SureSeq

A Sysmex Group Company

CLL + CNV Panel

Features

Unparalleled uniformity and high depth of coverage

- Detect low-frequency SNVs and indels with confidence

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, 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 copynumber variations (CNVs), including trisomies.

The SureSeq™ CLL + CNV Panel has been designed in collaboration with recognised cancer experts to detect 12 key genes and 5 chromosomal regions implicated in CLL progression (Table 1). The SureSeq CLL + CNV 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. Structural abnormalities are common in CLL and found in more than 80% of CLL cases, 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].

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 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*, *PLCG2*, *BIRC3*, *BRAF*, *TP53*, *XPO1*, *SF3B1*, *KRAS*, *MYD88*, *SAMHD1*, *NOTCH1* and *BTK*.
CNVs	7p (covering *TP53*), 11q (covering *ATM*), 13q (covering *RB1/DLEU2/DLEU7*), 6q (6q23.2-6q23.3 covering *MYB*) and Trisomy 12.
Sample tracking	*CXCR4* and *SRY* + 24 SNP profiling panel[3]

Table 1: The SureSeq CLL + CNV Panel targets the 5 most common chromosomal regions implicated in CLL and 14 genes, including 2 genes 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, offering confident detection of low frequency SNVs and indels down to 1% variant allele frequency (VAF) in 14 genes (Figure 1), including 2 genes and 24 SNPs to allow for easy sample tracking[3].

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CLL + CNV Panel

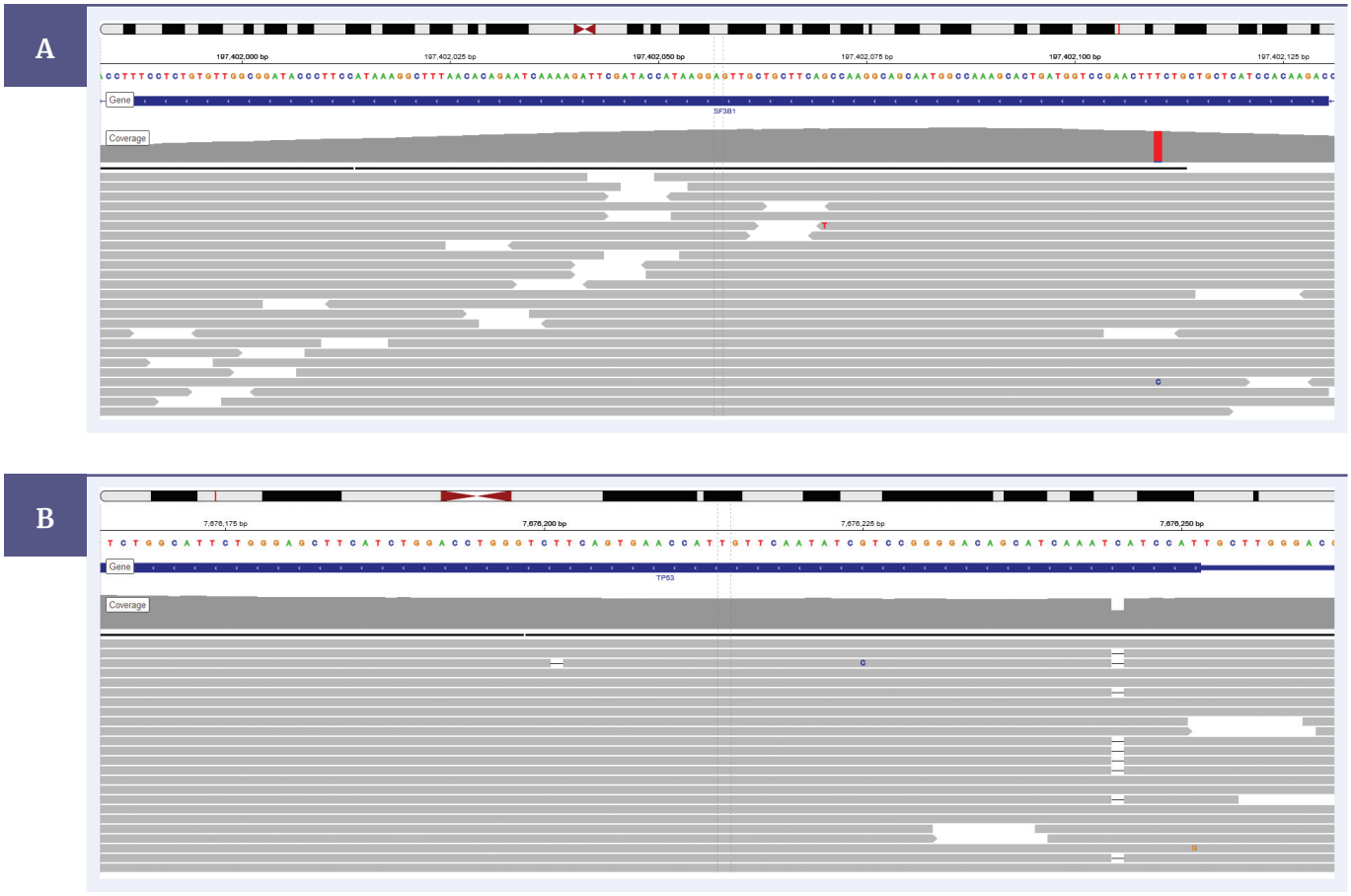
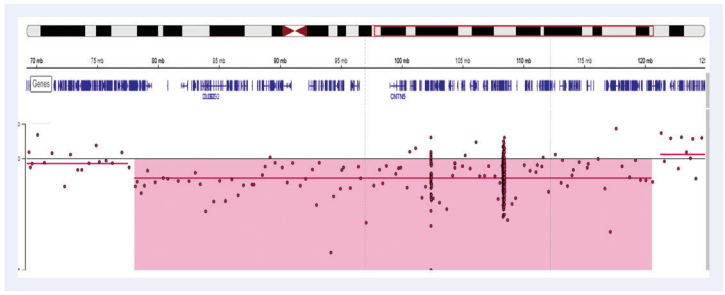


