Converge[™] Software v2.1 Release Notes Case Management, Kinship and NGS Data Analysis Modules for STR, SNP and Mito

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PRODUCTS AFFECTED

- Converge Software v2.1
 - HID Genotyper Plugin v2.1
 - Next-Generation Sequencing Module for STR, SNPs and Mito Converge-NGS-1.1.zip
 - Upgrade Installer Files ConvergeUpgrade-2.1-0.x86_64.rpm, upgradecvg
 - Precision_ID_Panel_Definitions.zip
- Precision ID mtDNA Panels
 - Precision ID mtDNA Whole Genome Panel
 - Precision ID mtDNA Control Region Panel
- Precision ID SNP Panels
 - Precision ID Ancestry Panel
 - Precision ID Identity Panel
- Precision ID STR Panel
 - Precision ID GlobalFilerTM NGS STR Panel v2
- Precision ID Manual Library Preparation Kits
- Precision ID DL8 Chef Kit
- ➢ NGS Run Template on TSS 5.10
 - Run Template Precision ID mtDNA Control Region Panel S5
 - Run Template Precision ID mtDNA Whole Genome Panel S5
 - Run Template Precision ID Ancestry Panel S5
 - Run Template Precision ID Identity Panel S5
 - Run Template Precision ID GlobalFiler STR Panel S5

SOFTWARE OVERVIEW

Converge v2.1 is a third release of a multi-phased product suite for Next Generation Software Platform. This release of Converge Software provides analysis support for all current NGS Panels (STR, mtDNA, ancestry, identity and YSNPs), in addition to Paternity and Kinship testing. The software is built on a modular platform offering data storage and workflow capabilities, genotype calling, in addition to downstream tertiary sample analysis tools after genotyping.

KEY FEATURES IN CONVERGE v2.1:

- Analysis Modules NGS analysis modules integrates with the Torrent SuiteTM Software v5.10 for automatic import of sample data. The following new modules are available.
 - NGS mtDNA module for mitochondrial DNA- Perform Secondary Analysis of Mito sample data.
 - EMPOP classification and haplogroup prediction using April 2017 EMPOP release..
 - IGV Developed version 1.01b
 - Mito Variant Caller version 1.01b



- NGS SNP module for single nucleotide polymorphisms Perform Secondary and Tertiary analysis of SNP sample data.
 - Torrent Variant Caller version 5.2.25.
 - Ancestry predictions based on ALFRED and Identity likelihood based on 1000 Genomes Phase 3.
 - Y Haplogroup prediction based on Phylotree ISOGG 2014
 - Exclusion of SNPs and reanalysis of Tertiary analysis workflow in Converge.
- ▶ Profile Dashboard—Manage NGS and/or GeneMapperTM ID-X Software profiles.
- Sample Dashboard—Manage NGS sample information.
- Batch Dashboard—Manage NGS Batches, Create a New Batch for a run.
- Manage Applications—Install and uninstall applications, such as the NGS modules STR, SNPs, Mito. (Manage Applications is located in the Admin Dashboard under Global Settings.)

SYSTEM REQUIREMENTS CONVERGE v2.1:

- ➤ TSS v5.10 / S5 / S5XLTM or Ion GeneStudio TM Series Sequencer
- Converge Software Server & its components
 - DellTM PowerEdgeTM T130 Tower Server, motherboard v2 or later
 - Red Hat[™] Enterprise Linux[™] operating system
 - ApacheTM TomcatTM application server that runs on Converge software
 - PostgreSQL database server that stores the data for the server and software
 - GoogleTM ChromeTM browser
 - Automatic configuration of IP, domain name service (DNS), and Windows internet name service (WINS) settings via dynamic host configuration protocol (DHCP)
- Converge Software Server Specifications
 - Processor Intel[™] Xeon[™] Processor E3 1270 v6, 3.8 GHz, 8M cache, 4C/8T,turbo (72 W)
 - Memory 16 GB of memory (2 × 8 GB), UDIMM, 2400 MT/s, Single Rank, x8 Data Width, DVD ROM, SATA, Internal
 - Hard Drive (2) 2 TB 7.2 K RPM NLSAS, 12 GB/s, 3.5-in cabled hard drive (RAID1)
 - Data Storage RAID 1; PERC H330 Integrated Controller for 3.5-inch cabled hard drive
 - Operating System Red HatTM Enterprise LinuxTM operating system
 - Browser Google Chrome[™] 66 or later
- Recommended Software (not provided)
 - AdobeTM Acrobat Reader
 - Microsoft Excel
- ▶ Verified Converge v2.1 TM software workflow on Google ChromeTM and MAC Safari browsers.

INSTALLATION / UPGRADE:

Refer to Converge Software v2.1 SETUP AND REFERENCE GUIDE - Publication Number 100039539, Rev D for following instructions

- > Initial setup and configuration of Converge Software Server and Converge Software.
- ➤ Managing the ConvergeTM Software Server and licenses.
- > In addition, following sections covers Upgrade and Fresh Install workflow plus enhanced troubleshooting section.
 - Appendix A Troubleshooting Server networking, Password Issues, Access to log files, Restart Services, Reset IP address, Account Configuration and Dell T110 USB recognition.
 - Appendix B Upgrade to Converge v2.1 on Dell T110 and T130 Appliance Servers.
 - Appendix C Fresh Installation of Converge v2.1 on Dell T130 Appliance Sever.

