non-coding RNAs (e.g., lncRNA biomarkers).

End-to-end Workflows for FFPE Transcriptomics

SPLIT One-Step FFPE RNA Extraction offers **rapid extraction from any FFPE tissue in under 2 hours,** and the resulting RNA can be directly channeled into RNA-Seq library preparation. Depending on the research goal, FFPE RNA can be assessed by gene expression profiling using QuantSeq FFPE, or through whole transcriptome sequencing using CORALL FFPE combined with rRNA depletion. Both workflows **include data analysis** on Lexogen's **web-based platform Kangooroo** (Fig. 3). If needed, residual DNA can be removed prior to library generation using the **DNA Removal Add-on,** which seamlessly integrates into the end-to-end workflow.

Figure 3 | End-to-end FFPE transcriptomics workflow solutions for FFPE RNA extraction, optional removal of residual DNA(*), FFPE expression profiling or whole transcriptome RNA-Seq and complementary data analysis on Kangooroo.

Cost-efficient Expression Profiling for FFPE

QuantSeq FFPE generates **one read at the 3' end of poly(A) transcripts.** It is, therefore, **ideal for expression profiling** from degraded FFPE material **using straightforward read counting**, as demonstrated by differential gene expression analysis of human kidney tumor vs. matched normal FFPE tissue (Fig. 4).

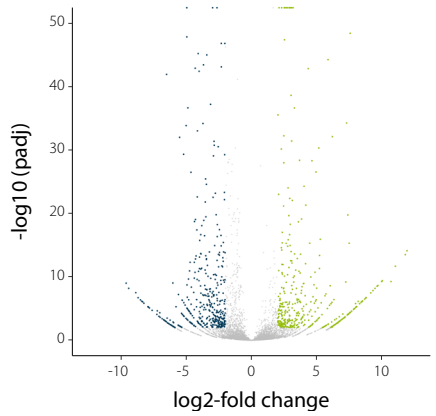

Figure 4 | Volcano plot of differentially expressed genes between human kidney tumor and normal FFPE tissue at a padj threshold of <0.01.

Robust Detection of Upregulated Marker Transcripts in Tumor FFPE Samples with CORALL FFPE

CORALL FFPE detects upregulation of tumor marker transcripts as exemplified by elevated coverage of Chemokine Receptor CXCR4 in kidney tumor FFPE samples associated with increased risk and the incidence of renal cell carcinoma progression (Fig. 5).

Key Benefits for FFPE RNA-Seq:

- Validated performance on various FFPE tissues and species, including mouse lung, colon, liver, spleen, and human liver, kidney, and brain.
- Accurate gene and transcript expression analysis with built-in UMIs.
- Easily scalable end-to-end workflows; from sample to sequencing-ready-libraries in only one day, including extraction.

In Need for Data Analysis?

Lexogen kits conveniently include data analysis codes for FFPE Expression Profiling and Whole Transcriptome Sequencing on Kangooroo to help you get to your results faster!

Full NGS Services available!

Trust your FFPE curls to Lexogen NGS Services and let our experts extract the best data possible for you.

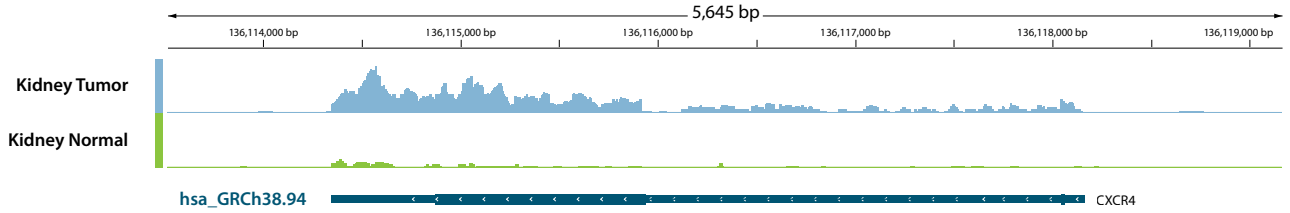

Figure 5 | Coverage of CRCX4, a known marker associated with renal cancer progression assessed by CORALL FFPE on human kidney tumor and normal FFPE tissue.

For more information and additional resources, please visit our website.

Ordering Information

Cat. №	Product Name
236	SPLIT One-Step FFPE RNA Extraction Kit
235	DNA removal Add-on
222 and 223	**QuantSeq FFPE 3' mRNA-Seq** Library Prep Kit with UDI 12 nt Set **A1** (222) and Set **B1** (223) **for FFPE Expression profiling**
219 and 220	**CORALL FFPE Whole Transcriptome RNA-Seq** Library Prep Kit with UDI 12 nt Set **A1** (219) and Set **B1** (220)
233 and 234	same as 219 and 220, **including RiboCop rRNA depletion**, UDI Set **A1** (233) and Set **B1** (234)