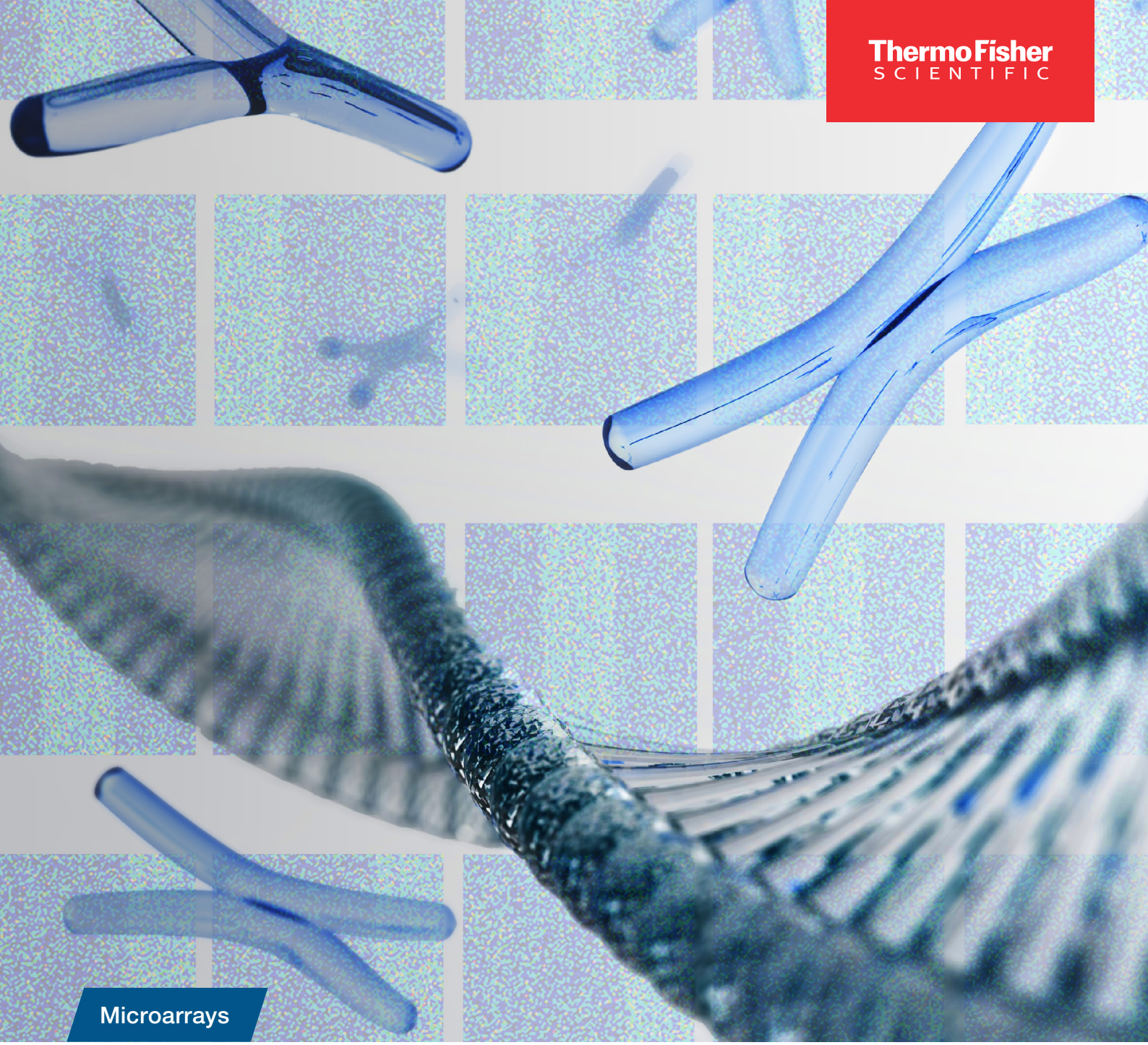
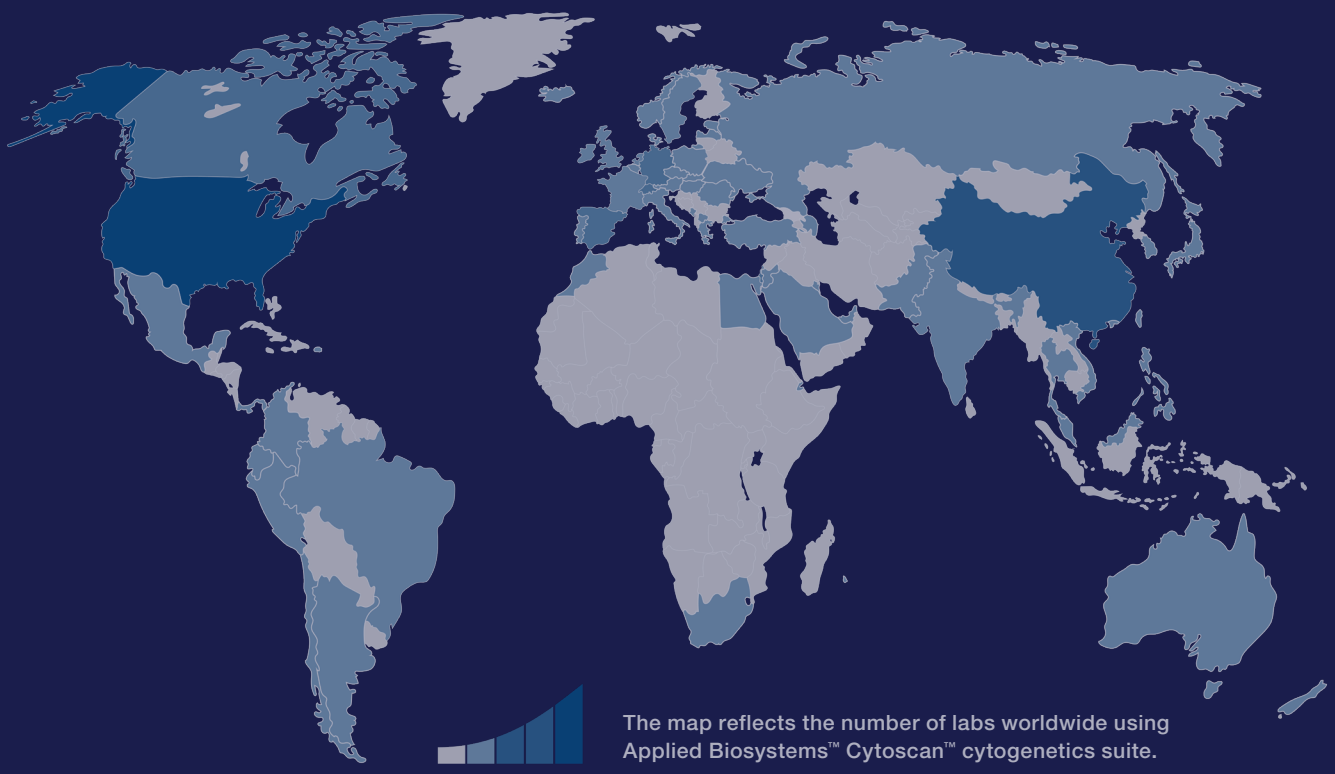