Steps below provide additional reference links for TSS upgrade to 5.10 and supplemental files that need to be downloaded prior to starting an end to end run from TSS and generating a batch file on Converge[™] Software.

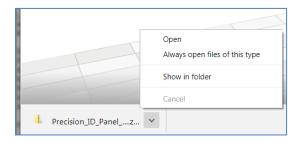
NOTE: In general, all the S3 Chrome Browser links provided below, downloads files to "Downloads" folder in your user account. When the download finishes, you'll see the linked file at the bottom of your Chrome window. To find a



file on your computer, next to the filename, click the arrow next to the file name > Show in folder link. Copy the downloaded files on to an external USB drive and insert into a readable port of the Converge appliance server for use.

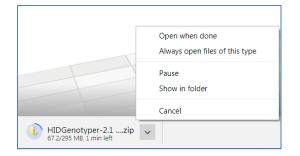
- TSS Upgrade your Torrent Server, Ion Chef, and Ion S5/S5 XL to TSS v5.10. For TSS v5.10 documentation, refer to the <u>TSS 5.10 User Guide</u> and <u>Release Notes</u>.
- Precision_ID_Panel_Definitions.zip Includes relevant Reference/BED and JSON Files and must be installed onto TSS v5.10 before analyzing data generated with Precision ID Chemistry. The zip file can be downloaded from <u>S3</u> or <u>TF.com</u> link.

Snapshot of the Downloaded Precision_ID_Panel_Definitions.zip file at bottom of your Chrome window. Click "Show in folder" to locate the file and copy it to an external USB drive and insert into a readable port of the Converge appliance server for use.



The Precision ID Panel definition.zip includes the following list of files:

- a. Mito Panel
 - Mito Reference Precision_ID_mtDNA_rCRS.fasta
 - Mito CR Target File Precision_ID_mtDNA_Control_Region_Panel_Targets_v1.0.bed
 - Mito WG Target File Precision_ID_mtDNA_Whole_Genome_Panel_Targets_v1.0.bed
 - Mito Analysis Parameter File Precision_ID_mtDNA_Panel_AnalysisParams_v1.0.json
- b. SNP Panel -
 - Ancestry Target File Precision_ID_Ancestry_Panel_Targets_v1.0.bed
 - Ancestry Hotspot File Precision_ID_Ancestry_Panel_Hotspot_v1.0.bed
 - Ancestry Analysis Parameter File Precision_ID_Ancestry_Panel_AnalysisParams_v1.0.json
 - Identity Target File Precision_ID_Identity_Panel_Targets_v1.0.bed
 - Identify Hotspot File Precision_ID_Identity_Panel_Hotspot_v1.0.bed
 - Identity Analysis Parameter File Precision_ID_Identity_Panel_AnalysisParams_v1.0.json
- c. STR Panel
 - 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
 - Precision_ID_GlobalFiler_NGS_STR_Control_Sample_9947A_v1.1.json
 - Precision_ID_GlobalFiler_NGS_STR_Control_Sample_NegCtrl_v1.1.json
 - Precision_ID_GlobalFiler_NGS_STR_Control_Sample_9947A_and_male007_and_NegCtrl_v1.1.json
- HID Genotyper v2.1 Plugin Download the plugin HIDGenotyper-2.1.zip from <u>S3 link</u> or <u>TF.com</u> for installation. Snapshot of the Downloaded HID Genotyper v2.1.zip file visible at bottom of your Chrome window is shown below. Click "Show in folder" to locate the file and copy it to an external USB drive.



Upload / configure plugin on supported Ion S5/S5XLTM or Ion GeneStudio Series Torrent Suite server. An example of successful configuration of HID Genotyper v2.1 Plugin with TSS and Converge v2.1 software is shown below.

Converge Account Configuration			
Converge Configura	ation	TSS Configuration	
User Name*:	converge@thermo.com	TSS User Name:	ionadmin
Password*:		API Key:	fdd5ab7043b6c1beb7717
URL*:	http://172.16.254.1/	Default Template:	Precision_ID_GlobalFil v
Default Instrument:			
		(*) Required fields	Submit
			Subline

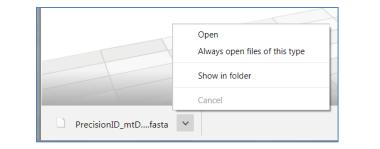
- Upgrade Installer Package Download following two files (Serial Number df70f6b-201808231621) from S3 link or <u>TF.com</u> for upgrading Converge v2.0.1 to Converge v2.1 software installed on Dell T110 or T130 Server.
 - ConvergeUpgrade-2.1-0.x86_64.rpm <u>S3 link</u>
 - upgradecvg <u>S3 link</u>

Snapshot of the Downloaded ConvergeUpgrade-2.1-0.x86_64.rpm and upgradecvg files at bottom of your Chrome window. Click "Show in folder" to locate the file and copy it to your local directory or an external USB drive and insert into a readable port of the Converge appliance server for use.

