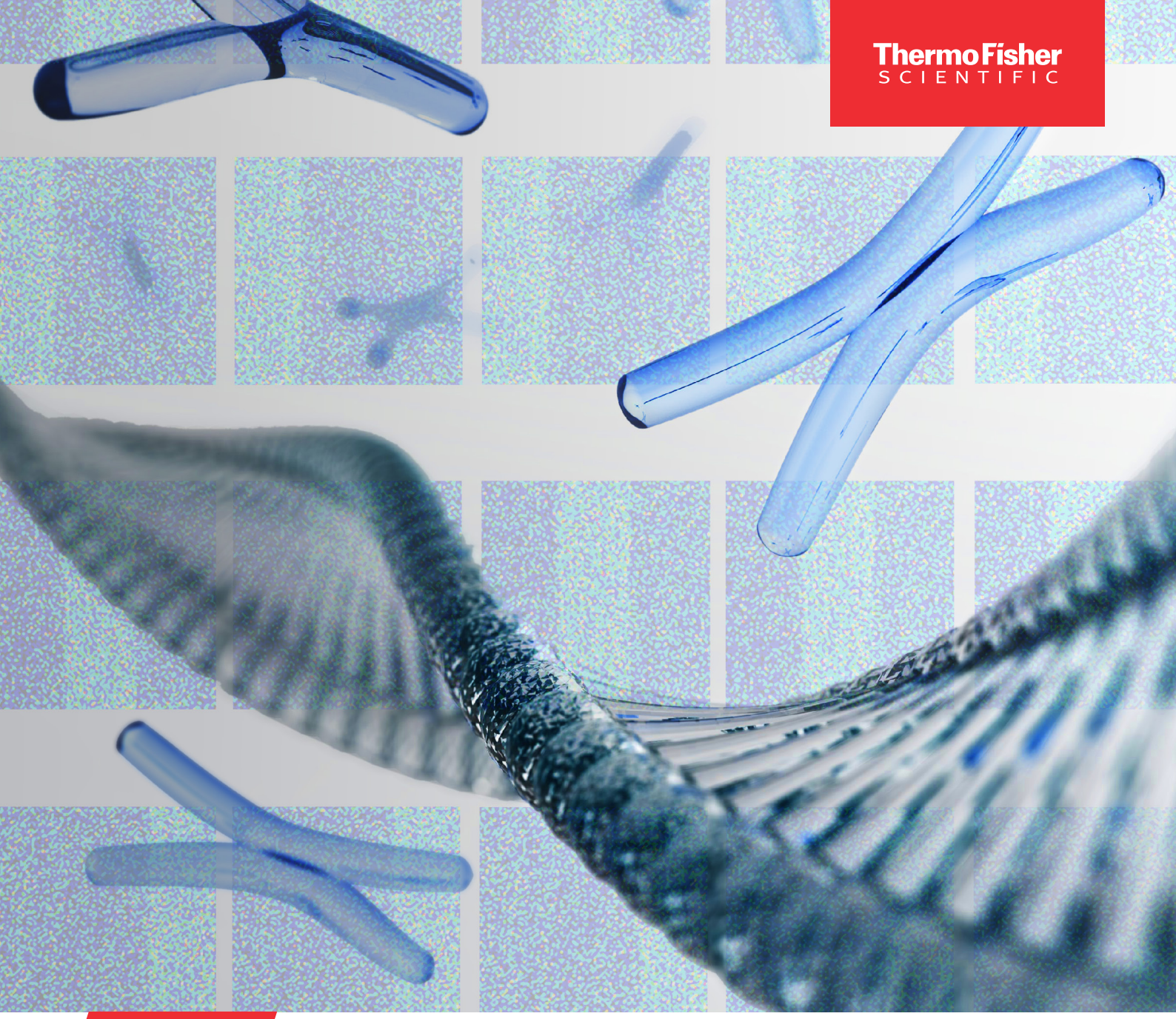
