RELEASE NOTES

November 15, 2017

Precision ID NGS System

Precision ID GlobalFiler NGS STR Panel v2 and Analysis Files
Converge™ Software 2.0 – Kinship and NGS Data Analysis Modules

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PRODUCTS AFFECTED

- A33114 Precision ID GlobalFiler NGS STR Panel v2 Analysis Files
- Converge Software 2.0
    - Kinship and Paternity Analysis Module
    - Next-Generation Sequencing Data Analysis Module

SOFTWARE OVERVIEW

Converge Software is a modular, enterprise platform that provides key analysis to perform next-generation sequencing (NGS) and complex kinship and paternity testing. The software serves as a central repository for case data and simplifies the daily complexities of forensic case management.

Converge NGS Data Analysis module is required to generate profiles from the Applied Biosystems Precision ID GlobalFiler NGS STR Panel v2. NGS analysis functionality includes information on Short Tandem Repeats (STRs) including allele calls, sequence motifs, Single Nucleotide Polymorphisms (SNPs) in flanking regions. NGS data uses Applied Biosystems GeneMapper ID-X Software inspired process quality values (PQVs) and flags such as allele number (AN), off-ladder allele (OL), peak height ratio (PHR), below stochastic threshold (BST), and control concordance (CC). Preconfigured analysis settings are provided and may be modified by the laboratory as needed. Additionally, full auditing functionality is included for chain of custody requirements. Using the NGS Data Analysis module with the Case Management application allows for simplified comparison of NGS and CE profiles.

Converge Kinship and Paternity module integrates with Converge Software and GeneMapper ID-X genotyping software to help enable automated analysis, reporting of routine paternity and other relationship testing cases, and allows for genetic likelihood ratio calculation, as well as reporting.

Case Management application supports case, subject, genotype profile, and laboratory data management, and allows for automated data transfer and integration with various forensic DNA laboratory systems.

NEW FEATURES

Modifications have been made to Precision ID GlobalFiler™ NGS STR Panel v2 and its analysis files.

INSTALLATION/UPGRADE

TSS

It is recommended that your Torrent Server, Ion Chef, and Ion S5/S5 XL remain on TSS 5.2.2. For TSS v5.2.2 support documentation, refer to the NGS Software Support page here.

BED/JSON Files

The following files must be installed onto TSS v5.2.2 before analyzing data generated with Precision ID GlobalFiler NGS STR Panel v2:

The following files have been updated to v1.1 (previously v1.0):

- Precision_ID_GlobalFiler_NGS_STR_Panel_Target_v1.1.bed
- Precision_ID_GlobalFiler_NGS_STR_Panel_Hotspot_v1.1.bed
- Precision_ID_GlobalFiler_NGS_STR_Panel_AnalysisParams_v1.1.json
- Precision_ID_GlobalFiler_NGS_STR_Control_Sample_male007_v1.1.json (Template-1002 in Converge)
- Precision_ID_GlobalFiler_NGS_STR_Control_Sample_9947A_v1.1.json (Template-1003 in Converge)
- Precision_ID_GlobalFiler_NGS_STR_Control_Sample_NegCtrl_v1.1 (Template-1004 in Converge)
- Precision_ID_GlobalFiler_NGS_STR_Control_Sample_9947A_and_male007_and_NegCtrl_v1.1 (Template-1005 in Converge)

Download the analysis files here.

Once the zip file has been downloaded, it can be unzipped and installed on the Torrent Suite server.

Under the “Admin” tab in Converge, in the “Add-ons” section, in the “Manage Add-ons” sub-section, please disregard the following files and refer to the newest versions provided in links.

- Precision_ID_GlobalFiler_NGS_STR_Panel_Target_v1.0
- Precision_ID_GlobalFiler_NGS_STR_Panel_Hotspot_v1.0
- Precision_ID_GlobalFiler_NGS_STR_Panel_AnalysisParams_v1.0

Under the “Admin” tab in Converge, in the “Global Settings” section, in the “Manage Templates” sub- section, please disregard the following templates and use the new versions of the files instead.

