PRODUCT BULLETIN

Human identification

Converge Software

A comprehensive forensic analysis platform that integrates answers for you

Key features and benefits

- Analyze next-generation sequencing data from the Applied Biosystems™ Precision ID NGS System
- Demonstrate concordance between CE and NGS profiles
- Streamline kinship and paternity analysis
- Centralize forensic data and analysis and case information in one place to help increase lab efficiency
- Customize information architecture, data inputs, and parameters to meet the needs of your laboratory

Converge software offers streamlined solutions for next-generation sequencing (NGS) analysis of short tandem repeat (STR) markers, capillary electrophoresis (CE)-to-NGS comparisons of STR profiles, kinship and paternity testing, and case management.

Introduction

For forensic laboratories, data management and analysis are daunting, requiring numerous procedural steps and complex decision-making. Many laboratories therefore rely heavily on their software systems to effectively manage their day-to-day operations.

Applied Biosystems™ Converge™ Software, an all-in-one modular enterprise platform from Thermo Fisher Scientific, integrates forensic DNA data management and analysis into a single software package designed to increase the efficiency of forensic and relationship DNA-testing laboratories. The system is highly configurable to fit specific laboratory workflows, not only for analysis parameters but also for incorporation of data fields according to a laboratory's standard operating procedures (SOPs). Laboratories can also integrate with an existing laboratory information management system (LIMS) using service-oriented architecture integration points that are built into Converge software.

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NGS analysis

With recent advances in NGS, crime laboratories are now able to analyze targeted and forensically relevant STR and single nucleotide polymorphism (SNP) markers to generate investigative leads and help determine the number of contributors in a mixture analysis. The application of NGS is particularly helpful with degraded samples that may not provide a full profile using traditional CE methods. The Converge NGS Analysis module is required to generate profiles from the Applied Biosystems™ Precision ID GlobalFiler™ NGS STR Panel v2. The NGS Analysis module functionality provides information on STR allele call, STR sequence motif, known SNPs in flanking regions, and isometric heterozygotes (alleles of the same fragment length but containing different sequences).

With an interface that is similar to that of Applied Biosystems™ GeneMapper™ *ID-X* Software, forensic analysts will be able to quickly evaluate NGS data using familiar process quality values (PQV) and flags such as allele number (AN), off-ladder allele (OL), peak height ratio (PHR), below stochastic threshold (BST), and control concordance (CC) (Figure 1). Preconfigured analysis settings are provided within the NGS module and may be modified as needed. Additionally, full auditing functionality is included for chain-of-custody requirements.

Sequence analysis of STRs also provides additional discrimination by resolving isometric heterozygotes (Figure 2) and shared STR alleles that contain SNPs in flanking regions (Figure 3). These additional sources of allelic diversity may be useful in both mixture analysis and kinship interpretation.

As forensic laboratories begin to adopt sequence analysis of STR markers into casework applications, validation and concordance studies may be required. Using both the NGS Analysis module and the Case Management module of Converge software allows for the easy comparison of NGS and CE profiles (Figure 4). This comparison ability will also be useful in the future when comparing a crime scene sample analyzed by NGS to a reference sample that has been processed using traditional CE methods.

