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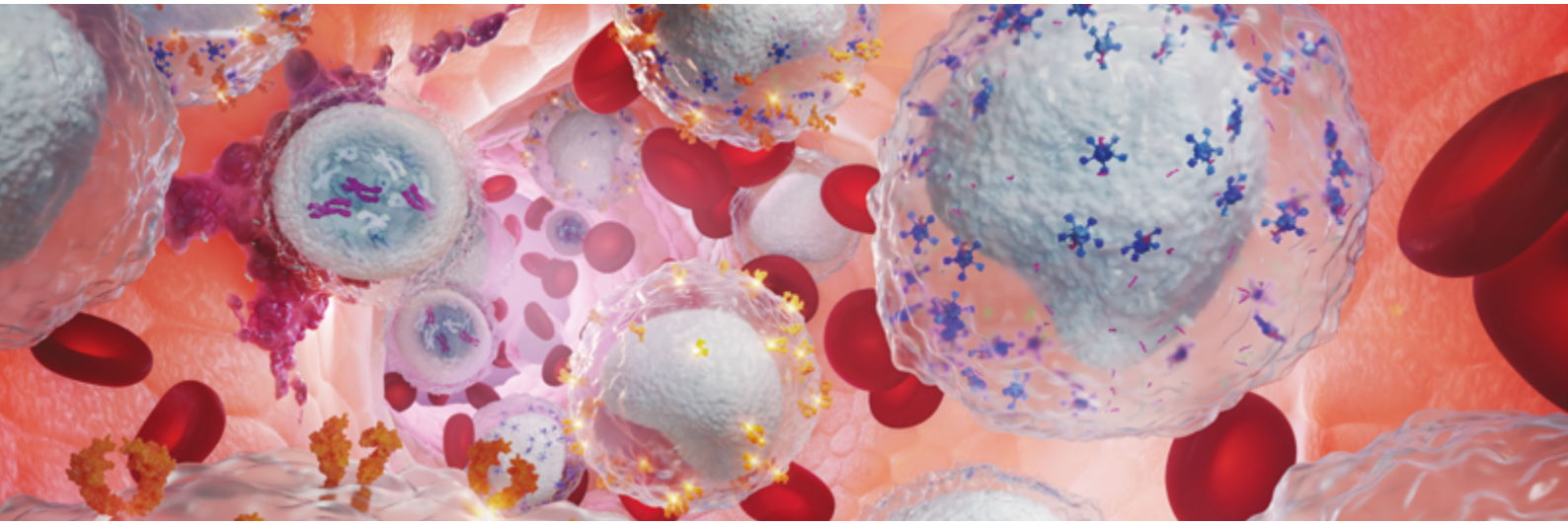
Lymphoid malignancy in focus

SureSeq™ NGS panels



Chronic lymphocytic leukaemia (CLL) is the most common type of leukaemia in adults in Europe. A wide range of chromosomal abnormalities are associated with CLL, from single nucleotide variants (SNVs) and insertions/deletions (indels) to large copy number variations (CNVs), including trisomies.

Designed in collaboration with leading cancer experts, the enhanced **SureSeq™ CLL + CNV V3 Panel** design provides more comprehensive genetic profiling of your samples. Our panel allows you to target 16 key disease-associated genes and five chromosomal regions implicated in CLL progression (Table 1), including enhanced *TP53* variant detection.

More comprehensive genetic profiling of your samples
with proprietary bait designs that provide CNV detection down to 20% tumour estimation and SNV detection down to 1% VAF for a wide range of disease-associated targets.

Enhanced CNV detection in the five most commonly aberrant regions in CLL
with reduced false positives and lower inter-run variability, using reference DNA for baseline CNV calling included as standard, for reliable and cost-effective sequencing results.

Reduce assay times and speed up your lab's sample-to-result process
with our streamlined workflow, which combines SNV detection across 16 key genes and CNV discovery for faster sample insights.

Easily analyse your NGS data without the need for additional bioinformatics resources
with Interpret, our complimentary easy-to-use analysis solution for accurate identification of all detected variants and CNVs.

Understanding CLL progression with the SureSeq™ CLL + CNV V3 Panel

- **Expert-led, evidence-based content:** The latest CLL discoveries and guidelines[1] are reflected in extended gene coverage for *TP53*, *BTK* and *PLCG2*, plus inclusion of *BCL2* and *NRAS*.
- **Superior coverage uniformity and variant detection:** Designed for detection down to 1% variant allele frequency (VAF) in 16 key genes.
- **Superior somatic CNV calling:** In the five most common CNVs down to 20% tumour content.
- **Sample tracking:** With the *SRY* gene and 24 SNPs.
- **Enhanced efficiency with SureSeq™ Reference Human DNA included:** For baseline CNV calling, reducing false calls caused by run-to-run variability, thus ensuring accurate sample characterisation.

Genes	*ATM, BCL2, BIRC3, BRAF, BTK, CXCR4, KRAS, MYB, MYD88, NOTCH1, NRAS, PLCG2, SAMHD1, SF3B1, TP53* and *XPO1*.
CNVs	del17p (covering *TP53*), del11q (covering *ATM*), del13q (covering *RB1/DLEU2/DLEU7*), del6q (6q23.2- 6q23.3 covering *MYB*) and trisomy 12. Reference DNA included to provide a baseline for CNV calling.

Table 1: The SureSeq™ CLL + CNV V3 Panel targets

Investigator's feedback

"The SureSeq™ CLL + CNV V3 Panel is invaluable for our research as it enables us to identify key CLL-associated biomarkers. The robust technical support provided by OGT makes the panel accessible to users with varying levels of expertise in molecular techniques. Additionally, the integration with bioinformatics software simplifies the data analysis process, providing clear and actionable results".

Anna Sobczyńska-Konefał
Head of the Department of Haemato-oncology Diagnostics
Lower Silesian Center for Oncology, Pulmonology and Haematology
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References

[1] **Alaggio, R., Amador, C., Anagnostopoulos, I.** *et al.* The 5th edition of the World Health Organization Classification of Haematolymphoid Tumours: Lymphoid Neoplasms. Leukemia 36, 1720–1748 (2022). https://doi.org/10.1038/s41375-022-01620-2

Consult your Sysmex representative and inquire about other SureSeq™ haematological malignancy NGS panels: **SureSeq™ Core MPN Panel, SureSeq™ Pan-Myeloid Panel, SureSeq™ Myeloid Plus Panel.**

SureSeq™ For Research Use Only; Not for Use in Diagnostic Procedures.

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