Cytogenetics

Enhance efficiency and productivity in cytogenetic analysis with the CytoScan HD Accel Suite

The complete solution

The advanced Applied Biosystems™ CytoScan™ Cytogenetics Suite for research includes:

- The fast, sensitive Applied Biosystems™ CytoScan™ HD Accel Array with a robust and reliable reagent kit
- The efficient, automated Applied Biosystems™ GeneChip™ System 3000 for array processing
- Intuitive, user-friendly Applied Biosystems™ Chromosome Analysis Suite (ChAS) software
- The evidence-driven, accelerated Applied Biosystems™ CytoScan™ Automated Interpretation and Reporting (AIR) solution

Summary

This white paper discusses the efficiency and productivity challenges that cytogenetics clinical research laboratories encounter in providing results quickly. Long assay workflows, staffing constraints, limitations of working with precious samples, and extensive data interpretation can all cause delays. The CytoScan HD Accel Suite is a powerful hybrid-SNP chromosomal microarray (CMA) research solution that can help overcome these challenges. The CytoScan HD Accel Array is designed to maximize speed with a two-day turnaround time (TAT), even with low input DNA. Laboratory efficiency and productivity are enhanced with updated content that delivers improved genome-wide coverage, an updated reference model that supports difficult sample types, and automated data interpretation and reporting capabilities.

Introduction

An efficient cytogenetics laboratory delivers time-sensitive results quickly and saves costs with reduced labor, resources, and operational expenses. Operational efficiency and productivity contribute to the success of a laboratory, providing benefits for clinical research and, ultimately, research study participants. Laboratories that generate results faster can process more samples in a given time period, increasing their testing throughput.

Minimizing TAT can be key to delivering results sooner

TAT, the length of time between sending a sample to the lab and obtaining results, is a key measure of laboratory efficiency. TAT can be particularly critical in prenatal and oncology research, where time is of the essence and faster access to reports enables researchers to make data-driven decisions more promptly. Any reduction in the TAT for CMA assay workflows can have a significant impact on research participants. Shorter incubation times, fewer PCR cycles, and fewer pipetting steps can all shorten the time required for a CMA assay workflow.

Shorter assay workflows may help drive staffing efficiencies

According to the U.S. Bureau of Labor Statistics, employment of clinical laboratory technologists and technicians in the United States is projected to grow by 5% from 2022 to 2032 [1]. A critical lack of adequately trained applicants for technologist positions in clinical genomics laboratories in the United States [2] could mean a risky reduction in the staff available to run assays. Workflows with shorter TATs might help to reduce the impact of staff shortages, potentially saving costs and enabling faster reporting. Time freed by running tests with shorter TATs may also allow staff to focus on other revenue-generating work. Optimizing workflows and reducing the time spent on each test enables a lab to allocate resources more efficiently.

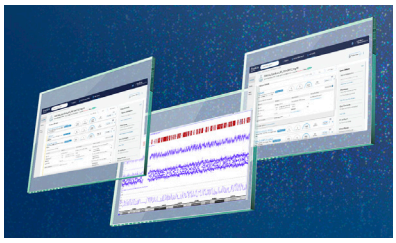
CytoScan HD Accel Suite—the complete chromosomal microarray (CMA) research solution with a two-day TAT

CytoScan HD Accel Array

Build trust in your lab with reliable, reproducible, and rapid results

GeneChip Scanner 3000

Efficient, safe, and updated microarray scanning supports genetic analysis applications



CytoScan AIR solution

Increase productivity with automated genetic data interpretation and reporting powered by AI

Chromosome Analysis Suite (ChAS)

Enhanced, intuitive features simplify cytogenetic investigations

"The relatively short TAT for CMA could be well suited to aid research studies in the prenatal setting where time is of the essence."