	Open when done			
	Always open files of this type			Open
	Pause			Always open files of this type
	Show in folder	_		Show in folder
	Cancel			Cancel
ConvergeUpgradrpm 29.1/438 MB, 2 mins left	~		😂 upgradecvg	~

Refer to Converge[™] Software v2.1 SETUP AND REFERENCE GUIDE - Publication Number 100039539, Rev D (Appendix B) for instructions on steps to upgrade to Converge v2.1 software

Download Mito reference file "Precision_ID_mtDNA_rCRS.fasta" (NCBI reference NC_012920) file from <u>S3 link</u> or <u>TF.com</u>. Snapshot of the Downloaded Precision_ID_mtDNA_rCRS.fasta file at bottom of your Chrome window. Click "Show in folder" to locate the file and copy it to an external USB drive. Upload the file onto TSS > Reference Page as shown below.



> Reference Sequences			Imp	ort Preloaded Ion R	eferences Import Custom Ref	ierence	
> Obsolete Reference Sequences	Reference Sequen	ces					
> Target Regions							
Hotspots	Short Name	Description	Notes	Enabled	Date v	Status	
Test Fragments Barcodes	HPV	GeneTree		true	Feb 19 2018	Successfully Completed	
Upload History	PrecisionID_mtDNA_rCRS	Mito		true	Aug 21 2017	Successfully Completed	
	hg19	Homo sapiens		true	Nov 5 2016	Successfully Completed	
	e_coli_dh10b	E. coli DH10B		true	Feb 14 2013	Successfully Completed	

- Readme.txt instructions can be downloaded from <u>S3 link</u> or <u>TF.com</u> to a USB and inserted into a readable port of the Converge appliance server for use. For any technical support on upgrade path, contact local FAS team member.
- Converge-NGS-1.1.zip Download Converge-NGS-1.1.zip file from <u>S3</u> or <u>TF.com</u> links. Snapshot of the Downloaded Converge-NGS-1.1.zip file at bottom of your Chrome window. Click "Show in folder" to locate the file and copy it to an external USB drive.

	Open Always open files of this type
	Show in folder
	Cancel
Converge-NGS-1.1z	~

- Post upgrade from Converge v2.0 / v2.0.1 > Converge v2.1 version, install Case management license at minimum, followed by uploading NGS Application Bundle package (Converge-NGS-1.1.zip) onto Converge > Admin > Manage Application Software page (snapshot shown below).
- Once installed proceed to install and activate NGS license downloaded from https://licensing.appliedbiosystems.com/web/login web portal.



- Admin 0 Manage Applications Kinship and Paternity LInstall Application Analysis Parameters Setting
 Manage Population Databas Installed Applications ŵ Converge-NGS-Bundle 1.1 Global Settings ed On: Sep-11-2018 7:23:46 PM NGS-STR NGS-SNP NGS-MH ** 8 11 NGS-Mito Ancestry Identity ELL 27) å Security Manage U m NGS-Batch 1.1 d On: Sep-11-2018 7:23:28 PM Audit NGS-Batch Manage Audit

NOTE:

- During upgrade from Converge v2.0 and v2.1, install NGS Application Bundle and NGS License prior to navigation through the Converge Software workflow. If user has not installed the NGS Application bundle and corresponding licenses, certain actions for example deletion of batches may lead to loss of user data.
- For Fresh Installation on Dell T130, Converge-NGS-1.1 application modules comes pre-installed by default.

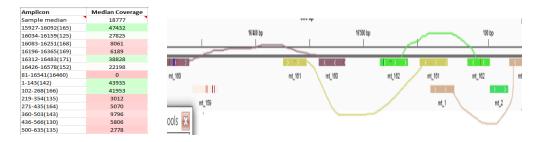
UPDATES TO CONVERGE™ SOFTWARE v2.1 HELP TOPICS

Refer to Converge[™] Software v2.1 Help contained in the software for following updates::

- New workflow and Analysis procedures.
 - NGS mtDNA & SNP workflow
 - Sample Dashboard
 - Profile Dashboard
 - Manage Applications
- Troubleshooting procedures.
 - o NGS Module workflow, Display Issues, Profile Management, and Kinship & Paternity features.

KNOWN ISSUES AND LIMITATIONS:

- Data Related:
 - Median Coverage of Amplicon calculation excludes overlapping amplicon read coverage, as such, when reads for overlapping amplicons are removed amplicon coverage is zeroed out (as seen in variant_colored.xls output file and screenshot below).

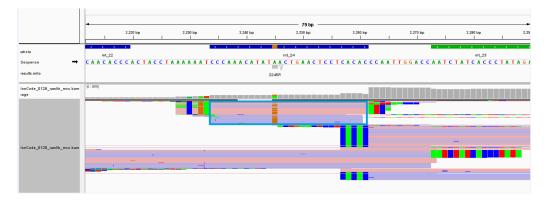


• For overlapping amplicons, the software selects only one amplicon coverage value for display even when there are significant coverage differences between the amplicons. Example: Software displays the coverage for position 263, spanned by 2 amplicons with coverages of 4839x and 542x. as of now it is considering the lesser of the two values which is 542x. In addition, comments in the variant colored xls sheet displays incorrect information on the coverage stats