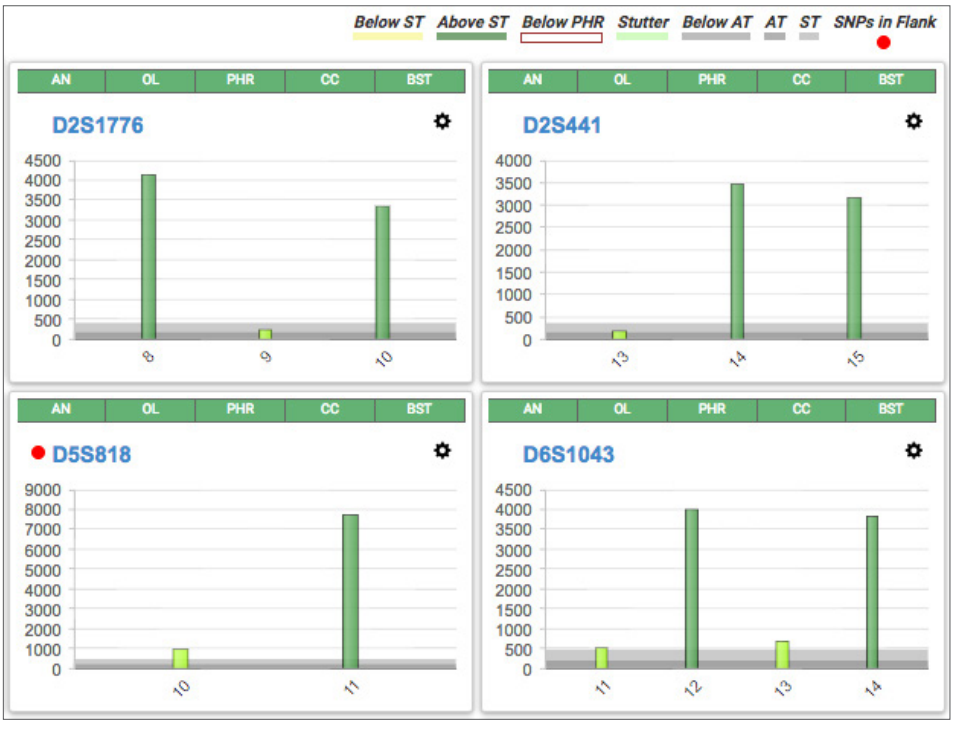

Figure 1. View of NGS secondary analysis results using Converge software.

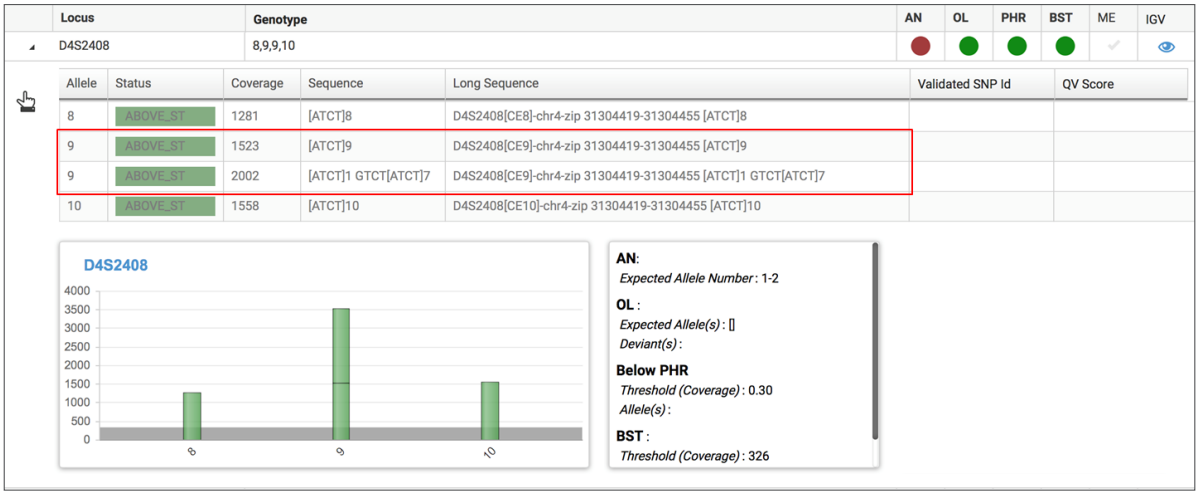

Figure 2. Detailed information from isometric heterozygote analysis with sequencing coverage and repeat motif structure.