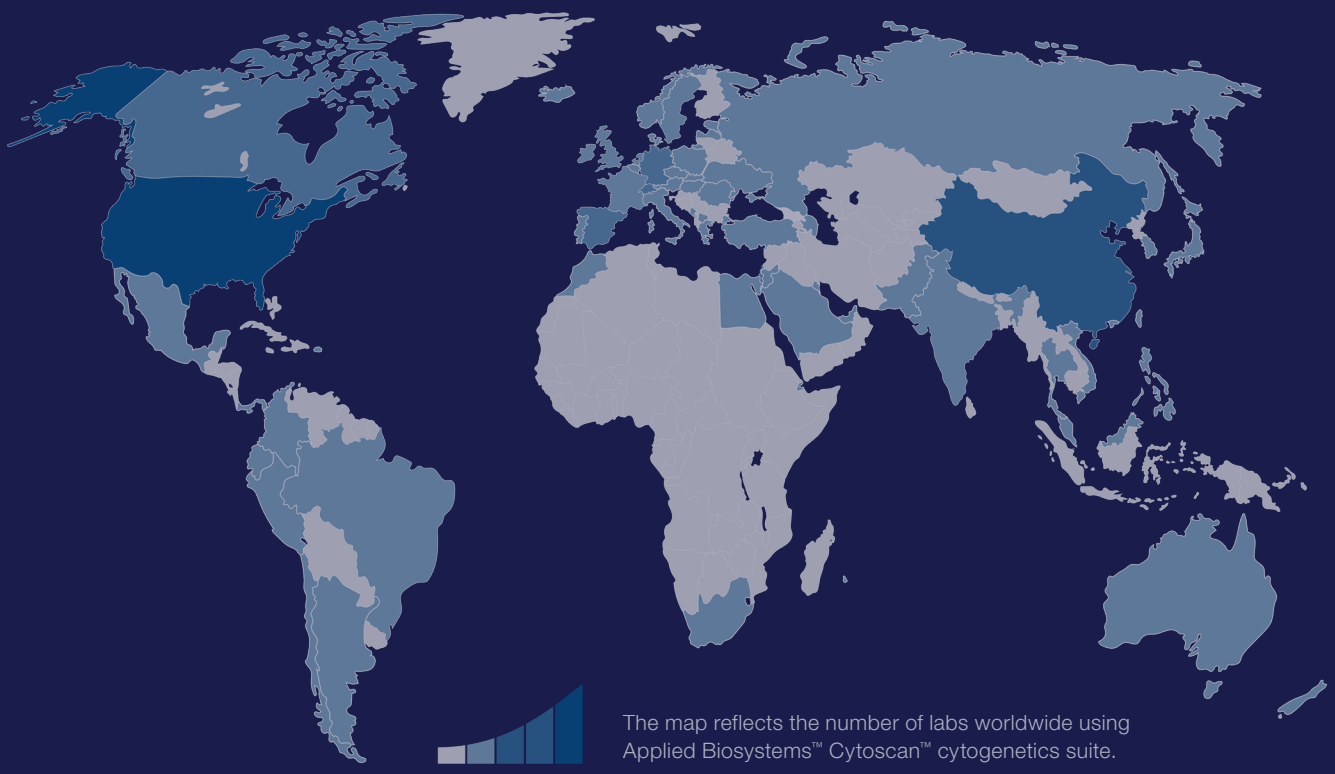


