

*The Affymetrix
SNP Array 6.0:
A solution for
molecular
cytogenetics*

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The Affymetrix® Genome-Wide Human SNP Array 6.0 enables cytogenetic researchers to capture more chromosomal aberrations with a streamlined solution and rapid results. The solution—which includes the SNP Array 6.0, an optimized assay, and state-of-the-art software—is the proven microarray platform for cytogenetics labs.

With more than 1.8 million markers on a single array, including 900,000 individual SNPs, the SNP Array 6.0 enables you to detect uniparental disomies (UPDs) and see chromosomal aberrations at an unprecedented resolution.

Power your cytogenetics study with the most comprehensive solution currently available, and the technology that's revolutionizing the field of cytogenetics.

The solution includes:

- The high-density SNP Array 6.0, with 1.8 million markers evenly distributed across the whole genome
- A streamlined assay
- Intuitive and easy-to-use Affymetrix Genotyping Console™ Software for summarizing aberrations across the genome

Features & benefits:

- Whole-genome coverage, including subtelomeric regions and pericentromeres
- More than 900,000 SNP probes for unmatched performance in detecting UPD, loss of heterozygosity (LOH), and regions identical by descent
- Confident and accurate detection of small gains and losses
- Precise determination of breakpoints to unequivocally determine which genes are affected



Applying microarrays to cytogenetics

The Affymetrix® SNP Array 6.0 allows cytogenetic researchers to capture more chromosomal aberrations with high-density SNPs and high-resolution copy number coverage on a single array.

The process requires only two primary steps: preparing the DNA for the microarray using the cytogenetics copy number assay, and analyzing the data using Genotyping Console™ Software.

As little as 500 ng of genomic DNA is required, and a clearly marked, pictorial manual will take you through the three-day assay from purified DNA to array data. Genotyping Console Software then makes it easy to move from data to results. All detected copy number changes are summarized in a segment report and displayed visually in a familiar karyoview.

Genotyping Console Software's chromosome view provides a closer view of these aberrations, by aligning copy number and LOH with annotated genes, CNVs, FISH clones, and any customized tracks. Within this single view, you'll be able to determine which genes are affected by the aberration, whether or not this region overlaps known CNVs, and which FISH clones may be used for confirmation, if desired.

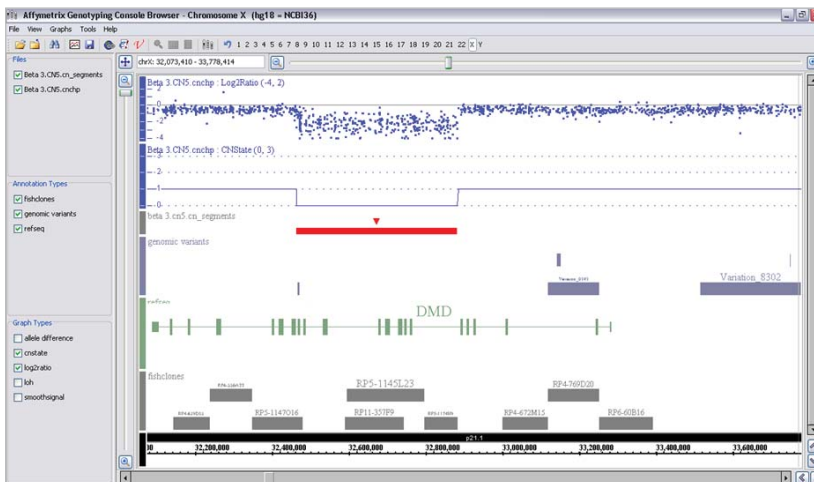


Illustration of a 419 kb deletion on Xp21.1 containing 372 markers.

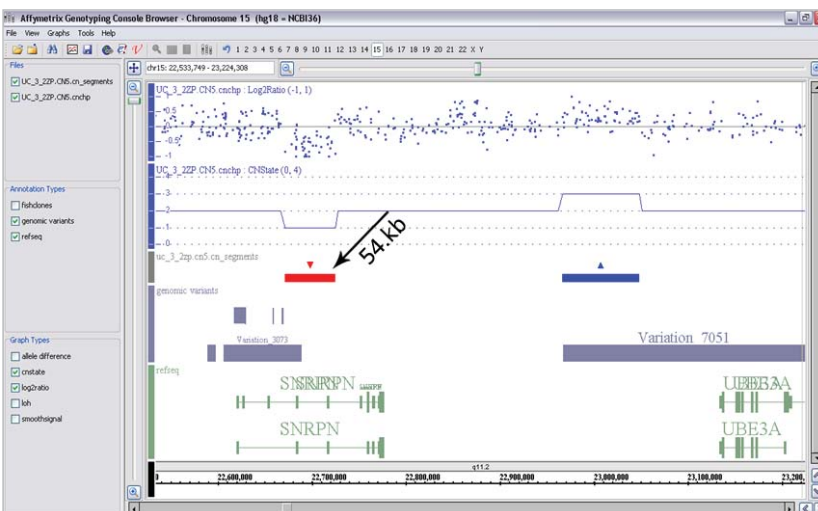


Illustration of a 54 kb deletion (on SNP Array 6.0) that was previously confirmed by FISH. This example shows the high resolution of the Affymetrix platform and the benefit of providing the segment and annotation tracks in the same view.

The SNP Array 6.0: Proven performance for cytogenetics studies

One array, multiple applications

The SNP Array 6.0 measures copy number, allele-specific copy number, and copy number-neutral LOH. The array contains more than 1.8 million markers evenly distributed across the entire genome, allowing the detection of small gains and losses. Of these probes, 906,600 target SNPs, and the remaining 945,826 target non-polymorphic sequences. Both types of probes are used to detect copy number changes, and the probes targeting SNPs are also used for measuring UPDs and consanguinity.