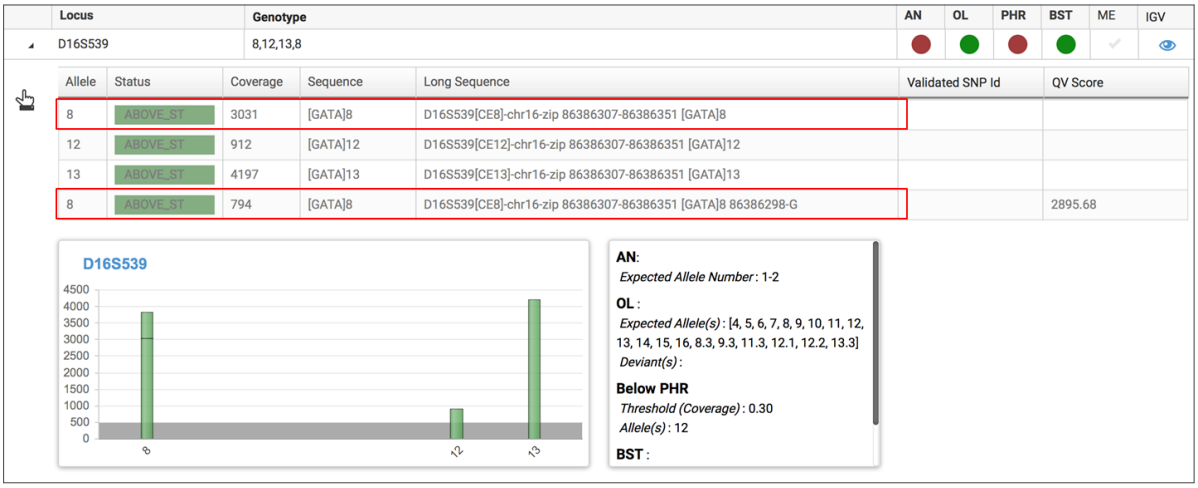

Figure 3. Detailed information on an SNP in a flanking region from a minor contributor. The SNP is identified with ISFG-recommended nomenclature. SNP information can be explored within public genomic databases via the Integrative Genomics Viewer (IGV).

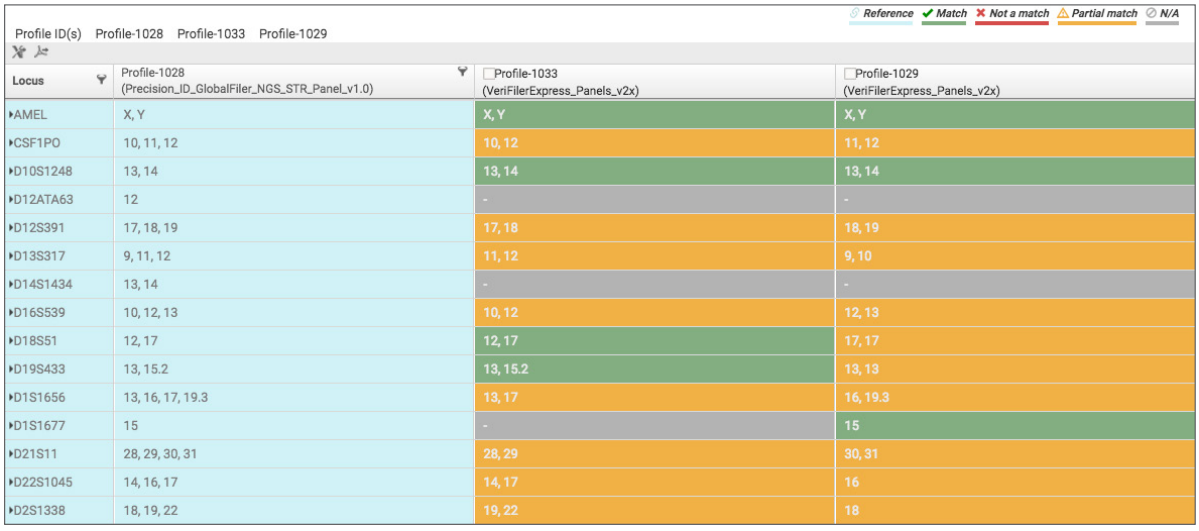

Figure 4. Comparison of NGS and two CE profiles (imported from GeneMapper *ID-X* Software) via the Case Management module. The NGS sample is a mixture of the two CE samples. The software displays marker-level profile comparisons as follows: (i) match, (ii) non-match, and (iii) partial match.

Kinship and paternity analysis

Kinship and paternity testing can be challenging in both the sheer volume of cases to be analyzed as well as the complexity of laboratory workflows and statistical analyses being performed. The Converge Kinship and Paternity module offers a comprehensive set of parameters to perform analysis, allowing laboratories to conduct various types of relationship testing in a fraction of the time compared to current methods.