— Jeanne Meck, PhD, FACMG,
Director, Cytogenetics and Prenatal
Diagnostic Services, GeneDx

Learn more

Leveraging performance advantages of CMA assays can help extract maximum insights from minimal sample

In CMA assays, insufficient or low-quality input DNA can yield inconclusive results. Unplanned test repeats waste time and increase costs.

Buccal swabs, saliva, and some prenatal fluids can be fundamental to cytogenetic tests, but high-quality DNA can be hard to obtain from these sample types. Saliva is also a highly complex fluid that includes buccal cells and microorganisms, which can confound data analysis. The use of a reference model file (RMF) that supports these challenging sample types can reduce detection noise and improve data quality.

Sample sources that are very small, such as those that might come from prenatal or cancer study subjects, may yield only limited amounts of relevant cells from which to extract DNA. Cells may need to be cultured, which can add several days to the TAT. If DNA is isolated from amniotic fluid cells or the mesenchymal core cells of chorionic villi and analyzed directly, culture is not required, saving time and avoiding culture artifacts [3]. An assay that requires less input DNA might help reduce the need for cell culture.

An additional advantage of being able to use less input DNA is that more tests could potentially be run on an individual sample. For prenatal, postnatal, and cancer analysis, researchers often perform multiple, different types of testing as complementary techniques or for orthogonal verification of results. For these valuable samples, the ability to use small amounts of DNA makes it possible to distribute the sample across several tests and avoid having to omit potentially informative tests.

In addition to properties of the samples themselves, the genomic content on a CMA can also contribute to the ability to gain greater insights from a single sample. As more CNVs are characterized, incorporation of content into CMA designs can help researchers broaden their investigations into rare variant alterations and potential relationships of genes and phenotypes in genetic constitutional disorders. Access to the latest available content can help improve laboratory efficiency by yielding more data from each sample run.

CNV software can streamline evidence-based data analysis and reporting

Time-consuming procedures for interpretation and reporting can also drain resources and contribute to increases in TAT. Analysis software that is fast, intuitive, and user-friendly can help to reduce analysis time and costs, and aid with interpretation. Some CNVs can be benign, platform-specific variants, or artifacts [4]. Managing analysis of datasets with unexpected variants can be simplified by creating and storing a database of previous laboratory microarray results and their interpretation.

CNVs that are currently without documented clinical significance can be particularly challenging to interpret [5]. Even interpretation of literature-reported clinically significant copy number changes can present uncertainties. Accurate interpretation of the potential clinical relevance of CNVs requires consistent methods of evaluating the genomic content of a CNV region and correlating clinical findings with those reported in medical literature, with the ultimate goal of producing consistent, evidence-based clinical classification across laboratories.

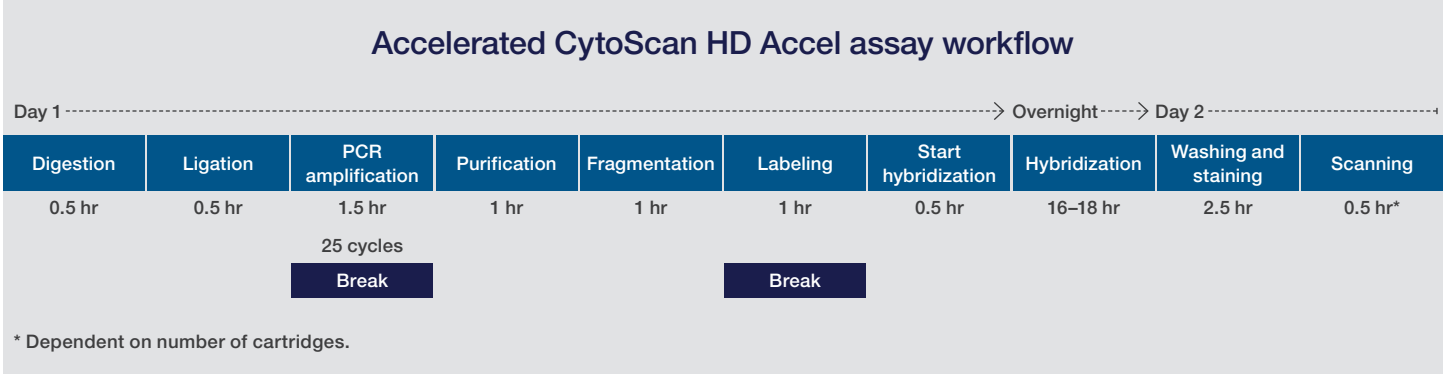


Figure 1. Accelerated CytoScan HD Accel assay workflow from DNA digestion through CMA scanning.