Microarrays

Powerfully efficient cytogenetics analysis

Whole-genome hybrid-SNP array research solutions

applied biosystems

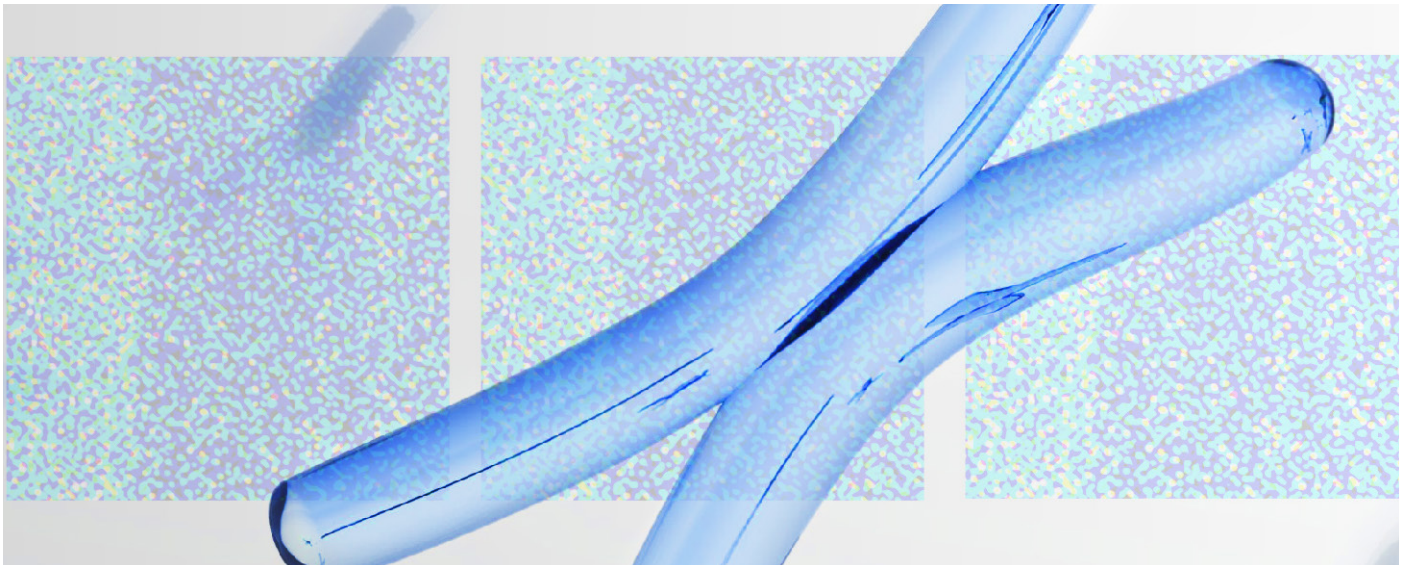


The map reflects the number of labs worldwide using Applied Biosystems™ Cytoscan™ cytogenetics suite.

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 that can lead to missed aberrations and delays or increased costs. Microarrays that include the latest available content for both **polymorphic and nonpolymorphic regions of the entire genome** with fast assays and artificial-intelligence (AI)-enabled variant identification can overcome some of these limitations and potentially boost discovery yield.

Contents



Boost efficiency and productivity in one complete solution

Complete chromosomal microarray (CMA) solution for genome-wide copy number analysis

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

The complete CMA platform for cytogenetic analysis for research includes arrays, fully kitted reagents, instrumentation, Applied Biosystems™ Chromosome Analysis Suite (ChAS) software, and Applied Biosystems™ CytoScan Automated Interpretation and Reporting (AIR) solution.