The Kinship and Paternity module incorporates data from GeneMapper *ID-X* Software or from the Converge NGS analysis of Precision ID GlobalFiler NGS STR Panel v2, which contains 32 multiallelic STR markers including Penta D and Penta E and gender determination markers. Converge software identifies and processes Trio Paternity, Trio Maternity, Duo Fatherless, and Duo Motherless kinship tests by automatically creating cases, adding subjects and profiles, running analyses, and generating reports. Users can quickly and easily create a variety of hypotheses by drawing pedigree trees and setting comprehensive analysis parameters, including application of mutation models and population substructures (Figure 5). It also allows for genetic likelihood ratio calculations, as well as the generation of reports for any complex relationship analysis. These analyses are conducted utilizing validated algorithms.

Through an intuitive interface, users can easily review detailed results, and also generate and electronically sign reports in a few simple steps. Converge software provides one default report template; however, laboratories can use existing tools to modify this template and adjust the report to their desired format. For trio and duo testing in paternity and maternity cases, the Quick Kinship Analysis (KA) functionality of the Case Dashboard integrates all of these steps on one screen, saving time within the laboratory.

Validation

Complex analysis parameters used in kinship analysis require validation in order to determine the appropriate settings for the thresholds governing the data interpretation. Therefore, it is important that the software be tested using a variety of samples that challenge each different relationship-testing scenario. Although default settings are suggested within the software, these can be adjusted based on the outcome of each laboratory's internal evaluation of Converge software. Optimizing any software will require an additional investment on the part of the laboratory. Extensive system verification has been performed at Thermo Fisher Scientific, and a summary of these verification studies is available as a reference guide for users interested in implementing the software.

