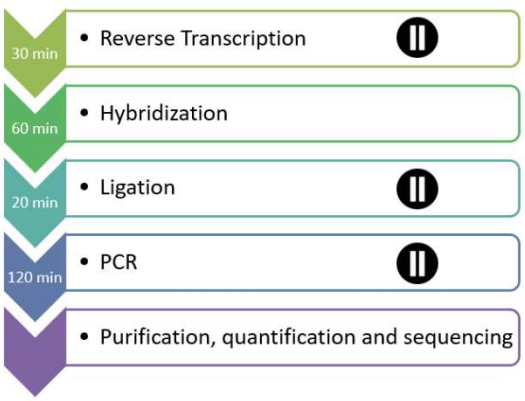
SarcomaFusion test

The **Genexpath SarcomaFusion** solution can highlight 140 fusion transcripts responsible for sarcomas. 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.

They are then processed using our RT-MIS software which provides details of any transcripts detected and the associated bibliography.

Using the test

The **GENEXPATH SarcomaFusion** 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 SarcomaFusion** 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.

RT-MIS also provides a bibliography for detected transcripts and thus offers a complete solution for cancer researchers.

Handling duration	5hrs30’
Actual working time	1hr-1hr30’
Type of nucleic acid	RNA
Input quantity	Between 50 and 500ng of RNA in a volume of 2µl
Type of cancer	Sarcoma
Contents of the reagent kit	Probes targeting more than 140 fusion transcripts, barcodes, sequence primers
Method	Ligation dependent RT-PCR
Description	Detects more than 140 transcripts of sarcoma-associated fusion in 1 single analysis.
Equipment compatibility	MiSeq, NextSeq 500, NextSeq 550 Illumina®
Type of samples	Tissue biopsies fixed and included in paraffin
Technology	Next Generation Sequencing

CE *In vitro diagnostic medical device according to Directive (EU) 98/79/EC*

IVD *For in vitro diagnosis use only. Please read the user manual before use.*

Contact

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Document last update : 01/06/2022