SOPHiA GENETICS™

Lymphoma Solution

The genomic application that streamlines the interpretation of complex genomic variants associated with different lymphoma types, by combining a capture-based target enrichment kit with the advanced analytical features of the SOPHiA DDM™ platform.

Main Features

SOPHiA GENETICS™ Lymphoma Solution covers **54 relevant genes** associated with many B- and T-cell lymphomas such as diffuse large B-cell, follicular, mantle cell and Burkitt lymphomas. Probe design is optimized to guarantee high on-target rate and coverage uniformity even in GC-rich regions. The technical limitations related to the analyses of key biomarkers such as CEBPA, ASXL1, and FLT3 (including detection of internal tandem duplications) are addressed.

Analytical Capabilities

The SOPHiA DDM™ platform analyzes complex NGS data by detecting, annotating and pre-classifying genomic alterations such as SNVs, Indels and gene amplifications in 47 genes of the panel to support experts with their data-informed decision making in the genes of this panel.

Analysis time[2] from FASTQ: from 4 hours

Gene Panel	Variants Called	Recommendations	Wet Lab
ARID1A, B2M, BCL2, CCND3, CD58, CHD2, CDKN2A, CDKN2B, CIITA, CXCR4, EP300, FOXO1, GNA13, ID3, IRF4, KMT2A, KMT2D, MAL, MEF2B, MYC, MYD88, NFKBIE, PAX5, PIM1, POT1, PRDM1, PTPN11, REL, SOCS1, TNFAIP3, TNFRSF14, TP53, ATM, BCL6, BIRC3, BRAF, BTK, CARD11, CCND1, CD79A, CD79B, CREBBP, EZH2, FBXW7, KRAS, NOTCH1, NOTCH2, NRAS, PLCG2, PTEN, SF3B1, STAT6, TCF3, XPO1	SNVs Indels Gene amplifications	**Starting material** 50 ng DNA **Sample type** FFPE, blood and bone marrow **Suggested Samples per run / Sequencer (Flow Cell / Ion Chip Kit)[3]** 4 for Illumina MiSeq® v2 (2x300bp)* 4 for Illumina MiSeq® V3 (2x150bp) 36 for Illumina NextSeq® 500/550 Mid Output v2 72 for Illumina NextSeq® 500/550 High Output v2	**Day 1:** Library Preparation **Day 2:** Capture and Sequencing **Total library preparation time: 1.5 days**

*2x150-cycle sequencing run (paired-end) is recommended

One Simple Intuitive Platform: Beyond Analytics

Accelerated assessment and reporting of genomic variants

The platform helps users to immediately focus on relevant genomic alterations. Several features facilitate their interpretation process:

- Hotspot screening
- Algorithm-supported variant pre-classification
- Fully customizable filters
- Comprehensive report

Confident decision-making

The SOPHiA DDM™ platform integrates the OncoPortal™. This feature provides the latest scientific evidence on the actionability and significance of each genomic alteration to support informed decision-making for research purpose.

Access to the SOPHiA GENETICS community

Through the SOPHiA DDM™ platform genomics experts from >1000 healthcare institutions interpret their findings and flag the pathogenicity level of variants. This highly valuable information enriches the variant knowledge base and is safely shared among the members of the community, supporting their decision-making process for research purposes.

1. Internal tandem duplications
2. Varies depending on the number of genes, samples multiplexed and server load.
3. Sequencing recommendations and specifications for other sequencing kits and instruments are available upon request. Number of samples per run is recommended for 1000x coverage depth.

Somatic gene variant annotations and related content have been powered by, without limitation, The Jackson Laboratory Clinical Knowledgebase (JAX-CKB™).

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