Figure 1: Illustration of the excellent uniformity and high depth of coverage allowing confident detection of A a *SF3B1* exon 15 hotspot variant Lys700Glu with 4.8% allele frequency and B a *TP53* exon 4 frameshift deletion (*TP53* c.124del) with frequency 38.9%.

The SureSeq CLL + CNV Panel covers the 5 most common CNVs in CLL and enables detection down to 10% VAF, corresponding to 20% tumour content. Compared to array data, often considered the gold standard for CNV detection, the events reported with the SureSeq CLL + CNV 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

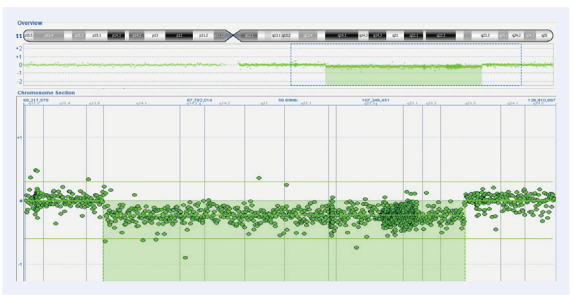


Figure 2: 42.7 Mb deletion of 11q covering *ATM*.

NGS

Array

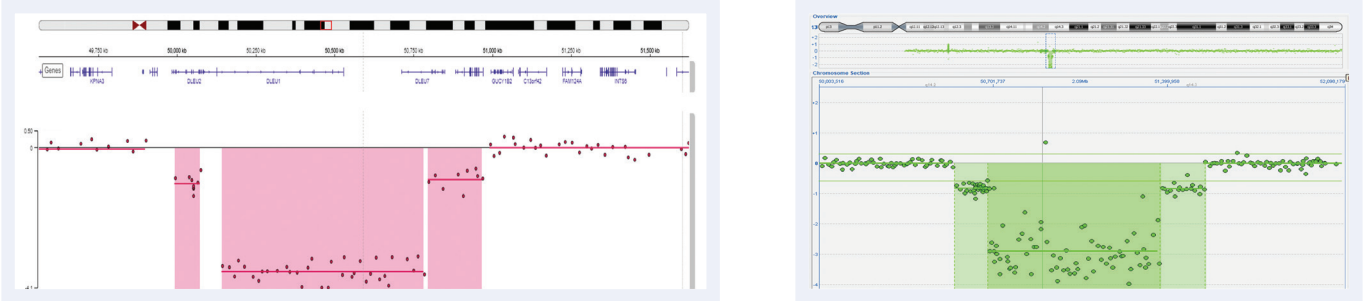


Figure 3: 0.6 Mb biallelic loss called within a larger ~1 Mb single allele deletion in the region covering *DLEU2/DLEU1/DLEU7* on chromosome 13q.

Complimentary Interpret software

Interpret 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 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).