Contact a Chromosome Microarray specialist

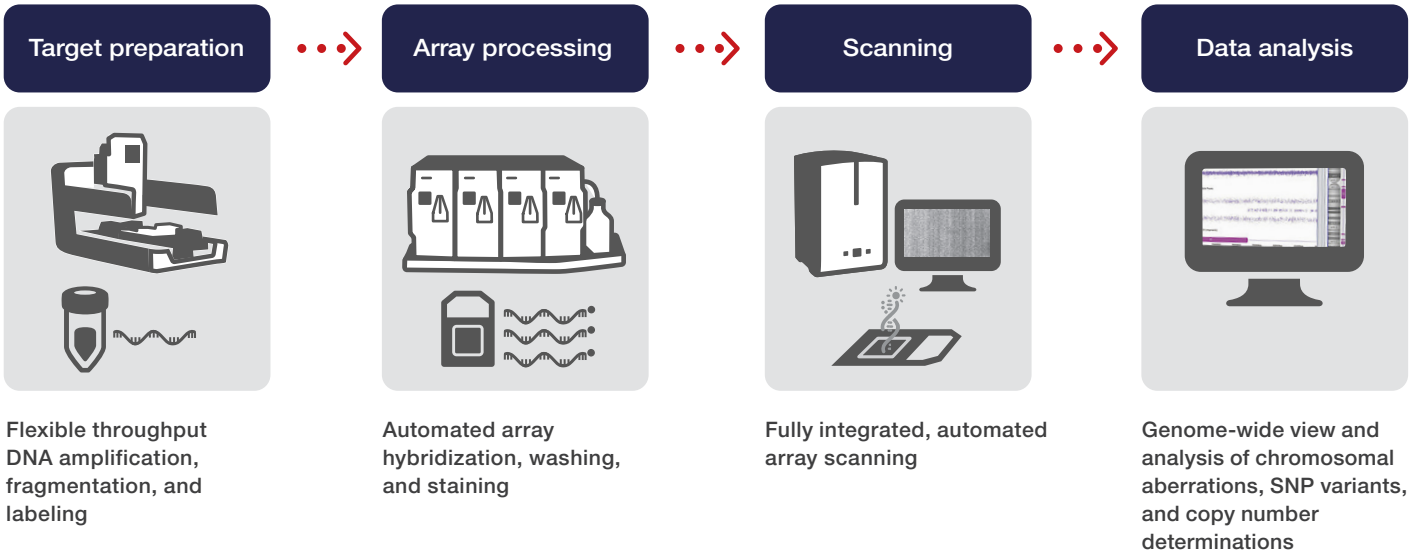


Figure 1. The robust workflow is aligned with your research laboratory workflow requirements, with intuitive processes to streamline data analysis and reporting.

Minimize the complexity of variant interpretation

The **CytoScan AIR** solution combines ChAS and Franklin (by Genoox) genetic data analysis software to simplify genomic variant pathogenicity research and reporting. Leverage AI for quick and precise variant identification, with rapid data interpretation and reporting in seconds.

Key features

- Enhanced evidence support with American College of Medical Genetics and Genomics (ACMG) classifications, phenotype matching, literature searches, and historical data
- Easy customization, reporting, evaluation, sign-off, and laboratory information management system (LIMS) export
- Evidence-based database development links evidence with observations
- Access to over 350,000 shared variant classifications and advanced findings from community-driven cytogenetics research