- Template-1002, Template-1003, Template-1004, Template-1005

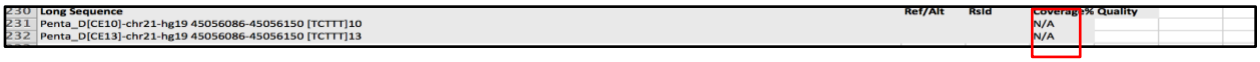
KNOWN ISSUES AND LIMITATIONS

Converge Software 2.0

1. Microsoft™ Excel files exported from the STR grid in the results page do not filter alleles showing zero coverage. The results page in the user interface accurately filters these instances.

23	DS5818	10, 13	PASS	PASS	PASS	
	Allele		Status	Coverage	Sequence	Long Sequence
	10		ABOVE_ST	3008	[AGAT]10	DS5818[CE10]-chr5-hg19 123111250-123111293 [AGAT]10
	10			0	[AGAT]10	DS5818[CE10]-chr5-hg19 123111250-123111293 [AGAT]10
	10			2999	[AGAT]10	DS5818[CE10]-chr5-hg19 123111250-123111293 [AGAT]10 123111306-G
	10			2	[AGAT]10	DS5818[CE10]-chr5-hg19 123111250-123111293 [AGAT]10 123111306-_
	10			5	[AGAT]10	DS5818[CE10]-chr5-hg19 123111250-123111293 [AGAT]10 123111306-G 123111309-_
	10			2	[AGAT]10	DS5818[CE10]-chr5-hg19 123111250-123111293 [AGAT]10 123111214-_ 123111306-G
	13		ABOVE_ST	2057	[AGAT]13	DS5818[CE13]-chr5-hg19 123111250-123111293 [AGAT]13
	13			0	[AGAT]13	DS5818[CE13]-chr5-hg19 123111250-123111293 [AGAT]13
	13			2046	[AGAT]13	DS5818[CE13]-chr5-hg19 123111250-123111293 [AGAT]13 123111306-G
	13			2	[AGAT]13	DS5818[CE13]-chr5-hg19 123111250-123111293 [AGAT]13 123111305-_ 123111306-G
	13			3	[AGAT]13	DS5818[CE13]-chr5-hg19 123111250-123111293 [AGAT]13 123111306-_
	13			6	[AGAT]13	DS5818[CE13]-chr5-hg19 123111250-123111293 [AGAT]13 123111306-G 123111309-_

2. Excel files exported from the STR grid in the results page display some alleles with coverage percentage as ‘N/A’. This occurs when the forward strand coverage of alleles is zero. The results page in the user interface has the correct coverage percentage displayed.