Microarrays

Powerfully efficient cytogenetics analysis

Whole-genome hybrid-SNP array research solutions

applied biosystems

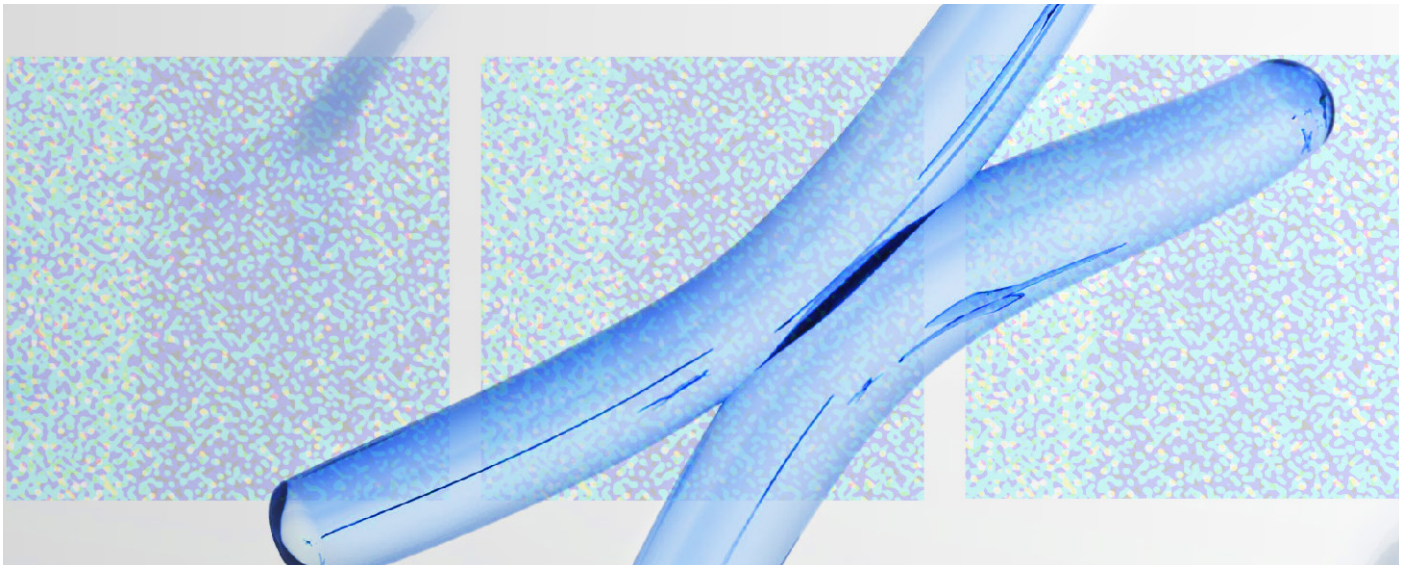


The map reflects the number of labs worldwide using Applied Biosystems™ Cytoscan™ cytogenetics suite.

