CytoSure

A Sysmex Group Company

Cancer +SNP Arrays

Features

- Unique SNP probe technology allowing the use of any reference sample with no restriction digest
- Unparalleled performance through design optimisation
- Fast and easy analysis using CytoSure Interpret software
- Versatile array designs across a choice of formats

Flexible arrays for reliable analysis of CNV and LOH using a single assay

OGT's range of CytoSure® Cancer +SNP arrays combine long-oligo probes for superior copy number variant (CNV) detection alongside single nucleotide polymorphism (SNP) probes – which function using OGT proprietary technology – for accurate identification of loss-of-heterozygosity (LOH).

Unique SNP probe technology allowing the use of any reference sample with no restriction digest

Array comparative genomic hybridisation (aCGH) using 60-mer oligonucleotide probes has been shown to offer higher signal-to-noise ratios, increased sensitivity and increased specificity compared to other technologies[1].

With other platforms, the use of 60-mer technology for LOH analysis typically requires a restriction digest, which can compromise sample quality, limits the target SNPs to those overlapping restriction sites, and requires a genotyped reference for comparison. However, due to OGT's unique SNP technology (Figure 1), there is no restriction digest required, the most informative SNPs can be targeted and any reference sample can be used (e.g. normal tissue from the same individual to enable constitutional abnormalities to be filtered out).

Combined with the *in silico* and empirical optimisation carried out across all OGT catalogue arrays as well as easy customisation to include any additional regions of interest, OGT's Cancer +SNP arrays deliver flexible and robust analysis of CNV and LOH combined in a single assay.

