

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 WHO¹, ICC², NCCN³, ESMO⁴.

>190'000
new CLL cases are identified per year⁵



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 software⁶** 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



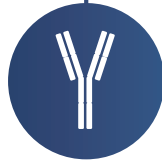
Accelerate your research with our powerful proprietary algorithms and versatile **SOPHiA DDM™ Platform**



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 FISH⁵

100%
Concordance
with Sanger⁵

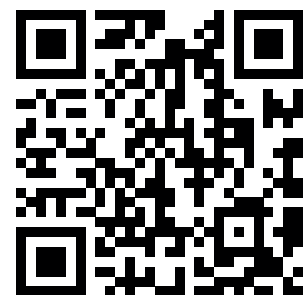
High reproducibility (**99.6%**) and repeatability (**99.8%**) is essential for **assay validation**[†] and **confident variant detection** across runs and samples.

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	<i>ATF1, ATM, BCL2, BIRC3, BTK</i> [‡] (15), <i>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</i>
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.

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