Expansive whole-genome cytogenetics research

Advancements in cytogenetic technologies are providing clinical researchers with powerful new approaches to investigate chromosomal aberrations such as **copy number variations (CNVs), chromosomal imbalances, and allelic imbalances**. However, test methods such as karyotyping, optical genome mapping (OGM), whole-exome sequencing (WES), whole genome sequencing (WGS), and low-resolution arrays each have constraints in genomic coverage, content, or resolution that can lead to missed aberrations and delays or increased costs of chromosomal variant investigations. Microarrays that cover both **polymorphic and nonpolymorphic regions of the entire genome** can overcome some limitations of alternative cytogenetic analysis technologies by enabling assessment of DNA copy number alterations at a much higher resolution.

Contents



Genome-wide copy number analysis in one complete solution

Identify aneuploidies, microdeletions, microduplications, and other types of chromosomal aberrations across the genome quickly and easily to support your research efforts. The Applied Biosystems™ CytoScan™ and Applied Biosystems™ OncoScan™ arrays offer a **highly reliable, consistent, and sensitive** genome-wide approach for high-resolution DNA copy number analysis to detect gains and losses that may be indicative loss of heterozygosity (LOH), absence of heterozygosity (AOH), copy-neutral loss of heterozygosity (cnLOH), uniparental disomy, regions identical by descent, and mosaicism.

The complete microarray platform for cytogenetic analysis for research includes arrays, Applied Biosystems fully kitted reagents, instrumentation, and Chromosome Analysis Suite (ChAS).

Contact reproductive health research specialist

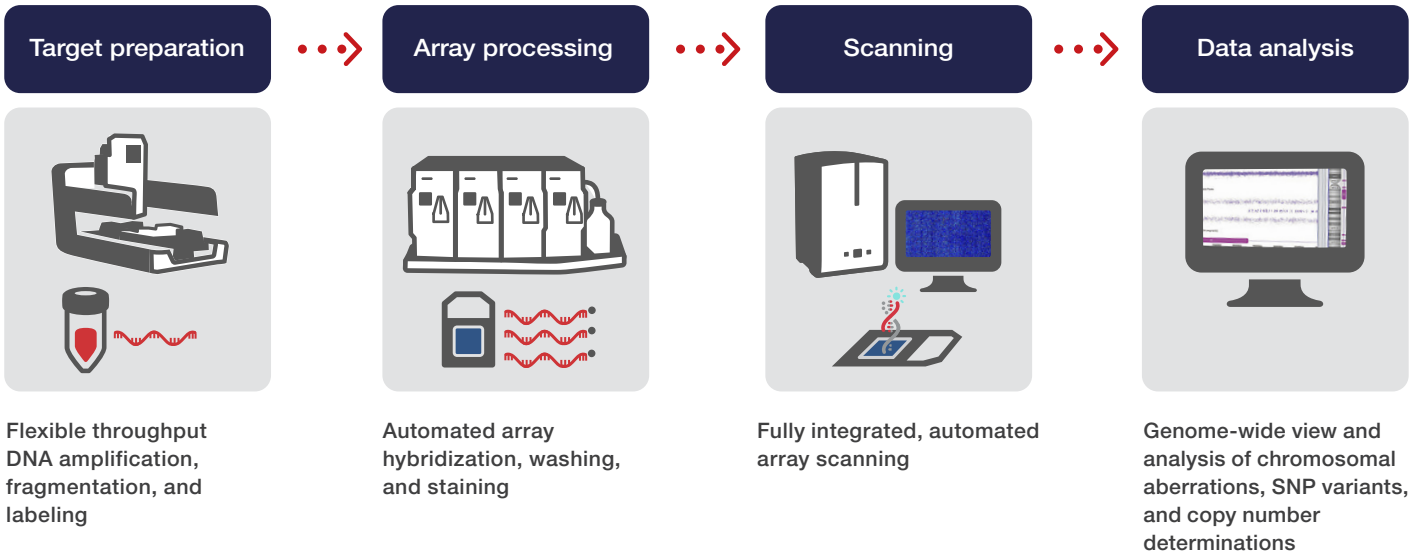


Figure 1. The robust workflow is aligned with your research laboratory workflow requirements, with processes that make it easy to obtain consistent and high-quality results.

All CytoScan arrays are hybrid-SNP chromosomal microarrays (CMAs) that contain large numbers of both SNP probes and non-polymorphic probes. Hybrid-SNP arrays, with more than 99% genotype accuracy, boost confidence in breakpoint determination and enable independent confirmation of copy number events throughout the entire genome.