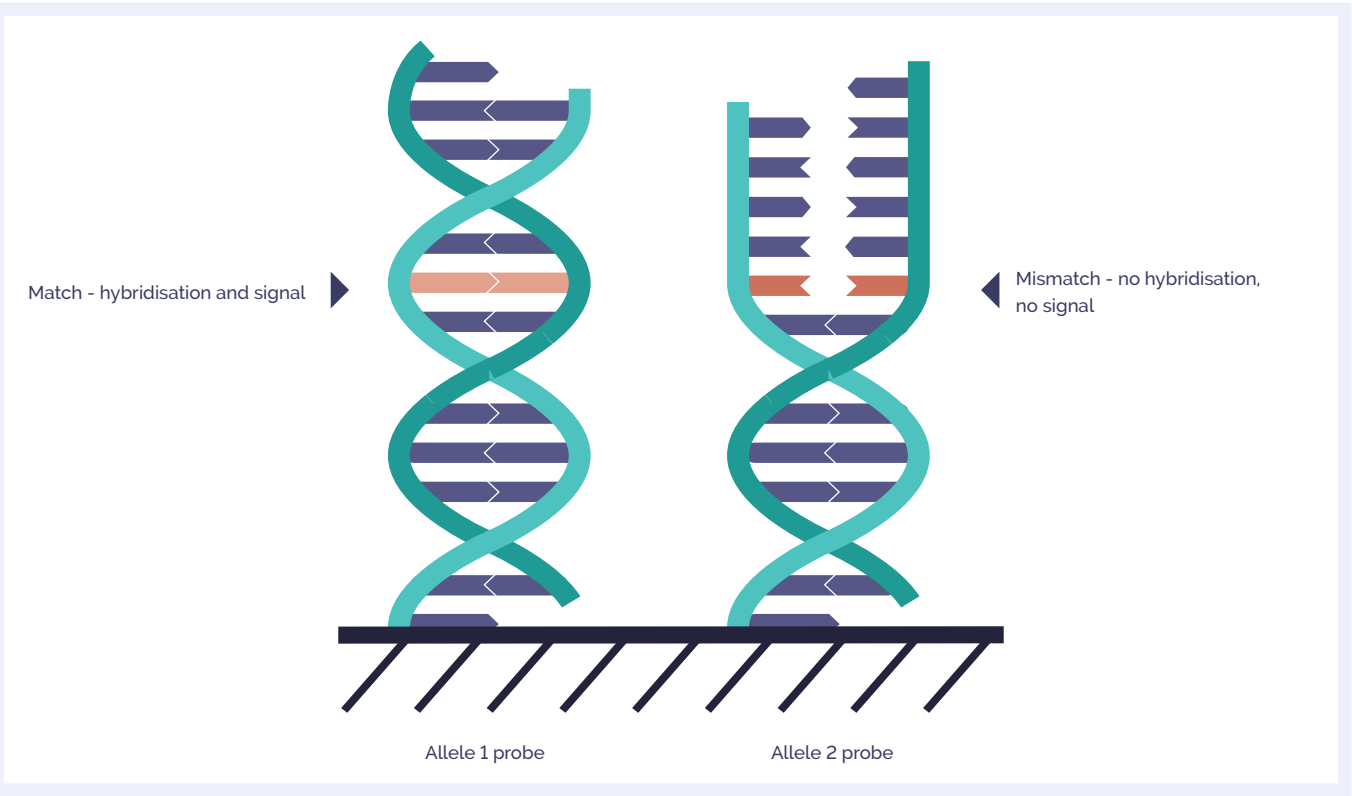


Figure 1. A schematic of the OGT SNP probe technology. Separate probes target both the reference (major) and non-reference (minor) allele. A fluorescent signal is only received from the probe if DNA fragments containing the respective alleles are present in the sample. By comparing fluorescence intensity between the two probes, the allelic status at each SNP position can be ascertained.

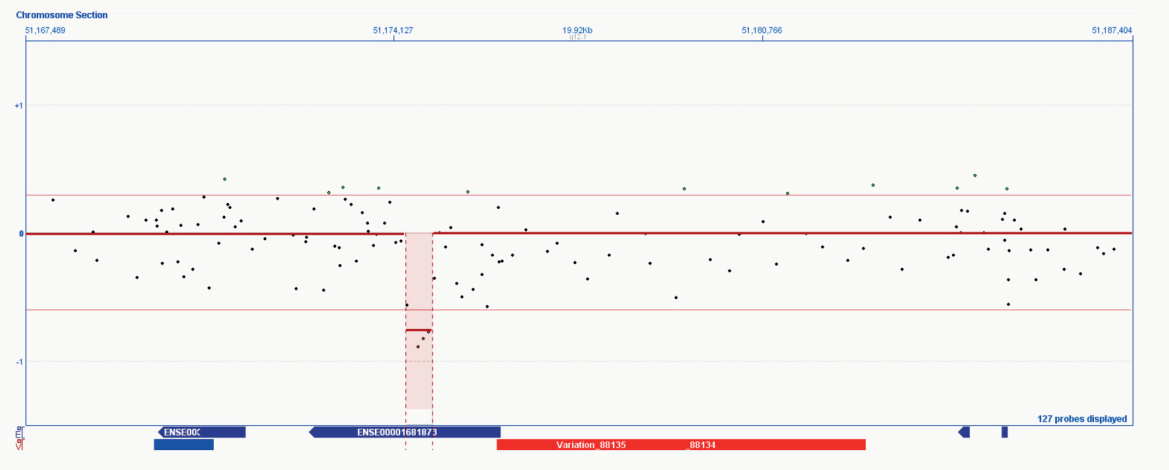
Unparalleled performance through design optimisation

The ability of a microarray to detect genetic aberrations accurately is highly dependent on achieving the best possible data quality. OGT leverage years of experience in microarray design to ensure excellent performance in all microarray products. A proprietary pipeline of perl scripts is used to design the best possible probes to target genomic regions of interest, followed by both *in silico* and empirical optimisation.

Customisation made simple

Additional targets relevant to your research can also easily be targeted by selecting probes from our Oligome™ database containing more than 26 million pre-optimised probes, including additional SNP probes to improve LOH resolution.