	A	В	C	Date Bam file									
1	Amplicon	Median Cov	erage	Sample	2_00	it.5850/mi	to/loncode	0149/result	ts/loncode	0149_rawl	b_mvc.bam		
2	Sample median	4017	er uge	Close haple Regions									
3	1-143(142)	6882		Position	Re			Artefact	Var Strand	Read Stran	EMPOP	Score	Comment
×	102-268(166)	4839		64			28.5	Point Heter		0.6	unexpected		no strand blas in variant reads;not listed in X2d1 or its subgroups; found 3.06% in EMPOP;
1-1-1-	and the second)	73		confirmed		True varian		0.6 0.5	unchecked unchecked		no strand bias in variant reads;73G is expected in X2d1 or its subgroups; found 76.26% in EMPOP;
~	219-354(135)	542		195		confirmed confirmed		True varian		0.5	unchecked		no strand bias in variant reads;195C is expected in X2d1 or its subgroups; found 20.78% in EMPOP; no strand bias in variant reads;204C is expected in X2d1 or its subgroups; found 6.1% in EMPOP;
6	271-435(164)	417	and second	1		confirmed confirmed		True varian		0.5	unchecked		no strand bias in variant reads;204C is expected in X2d1 or its subgroups; found 6.1% in EMPOP; no strand bias in variant reads;207A is expected in X2d1 or its subgroups; found 4.52% in EMPOP;
7	360-503(143)	541					, · · · ·	_		,		ſ	no strand bias in variant reads; The coverage is only 544 compared to the median 3686 for this
8	436-566(130)	490		263		confirmed	100	True	0.5	0.6	unchecke d	0.903	amplicon (might be sequencing artefact);263G is expected in X2d1 or its subgroups; found 96.88% in EMPOP:
•	430-300(130)			309	:			Length Het		0.7	confirmed		The reference has HP 7 (might be indel artefact): (the sample sequence might have HP 8): no strand bia
9	500-635(135)	196		315		likely	56.2	Length Het	0.9	5.7	confirmed	0.693	The reference has HP 5 (might be indel artefact); (the sample sequence might have HP 6); no strand bia
				709		confirmed	99.1	True varian	0.5	0.5	unchecked	1	no strand bias in variant reads;709A is expected in X2d1 or its subgroups; found 14.33% in EMPOP;
10	571-732(161)	5428		750		confirmed		True varian		0.5	unchecked	1	no strand bias in variant reads;750G is expected in X2d1 or its subgroups; found 98.96% in EMPOP;
11	663-830(167)	4798		1438		confirmed		True varian		0.6	unchecked		no strand bias in variant reads;1438G is expected in X2d1 or its subgroups; found 95.74% in EMPOP;
				1719		confirmed		True varian		0.6	unchecked		no strand bias in variant reads;1719A is expected in X2d1 or its subgroups; found 5.75% in EMPOP;
12	771-930(159)	5347		2706		confirmed		True varian		0.7	unchecked		no strand bias in variant reads;2706G is expected in X2d1 or its subgroups; found 79.31% in EMPOP;
		2450		4769		confirmed		True varian		0.5	unchecked		no strand bias in variant reads;4769G is expected in X2d1 or its subgroups; found 98.39% in EMPOP;
13	868-1029(161)	2450		4929		possible confirmed		True varian			unknown i		no strand bias in variant reads; not listed in X2d1 or its subgroups;
14	964-1138(174)	4717		5186		confirmed		True varian True varian		0.7 0.5	unchecked		no strand bias in variant reads;5186G is expected in X2d1 or its subgroups; found 0.16% in EMPOP;
				6221		confirmed		True varian		0.5	unchecked unchecked		no strand bias in variant reads;6221C is expected in X2d1 or its subgroups; found 3.1% in EMPOP;
15	1092-1266(174)	3687		6791		confirmed		True varian		0.6	unchecked		no strand bias in variant reads;6371T is expected in X2d1 or its subgroups; found 1.58% in EMPOP; no strand bias in variant reads;6791G is expected in X2d1 or its subgroups; found 0.17% in EMPOP;
10	1212 1222/1051	7844		7028		confirmed		True varian		0.5	unchecked		no strand bias in variant reads;079201s expected in X201 of its subgroups; found 0.17% in EMPOP; no strand bias in variant reads;7028T is expected in X201 of its subgroups; found 80.48% in EMPOP;
10	1212-1377(165)	/844		8503		confirmed		True varian		5.9	unchecked		no strand bias in variant reads; 7020 is expected in X201 or its subgroups; found 0.18% in EMPOP; no strand bias in variant reads;8503C is expected in X201 or its subgroups; found 0.18% in EMPOP;
17	1317-1491(174)	7918		8860		confirmed		True varian		0.5	unchecked		no strand bias in variant reads;8360G is expected in X2d1 of its subgroups; found 9:46% in EMPOP; no strand bias in variant reads;8860G is expected in X2d1 of its subgroups; found 9:46% in EMPOP;
- '		/ 510		11719		confirmed		Truevarian		h s	unchecked		no strand blac in variant reads:11719A is expected in ¥2d1 or its subgroups; found 76,81% in FMPOP

• In certain samples with low amount of DNA (< 0.1ng) or degraded DNA and / or high amount of primer dimer, not all primer sequence get removed. In these cases, both the target sequence that contributes to the variant call and primer sequences are used to determine the variant classification.



• Excluded region in IGV is off by 1 base, independent of what "virtual kit"/ regions analysed is selected. Note -The beginning of the marker (highlighted in red in IGV, where start position 578 instead of 577, is off by 1. All the end positions are correctly displayed though.

