SOPHiA GENETICS™

Accelerate your analysis of Chronic Lymphocytic Leukemia (CLL)

Discover an application developed and tested by European Hemato-Oncology experts of the SOPHiA GENETICS' Community.

SOPHiA DDM™ Community CLL Clonality Solution is an all-in-one application enabling the characterization of the most scientifically-relevant genomic & immunogenetic biomarkers in CLL, recommended by major international guidelines such as WHO[1], ICC[2], NCCN[3], ESMO[4].

>190'000
new CLL cases are identified per year[5]

Guidelines recommended[1,2,3,4] CLL biomarkers

Full *TP53* mutational status, and capture of *IGH* rearrangements (clonality) and cytogenetic abnormalities

Analytical perf. powered by SOPHiA DDM™

Easy variants visualization and filtering, access to the latest scientific evidence, and customized reporting

Developed with clonality companion software

Peer-reviewed **IgCaller software[6]** to detect somatic hypermutation status and V(D)J- recombination

Benefits of SOPHiA DDM™ community CLL Clonality Solution

- Replace the routine multiple gold standard assays (FISH, Sanger and *IGH*-specific)[7] by an **all-in-one NGS workflow**
- Identify approved CLL biomarkers and **stay ahead of guidelines** with additional insight into CLL-associated genes
- Accelerate your research with our powerful proprietary algorithms and versatile **SOPHiA DDM™ Platform**

Capture the recommended biomarkers

Gather insights on CLL-associated genes and latest scientific evidence

Annotate the *IGH* region with tier tools

Advance your reporting capacities

ADVANCED ANALYTICAL PERFORMANCES*

SOPHiA DDM™ Community CLL Clonality Solution
shows excellent analytical performances and provides experts with the required confidence in their NGS results.

100% sensitivity

100% specificity

99% Concordance with FISH[5]

100% Concordance with Sanger[5]

High reproducibility **(99.6%)** and repeatability **(99.8%)** is essential for **assay validation**[†] and **confident variant detection** across runs and samples.

Excellent coverage uniformity **(>99.6%)** across AT- and GC-rich regions allows **multiplexing** and makes each sequencing exceptionally **cost-efficient.**

Product Specifications

23 genes covered	*ATF1, ATM,* ***BCL2****, BIRC3, BTK*[‡] *(15), CDK4, CUL4A (1-5), CXCR4 (2), DLEU1, EGR2, FBXW7, KLF5, KRAS, MYD88, NFKBIE,* ***NOTCH1*** *(34), PLCG2 (19,20,24), POT1, PROZ, RB1, SF3B1 (14-16,18),* ***TP53****, XPO1 (15,16)* **+** ***IGH*** **rearrangement**
Sample type	Blood and Bone marrow
Starting material	200 ng DNA
Samples /run for 1000x coverage depth	24 on MiSeq® v3 (3x300bp) 16 on MiniSeq® High-Output (2x150bp)
Product codes	CS2462ILLRSMY01-16 CS2462ILLRSMY01-32 CS2462ILLRSMY01-48

Want to learn more?

Or contact us at:
info@sophiagenetics.com

CLL, chronic lymphocytic leukemia; ESMO, European society for medical oncology; FISH, fluorescence in situ hybridization; ICC, international consensus classification; IGH, immunoglobulin heavy locus; NCCN, national comprehensive cancer network; NGS, next-generation sequencing; WHO, world health organization.

*Data on file; †SOPHiA GENETICS does not provide aid in the validation of custom/community panels for clinical use; ‡Excluded from CNVs analysis.

[1]Alaggio et al., *Leukemia*, 2022; [2]Campo et al., *Blood*, 2022; [3]Wierda et al., *J Natl Compr Canc Netw.*, v2.2023; [4]Eichhorst et al., *Ann Oncol.*, 2021; [5]Sung et al., *CA Cancer J Clin.*, 2021; [6]Nadeu et al., *Nat Commun.*, 2020; [7]Nadeu et al., *ERIC International Meeting*, 2022.

The information provided in this document is for informational purposes only. Full details of the panel should be confirmed. Please contact us to obtain appropriate further information.