SureSeq

A Sysmex Group Company

CLL + CNV V3 Panel

Coming soon

Features

Gain a more complete understanding of CLL progression

- Accurately detect low-frequency SNVs and indels in 16 key CLL-implicated genes, including *TP53*, *BTK*, *PLCG2*, *BCL2* and *NRAS*

Enhanced CNV detection ranging from loss of single exons to full chromosome arms and trisomy 12

- Profile your samples for CNVs in the 5 most commonly aberrant regions in CLL

Time savings

- Replace multiple assays with a single NGS panel, increasing throughput and reducing turnaround time

Complimentary data analysis software

- Analyse your data with Interpret NGS Analysis Software, OGT's powerful and easy-to-use analysis solution for accurate identification of all variants 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.

The SureSeq™ CLL + CNV V3 Panel has been designed in collaboration with recognised cancer experts to detect 16 key genes and 5 chromosomal regions implicated in CLL progression (Table 1). The SureSeq CLL + CNV V3 Panel alleviates the burden of running multiple assays and streamlines your CLL research to deliver a comprehensive genomic profile for each CLL sample using a single workflow.

Contains the latest 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. 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	17p (covering *TP53*), 11q (covering *ATM*), 13q (covering *RB1/DLEU2/DLEU7*), 6q (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 expert bait design delivers outstanding uniformity and depth of coverage, capable of detecting low frequency SNVs and indels down to 1–2.5% variant allele frequency (VAF) in 16 genes (Figure 1), plus the *SRY* gene and 24 SNPs to allow for easy sample tracking[3]. Reference DNA is also included to provide a baseline for CNV calling, reducing spurious calls due to run-to-run variability.

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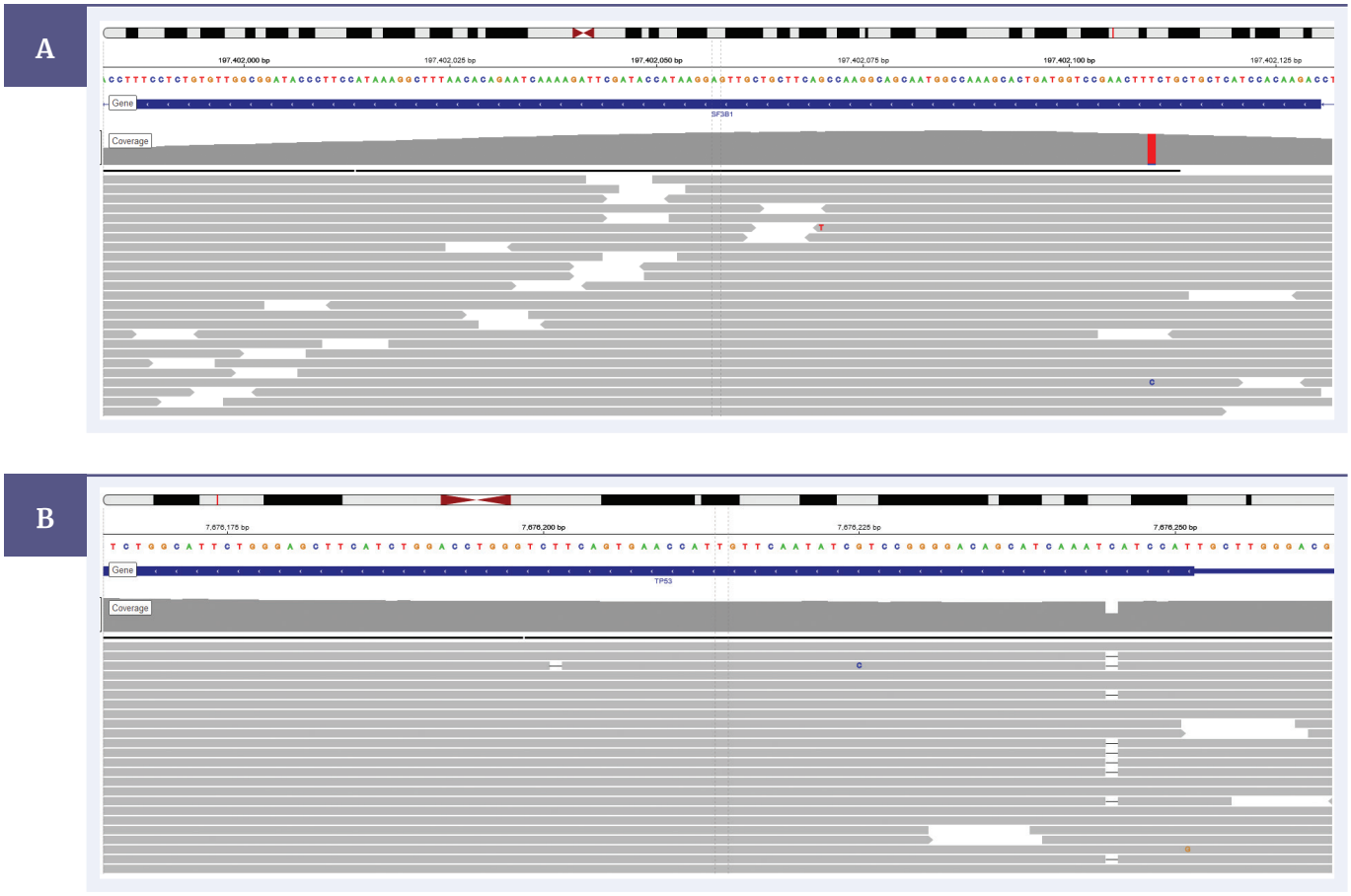