PrecisionID_mt \$	chrM 🗘	chrM:550-601	Go	₫ • →	🗟 🥱 🍖 🤅) 🛛 X 🗖	l 🛟 🔲 🦉 🗽 (j) 📰 🔌 EM 🛛 📄 I I	
	•					52 bp			,
<	50 bp	I	560 bp	I	570 bp	1	580 bp	590 bp	600 bp
Sequence →	AACC	AAACC	C C A A	AGAC	ACCCC	C C A C A G	Location: 578 Click and drag to zoom	A G C T T A C C T C	CTCAAA

• Confirmed variants are used for mtDNA haplotype profile comparisons at the batch and case level. In some instances, match results may differ between batch and case levels. In the example below, the reference is missing a variant at position 150 that is present in the unknown profile; the variant is considered for match% calculation, and the software displays this as a mismatch for the case level comparison.

applied biosystems

For the same comparison at the batch level, position 150 is ignored

Batch Level Comparison Match % (4/10 = 40%)

Case Level Comparison Match %	(4/15 = 26.7%)
-------------------------------	----------------

			Position 9	Profile-1326	Profile-1327
Manual_Mt-CR_CHR_Rep1 (N)	Manual_Mt-CR_HL60_Rep2 (J2b1a1a)	1		(Precision_ID_mtDNA_Control_Region_Panel_v1.0)	(Precision_ID_mtDNA_Control_Region_Panel_v1.0)
(N) 64Y			73	73G	73G
	Meta Data		195	195C	
736	Percentage Natch: 40		204	204C	
195C					
204C			207	207A	•
207A	•		263	263G	263G
263G	263G		16189	16189C	•
309c	309c		16278	16278T	16278T
309.1C	•		16519	16519C	-
315.1C	315.1C		16642	16642G	16642G
16183C	÷			_	
16189C			150	·	150T
16193.1C	•		152	•	152C
16223Y	-		295	·	295T
16224Y			489	·	489C
16079T	16079T		Variant Match %		26.7%

- Converge software calls variants in accordance with ISFG and IUPAC recommendations. As such, lower case variants should be displayed as "del". The following examples highlights inconsistencies in nomenclature for certain software displays.
 - a. 16640g is incorrectly displayed in the variant grid and should be "16640del" with a "-" deletion icon.

S-1065	.1 (DLI	B_Mt-C	R_GM099474	Rep	2) ^											0
Median C Concords Batch ID: Last Mod	1-610, 15	1508 N/A 00 Jul-18-3	018 10:26:43 AM 9		Case ID: Closest H Profile Co Status: In Created B	oncordan Progres	ice: N/A			Profile Ger Sample Co	nder: N/ incorda arameti	nce: N/A ere: Analysis Pr		Semple Type: Unknow Sample Gender: N/A Secondary Analysis R Greated Date: Jul-18-2	eview:	
								-	Compare	@ Upload	~ A	sprove × Re	gent M Apply C	hanges 👘 🏝 Load Data From		Collapse All
- G	rid															0
- G		called Vi	wiants Unexpr	soted Var	riants E	ischuded 1	Variants								O meetier	e Defetion
	yte Lle	called V	arlants Unexpe	roted Var	rients E	Linchuded 1	Variants								O meertier	
Variar	yte Lle	called V	Frequency O	ected Var	lients E Status	Lachaded	Variants EMPOP State	~]	Var Strand Bi	ian O		Classification		Variant Goverage 😝	O Assertion	• O Defetion
Variar	16 U	called V							Var Strand Bi	las O	×	Classification True Varian	4	Varient Coverage @		• O Defetion
Variar Nr Je	to Ui e Variant		Frequency O		Status	ed eat	EMPOP State			las 0	4				U Quality S	• O Defetion
Variar Nr Je	vie Ui e Variant 936		Frequency O		Status O Confirme	~ ed	EMPOP State Unchecked		0.5	lan O	*	O True Varian		19030	U Quality S	• O Defetion
Variar Nr 2-	Variant 03C	~	Frequency 0 99.12 99.61		Status Confirms Confirms Confirms	v ed ed	EMPOP State Unchecked Unchecked		0.5	int O	*	O True Varian	*	19030	U Quality S	• O Defetion
Variar Nr 2-	Vie Li Verlant 03G 195 214 263 0 309	~ 1 1 1 0	Frequency O 00.12 00.61 00.53	•	Status Confirms Confirms Confirms Confirms Confirms	ed ed ed	EMPOP State Unchecked Unchecked Unchecked		0.5 0.5 0.5 0.5 0.5	ian Q	×	True Varian True Varian True Varian True Varian	4 4	19030 37328 37176	Quality 5	• O Defetion
Variar N° 25	vis Ui e Variant 93G 195 214 263	~ 1 1 1 0	Frequency () 00.12 00.61 00.53 00.04	•	Status Confirms Confirms Confirms	ed ed ed	EMPOP State Unchecked Unchecked Unchecked Unchecked		0.5 0.5 0.5	ini O	*	True Varian True Varian True Varian True Varian True Varian	e eroplasmy	19030 37328 37176 3352	- Quality 5 1 1 1 1 1	• O Defetion
Variar St Ja	Vie Li Verlant 03G 195 214 263 0 309		Prequency () 00.12 00.61 00.53 00.04 85.77	•	Status Confirms Confirms Confirms Confirms Confirms	ed ed ed ed	EMPOP State Unchecked Unchecked Unchecked Unchecked Confirmed		0.5 0.5 0.5 0.5 0.5	hat O	*	C True Varian True Varian True Varian True Varian Length Hee Length Hee True Varian	e eropiasmy eropiasmy eropiasmy	19030 37328 37176 3352 2795	Quality 5	• O Defetion
Variar 34 34	Viri Ui Variant 930 1950 2140 2630 0 309 0 315	× 3 3 10 10 10 90	Frequency 0 99.12 99.53 99.94 35.77 48.34	*	Batus Confirms Confirms Confirms Confirms Likely Possible	ed ed ed ed ed ed	EMPOP State Unchecked Unchecked Unchecked Confirmed Confirmed		0.5 0.5 0.5 0.5 0.55 0.9	int O	~	C True Varian True Varian True Varian True Varian Length Het Length Het	e eropiasmy eropiasmy eropiasmy	19030 37328 37176 3852 2795 3754	Quality 5	• O Defetion