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

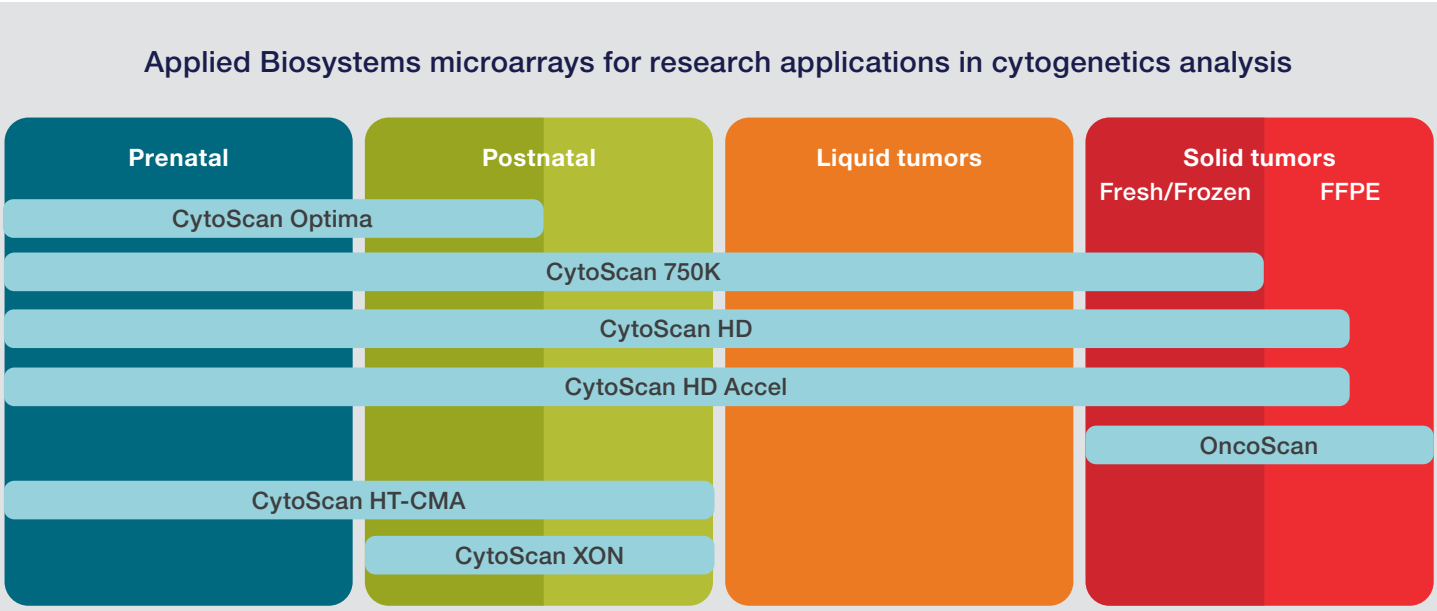


Figure 2. Applied BioSystems microarrays enable a wide range of cytogenetics research application areas.

Hybrid-SNP arrays can detect these types of genetic conditions[1] for research applications:

- Suspected 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 research applications

Advances in human genetic analysis technologies can potentially enable detection of certain causative DNA aberrations associated with genetic disorders, thus helping provide valuable insights into chromosomal abnormalities in constitutional and oncology 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 following birth.
- **Product of conception (POC)** genetic testing of fetal tissue after the loss of a pregnancy helps clinical researchers study chromosomal anomalies associated with miscarriage.
- **Oncology** genetic testing of tumor samples helps clinical researchers study chromosomal aberrations associated with cancer.

Boost productivity with tailored cytogenetic analysis

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.

- 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.
- Boost your discovery yield with the evidence-based CytoScan AIR solution.

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.

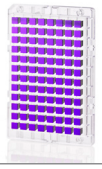
Watch the webinars

Scientific spotlight:
Learn why GeneDx, a leader in testing for rare genetic disorders, switched to high-resolution whole-genome 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 Accel	CytoScan HD	CytoScan 750K	CytoScan Optima	CytoScan HT-CMA	CytoScan XON
Research applications						
	Fast turnaround with latest available content for prenatal, postnatal, and oncology research	High genome-wide resolution of CNVs for applications in prenatal and postnatal research	High genome-wide resolution to analyze copy number gains and losses for prenatal and postnatal research	Low-cost genome-wide platform to detect aneuploidies and copy number losses and gains at lower resolution, optimized for constitutional cytogenetics research	High-throughput, cost-effective, genome-wide copy number analysis for constitutional cytogenetics research and testing of relevant SNP variants	Sensitive, high coverage, whole genome, single exon-level copy number analysis. 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, POC, and fresh, frozen, or FFPE tissue	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	Blood, uncultured or cultured cells, chorionic villi, amniocytes, and POC	Blood, buccal swabs, saliva, uncultured or cultured cells, chorionic villi, amniocytes, and POC	Blood (Custom-built reference file enables other sources of DNA)
Size of aberration* (analytical claims)	Losses: 25 kb Gains: 50 kb LOH/AOH: 3 Mb Mosaicism: >15% (approximately)	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 to study exon-level CNVs Whole genome coverage, with increased coverage in 7,000 clinically relevant genes
Input DNA	100 ng	10–250 ng**	10–250 ng**	10–250 ng**	100 ng	100 ng
Probe structure	2.8 million markers for whole genome coverage 2 million nonpolymorphic markers ~750,000 SNP probes for LOH/AOH analysis, duo-trio assessment, and sample tracking	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 markers 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	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	2 days	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

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).