Figure 1: Illustration of the excellent uniformity and high depth of coverage allowing confident detection of A a *SF3B1* exon 15 hotspot variant Lys700Glu with 4.8% allele frequency and B a *TP53* exon 4 frameshift deletion (*TP53* c.124del) with frequency 38.9%.

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. With a CNV size detection range from single exon to whole gene, up to complete loss of a chromosomal arm and whole chromosome gains (trisomy 12), your data provides a more comprehensive genetic picture for each sample from a single assay.

NGS

Array

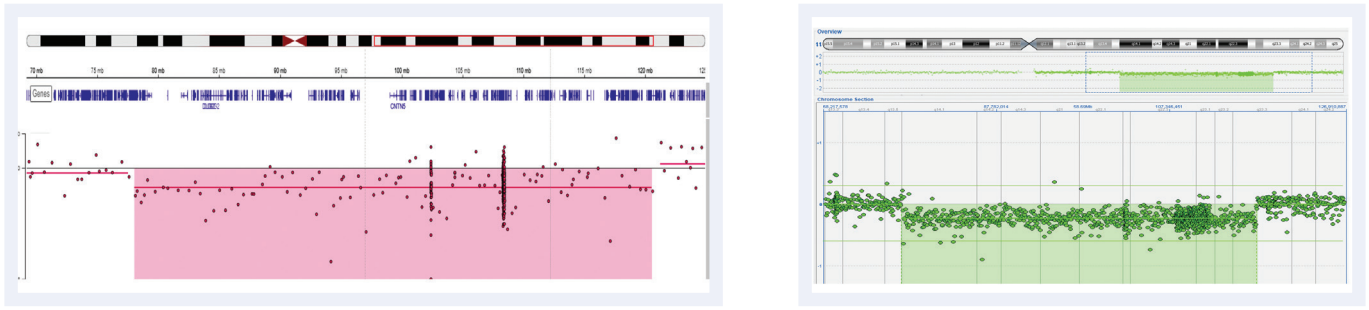
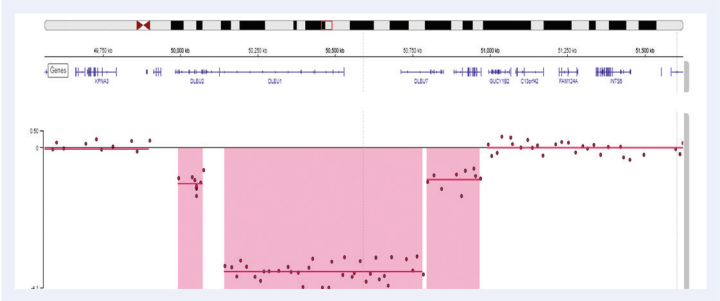


Figure 2: 42.7 Mb deletion of 11q covering *ATM*.

NGS



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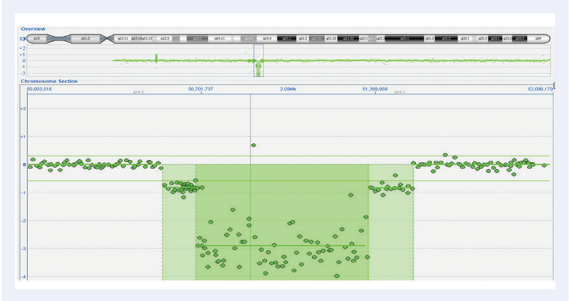

Figure 3: 0.6 Mb biallelic loss called within a larger ~1 Mb single allele deletion in the region covering *DLEU2/DLEU1/DLEU7* on chromosome 13q.

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).