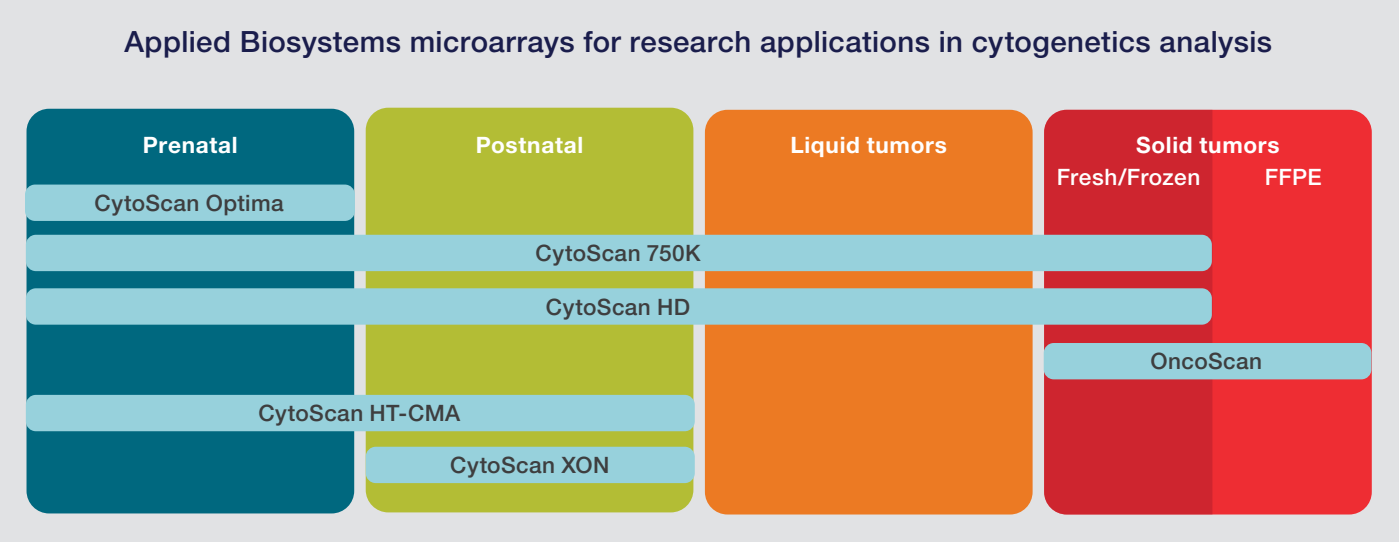


Figure 2. Applied BioSystems microarrays enable a wide range of cytogenetics research application areas.

Hybrid-SNP arrays can detect these types of genetic conditions1 for research applications:

- Suspected uniparental disomy (UPD), whole genome UPD, cnLOH, or AOH
- Mosaicism
- Zygosity
- Consanguinity
- Parent of origin (requires parental genomic analysis)
- Twin-twin or maternal cell contamination
- Allele-specific changes
- Sample heterogeneity, clonal diversity
- Genomic contamination

SNP analyses are also used for:

- Breakpoint determination
- Mendelian consistency checking
- Confirmation of CNV events

Download whitepapers: Learn how high-resolution SNP arrays detect inherited chromosomal anomalies

Cytogenetic applications

With advances in human genetic analysis technologies, various types of causative genetic aberrations associated with disorders can be detected thus helping provide valuable insights into chromosomal abnormalities in constitutional and oncological samples.

- **Prenatal** genetic testing helps clinical researchers study congenital anomalies or genetic disorders in the fetus.
- **Postnatal** genetic testing helps clinical researchers study congenital anomalies, diseases, and developmental delays in cases following birth.
- **Product of Conception (POC)** genetic testing of fetal tissue after the loss of a pregnancy helps clinical researchers study if the miscarriage was caused by a chromosomal anomaly.
- **Oncological** genetic testing of tumor samples helps clinical researchers study chromosomal aberrations to guide investigations of potential cancer treatments.

Tailored cytogenetic analysis with chromosomal microarrays

Constitutional applications

Select a CytoScan hybrid-SNP array that is tailored to your application and detection sensitivity requirements. CytoScan assays feature Applied Biosystems™ GeneChip® cartridge microarrays designed specifically for prenatal and postnatal research applications.

CytoScan arrays are manufactured using photolithography technology, which produces arrays with **very high batch-to-batch reproducibility without probe dropouts** that are inherent in some other array manufacturing techniques.

- Chromosomal microarray (CMA) is the recommended first line test by ACMG guidelines and is used by the cytogenetics community worldwide[2,3].
- Detect chromosomal aberrations at high resolution with a genome-wide gene-centric design containing high density SNP and CNV probes.
- Analyze your data with the powerful and intuitive ChAS software with enhanced analysis features, included free-of-charge.
- Maximize operational time with the assistance of our world class support team and dedicated specialists.

