SureSeq

A Sysmex Group Company

CLL + CNV V3 Panel

Features

- **More comprehensive genetic profiling of your samples** with proprietary bait designs that unlock CNV detection down to 20% tumour estimation and SNV/indel detection designed down to 1% VAF for an expansive array of disease-associated targets
- **Enhanced CNV detection in the 5 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 that combines SNV detection across 16 key genes and CNV discovery for faster sample insights
- **Easily analyse your NGS data without the need for additional bioinformatic resource** with Interpret, our complimentary easy-to-use analysis solution for accurate identification of all detected SNVs, indels and CNVs

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Introduction

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

Designed in collaboration with leading cancer experts the enhanced SureSeq™ CLL + CNV V3 Panel enables more expansive genetic profiling of your samples. Our panel allows you to target 16 key disease-associated genes and 5 chromosomal regions implicated in CLL progression (Table 1), including enhanced *TP53* variant detection.

Expert-led, evidence-based content

Investigating both chromosomal aberrations and SNVs/indels is imperative to advance research into CLL progression and treatment. Cytogenetic abnormalities are present in more than 80% of patients with previously untreated CLL, the most frequent being del(13q), del(11q), del(17p), del(6q) and trisomy 12[1]. Some of these CNVs cover important tumour suppressors, such as del(17p) resulting in the loss of the *TP53* gene and del(11q) resulting in loss of *ATM*. More recently, other genes have also been found to be mutated in CLL, including *NOTCH1*, *SF3B1*, *MYD88* and *BIRC3*, adding to the genomic complexity of this leukaemia[2]. Together with leading cancer experts, we continue to monitor the latest CLL research, which is reflected in the latest V3 panel design through enhanced gene coverage for *BTK* and *PLCG2*, plus the inclusion of baits for *BCL2* and *NRAS* genes.

Due to this genetic heterogeneity, current analysis strategies for CLL require multiple methods to obtain a comprehensive genetic picture, often using microarray or fluorescence *in situ* hybridisation (FISH) to detect structural abnormalities in combination with NGS for somatic variants. With OGT's SureSeq CLL + CNV V3 Panel, you can now obtain a more complete understanding of the genetic makeup of CLL progression in each sample using a single assay.

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 is included to provide a baseline for CNV calling.

Table 1: The SureSeq CLL + CNV V3 Panel targets the 5 most common chromosomal regions implicated in CLL and 16 genes, plus the *SRY* gene and 24 SNPs for easy sample tracking.

Superior coverage uniformity allowing reliable variant and somatic CNV detection

OGT's pioneering experience in hybridisation-based technology means the SureSeq CLL + CNV V3 Panel provides you with better coverage uniformity, fewer false positives, and superior variant detection. Designed for detection down to 1% variant allele frequency (VAF) in 16 key genes (Figure 1) plus the *SRY* gene and 24 SNPs, to allow for easy sample tracking[3], you can be confident you're getting the full genetic profile of your sample. Additionally, we have enhanced this panel with the inclusion of reference DNA for baseline CNV calling, to increase your labs efficiency with reduced false positives and lower inter-run variability assuring you of accurate sample characterisation.