Variant assessment can be time-consuming. Evaluation may require manually querying multiple databases with different questions. To use internal resources efficiently, some laboratories may outsource analysis, which adds extra cost and data handling steps. Other laboratories may develop their own reporting solutions, potentially requiring different resources or distraction from the primary objectives of the lab.

To evaluate the potential clinical relevance of variants from a sample, test results must be integrated with previously reported information to see whether the variant has been indicated as benign, likely benign, a variant of uncertain significance (VOUS), likely pathogenic, or pathogenic.

Not all laboratory information management system (LIMS) solutions can accommodate the complexity of genetic testing results and reports required for some cytogenetic research. An internal database that accounts for local variation and identifies previous cases with the same variant is critical.

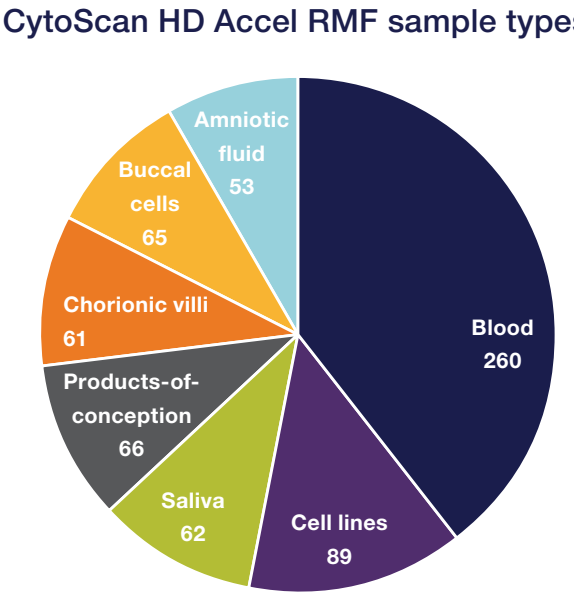


Figure 2. CytoScan HD Accel RMF sample types (656 samples, 535 unique).

Internal databases can provide a more accurate assessment of variants in the tested population than is provided by external databases built with data from hundreds of other laboratories or unrelated populations.

The growing volume of data generated in cytogenetics laboratories has led to a focus on structured and concise reporting. Laboratories strive for standardized output that enhances the quality of the report [6]. Quick and intuitive report generation workflows that automate data analysis and deliver easily interpreted reports can enable large savings in TAT and increase efficiency, while allowing researchers to remain up-to-date with rapidly advancing applications.

Improving productivity and efficiency with the CytoScan HD Accel Array

The CytoScan HD Accel Array has been designed to deliver robust results with a TAT of just two days (Figure 1). The faster assay time is enabled by short incubation times and fewer PCR cycles. The assay only requires 100 ng of input DNA, which may help to mitigate the challenges of small or precious source samples and potentially eliminate the time and costs associated with cell culture.

Plate-based purification saves time by reducing the number of pipetting steps required. It also reduces the risk of unintended sample swaps, which can occur any time the sample is out of the plate, and then adds time and costs. By reducing risks inherent to sample swapping, laboratories can maximize efficiency in control procedures required to ensure correct tracking.

The CytoScan HD Accel Array is a hybrid-SNP array that includes both probes for single nucleotide polymorphisms (SNPs) and nonpolymorphic probes to support prenatal, postnatal, and oncology assays. Updated content in more than 5,000 critical genome regions gives balanced genomic coverage, improving discovery yield and potentially reducing the time required to deliver a result with confidence.