Hybrid-SNP array: A practical approach to complex problems in era of NGS

Dr. Catherine Rehder, Director
Clinical Cytogenetics Laboratory, Duke University

Determining the genetic cause of disease by application of single exon array as a complement to exome sequencing
Dr. Benjamin Hilton, Assistant Director
Cytogenetics Laboratory, Greenwood Genetic Center

Challenging microarray cases and the approaches for analysis of unusual findings

Dr. Stuart Schwartz, Strategic Director, Cytogenetics
Women's Health and Genetics, Labcorp

Learn more about how hybrid-SNP arrays are facilitating resolution to unsolved clinical research questions in prenatal and postnatal testing.

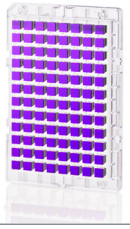
Watch the webinars

Scientific Spotlight: Learn why GeneDx, a leader in testing for rare genetic disorders, switched to high-resolution whole-genome chromosomal microarrays (CMAs) for prenatal and postnatal research applications.

"The hybrid SNP microarray requires **less DNA**. This is especially good for **buccal** and **uncultured prenatal samples**. We have been able to **reduce the amount of sample necessary by 40%**. We see fewer inconclusive results and fewer repeats compared to our prior platform. This **saves GeneDx time, money**, and **resources**."

– Dr. Jeanne Meck,
Director, Cytogenetics and Prenatal Diagnostic Services, GeneDx

Table 1. CytoScan Suite specifications

	CytoScan HD	CytoScan 750K	CytoScan Optima	CytoScan HT-CMA	CytoScan XON
Research applications					
	The benchmark in cytogenetics research with highest genome-wide resolution of CNVs for applications in prenatal and postnatal research	High genome-wide resolution for the analysis of copy number gains and losses for prenatal and postnatal research	A low-cost genome-wide platform for detection of aneuploidies and copy number losses and gains at lower resolution, optimized for constitutional cytogenetics research	A solution for high-throughput, cost-effective genome-wide copy number analysis for constitutional cytogenetics research applications, as well as testing of relevant SNP variants	Sensitive single exon-level copy number analysis with outstanding coverage within exons across the whole genome. Use as a stand-alone research tool or to confirm CNV findings with alternative technologies like next generation sequencing
Sample types	Blood, buccal swabs, saliva, uncultured or cultured cells, chorionic villi, amniocytes, and POC	Blood, buccal swabs, saliva, uncultured or cultured cells, chorionic villi, amniocytes, and POC	Amniocytes, chorionic villi, POC, blood, uncultured or cultured cells	Blood, buccal swabs, saliva, uncultured or cultured cells, chorionic villi, amniocytes, and POC	Blood. Other sources of DNA can be used upon building a customized reference file
Size of aberration* (analytical claims)	Losses: 25 kb Gains: 50 kb LOH/AOH: 3 Mb Mosaicism: >15% (approximately)	Losses: 100 kb Gains: 400 kb LOH/AOH: 5 Mb Mosaicism: >15%–20% (approximately)	Losses: 1 Mb Gains: 2 Mb AOH: > 5 Mb Mosaicism: >20% (approximately) 400 genes at 100 kb resolution	Gains/losses (except for OMIM genes): 400 kb Gains/losses (OMIM genes): 100 kb LOH/AOH: 3 Mb Mosaicism: >15%–20%	95% sensitivity for the detection of exon-level CNVs Designed to cover the whole genome, with increased coverage in 7,000 clinically relevant genes
Input DNA	10–250 ng**	10–250 ng**	10–250 ng**	100 ng	100 ng
Probe structure	2.67 million markers for whole genome coverage 1.95 million nonpolymorphic markers ~743,000 SNP probes for LOH/AOH analysis, duo-trio assessment, and sample tracking	750,000 markers for whole genome coverage 550,000 nonpolymorphic markers ~200,000 SNP probes for LOH analysis, duo-trio assessment, and sample tracking	Whole genome coverage 315,000 features covering control, CNV and SNP probes ~148,000 SNP probes for LOH analysis, duo-trio assessment, and sample tracking	750,000 markers for whole genome coverage 550,000 nonpolymorphic markers ~200,000 SNP probes for LOH analysis, duo-trio assessment, and sample tracking. SNP probes for 178 variants across 36 genes such as *SMN1* and *SMN2*	6.85 million empirically selected probes for whole-genome coverage including: 6.5 million copy number probes 300,000 SNP probes for LOH analysis, duo-trio assessment, and sample tracking
Protocol	3–4 days	3–4 days	As little as 2.5 days	4 days	4 days
Click on each icon to download datasheets					

*Size of aberration—The size of the segment call depends on the average marker spacing in the region. Best performance can be achieved in regions with higher marker coverage. Mosaicism detection may depend on the size of the altered segment and the type of aberration involved.