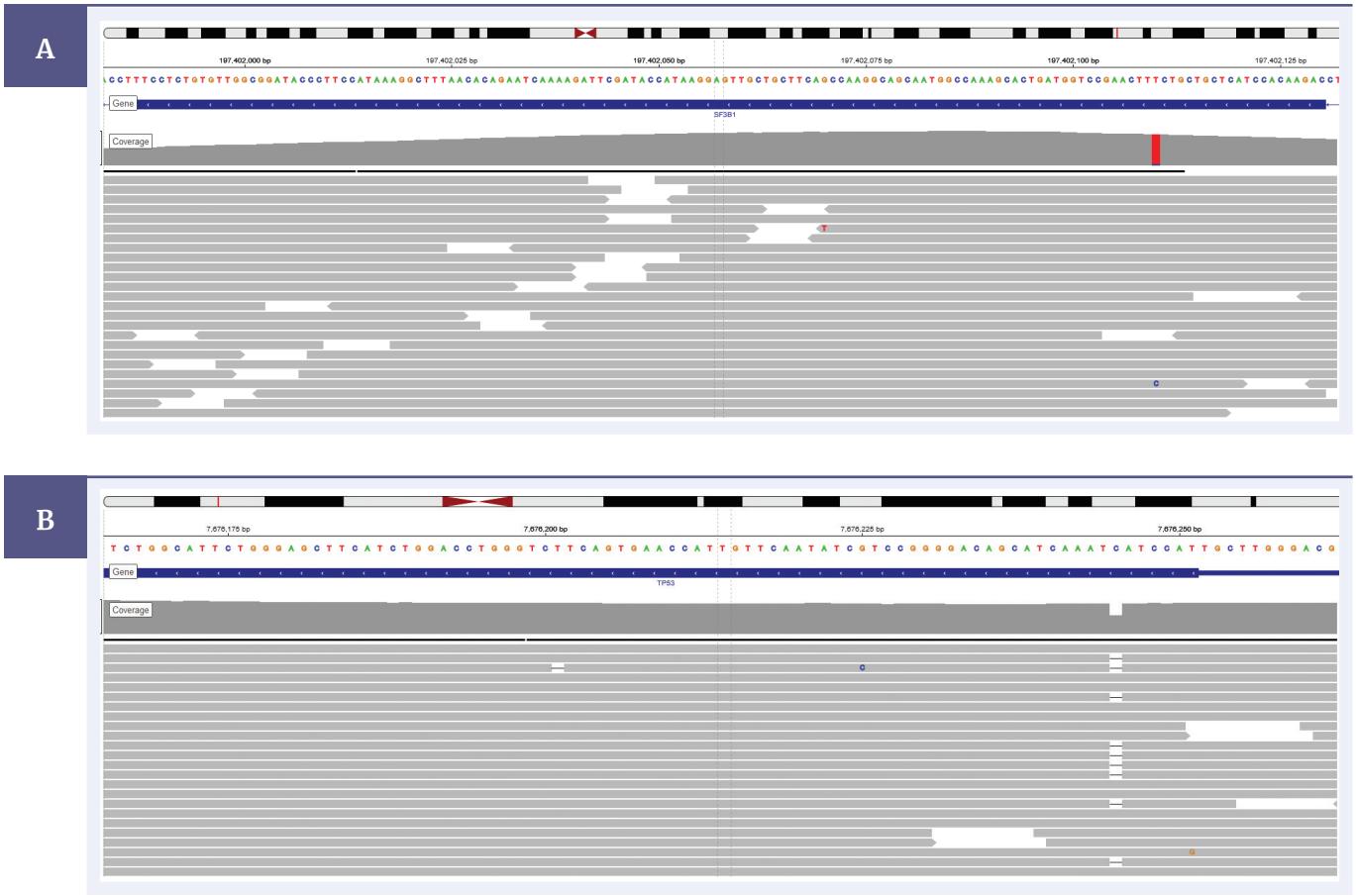


Figure 1: Illustration of the excellent uniformity and high depth of coverage allowing confident detection of A a *SF3B1* exon 15 hotspot variant Lys700Glu with 4.8% allele frequency and B a *TP53* exon 4 frameshift deletion (*TP53* c.124del) with frequency 38.9%.

The SureSeq CLL + CNV V3 Panel covers the 5 most common CNVs in CLL. Compared to array data, often considered the gold standard for CNV detection, the events reported with the SureSeq CLL + CNV V3 Panel were 100% concordant, even in genomic regions containing multiple aberrations (Figures 2 - 3). More so, facilitated by OGT's excellent bait design, loss-of-heterozygosity (LOH) can be identified and support CNV calls. With a CNV size detection ranging from small CNVs through to complete loss of a chromosomal arm and whole chromosome gains (trisomy 12), your data provides a more comprehensive genetic picture for each sample, all in a single assay.