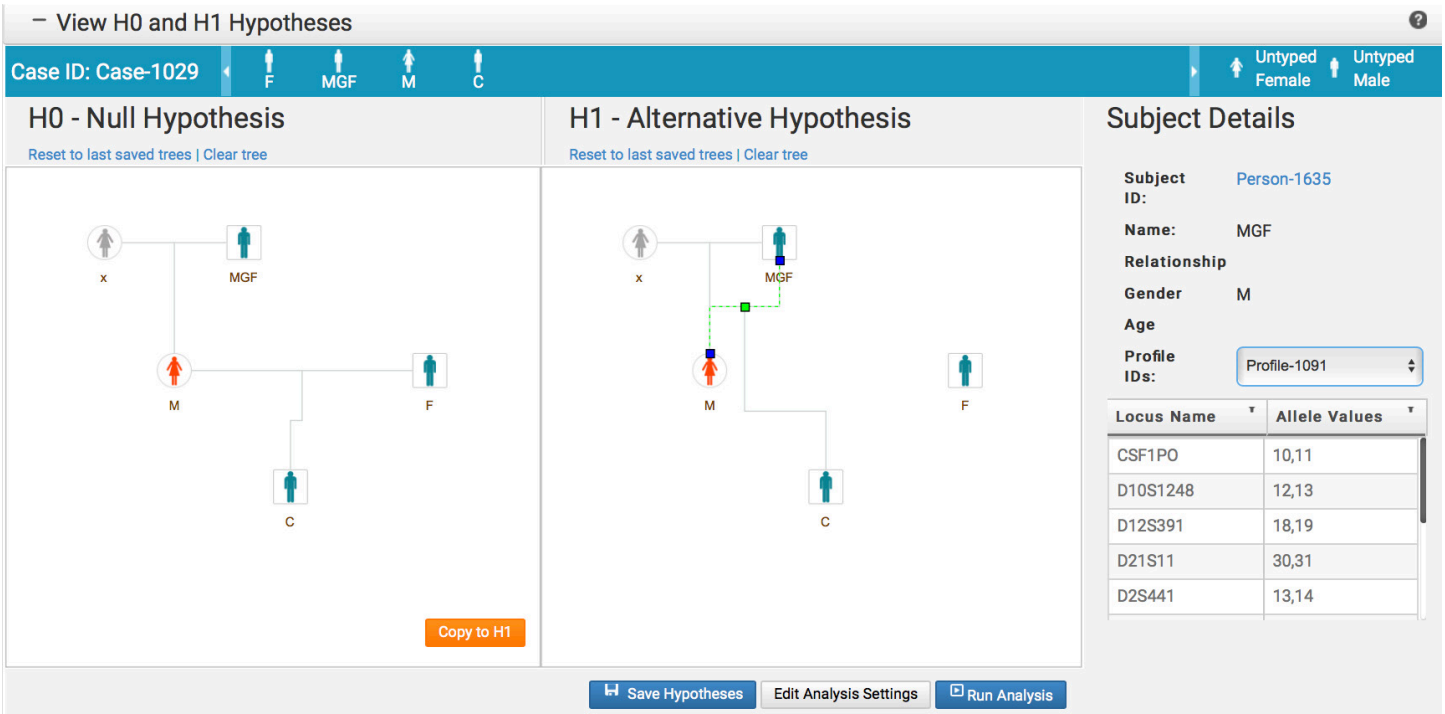

Figure 5. The Kinship and Paternity module offers an intuitive user interface to quickly perform relationship testing.

Case management

Underlying the centralization of data creation, analysis, and storage to one easy-to-access location, the Converge Case Management module supports case, subject, genotype profile, and laboratory data management. It also allows for automated data transfer between various forensic DNA laboratory systems and efficient management of daily operations. The module serves the needs of various users such as laboratory managers and analysts, providing intuitive data views and reports that can be configured and saved for each user. These features are easily accessible through a secured web browser under the protection of the laboratory's IT department. The information management configurability allows the user to focus on pertinent information and adapt to a laboratory's specific needs by adding new data fields. Case data management includes metadata related to the case, subjects, DNA profiles, and attachments, with extensive data fields available to track all required information.

Case dashboard

Ideal for quickly reviewing case status and accessing case reports, the Case Dashboard functionality provides an at-a-glance overview of the case (Figure 6). Extensive search and filtering capabilities on many data elements allow faster access to relevant information, saving time and effort. Once performed, searches can be saved and viewed at a later date. Cases can also be exported for external sharing and storage and can be imported back as needed. Archiving can be scheduled or performed manually, to remove closed cases from the active dashboard. Should the need arise, archived cases can always be retrieved in the Case Dashboard.

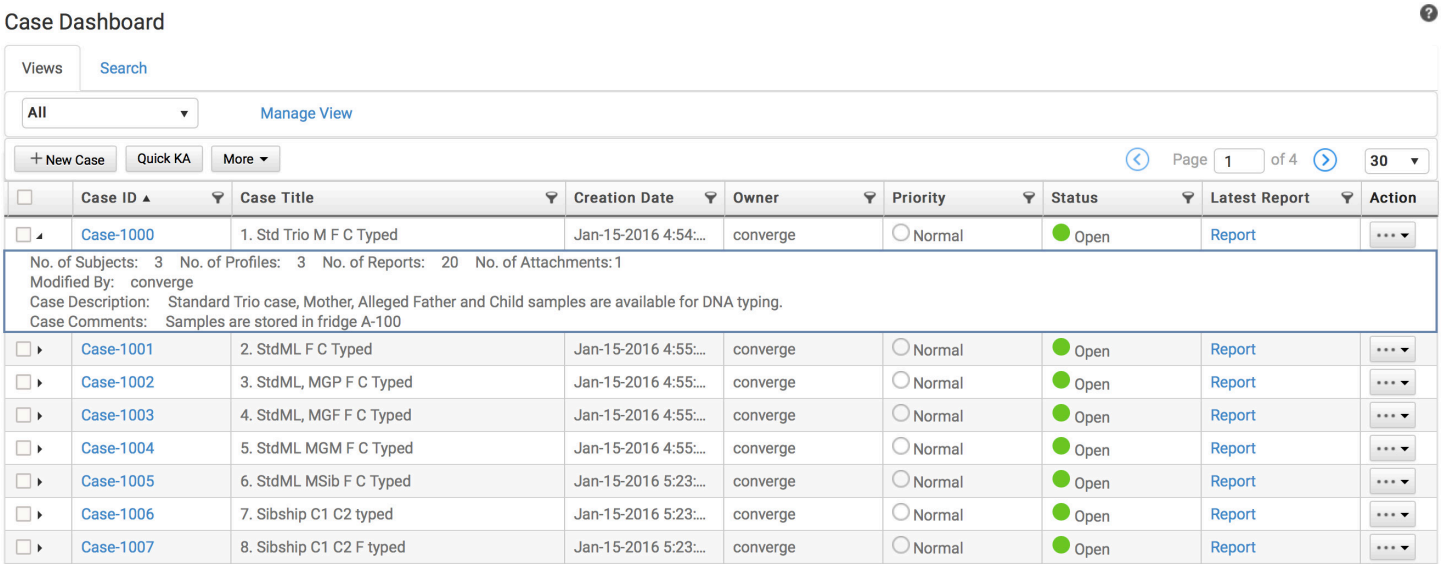

Figure 6. The Case Dashboard centralizes information on all cases in one view, allowing for a quick review.