**250 ng is optimal but users have reported success using as little as 10 ng starting DNA.

Oncology applications

Microarray analysis is a powerful genomic tool that can provide critical genome-wide information to help guide investigation of potential future cancer treatments. Unlike constitutional applications of microarray analysis, which are performed on whole blood samples, microarray analysis of solid tumors is challenging because tumor tissues are typically formalin fixed and paraffin embedded (FFPE).

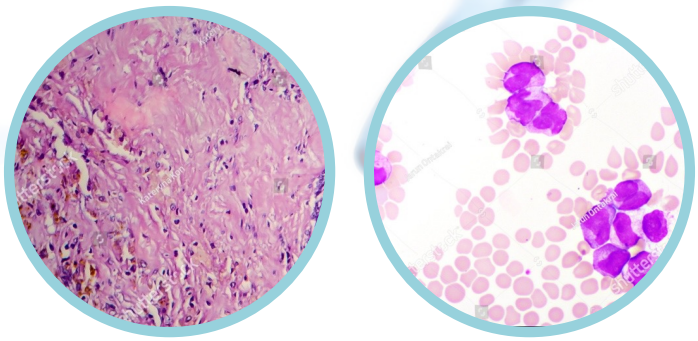


Figure 3. Solid tumors refer to a solid mass of cancer cells that grow in organ systems and can occur anywhere in the body, for example breast cancer **(left)**. Liquid tumors occur in the blood, bone marrow or lymph nodes and include types of leukemia, lymphoma and myeloma **(right)**.

"CytoScan HD array analysis allows detection of copy number variations and regions of copy-neutral loss of heterozygosity across the genome during clinical research work-up of hematologic neoplasms."

– Madina Sukhanova, PhD, FACMG, Assistant Professor of Pathology, Northwestern University, Feinberg School of Medicine

CytoScan HD Suite for hematologic malignancies research

Capture chromosomal abnormalities and genomic instability, which are some of the most important aberrations in tumors. The CytoScan HD Suite assay is designed with 2.67 million markers for copy number analysis, facilitating comprehensive coverage at the exceptional resolution so you do not miss important aberrations.

OncoScan assays for solid tumors research

Detect deletions, duplications, LOH, cnLOH, breakpoint determination, ploidy, mosaicism, and unbalanced translocations with Applied Biosystems™ OncoScan™ CNV assay and Applied Biosystems™ OncoScan™ CNV Plus Assay (previously known as Applied Biosystems™ OncoScan™ FFPE Assay). OncoScan assays are whole-genome copy number assays designed to detect structural variants that are not well characterized by short-read sequencing or targeted sequencing.

Key features

- **Exceptional flexibility**—detect chromosomal arm aberrations, gains, losses, focal changes, LOH, and cnLOH in a single assay, helping to reduce costs and processing times
- **Comprehensive coverage**—whole-genome analysis of genes with established significance in cancer and tumor progression as well as those with emerging evidence
- **Robust performance**—obtain consistent results from lot to lot and operator to operator
- **Broad somatic mutation panel**—covering 64 mutations in 9 genes (*BRAF, EGFR, IDH1*, *IDH2, KRAS, NRAS, PIK3CA, PTEN,* and *TP53*)
- **Low sample input and fast results**—get results in 72 hours from only 80 ng of FFPE-derived DNA
- **Rapid analysis**—included software provides intuitive data visualization for hundreds of samples in minutes
- **OncoScan CNV Plus Assay offers a high-resolution copy number detection in priority cancer genes**—accurate identification of very small (50–125 kb) to large (Mb) CNVs

Learn how Dr. Madina Sukhanova used CMA combined with NGS assays to identify and research genetic aberrations associated with specific prognoses in different types of cancer.

Watch the webinar

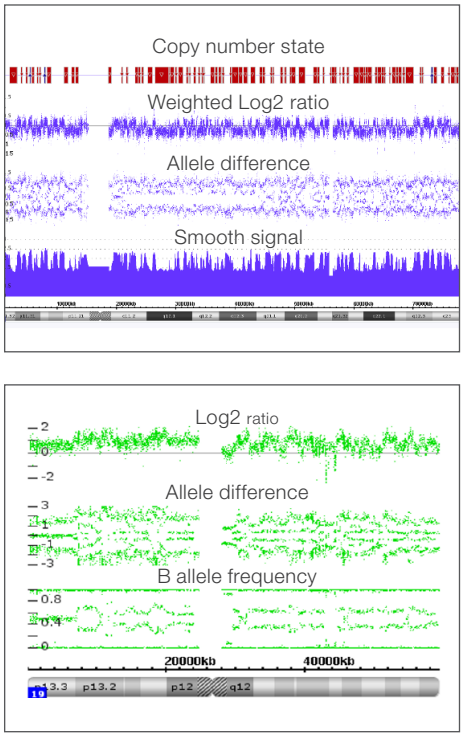


Figure 4. Chromothripsis detected on chromosome 18 using CytoScan HD (top) and on chromosome 19 using OncoScan (bottom), revealed by the sequential copy number changes and the multiple breakpoints seen in the different tracks.