Copy number resolution

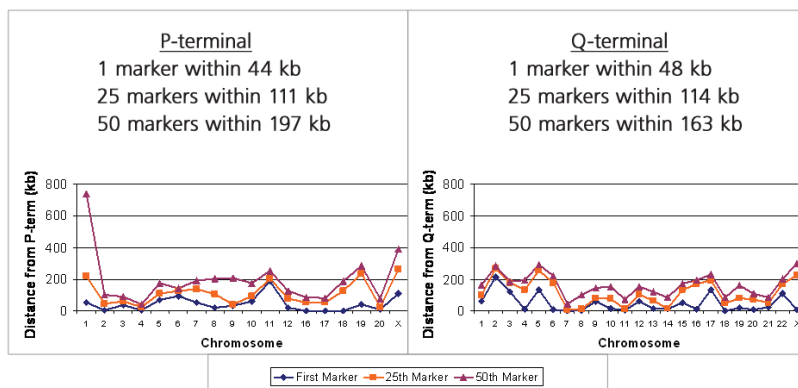
With an intermarker spacing of 696 base pairs, the SNP Array 6.0 offers the highest resolution of copy number changes. This array will enable you to detect even the smallest changes with confidence and fine-map the breakpoints of observed aberrations.

Copy number-neutral LOH

Copy number-neutral LOH can expose important recessive mutations and regions affected by imprinting. The SNP Array 6.0 measures sequence within the polymorphic regions to derive allelic information. Even if the copy number within a chromosomal region is normal, the sequences could still be severely abnormal. This can only be determined by also looking at the sequence, which the SNP Array 6.0 is uniquely able to measure. This information is then used to uncover UPDs.

Allele-specific copy number

Imprinting leads to the differential expression of genes. Depending on whether they were inherited maternally or paternally, allele-specific copy number can determine the parent of origin and indicate if the gain is associated with allelic loss or retention.



Subtelomeric coverage of SNP Array 6.0 markers across all chromosomes.

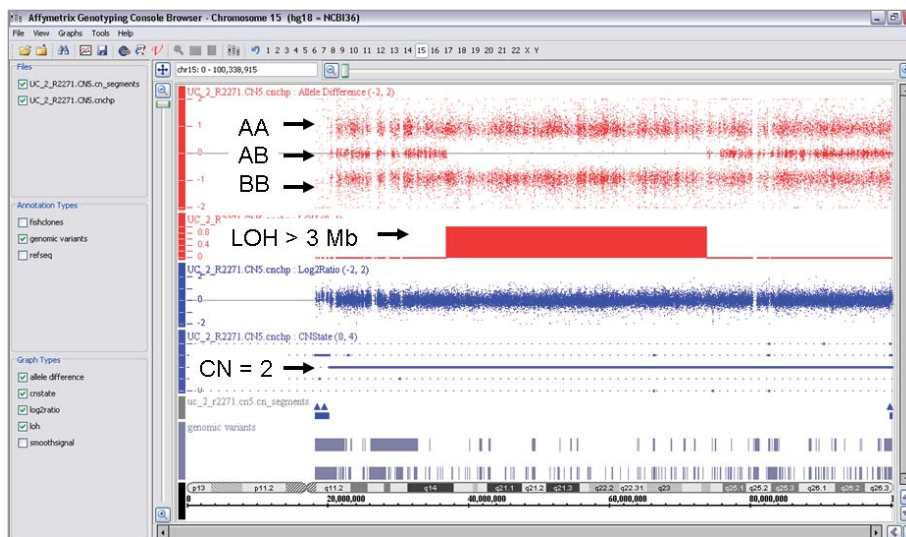
Two experiments in one

Affymetrix SNP arrays provide genotype and allow the detection of copy number-neutral LOH, which enables:

- Detection of UPD
- Paternity confirmation
- Parent-of-origin analysis (for UPD and deletions)
- Homozygosity mapping
- Determination of consanguinity

The following events cannot be detected when looking at copy number alone:

- 30 percent of Prader-Willi = mUPD of 15q
- 2-3 percent of Angelman syndrome = pUPD of 15q
- 10-30 percent of Beckwith-Wiedemann syndrome = pUPD of 11p15
- 5 percent of Silver-Russell syndrome = mUPD of chr7
- UPD of chromosome 14 is known to cause distinct disorders



This figure highlights the SNP Array 6.0's ability to measure structural changes (copy number) and sequence variations (UPD) across the entire genome. Regions of LOH greater than 3 Mb are summarized in the red block. The LOH region is copy number neutral, as illustrated by the blue data points of log₂ ratios and copy number state. This entire chromosome would be considered structurally normal, yet it is severely abnormal from a sequence perspective.

Ordering information

Part number	Description
Affymetrix® Genome-Wide Human SNP Array 6.0	
901182	Contains 2 arrays
901153	Contains 6 arrays
901150	Contains 30 arrays
Affymetrix® Genome-Wide Human SNP Nsp/Sty Assay Kit 5.0/6.0	
901013	Contains 30 arrays
User's Guide, Affymetrix® Cytogenetics Copy Number	
702607	

Please visit our web site, www.affymetrix.com, for additional ordering information.





Affymetrix, Inc. Tel: +1-888-362-2447 ■ Affymetrix UK Ltd. Tel: +44-(0)-1628-552550 ■ Affymetrix Japan K.K. Tel: +81-(0)3-5730-8200
Panomics Products Tel: +1-877-PANOMICS www.panomics.com ■ USB Products Tel: +1-800-321-9322 www.usb.affymetrix.com

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