b. Deletion variants are being saved with upper case "DEL" and lower case "del", although they reflect the same deletion w.r.t to comparison but is different w.r.t to frequency/display..

				C	onvera	e				
		Compare Pro	files					>		
	- Profile(s)	Profile ID(r)	ofile-1006 Profile-1	007 Profile-1008	Profile-1009 Profil		h 🗙 Not a match 📥	Partial match ON/A		
	+ New Profile More -	Nr Ja	one root rrome r	007 110110 1000	1101110 1005 111011	- 1010 11000-101				
X	e se	Position ¥	Profile-1006 ¥ (Precision_ID_mtDN	Profile-1007	Profile-1008 (Precision_ID_mt	Profile-1009 (Precision_ID_mt	Profile-1010 (Precision_ID_mt	Profile-1011 (Precision_ID_mt	Page 1 of 1	20 .
	Profile ID *	73	73G	73G	73G	73G	736	73G	Sample Name 🛛 🌱	Action
	Profile-1000	195	195C	195C		•		195C	DL8_Mt-CR_HL60_Rep1	
	Profile-1001	204	204C	204C	-			204C	DL8_Mt-CR_CHR_Rep2	• • • •
	Profile-1002	207	207A	207A				207A	DL8_Mt-CR_NA10742A	
	Profile-1003	263	263G	263G	263G, 263T	263G	263G	263G	DL8_Mt-CR_CHR_Rep1	• • • •
	Profile-1004	309	309c	309c	309DEL	309DEL	309DEL	309c	DL8_Mt-CR_NA10742A	
	Profile-1005	16189	16189C	16189C	-			16189C	DL8_Mt-CR_HL60_Rep1	• • • •
	Profile-1006	16223	16223T	16223T				16223T	DL8_Mt-CR_CHR_Rep2	
	Profile-1007	16278	16278T	16278T	16278T			16278T	DL8_Mt-CR_CHR_Rep1	
	Profile-1008	16519	16519C	16519C				16519C	DL8_Mt-CR_HL60_Rep1	
	Profile-1009	16642	16642G	16642G	16642G	16642G	16642G	16642G	DL8_Mt-CR_NA10742A	
	Profile-1010	150			150T	•		*	DL8_Mt-CR_NA10742A	
	Profile-1011	152		-	152C			-	DL8_Mt-CR_CHR_Rep1	
	 Sample 	Variant Match %		100%	22.2%	15%	15%	100%		•
	More -							OK		
X	e , , , , , , , , , , , , , , , , , , ,							O	Page 1 of 1) 10 -
	Sample ID		Υ.	Sample Name			Y Sample Type		`	Action
	\$-1024.1			DL8_Mt-CR_HL60_R	Rep1		Unknown			
	S-1027.1			DL8 MI-CR NA1074			Unknown			

• Mito Results Page > Variants classified as Degraded in "Grid>Unexpected" tab are not captured in "variant_colored.xls" excel output file..

Variants	Uncalled Variants	Unexp	ected Variants	Excluded Variants						
Xx										
Variant	- Frequency 0	v	Status 🗸	Var Strand Bias 0	Classification 🛓 🗸 🗸					
16319R	11.29		O False	0.8	O Degraded	Unexpect	ed variants o	f l2b1a1ati	hat were list	ed
16320Y	12.86		🕄 False	0.77	O Degraded	onexpect	eu variarits e		at were not	
16327Y	20.29		C False	0.6	O Degraded	Variant	Frequency	State	Var Strand	EMPOP state
🖨 309del	67.29		🖲 Unclear	0.87	9 Length Heteroplasmy	309del	67.3	unclear	0.9	UNEXPECTED
16325Y	14.96		🖲 Unclear	0.73	Point Heteroplasmy	16325Y	15	unclear	0.7	UNEXPECTED

• Mito Quality Scores are rounded off up to 2 decimal places but original values are used for state determination For e.g. Calls with score 0.82 has state as "Likely" when score >= 0.82 maps to "Confirmed" & < 0.82 maps to "Likely" state. The reason is that the actual score is 0.815 (as seen in variant_colored.xls output file) but it is rounded up to 2 decimal places & displayed as 0.82.