NGS

Array

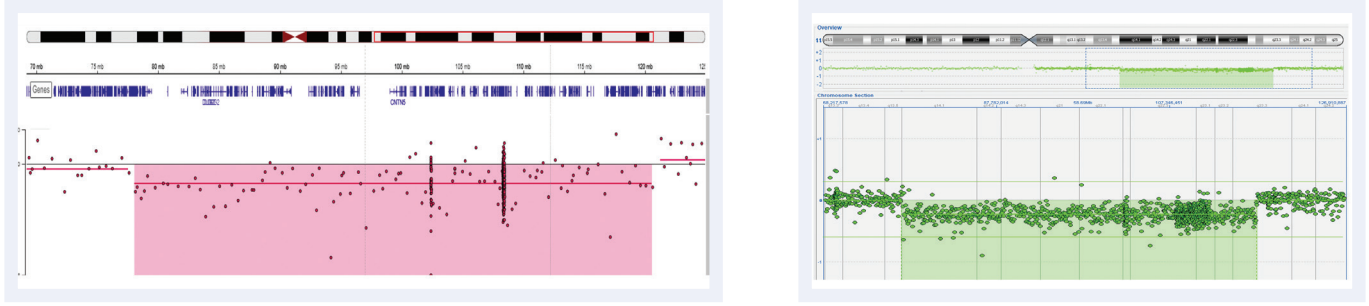
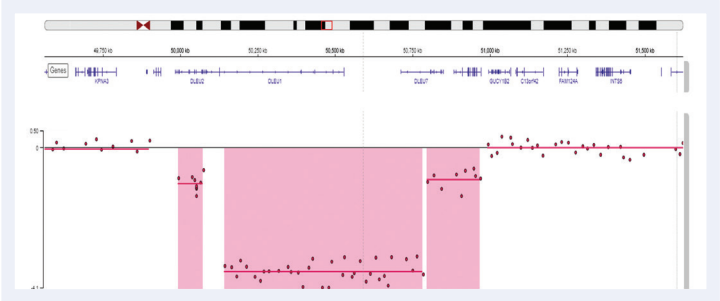


Figure 2: 42.7 Mb deletion of 11q covering *ATM*.

NGS



Array

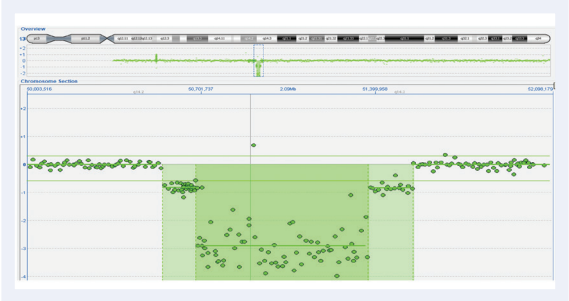


Figure 3: 0.6 Mb biallelic loss called within a larger ~1 Mb single allele deletion in the region covering *DLEU2/DLEU1/DLEU7* on chromosome 13q.

Complimentary analysis software

Interpret NGS Analysis Software is OGT's powerful and easy-to-use data analysis solution, facilitating analysis and visualisation of a wide range of somatic variants and structural aberrations. Designed to work seamlessly with all SureSeq panels, Interpret perfectly complements the SureSeq CLL + CNV V3 Panel, delivering fast and accurate detection of all SNVs, indels, LOH and CNVs covered by the panel. Following detection, all events can be readily visualised in the user-friendly variant browser, for an effortless translation of all your CLL data into meaningful results (Figure 4).