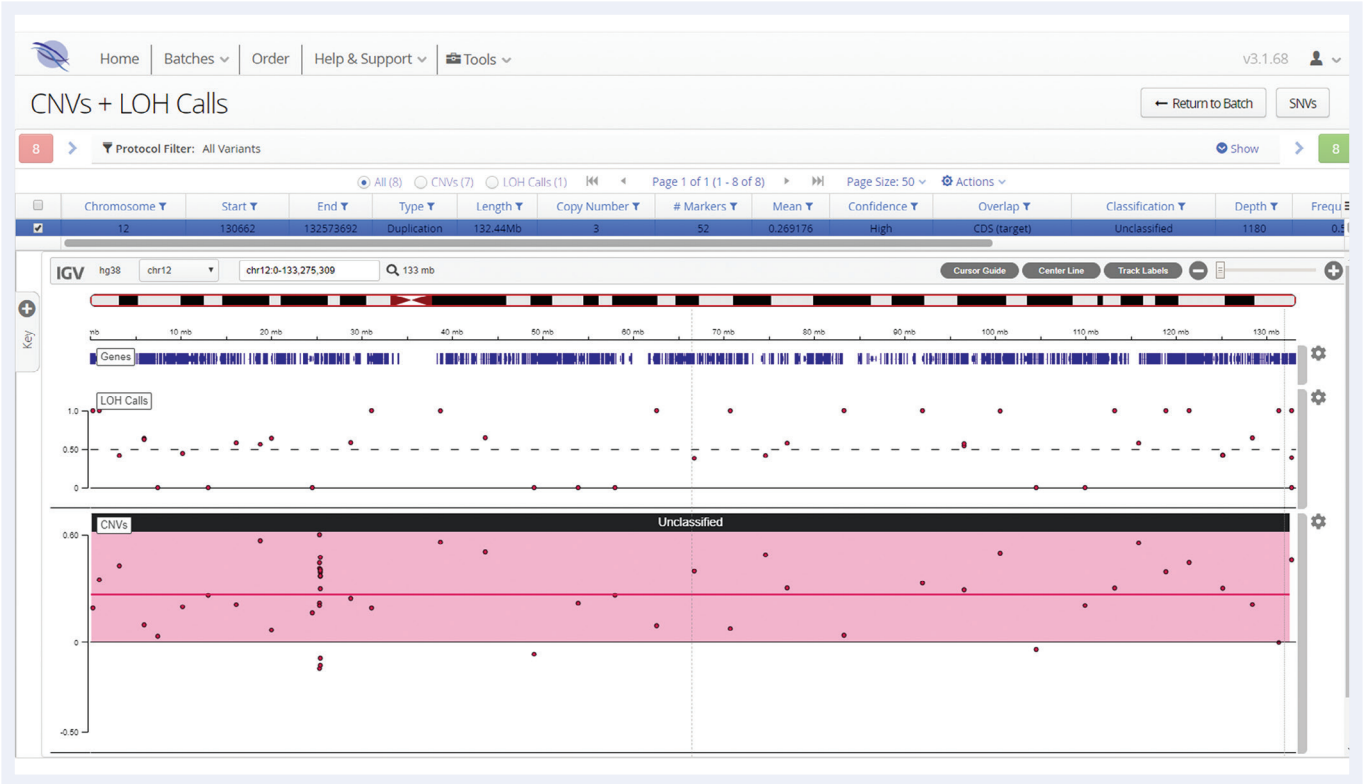

Figure 4: Following analysis, all variants and CNVs are visualised for easy interpretation in OGT's Interpret NGS Analysis Software. In this example a trisomy 12 is detected, showing a reliable gain call across the whole chromosome.

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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

Does the SureSeq CLL + CNV V3 Panel not meet your exact requirements? With OGT, you never have to sequence genes you're not interested in and can always modify each panel to what's most relevant for your research. Choose from our regularly updated, expert-curated library of pre-optimised cancer content to create your ideal custom SureSeq myPanel™ CLL Panel.

The SureSeq CLL + CNV V3 Panel in numbers

Feature	Specification	
Number of genes	16	
Panel size	142 kb	
DNA input recommended	>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	17p (covering *TP53*), 11q (covering *ATM*), 13q (covering *RB1/DLEU2/DLEU7*), 6q (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
CNV detection size	11q:	- single exon to whole gene of *ATM*, whole 11q arm
	17p:	- single exon to whole gene of *TP53*, whole 17p arm
	13q:	- del(13)(q14) type I (short) and del(13q)(q14) type II (larger) events covering *RB1/DLEU2/DLEU7*, whole 13q arm
	6q:	- (6q23.2-6q23.3) covering *MYB* gene
	Trisomy 12:	- whole chromosome
LOH detection size	CN-LOH ≥10 Mb	
SureSeq Reference Human DNA	DNA: SureSeq Reference Human 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	780106-24
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	780106-96
SureSeq CLL + CNV V3 Panel (24)	Enrichment baits sufficient for 3 x 8-sample pools. SureSeq Reference Human DNA. Interpret NGS Analysis Software	770027-24
SureSeq CLL + CNV V3 Panel (96)	Enrichment baits sufficient for 12 x 8-sample pools. SureSeq Reference Human DNA. Interpret NGS Analysis Software	770027-96
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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