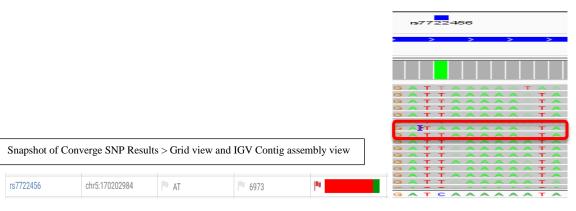
16311C	93.11	Likely	Unchecked	0.53	True Variant	2758	0.82

• Both LHP & PHP variants get reported at same location for single source. Example two calls observed at position 16192 - 16192Y & 16192.1T. For a single source it is not expected to have variants classified as both LHP & PHP. As seen in the variant_colored.xls export file (snapshot below), 23.5% of T inserts ideally should be classified as a sequence artefact and not a true positive call for a single source.

Position	Ref	Sam	p Varia	a Var Freq	Туре	Read Co	ve Read Co	ove Allele C	ov Allele	Cov Alle	l(G%	A%	Т%	C%	N%	ins%	del%	Polymorp	Control R	e State	Freque	ency Artefact	Var Stra	nc Read Stra
16192	С	T	Y	60.5	SNP	227	747	589	134	455	0	0.1	60.5	35.4	0	0.1	4	16192Y	16192Y	possible	60.5	Point Het	0.5	0.8
16192	С	+	T	21.3	INS	227	748	208	56	152	0	0	0	0	0	23.5	0	16192.1T	16192.1T	possible	21.3	Length He	0.5	0.8
																					_			
				~	с	с	с	c	с					с	_	c	c	•	т	G				
				-	-	-	~	~		1618		5		-		-	-	-						
															161	192	Y S				L			
														1	61	92.	1 T							
			-																					
			_																					
					_	-															1			
																		-	-					

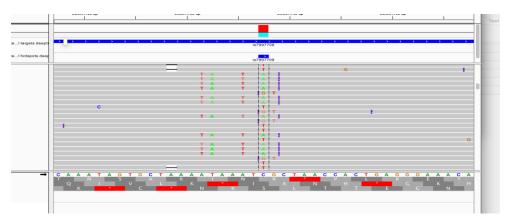
- Consensus.fasta downloaded from Mito Results grid contains the entire reference genome as opposed to three different contigs covering HV1, HV2, HV123 or intervening regions should have been masked with an "N" calls.
- Genotype errors are around homopolymer regions with too many wrong A reads. For example rs7722456 (aiSNP) which lies near homopolymer region (6As) because of which some A bases incorrectly align with rs7722456 position & hence, "A" Genotype call is added. ~15% of reads show an "A" call as seen in the contig assembly snapshot in IGV Browser and could be due to a sequence artefact around homopolymer regions.

applied biosystems



Additional SNP id's with similar noise issues -

- rs772262 C noise is added to this SNP position because of poly Cs (5Cs)
- rs13400937- T noise is added to this SNP position because of poly Ts (4 Ts)
- rs7997709 A & G noise added due to polyA region close by (screenshot below)



- The following aiSNPs do not have frequency values in the seeded population table and thus excluded from tertiary calculations: rs6541030, rs2814778, rs13400937, rs1369093, rs3811801, rs6556352, rs7722456, rs6422347, rs731257, rs6464211, rs3943253, rs2306040, rs2073821, rs4918842, rs214678, rs9319336, rs17642714, rs7238445, rs3907047, rs310644.
- SNPs are assumed to be bi-allelic; we rarely observe a third allele for some SNPs (e.g., rs1503767). Since we don't have frequencies for these alleles, they are ignored from the calculation.



• SNP ID rs938283 from the Identity Panel does not have frequency values in 1000 Genomes population table and hence ignored in Random Match Probabilities (RMP) calculations.

- General Functionality, IGV and TSS Workflow:
 - Converge v2.1 does not have audit capability features enabled for the supported mtDNA analysis workflow.
 Further, Mito IGV contains advanced user analysis settings in an unsupported workflow. Variant edits made in Mito IGV are auditable (steps & screenshot below) to a limited extent; changes to advanced analysis settings are not auditable. Steps to perform the Mito IGV analysis workflow are as follows:
 - a. Launch IGV > Make edits > Right click in the variants track
 - b. Select "Save results.mito" > Right click again > Select "Export Mito Data to"
 - c. Followed by "Excel colored file with all variants"



- Grid "Preference Settings" for Batch Details > Mito Results Card does not have options to be configured and saved.
- "Export Results" from Batch Details > Mito Results Card works only for a smaller set of sample results (up to 10).
- A user may reanalyse samples in IGV with modified parameters using "Load from IGV" workflow in Converge. Post Reanalysis in IGV with modified parameters, the analysis parameters on Converge > Mito Results > Summary Pane does not get updated although genotype changes get recorded.