Table 2. Suite specification for oncological clinical research sample profiling solutions

	CytoScan HD Suite	OncoScan CNV Assay OncoScan CNV Plus Assay*
Research application	High resolution analysis of genome wide CNVs in liquid and solid tumors	High resolution analysis, up to 50 kb in top cancer genes and 300 kb across whole genome in FFPE and fresh frozen tissues
Sample types	Blood, bone marrow, and fresh and frozen tissue	FFPE, fresh and frozen tissue
Size of aberration (analytical claims)**	Gains: 50 kb Losses: 25 kb LOH/AOH: 3 Mb Mosaicism (% aberrant cells): approximately >15%†	Gains: 50 kb Losses: 50 kb LOH/AOH: 10 Mb Mosaicism (% aberrant cells): 15%†
Input DNA	10-250 ng‡	80 ng
Probe structure	2.67 million markers for whole genome coverage 1.95 million nonpolymorphic markers ~743,000 SNP probes for LOH/AOH analysis, and sample tracking	220,000 molecular inversion probes (MIPs), whole genome coverage 5,700 non-polymorphic probes 216,000 SNP probes
Protocol	3–4 days	2–3 days
Click on each icon to download product literature		

*OncoScan CNV Plus Assay includes somatic mutation panel covering 64 mutations in 9 genes (*BRAF, EGFR, IDH1 and 2, KRAS, NRAS, PIK3CA, PTEN*, and *TP53*)

**Size of aberration—The size of the segment call depends on the average marker spacing in the region. Best performance can be achieved in regions with higher marker coverage. Mosaicism detection may depend on the size of the altered segment and the type of aberration involved.

†Mosaicism in cancer is classified by % aberrant cells in the sample and is called in ChAS software.

‡250 ng is optimal but users have reported success using as little as 10 ng starting DNA.

Fully integrated, high-throughput array processing

The Applied Biosystems™ GeneChip™ System 3000 is a fully integrated platform for conducting your research using CytoScan or OncoScan arrays.

The GeneChip System 3000 combines advanced design and automation to deliver high resolution scanning with minimized hands-on time. This comprehensive system includes the Applied Biosystems™ GeneChip™ Scanner 3000 7G, Applied Biosystems™ GeneChip™ Fluidics Station 450, Applied Biosystems™ GeneChip™ Hybridization Oven 645, and a powerful computer workstation installed with instrument control software.

When used with the optional Applied Biosystems™ GeneChip™ AutoLoader Carousel, the system helps provide complete walk-away freedom for scanning your arrays. The GeneChip Scanner 3000 7G uses a solid-state laser so it needs no external laser power supply or special cooling system and fits easily into a laboratory benchtop. Accurate gridding improves data integrity. Highly consistent scanner-to-scanner performance facilitates data sharing among collaborators.

Highlights

- **Higher-resolution scanning** from 0.51 to 2.5 µm pixels automatically selected by array type
- **Optimal image uniformity and collection efficiency** across the entire scan area with proprietary Applied Biosystems™ Flying Objective™ Lens technology
- **Compatible with the AutoLoader Carousel** for complete walk-away scanning of up to 48 arrays at a time
- **Cost-effective** approach enabling multiple assays on a single flexible instrument
- **Compact size** for better space utilization
- **No laser drift** and reduced scanner-to-scanner variability
- **Automatic adjustments** of residual arc correction and x-linearity

Chromosome Analysis Suite (ChAS) software supports analysis for challenging genes

View and summarize chromosomal aberrations across the genome, including copy number gain or loss, LOH, and mosaicism. Developed with input from leading experts, **ChAS is designed specifically for copy number and cytogenetics research analysis and reporting**. We work with our customers, listen to their valuable feedback, and continually empower them with enhanced features to make data analysis for their research simpler and more intuitive.

Key features

- Analyze copy number, mosaicism, and LOH segment data at different levels of resolution
- Automatically prioritize segment data using ACMG-inspired scoring
- Customize and load your own annotations and regions for focused analysis
- Store, query, and display historic sample data and annotations for streamlined analysis
- Directly access NCBI, UCSC Genome Browser, DECIPHER, ClinVar, ClinGen, Ensembl, and OMIM databases and others
- Export user-selected data in formats like browser extensible data (BED), Applied Biosystems™ Affymetrix™ extensible data (AED), and variant call format (VCF) files
- APIs to push and pull segment coordinates in and out of ChAS software
- Automatic results file generation with zero manual set-up required
- Export data in ClinVar format for easy uploading into ClinVar
- Annotation track to complete the OMIM morbidity map

View ChAS training modules

Request a ChAS demo

Maximize your CytoScan expertise, minimize your start-up time

Our commitment to your success in cytogenetics research goes beyond tools and technologies. Leverage our comprehensive onboarding service and support offerings for the CytoScan Suite solution to maximize your expertise and minimize the time needed to ramp up your cytogenetics research investigations. The team of experienced professionals at Thermo Fisher Scientific, including technical sales specialists, field service engineers, field application scientists, and clinical application consultants, will support you with **comprehensive support from initial planning to routine implementation**.