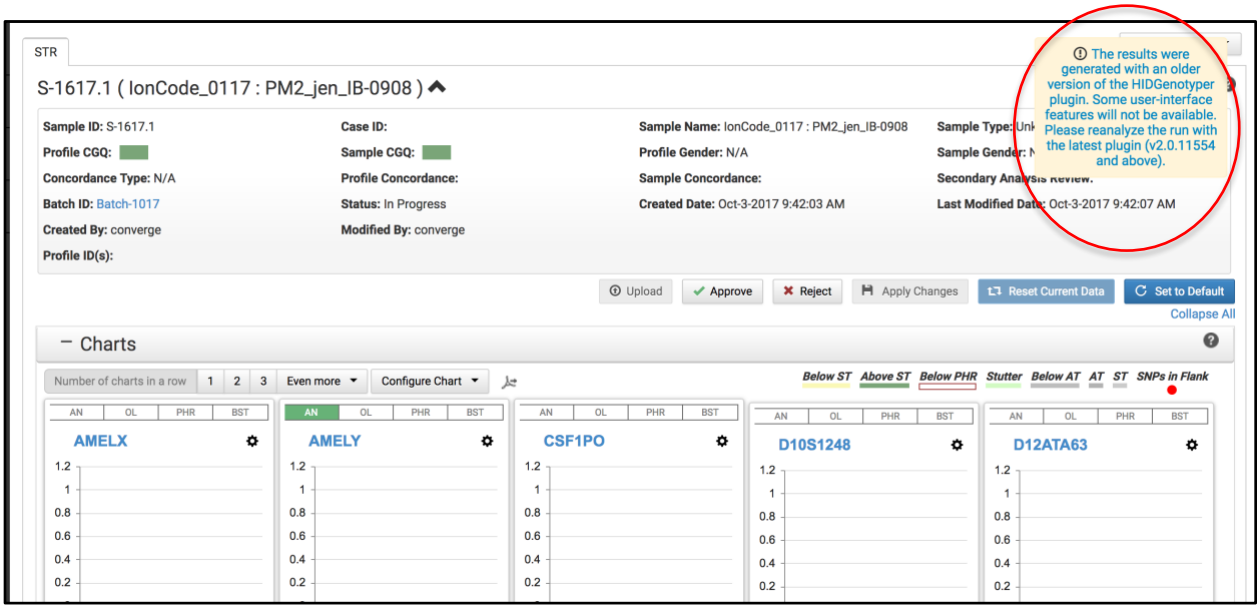


	Long Sequence	Ref/Alt	Rsid	Coverage	% Quality
231	Penta_D[CE10]-chr21-hg19 45056086-45056150 [TCTTT]10			N/A	
232	Penta_D[CE13]-chr21-hg19 45056086-45056150 [TCTTT]13			N/A	

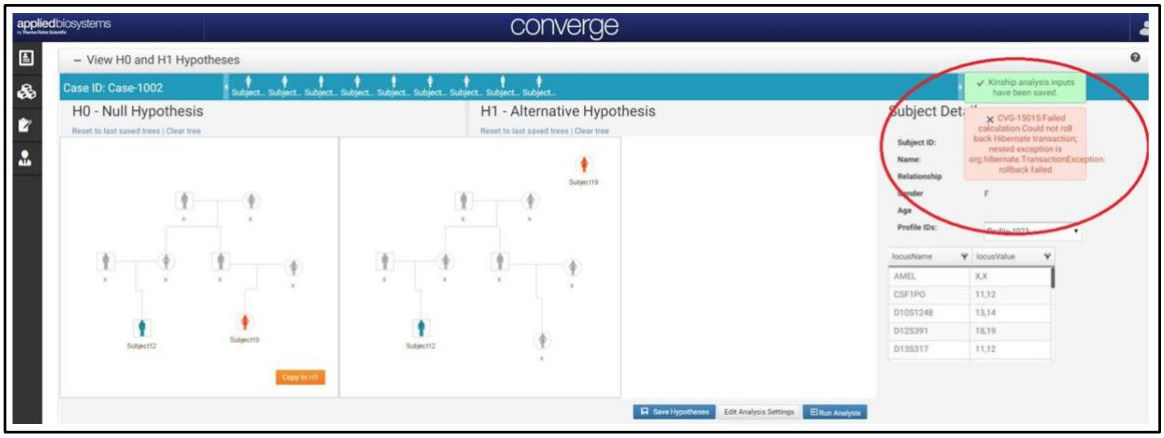
3. When a sample has no data after secondary analysis, Converge user interface displays the following message:

> ‘The results were generated with an older version of the HIDGenotyper plugin. Some user interface features will not be available. Please analyze the run with the latest plugin (v2.0.11554 and above).’

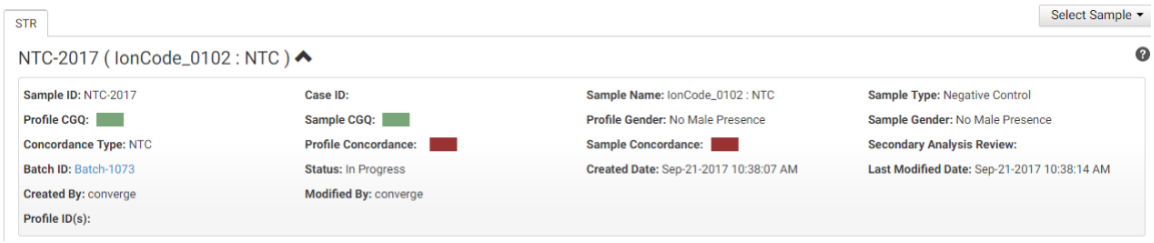
This error message is incorrect and should be ignored.