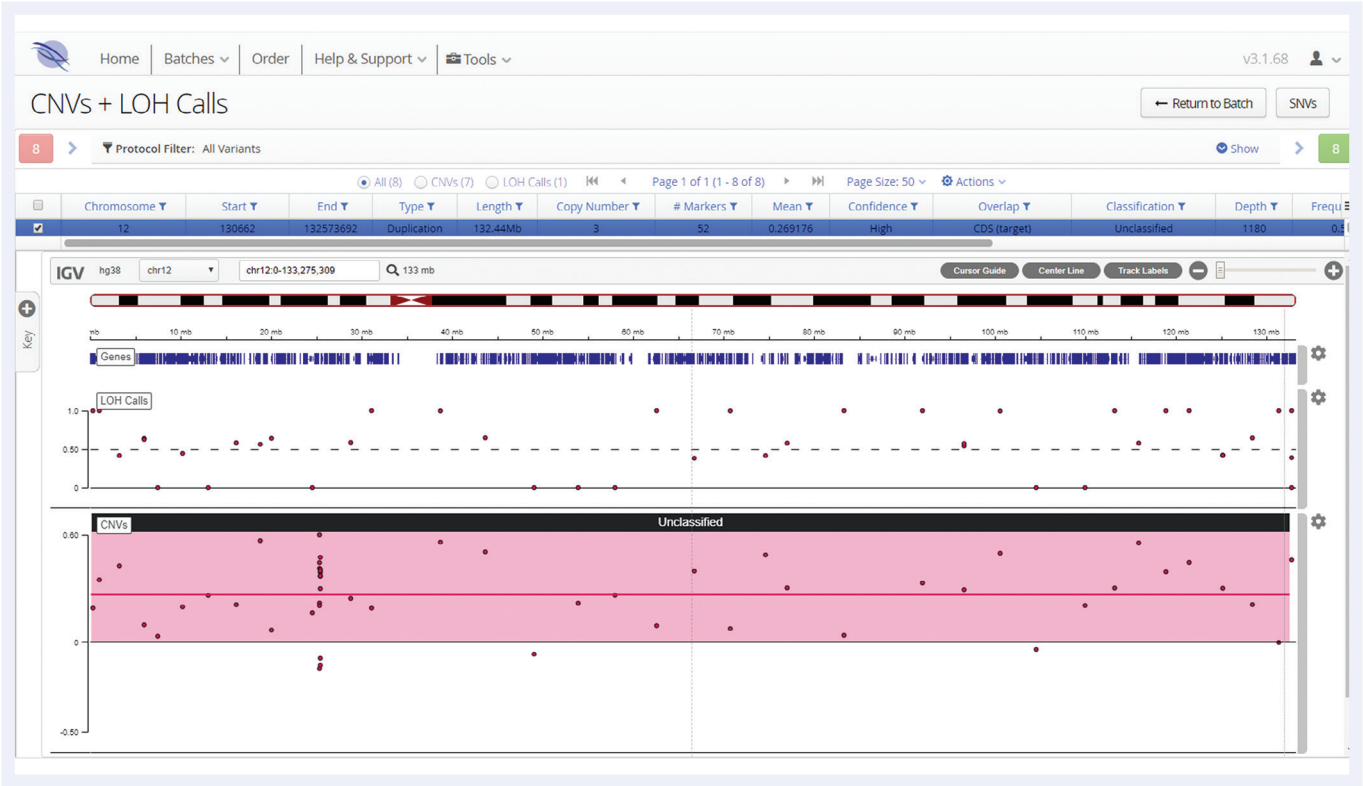


Figure 4: Following analysis, all variants and CNVs are visualised for easy interpretation in OGT's Interpret NGS Analysis Software. In this example a trisomy 12 is detected, showing a reliable gain call across the whole chromosome.

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The OGT Partnership

Behind every sample is a life that can be improved through the right care decisions. The OGT partnership approach is key to providing the highest level of service, working closely with you to understand your unique challenges, customising our approach to meet your exact needs.