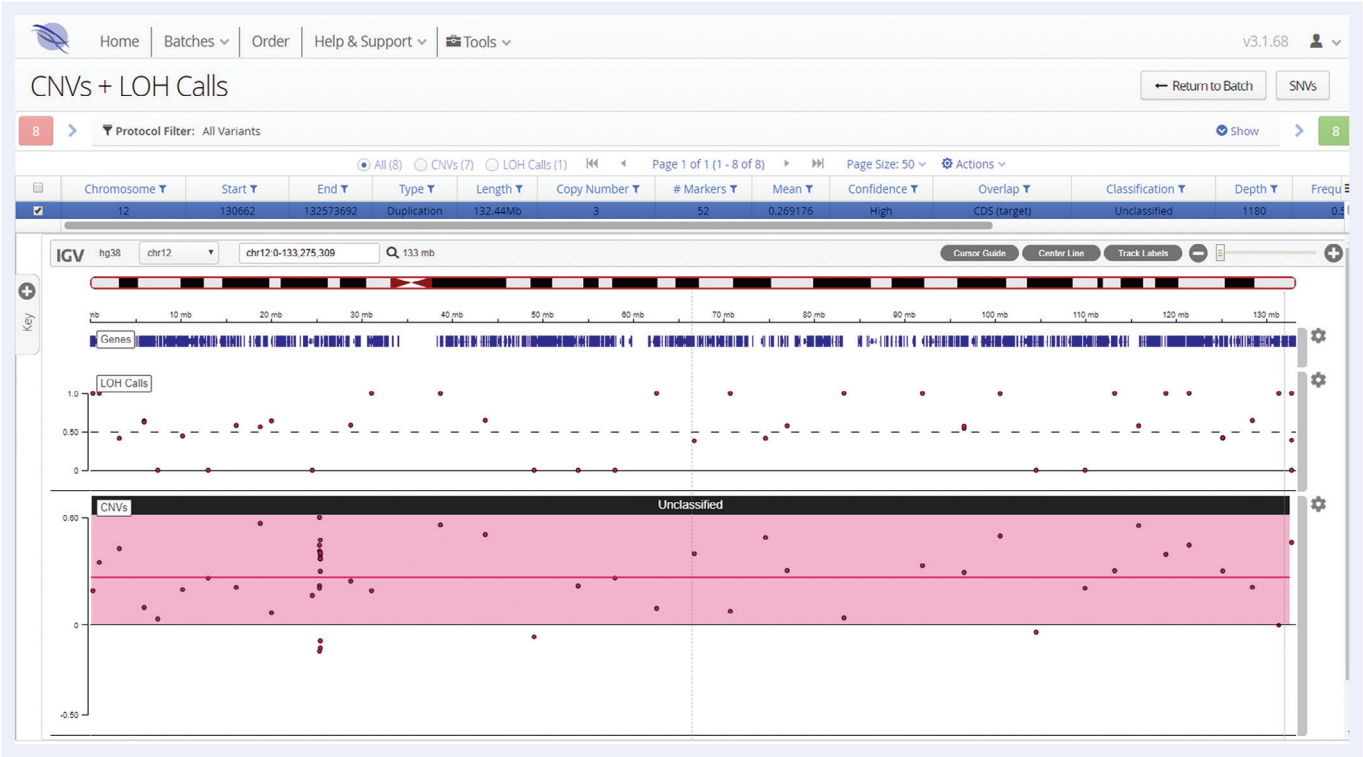


Figure 4: Following analysis, all variants and CNVs are visualised for easy interpretation in OGT's Interpret. In this example a trisomy 12 is detected, showing a reliable gain call across the whole chromosome.

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Bespoke panel content

Does the SureSeq CLL + CNV 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, or order the SureSeq CLL + CNV Panel right off the shelf.

The SureSeq CLL + CNV Panel in numbers

Feature	Specification	
Number of genes	14	
Panel size	117 kb	
Uniformity Coverage	>99% of bases at >20% of the mean target coverage	
Mean target coverage	>1000x	
DNA input recommended	>500ng high quality DNA	
Gene list	*ATM, PLCG2, BIRC3, BRAF, TP53, XPO1, SF3B1, KRAS, MYD88, SAMHD1, NOTCH1* and *BTK*	
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	*CXCR4* and *SRY* + 24 SNP profiling panel[3]	
Limit of Detection	SNVs/indels: CNVs:	VAF of 1% within the 14 genes VAF of 10% within the 5 chromosomal regions
CNV detection size	11q:	- single exon to whole gene of *ATM* - > 5-10 Mb for the rest of the 11q arm
	17p:	- single exon to whole gene of *TP53* - > 5-10 Mb for the rest of the 17p arm
	13q:	- del(13)(q14) type I (short) and del(13q)(q14) type II (larger) events covering *RB1/DLEU2/DLEU7* - > 10-20 Mb for the rest of the 13q arm
	6q (6q23.2-6q23.3):	- single exon to whole gene of *MYB* plus 1 Mb flanking sequence on either side
	Trisomy 12:	- whole chromosome
LOH detection size	11q and 17p: 5-10 Mb 13q: 10-20 Mb	
Samples per MiSeq® v2 run	16 samples/ run	

Ordering information

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Product	Contents	Cat. No.
SureSeq CLL + CNV Panel (16 reactions)	Enrichment baits sufficient for 16 samples; Interpret Software	602022-16
SureSeq CLL + CNV Panel (96 reactions)	Enrichment baits sufficient for 96 samples; Interpret Software	602022-96
SureSeq NGS Library Preparation Complete Solution (16)	Bundle of 1x SureSeq NGS Library Preparation Kit (16), containing adaptors, PCR primers and enzymes, 1x SureSeq NGS Index Kit – Collection A, 1x SureSeq NGS Hyb & Wash Kit (16), 1x Dynabeads M270 Streptavidin (2ml) and 1x AMPure XP beads (10ml). Sufficient for 16 samples	500084
SureSeq NGS Library Preparation Complete Solution (48)	Bundle of 1x SureSeq NGS Library Preparation Kit (48), containing adaptors, PCR primers and enzymes, 1x SureSeq NGS Index Kit – Collection B, 3x SureSeq NGS Hyb & Wash Kit (16), 3x Dynabeads M270 Streptavidin (2ml) and 3x AMPure XP beads (10ml). Sufficient for 48 samples	500085

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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