Unoptimised – wrong aberration size



Optimised – correct aberration size

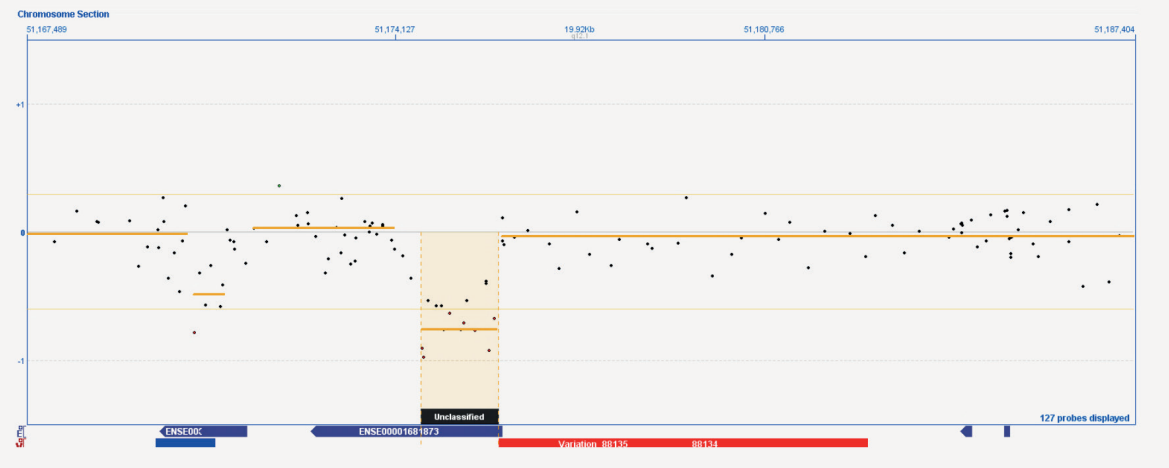


Figure 2. Screenshots from CytoSure Interpret, displaying results from an unoptimised and optimised array on the same sample with a confirmed ~1600 bp deletion. All CytoSure catalogue arrays go through stages of both in silico and empirical optimisation.

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Fast and easy analysis using CytoSure Interpret Software

OGT's CytoSure Interpret Software, which accompanies all CytoSure arrays, is a powerful and easy-to-use package for straightforward analysis of CNV and SNP data (Figure 3), delivering:

- Feature-rich, highly-customisable analysis workflows to meet any lab's requirements
- Automation of the data analysis processes, including batch upload of LIMS information to the database
- Extensive cancer-specific annotation tracks including regions from the Mitelman Database, the Cancer Gene Consensus Genes, the Atlas of Genetics and Cytogenetics in Oncology and Haematology and the Hurles Haploinsufficiency data[2]

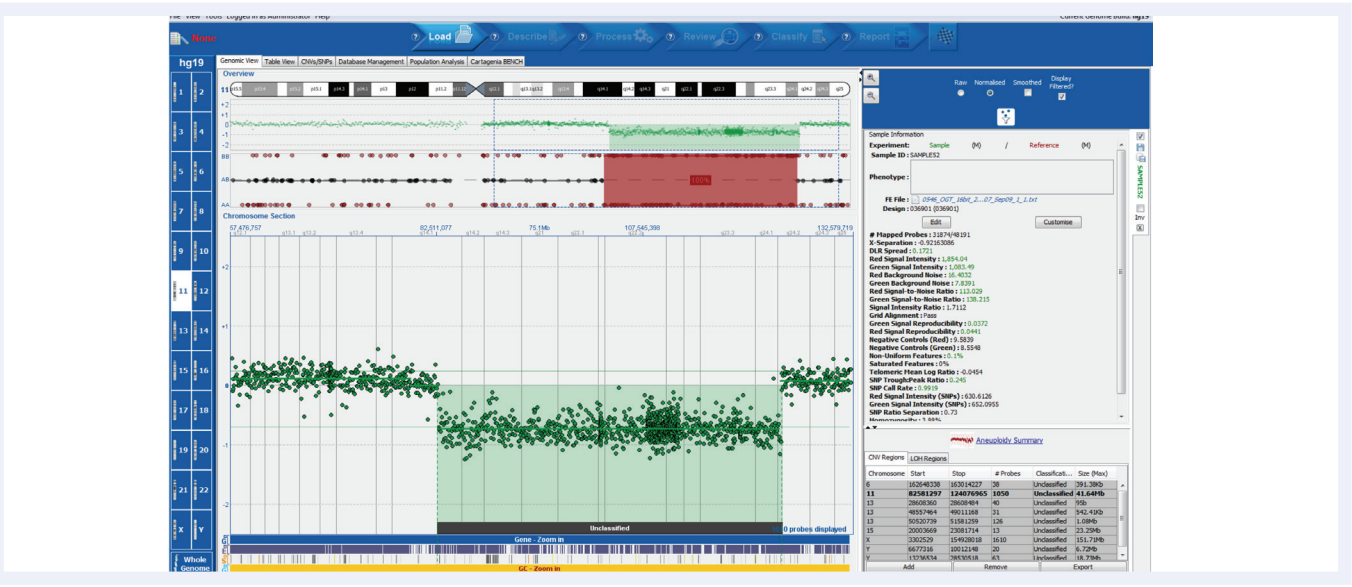

Figure 3: Shown here is a CLL research sample run on the CytoSure Consortium Cancer +SNP array (8x60k) with a deletion and corresponding LOH. CytoSure Interpret offers an intuitive user interface for easy interpretation of genetic findings. Samples kindly provided by Dr Jon Strefford, University of Southampton.