Bespoke panel content

With our NGS customisation service you can tailor your panel using OGT's regularly updated, expert-curated library of pre-optimised cancer content. Add or remove targets to meet your specific analytical needs, ensuring maximum efficiency and focus on the most relevant insights for your research.

The SureSeq CLL + CNV V3 Panel in numbers

Feature	Specification
Number of genes	16
Panel size	142 kb
DNA input recommended	200-500ng high-quality DNA
Gene list	*ATM, BCL2, BIRC3, BRAF, BTK, CXCR4, KRAS, MYB, MYD88, NOTCH1, NRAS, PLCG2, SAMHD1, SF3B1, TP53* and *XPO1*
CNV list	del17p (covering *TP53*), del11q (covering *ATM*), del13q (covering *RB1/DLEU2/DLEU7*), del6q (6q23.2-6q23.3 covering *MYB*) and Trisomy 12
Sample tracking	*SRY* + 24 SNP profiling panel[3]
Limit of detection	SNVs/indels: capable of VAF of 1 - 2.5% within the 16 genes. CNVs: capable of detecting CNVs down to 20% tumour content
SureSeq Reference Human DNA	DNA: SureSeq Reference Female DNA, SureSeq Reference Male DNA

Ordering information

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Product	Contents	Cat. No.
SureSeq CLL + CNV V3 Complete NGS Workflow Solution V2 (24)	Enrichment baits sufficient for 3 x 8-sample pools. Bundle of 1 x Universal Library Preparation Kit (24), containing PCR primers and enzymes. 1 x Universal Hybridisation & Wash Kit V2 (24). 1 x Pre-PCR Universal Bead Kit (24). 1 x Post-PCR Universal Bead Kit (24). 1 x Universal Index Adapter Kit (24). SureSeq Reference Human DNA. Interpret NGS Analysis Software	780108-24
SureSeq CLL + CNV V3 Complete NGS Workflow Solution V2 (96)	Enrichment baits sufficient for 12 x 8-sample pools. Bundle of 1 x Universal Library Preparation Kit (96), containing PCR primers and enzymes. 1 x Universal Hybridisation & Wash Kit V2 (96). 1 x Pre-PCR Universal Bead Kit (96). 1 x Post-PCR Universal Bead Kit (96). 1 x Universal Index Adapter Kit (96). SureSeq Reference Human DNA. Interpret NGS Analysis Software	780108-96
SureSeq CLL + CNV V3 Panel (24)	Enrichment baits sufficient for 3 x 8-sample pools. SureSeq Reference Human DNA. Interpret NGS Analysis Software	771027-24
SureSeq CLL + CNV V3 Panel (96)	Enrichment baits sufficient for 12 x 8-sample pools. SureSeq Reference Human DNA. Interpret NGS Analysis Software	771027-96
Universal NGS Workflow Solution V2 (24)	Bundle of 1 x Universal Library Preparation Kit (24), containing PCR primers and enzymes. 1 x Universal Hybridisation & Wash Kit V2 (24). 1 x Pre-PCR Universal Bead Kit (24). 1 x Post-PCR Universal Bead Kit (24). 1 x Universal Index Adapter Kit (24)	770510-24
Universal NGS Workflow Solution V2 (96)	Bundle of 1 x Universal Library Preparation Kit (96), containing PCR primers and enzymes. 1 x Universal Hybridisation & Wash Kit V2 (96). 1 x Pre-PCR Universal Bead Kit (96). 1 x Post-PCR Universal Bead Kit (96). 1 x Universal Index Adapter Kit (96)	770510-96

Request a quote at www.ogt.com or contact one of our experts at contact@ogt.com.

References

1. Döhner *et al.*, N Engl J Med 2000;343:1910–1916
2. Rossi *et al.*, Blood 2013;121:1403–1412
3. Pengelly *et al.*, Genome Med 2013;5:89

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What binds us, makes us.

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