

# **LymphoTrack**<sup>®</sup> Flex

## Clonality, SHM, & Ultra-High Sensitivity MRD

### HIGH-THROUGHPUT SOLUTION

Designed to meet the growing demand for flexible, high-throughput and automation-ready solutions, **LymphoTrack Flex Assays** deliver precise, sequence-level identification of B- and T-cell clonality, somatic hypermutation (SHM), and ultra-high sensitivity (UHS) measurable residual disease (MRD). With the ability to multiplex targets and samples on high-throughput sequencing platforms, these assays provide input volume flexibility, apply scalability, and maximize workflow efficiencies.

Sequencing results can be analyzed using desktop or a fully automated Linux-based bioinformatics software. LymphoTrack Enterprise Software is a powerful application built for automated, high-throughput labs with LIMS integration, while desktop software offers the same intuitive analysis without the need for bioinformatics expertise. Data stays fully within the user's control and safely on-premises with both software applications.

### KEY BENEFITS

- » **Standardized Workflow** reduces errors and enables automated lab environments
- » **Objective Reporting** of clonality and MRD results
- » **Scalability** using up to 96 indices per target
- » **Optimized Design** provides flexibility for additional applications
- » **Flexible Software** options from intuitive desktop analysis to LIMS-integrated pipelines

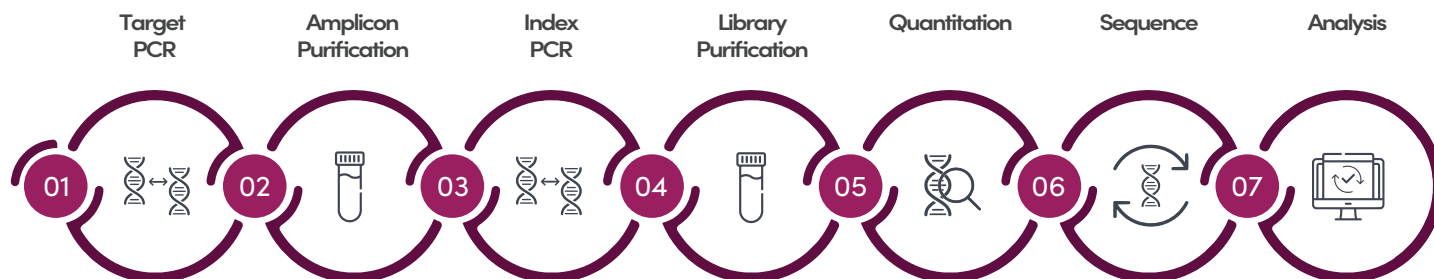
### BACKGROUND

Identifying clonality and determining the frequency of immunoglobulin (Ig) and T-cell receptor (TCR) gene rearrangements is crucial in understanding lymphoproliferative diseases.<sup>1</sup> These gene rearrangements serve as markers for clonal lymphocyte populations, aiding in the detection of blood cancers.<sup>2,3</sup>

The introduction of next-generation sequencing (NGS) has enhanced sensitivity and specificity in clonality assessment, allowing a more comprehensive analysis of Ig and TCR gene rearrangements, facilitating the detection of clonal populations even in samples with low tumor cell content. Recent improvements in NGS clonality assays include providing molecular evidence of clonality in malignant or suspect lymphoproliferative disorders and facilitating measurable residual disease (MRD) assessment.<sup>1,4</sup>



## WORKFLOW



LymphoTrack Flex Assays follow a basic NGS workflow in which high-quality genomic DNA (gDNA) is used as the assay input. The gDNA template is amplified via PCR using target-specific primers (PCR1), undergoes purification, then sequencing adapters and unique dual indices (UDIs) are added to the target amplicons (PCR2). The purified, target-specific, UDI-labelled amplicons are then pooled into Single-Target Libraries, which are then purified and quantified. The Single-Target Libraries are then diluted and combined into a Final Library, which is then sequenced. After the sequencing run is complete, LymphoTrack Software is used to analyze the resulting data.

## ORDERING INFORMATION

| Catalog # | Products                                  |
|-----------|-------------------------------------------|
| 7100003   | LymphoTrack Flex <i>IGH</i> FR1 Assay     |
| 7100005   | LymphoTrack Flex <i>IGH</i> FR2 Assay     |
| 7100006   | LymphoTrack Flex <i>IGH</i> FR3 Assay     |
| 7100004   | LymphoTrack Flex <i>IGHV</i> Leader Assay |
| 7100008   | LymphoTrack Flex <i>IGK</i> Assay         |
| 7100007   | LymphoTrack Flex <i>TRB</i> Assay         |
| 7100002   | LymphoTrack Flex <i>TRG</i> Assay         |
| S100003   | LymphoTrack Enterprise Software           |
| S100010   | LymphoTrack Desktop Software              |

LymphoTrack Flex Assay kits include PCR master mixes (PCR1-amplifies the target and PCR2-adds index primers), positive and negative controls to process a total of 96 samples and controls.

## REFERENCES

1. Groenen, PTJA et al. *Fron. Oncol.* 2023 Feb 07;13:2234–2243.
2. Fan, H, Robetorye, RS. *Methods in Molecular Biology* 2013;999:151–67.
3. Teramo A, et al. *Nat Commun* 2022 Jun 8;13(1):3298.
4. Faham M, et al. *Blood.* 2012 Dec 20;120(26):5173–80.

Ready for a flexible, high-throughput  
sequencing solution?