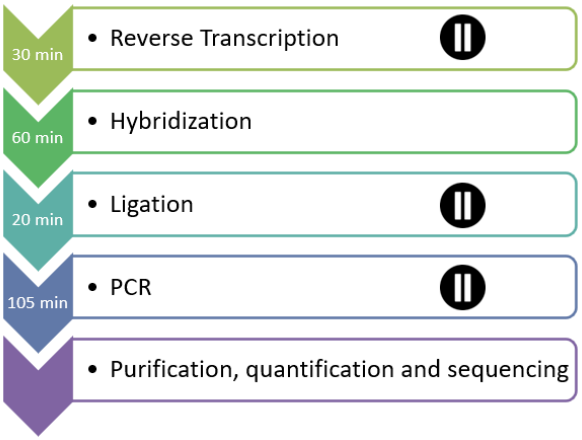
LymphoTranscript Test

The **LymphoTranscript** solution can highlight fusion transcripts de fusion associated to peripherical T-cell Lymphomas. It is applicable to low-quality RNA samples extracted from sections of FFPE biopsies, fixed and included in paraffin, obtained in the clinic. A needle biopsy is also possible to obtain a sample of sufficient quality. Data are generated using a next-generation sequencer and require only 10^5 reads per sample.

The bioinformatics analysis is carried out using our RT-MIS software which provides details of any fusion transcript detected.

Using the test

The **GENEXPATH LymphoTranscript** test is based on a ligation-dependent RT-PCR (LD-RT-PCR) method. This semi-quantitative technique makes it possible to simultaneously evaluate the expression levels of a large number of genetic markers and more precisely for this test, chromosomal translocations using pairs of oligonucleotide probes specific to each of these markers.



A simple and fast protocol

From a total RNA extract, four steps are sufficient to obtain the libraries.

1. A reverse transcription step.
2. A step of hybridization of oligo-nucleotide probes.
3. A ligation step.
4. A PCR amplification step.
5. Then sequencing the libraries

No purification is necessary until the libraries are obtained, which limits the loss of material and ensures a very good sensitivity to this technique. In addition, the genetic sequences targeted by the probes are particularly short (between 40 and 60 bases) which ensures a very good robustness against the degradation of RNAs.

LD-RT-PCR is therefore a particularly suitable approach for the analysis of difficult biological samples such as tissue biopsies fixed and included in paraffin.

For each sample, about 10^5 sequences are sufficient to obtain an analyzable expression profile, which makes it possible to test a large number of samples in parallel on the same sequencing FlowCell.

To optimize costs**, GENEXPATH LymphoTranscript** libraries can also be loaded at the same time as other sequencing libraries, generated by other methods.

Post-PCR analysis based on dedicated software

Once the sequencing is complete, the FASTQ file can be uploaded to the RT-MIS platform which, after a few minutes of analysis, delivers a file containing the detected merge transcripts.

Duration of handling	5H30
Actual working time	1h-1h30
Type of nucleic acid	RNA
Input quantity	Between 50 et 500ng of RNA
Type of cancer	Peripherical T-cell Lymphomas
Contents of the reagent kit	Probes targeting fusion transcripts, somatical mutations, virus HTLV1, barcodes, sequencing primers.
Method	Ligation dependent RT-PCR
Description	Detect fusion transcripts associated to peripherical T-cell Lymphomas in 1 analysis.
Hardware compatibility	MiSeq, NextSeq 500, NextSeq 550 Illumina®
Type of samples	Tissue biopsies fixed and included in paraffin
Technology	Next Generation Sequencing

This product is reserved for research use in the field of molecular biology. Do not use for medical diagnostic procedures.

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