Versatile array designs across a choice of formats

Three fully customisable Cancer +SNP designs are available (Table 1), designed using different formats to suit any analysis and throughput requirement.

Array	Copy number resolution		LOH resolution
	Backbone	Average gene resolution (Hg19)	
CytoSure Haematological Cancer +SNP (8x60k)	1 probe every 117 kb	1 probe every 68 kb	30 Mb
CytoSure Cancer +SNP (4x180k)	1 probe every 44 kb	1 probe every 25 kb	20 Mb
CytoSure Consortium Cancer +SNP (4x180k)	1 probe every 36 kb	1 probe every 23 kb	10 Mb

Table 1. CytoSure Cancer +SNP arrays selection guide. For a complete list of genes covered by each array, email support@ogt.com.

CytoSure Haematological Cancer +SNP array (8x60k)

This design offers a balance between throughput and resolution, allowing investigation of large CNV and LOH in a cost-effective manner. This array delivers:

- Whole-genome coverage for CNV and LOH analysis
- Enhanced resolution across regions relevant for research into CLL, MM, MPN and MDS (Chronic Lymphocytic leukaemia, Multiple Myeloma, Myeloproliferative Neoplasms, Myelodyspastic Syndromes)

CytoSure Cancer +SNP array (4x180k)

This design, developed in collaboration with Dr Jacqueline Schoumans (Head of the Cancer Cytogenetic Unit at Lausanne University Hospital), focuses on CNV detection across the target regions and delivers:

- Whole-genome coverage for CNV and LOH analysis
- Whole-gene CNV resolution across more than 1500 cancer-associated genes
- Exon resolution across 18 genes (Table 2)

CDKN2A	*CDKN2B*	*CEBPA*	*EBF1*	*ETV6*	*FLT3*
IKZF1	*IK2F2*	*JAK2*	*KIT*	*MPL*	*NF1*
NRAS	*PAX5*	*RB1*	*RUNX1*	*TET2*	*WT1*

Table 2. Genes covered at single-exon resolution on the CytoSure Cancer +SNP array.

CytoSure Consortium Cancer +SNP array (4x180k)

This design focuses on the content recommended by the Cancer Cytogenetics Microarray Consortium (CCMC) now known as the Cancer Genomics Consortium (CGC), with more probes dedicated to SNP analysis than the other arrays. The recommended content is intended to help standardise research across cancer genomics, similar to the successful model introduced by ISCA/ICCG, now known as ClinGen. The array delivers:

- Whole-genome coverage for CNV and LOH analysis
- Enhanced coverage of 130 cancer-associated genomic regions
- Whole-gene CNV resolution of more than 500 cancer-associated genes

Ordering information

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Product	Contents	Cat. No.
Sure Haematological Cancer +SNP (8x60k)	Slide with eight arrays of 60,000 spots; CytoSure Interpret analysis software	020070
CytoSure Cancer +SNP (4x180k)	Slide with four arrays of 180,000 spots; CytoSure Interpret analysis software	700090
CytoSure Consortium Cancer +SNP (4x180k)	Slide with four arrays of 180,000 spots; CytoSure Interpret analysis software	020071
CytoSure Genomic DNA Labelling Kit	24 reactions: dyes, nucleotide mix, random primers, enzyme	020020
CytoSure HT Genomic DNA Labelling Kit	96 reactions: dyes, nucleotide mix, random primers, enzyme	500040
Clean-up Columns	24 columns for the clean-up of DNA	500020
Clean-up Plates	96-well plate for the clean-up of DNA	500041
CytoSure Interpret Software	Class-leading data analysis software provided with CytoSure arrays Complimentary with all array purchases	020022

References

1. Curtis, C. *et. al*, (2009) The pitfalls of platform comparison: DNA copy number array technologies assessed. BMC Genomics 10, 588-610
2. Hurles, M. *et. al*, (2010) Characterising and predicting haploinsufficiency in the human genome. PLoS Genetics 6, 10, e1001154 1-11.

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What binds us, makes us.

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