Contact a reproductive health research specialist

Ordering information

Product	Description	Cat. No
CytoScan HD		
CytoScan HD Kit Plus 24	Arrays and reagents sufficient for 24 reactions and CytoScan Amplification Kit sufficient for 96 reactions	905824
CytoScan HD Kit Plus 96	Arrays and reagents sufficient for 96 reactions and CytoScan Amplification Kit sufficient for 96 reactions	905896
CytoScan HD Array Kit and Reagent Kit Bundle	Arrays and reagent sufficient for 24 reactions plus training materials	901835
CytoScan HD Training Kit	Arrays and reagent sufficient for 24 reactions plus training materials	901834
CytoScan 750K		
CytoScan 750K Kit Plus 24	Arrays and reagents sufficient for 24 reactions and CytoScan Amplification Kit sufficient for 96 reactions	905924
CytoScan 750K Kit Plus 96	Arrays and reagents sufficient for 96 reactions and CytoScan Amplification Kit sufficient for 96 reactions	905996
CytoScan 750K Array and Reagent Kit Bundle	Arrays and reagent sufficient for 24 reactions	901859
CytoScan 750K Training Kit	Arrays and reagent sufficient for 24 reactions plus training materials	901860
CytoScan Optima		
CytoScan Optima Kit	Arrays and reagent sufficient for 24 reactions	902533
CytoScan Optima Training Kit	Arrays and reagent sufficient for 24 reactions plus training materials	902534
CytoScan HT-CMA		
CytoScan HT-CMA 96F Assay Kit	Arrays and reagent sufficient for 96 reactions	906025
CytoScan HT-CMA 96F Assay Training Kit	Arrays and reagent sufficient for 96 reactions plus training materials	906027
CytoScan XON		
CytoScan XON Assay Kit	Arrays and reagent sufficient for 24 reactions	931311
CytoScan XON Assay Training Kit	Arrays and reagent sufficient for 24 reactions plus training materials	931312
OncoScan		
OncoScan CNV Plus Assay	Arrays and reagent sufficient for 24 reactions	902293
OncoScan CNV Plus Training Kit	Arrays and reagent sufficient for 18 reactions plus training materials	902305
OncoScan CNV Assay	Arrays and reagent sufficient for 24 reactions	902695
OncoScan CNV Training Kit	Arrays and reagent sufficient for 18 reactions plus training materials	902693

Ordering information (continued)

Product	Description	Cat. No
Support products		
Chromosome Analysis Suite (ChAS)	Available as a free download from thermofisher.com/chas	NA
Reproductive Health Research Analysis Suite (RHAS)	Available as a free download from thermofisher.com/chas	NA
GeneChip Scanner 3000 System with Workstation and AutoLoader	Includes: GeneChip Scanner 3000 7G with AutoLoader and Electronic Barcode Reader GeneChip Fluidics Station 450 GeneChip Hybridization Oven 645 Computer workstation with Instrument Control Software and monitor	00-0218
GeneChip Scanner AutoLoader with Electronic Barcode Reader	Can be ordered separately	00-0129
GeneChip Scanner 3000 7G	Can be ordered separately	00-0210
GeneChip Fluidics Station 450	Can be ordered separately	00-0079
GeneChip Hybridization Oven 645	Can be ordered separately	00-0331
Computer Workstation with Instrument Control Software	Can be ordered separately	90-0740
GeneTitan MC Instrument	Automated array-processing instrument required to hybridize, wash, stain, and scan arrays	00-0373
NIMBUS Target Preparation Instrument	Robotics workstation and laptop	00-401
NIMBUS™ CytoScan™ Training Kit	Sample preparation reagents to be used with robotics workstation	902169

References

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2. Manning M, Hudgins L; American College of Medical Genetics and Genomics (ACMG) Professional Practice and Guidelines Committee. Addendum: Array-based technology and recommendations for utilization in medical genetics practice for detection of chromosomal abnormalities. Genet Med. 2020 Dec;22(12):2126. doi: 10.1038/s41436-020-0848-8. Epub 2020 Jun 8. Erratum for: *Genet Med.* 2010 Nov;12(11):742-5. PMID: 32514088.
3. Shao L, Akkari Y, Cooley LD, Miller DT, Seifert BA, Wolff DJ, Mikhail FM; ACMG Laboratory Quality Assurance Committee. Chromosomal microarray analysis, including constitutional and neoplastic disease applications, 2021 revision: a technical standard of the American College of Medical Genetics and Genomics (ACMG). *Genet Med.* 2021 Oct;23(10):1818-1829. doi: 10.1038/s41436-021-01214-w. Epub 2021 Jun 15. PMID: 34131312.

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