Case details

The Case Details feature presents all information on a specific case in one view and allows access to case metadata such as case ID, requesting organization, description, priority, status, creation date, and owner (Figure 7). Added functionality allows the user to create and manage subjects through extensive subject details, capturing all necessary information that is saved, tracked, and retrieved. Subject details include, but are not limited to, name, date of birth, ethnicity, address, phone number, and government-issued identification. Additionally, exported DNA profiles from the NGS Analysis module and GeneMapper *ID-X* software can be imported and stored in Converge software. The DNA profile along with its metadata, including the kit used to generate the data, is preserved. Multiple profiles can be generated by kits using different chemistry and be associated with the same subject. Lastly, the attachments feature allows easy uploading of files like pictures, Microsoft™ Word™ documents, and Microsoft™ Excel™ files, organizing all case information in one location.

Rely on our experienced team

To help labs integrate, validate, and implement new technologies, our Human Identification Professional Services (HPS) team offers services designed to help customers successfully navigate the validation process. Through a consultative approach, the HPS team of forensic experts can work with you to integrate Converge software seamlessly in your laboratory.

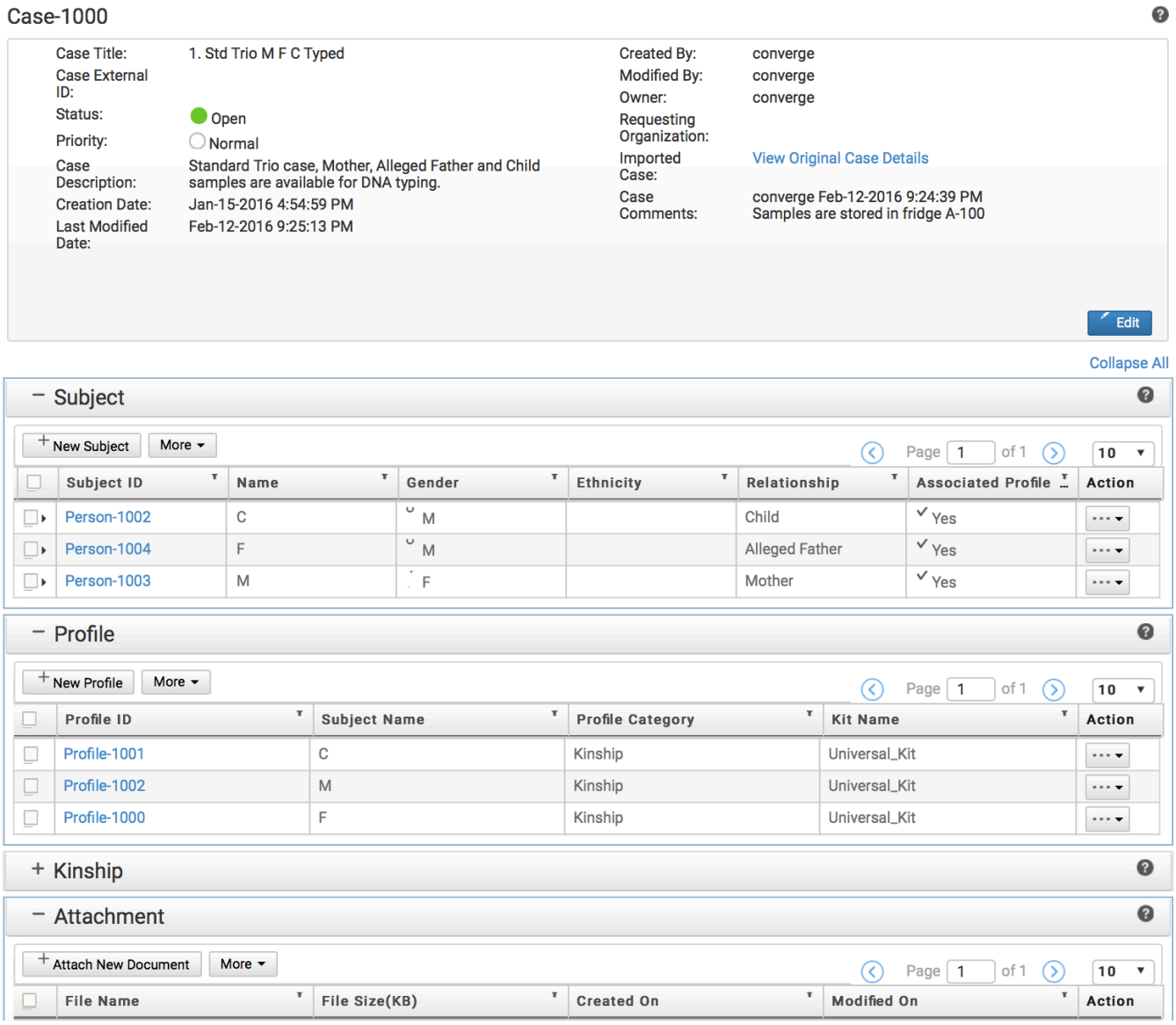

Figure 7. Case Details allows easy access to all metadata for a case.

Security

Easily accessible through a web browser, data can be accessed from any computer with connectivity privileges to the Converge software server and are deployed within a laboratory's own intranet. Access to data within the software is secured through various security policies, including password expiration and account suspension. Backup and restore functionalities allow laboratories to securely maintain data and manage disaster recovery situations.

Converge software server

The Converge software server, based on the Linux™ operating system, hosts Converge software using an internet protocol (IP) address configured in the system. The Converge software server requires an administrator to manage user accounts and comes preconfigured with the following components and settings:

- Dell™ PowerEdge™ T110 II base unit
- Red Hat™ Enterprise Linux™ operating system
- Apache™ Tomcat™ application server that runs Converge software