CytoScan HD Suite for hematologic malignancies research

Capture chromosomal abnormalities and genomic instability, which can be 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.

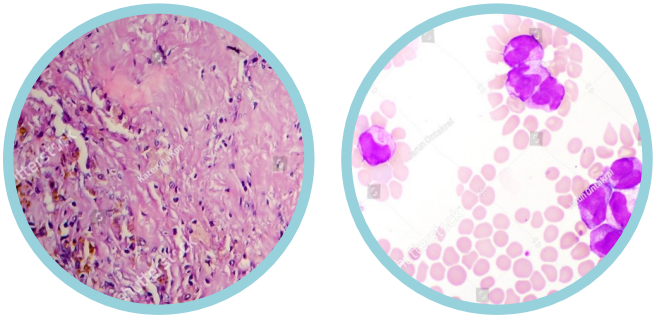


Figure 3. CytoScan and OncoScan hybrid-SNP arrays enable investigation of a wide range of solid **(left)** and liquid **(right)** tumors.

"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

The new Applied Biosystems™ CytoScan™ HD Accel Array incorporates updated coverage in more than 5000 regions as categorized by industry databases. The two-day assay workflow and lower input sample requirement help boost laboratory efficiency.

OncoScan assays for solid tumors research

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.

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).

Key features boost productivity and efficiency

- **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 with the latest content 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 as little as two days from only 80 ng of FFPE-derived DNA
- **Rapid analysis**—included software provides intuitive data visualization for hundreds of samples in minutes
- **Evidence-based database development**—link evidence with observations for internal database management and expansion
- **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 (Mbs) 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

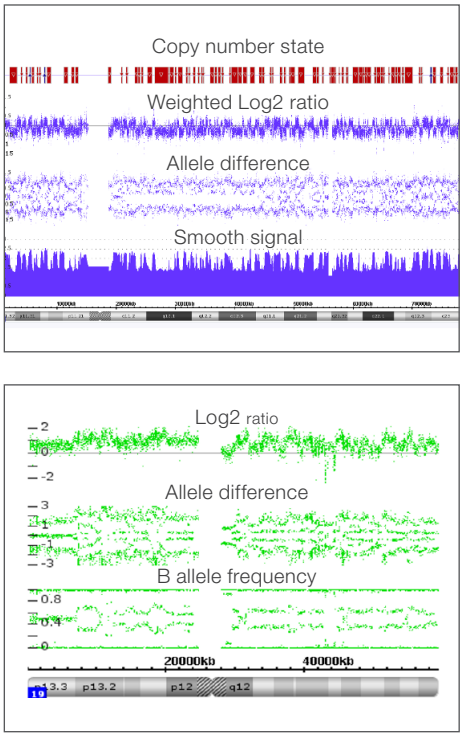


Figure 4. Chromothripsis detected on chromosome 18 using CytoScan HD arrays **(top)** and on chromosome 19 using OncoScan arrays **(bottom)**, revealed by the sequential copy number changes and the multiple breakpoints seen in the different tracks.

