SOPHiA™

SOPHiAGENETICS.COM

SOPHiA LYMPHOMA SOLUTION™

The genomic application that bundles a capture-based target enrichment kit with the analytical power of SOPHiA™ AI and full access to the SOPHiA DDM™ platform.

SMART KIT DESIGN

SOPHiA 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 coverage uniformity throughout the entire target regions.

Gene panel

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 (57-63), BCL6 (8,9), BIRC3 (all,ex.2), BRAF (15), BTK (15), CARD11 (4-9), CCND1 (1), CD79A (4,5), CD79B (5,6), CREBBP (27-30), EZH2 (16,18), FBXW7 (9,10), KRAS (2,3), NOTCH1 (34), NOTCH2 (26-28,34), NRAS (2,3), PLCG2 (17-23), PTEN (5), SF3B1 (14,15), STAT6 (9-14), TCF3 (17-19), XPO1 (15-18)

Recommendations

Starting material: 50 ng DNA
Sample source: FFPE, blood and bone marrow
Samples per run: Depending on sequencing platform(1)

Sequencer	Flow Cell/ Ion Chip Kit	Recommended samples per run (for 1000x coverage depth)
Illumina MiSeq®	v3 (2x300bp)*	4
	v2 (2x150bp)	4
Illumina NextSeq®	Mid Output	36
	High Output	72

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

Wet lab

Day 1: DNA Library Preparation
Day 2: Capture and Sequencing
Total library preparation time: 1.5 days

ANALYTICAL POWER

SOPHiA 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.

SOPHiA reaches advanced analytical performance:

	Observed
Sensitivity	99.85%
Specifity	99.99%
Accuracy	99.99%
Repeatability	99.96%
Reproducibility	99.98%
Medium on-target rate	> 80%
Medium coverage uniformity	> 99%
Average % of target region with depth > 1000x	> 99%

Analysis time from FASTQ files: 4 hours(2)

(1) Sequencing recommendations and specifications for other sequencing kits and instruments available upon request. Delivery time may vary according to the selected sequencing platform.
(2) Analysis time may vary depending on the number of genes, samples multiplexed and server load.

UNIVERSAL PLATFORM

The results are presented in SOPHiA DDM, the platform of choice for experts performing genomic testing. Its intuitive user interface and advanced features facilitate the visualization and interpretation of genomic alterations. Data are kept safe by applying the highest industrial standards of encryption.

Main features

SOPHiA DDM offers several features that make variant analysis more efficient. With variant pre-classification and customized filtering options, experts can easily accelerate the data interpretation process.

OncoPortal™

SOPHiA DDM integrates the OncoPortal, a decision support functionality based on precision medicine intelligence. It enables experts to access relevant therapeutic, prognostic and diagnostic information to help determine actionability and clinical significance of detected genomic alterations. Moreover, the OncoPortal uses genes and disease association to maximize clinical trial matching.

Access to SOPHiA's Community

In SOPHiA DDM, experts from hundreds of healthcare institutions interpret the results and flag the pathogenicity level of variants according to their knowledge and experience. This highly valuable information feeds the variant knowledge base and is anonymously and safely shared among the members of the community.

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