- PostgreSQL database server that stores the data for the server and software
- Google™ Chrome™ browser
- Automatic configuration of IP, domain name service (DNS), and Windows internet name service (WINS) settings via dynamic host configuration protocol (DHCP)

Note: See the manufacturer's documentation accompanying the server or the manufacturer's website for network requirements, specifications, and product details.

Supported browsers

Converge software is supported for use with the following browsers:

- Apple™ Safari™ v8
- Microsoft™ Internet Explorer™ v11
- Google™ Chrome™ v45

Note: Google Chrome is the only browser available on the Converge software server.

Converge software server components

Description
Dell PowerEdge T110 II Tower Server
Dell Flat Panel Monitor, 23 inch (or equivalent) with cable
Dell Quiet Key USB Keyboard
Dell Laser USB Mouse
4 GB USB drive
Power cord*
RJ45 CAT6 Ethernet cable
USB drive (Converge software)
USB drive (Converge software documentation)

* Supplied with the server and monitor. Supplies 13 A/125 V depending on the geographic location of the installation.

Converge software server specifications

Specification	Description
Processor	Intel™ Xeon™ processor E3-1230 v2 (8 MB cache, 3.30 GHz, Intel™ Turbo Boost™ technology, quad core/8 threads/69 W TDP)
Memory	16 GB memory (2 x 8 GB); 1,600 MHz; dual rank, low-voltage UDIMM
Hard drive	2 x 2 TB, 7,200 RPM, SATA 3 GB/s, 3.5-inch cabled hard drive
Data storage	RAID 1 with add-in H200 (SAS/SATA) controller, 2 hard drives

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Ordering information

Description	Cat. No.
Converge Software with server v2.0	A35131
Case Management and NGS Analysis modules (1 user, 3-year license)	A35987
Case Management and NGS Analysis modules (5 users, 3-year license)	A36237
Case Management and Kinship & Paternity Analysis modules (1 user, 1-year license)	A31001
Case Management and Kinship & Paternity Analysis modules (1 user, 3-year license)	A31002
Case Management and Kinship & Paternity Analysis modules (5 users, 3-year license)	A31005

Additional configurations of software licenses are available. Please contact your local representative for more information.

Find out more at **thermofisher.com/converge**

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For Research, Forensic, or Paternity and Cell Line Authentication. Not for use in diagnostic and therapeutic applications.

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