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

	CytoScan HD Suite	OncoScan CNV Assay OncoScan CNV Plus Assay*	CytoScan HD Accel
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 the whole genome in FFPE and fresh frozen tissues	Fast turnaround with latest available content for prenatal, postnatal, and oncology research
Sample types	Blood, bone marrow, and fresh and frozen tissue	FFPE, fresh and frozen tissue	Blood, bone marrow, and fresh, frozen, or FFPE tissue
Size of aberration (analytical claims)**	Gains: 50 kb Losses: 25 kb LOH/AOH: 3 Mb Mosaicism (% aberrant cells): >15% (approximately)†	Gains: 50 kb Losses: 50 kb LOH/AOH: 10 Mb Mosaicism (% aberrant cells): 15%†	Losses: 25 kb Gains: 50 kb LOH/AOH: 3 Mb Mosaicism: >15% (approximately)
Input DNA	10-250 ng‡	80 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 and sample tracking	220,000 molecular inversion probes (MIPs) for whole genome coverage 5,700 non-polymorphic probes 216,000 SNP probes	2.8 million markers for whole genome coverage 2 million nonpolymorphic markers ~750,000 SNP probes for LOH/AOH analysis, duo-trio assessment, and sample tracking
Protocol	3–4 days	2–3 days	2 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.

Enhance efficiency with fully integrated array processing

The Applied Biosystems™ GeneChip™ System 3000 is a fully integrated platform to boost your research productivity 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.

The pre-assembled internal autoloader helps enable complete walk-away freedom for scanning your arrays and supports more efficient installation. 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
- **Complete walk-away scanning** of up to 48 arrays at a time with pre-assembled autoloader
- **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
- **Easier and safer operation** with new scanner lid features
- **Maximized longevity** with updated internal components

Streamline analysis, interpretation, and reporting for challenging genes

View and analyze chromosomal aberrations across the genome, including copy number gain or loss, LOH, and mosaicism. Developed with input from our customers and leading experts, **Applied Biosystems™ Chromosome Analysis Suite (ChAS) software is designed specifically for analysis and reporting in chromosomal aberration research.** Enhanced, intuitive features simplify cytogenetics investigation.

Key features

- Whole-genome support for CytoScan Suite
- CN state for CytoScan Suite
- LIMS APIs
- Analyze data at different levels of resolution
- Automatically prioritize segmented data using scoring inspired by the ACMG
- 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

View ChAS training modules

Request a ChAS demo

Maximize your CytoScan expertise for greater laboratory efficiency

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, support you with **comprehensive support from initial planning to routine implementation**.

Contact a Chromosome Microarray specialist

Ordering information

Product	Description	Cat. No
CytoScan HD Accel		
CytoScan HD Accel Kit Plus 24	Arrays and reagents for 24 reactions with amplification kit	952465
CytoScan HD Accel Kit Plus 96	Arrays and reagents for 96 reactions with amplification kit	952466
CytoScan HD Accel Array Kit and Reagent Kit Bundle	Arrays and reagents sufficient for 24 reactions	952460
CytoScan HD Accel Training Kit	Arrays and reagents sufficient for 24 reactions to perform assay training	952461
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

Ordering information continued

Product	Description	Cat. No
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
Analysis software		
Chromosome Analysis Suite (ChAS)	Available as a free download from thermofisher.com/chas	NA
CytoScan Automated Interpretation and Reporting (AIR) Tokens	24 tokens	00.1001
	96 tokens	00.1003
	384 tokens	00.1004
Support products		
Reproductive Health Research Analysis Suite (RHAS)	Available as a free download from thermofisher.com/chas	NA
GeneChip System 3000	Includes: GeneChip Scanner 3000 with AutoLoader GeneChip Fluidics Station 450 GeneChip Hybridization Oven 645i Workstation with GeneChip Data Collection Software	00-0218
GeneChip Fluidics Station 450	Single station available for purchase separately from the GeneChip System 3000	00-0079
GeneChip Hybridization Oven 645i	Single unit available for purchase separately from the GeneChip System 3000	00-0331
GeneTitan MC Fast Scan 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

1. Levy B, Wapner R. Prenatal diagnosis by chromosomal microarray analysis. *Fertil Steril.* 2018 Feb;109(2):201-212. doi: 10.1016/j.fertnstert.2018.01.005. PMID: 29447663; PMCID: PMC5856154.
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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