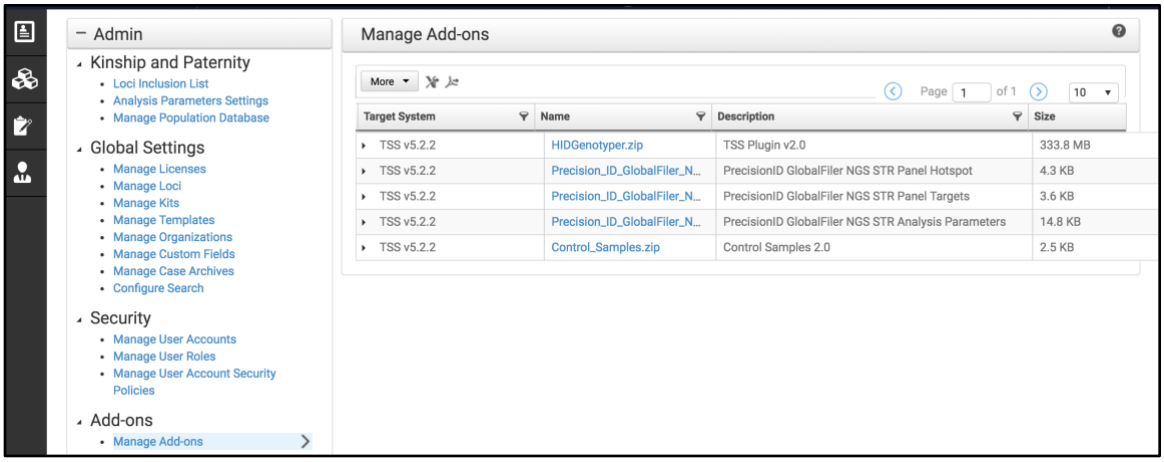
4. Transaction time out error might occur when using the kinship module for analysis that may exceed 1 minute.



5. CGQ flag does not account for the result of the concordance check. When the concordance (profile, sample level) has failed, indicated by red flag, on the results page on Converge, the CGQ (profile/sample level) is green, it should be red instead.



6. Under the “Admin” tab in Converge, in the “Add-ons” section, in the “Manage Add-ons” sub-section, please disregard the following: target, hotspot and analysis parameters files. To obtain these, refer to the URL provided in the installation/upgrade section above.



SYSTEM REQUIREMENTS

TSS

- TSS v5.2.2

Converge Software Server

- Dell™ PowerEdge™
- Red Hat™ Enterprise Linux™ operating system
- Apache™ Tomcat™ application server that runs on Converge software v2.0
- 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)

Supported Browsers

- Microsoft™ Internet Explorer™ v11
- Google Chrome™ 55
- Apple™ Safari™ v8

Recommended Software (not provided)

- Adobe™ Acrobat Reader
- Microsoft Excel

RELEASE & COMPATIBILITY SUMMARY

Updates in **BOLD** below.

SYSTEM	TYPE	DESCRIPTION	CURRENT VERSION	PREVIOUS VERSION
TSS	Software	TSS Compatibility	v5.2.2	N/A
Genotyper	Plugin	HIDGenotyper	v2.0_r16121	N/A
Control Publisher	Publisher	Control_Samples	v1.01	N/A
	Control File	**Precision_ID_GlobalFiler_NGS_STR_Control_Sample_male007**	**v1.1**	N/A
	Control File	**Precision_ID_GlobalFiler_NGS_STR_Control_Sample_9947A**	**v1.1**	N/A
	Control File	**Precision_ID_GlobalFiler_NGS_STR_Control_Sample_NegCtrl**	**v1.1**	N/A
	Control File	**Precision_ID_GlobalFiler_NGS_STR_Control_Sample_9947A_and_male007_and_NegCtrl**	**v1.1**	N/A
BED/ JSON File	Target	**Precision_ID_GlobalFiler_NGS_STR_Panel_Target.bed**	**v1.1**	v1.0
	Hotspot	**Precision_ID_GlobalFiler_NGS_STR_Panel_Hotspot.bed**	**v1.1**	v1.0
	Analysis Parameters	**Precision_ID_GlobalFiler_NGS_STR_Panel_AnalysisParams.json**	**v1.1**	v1.0
Converge	Platform	Platform	Serial No. 16151	N/A
	License	Platform	2.0	1.0
	Module	Case Management	2.0	2.0
	Module	Kinship and Paternity Analysis	1.0	1.0
	License	Kinship	1.0	1.0
	Module	Next-Generation Sequencing	1.0	N/A
	License	NGS	1.0	N/A

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