A reference model file (RMF) improves data quality for a diversity of sample types, including blood, products-of-conception, buccal cells, saliva, amniotic fluid, chorionic villi sampling, and cell lines (Figure 2).

The CytoScan Cytogenetics Suite raises your **productivity** and **efficiency** to a whole new level

CytoScan Automated Interpretation and Reporting (AIR) solution

The CytoScan AIR solution leverages the power of AI for quick and precise variant identification. Streamlined interpretation and reporting for genetic data analysis can save time and increase efficiency, helping enable fast and accurate in-house analytics (Figure 3). The data and evidence used to generate reports are ready to review in just a few seconds, so researchers can focus on discovery and interpretation rather than file administration.

Enhanced and accelerated interpretation allows specialists to invest more time analyzing information instead of manually searching for information to interpret their results.

With the intuitive interface of the CytoScan AIR solution, reports can be customized and exported to a LIMS system. Standardized reports can be prepared using templates that automatically generate consistent reports in a specified format. Clear visualization of the results allows the report recipients to identify important information rapidly.

All reports are efficiently compiled on the same database to enable easy management of cases for reevaluation, assignment, status checking, validation, reporting, evaluation, and sign-off.

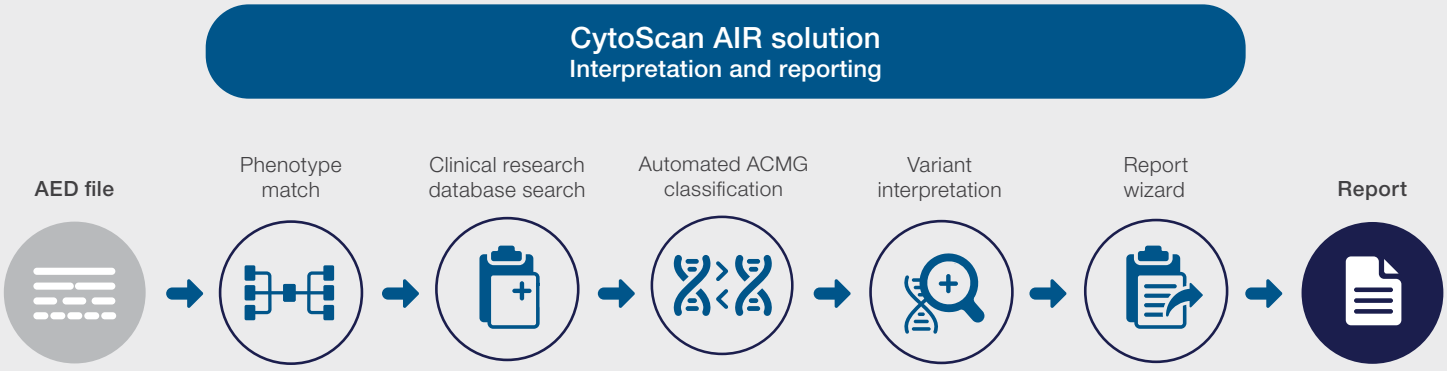


Figure 3. CytoScan AIR solution for variant interpretation and reporting.

Conclusion

Solving common cytogenetics laboratory challenges by shortening assay workflows, maintaining staff focus, mitigating limitations of working with precious samples, and streamlining data interpretation can help maximize laboratory output to enable faster delivery of results. The CytoScan HD Accel Suite increases efficiency and productivity for cytogenetics laboratories by featuring a short TAT and a streamlined workflow that provides robust and reliable data. The CytoScan AIR solution provides automated interpretation and reporting as well as easier variant classification. The two-day TAT, updated coverage, and automated interpretation and reporting all contribute to faster data availability so researchers can make informed decisions, collaborate effectively, and accelerate scientific discovery.

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