edbiosystems		Analysis Para	ametere		/erae		~			
\$-1117.1 (1	damual Mt.C	,								
		Sta	ndard				- 8			
Sample ID: S-11 Median Covera		Min total read or	overage per posi	tion	20		Unknown w: N/A elysis Review:			
Concordance T	pe: N/A	Min variant cove	rage to call		20					
Batch ID: Batch		Coverage thresh	old to mark regi	n	20	A.0	Aug-24-2018 12:31:20 PM			
Region: 1-576 .	ate: Aug-24-2018	Min coverage pe	roent compared	to the median of the amplicon	5	- 8				
Profile ID(s):		Threshold for co	onfirmed call		96	- 8				
		Threshold for PF	HP call		10	F10	Collapse AJ			
		Threshold for in	sertion call		20	- 8				
- Grid		Threshold for de	eletion call		30	- 8				
Variants		Remove contam	inant reads		0	- 8				
XX		Include variants	flagged as NUM	T or DEGRADED	0	- 8				
Variant	. Frequency	Show input BAM	t in IGV		•	- 8		Quality Score		
© 309del	67.29	Regions to analy	/ze		control		- 8		0.34	
16319R	16319R 11.29					- 1		0.03		
16320Y	12.86					Cancel		0		
16325Y	14.96		O Unclear	0.73	O Point Heteroplasmy	473	_		0.35	
16327Y	20.29		O False	0.6		636			0	

- Profile comparison grid does not export the entire grid (pdf format) and screen captures are required to capture the entire grid.
- User Defined Custom Templates created in Converge 2.0 version needs to be reimported using "Admin > Manage Template" Workflow, post upgrade from Converge v2.0 > v2.1.
- Batch (.bef) file generation fails if TSS is offline mode, since Converge Software fails to fetch valid host IP. Meaning if TSS server runs as a stand-alone (non-networked) server where the plugins are hosted, then the HIDGenotyper plugin would fail while trying to fetch the host id of the server. And though the analysis will complete for all the samples involved, but the previous exceptions would prevent it from generating the .bef

(batch export file).

This known issue will be addressed in subsequent release of HID Genotyper Plugin.

• In certain network topology, S5 Data Collection system does not automatically sync the run plan on the chip. There is hence a delay in Data Collection server updating run plan on TSS v5.10 server and hence expected run plans do not get updated. The workaround is to restart Data Collection server and restart S5 sequence analysis workflow.

This known issue will be addressed in next patch release of Data Collection and TSS server v5.10.1.

Steps to be taken and workaround -

a. In the run selection page, notice that S5 does not automatically sync the run plan in the "Planned run field" when the chip barcode gets displayed (snapshot below)



b. Workaround , is to keep chip in S5 > Restart Data Collection > Run > selecting "Next" in "Load Chip" screen > S5 automatically selects correct run plan



RELEASE & COMPATIBILITY SUMMARY:

SYSTEM	ТҮРЕ	DESCRIPTION	VERSION / DATE STAMP
	Software	TSS Compatibility	v5.10
		Precision ID mtDNA Control Region Panel - S5	June 23 rd 2018
TSS		Precision ID mtDNA Whole Genome Panel - S5	June 23 rd 2018
	Run Templates	Precision ID Ancestry Panel - S5	June 23 rd 2018
		Precision ID Identity Panel - S5	June 23 rd 2018
		Precision ID GlobalFiler STR Panel - S5	June 23 rd 2018
	Publisher	Control_Samples	v1.01
		Precision_ID_GlobalFiler_NGS_STR_Control_Sample_male007	v1.1
TSS Control	STR Control	Precision_ID_GlobalFiler_NGS_STR_Control_Sample_9947A	v1.1
Publisher	Files	Precision_ID_GlobalFiler_NGS_STR_Control_Sample_NegCtrl	v1.1
		Precision_ID_GlobalFiler_NGS_STR_Control_Sample_9947A_and_male 007_and_NegCtrl	v1.1
		Precision_ID_mtDNA_Whole_Genome_Panel_Targets_v1.0.bed	v1.0
	NGS mtDNA Module	Precision_ID_mtDNA_Control_Region_Panel_Targets_v1.0.bed	v1.0
		Precision_ID_mtDNA_Panel_AnalysisParams_v1.0.json	v1.0
BED/	NGS SNP Module	Precision_ID_Ancestry_Panel_Targets_v1.0.bed	v1.0
JSON File		Precision_ID_Ancestry_Panel_Hotspot_v1.0.bed	v1.0
		Precision_ID_Identity_Panel_Target_v1.0.bed	v1.0
		Precision_ID_Identity_Panel_Hotspot_v1.0.bed	v1.0
		Precision_ID_GlobalFiler_NGS_STR_Panel_Target	v1.1
	NGS STR Module	Precision_ID_GlobalFiler_NGS_STR_Panel_Hotspot	v1.1
		Precision_ID_GlobalFiler_NGS_STR_Panel_AnalysisParams	v1.1
HID Genotyper	Plugin	HIDGenotyper-2.1 (Serial No.)	2.1_df70f6b
	Software	About (Serial No.)	df70f6b- 201808231621
	Module	Platform	v2.1
	License	Case Management	v1.0
	Module	Kinship and Paternity Analysis	v1.0
Converge	License	Converge Kinship	v1.0
Software	Module	NGS Application	v1.1
	License	Converge NGS	v1.0
	Upgrade Installer	ConvergeUpgrade-2.1-0.x86_64.rpm (Serial No.)	df70f6b-
	Components	upgradecvg (Serial No.)	201808231621
	Supplemental	Converge-NGS-1.1.zip	v1.1



Files Precision_ID_Panel_Definitions.zip

Oct 15th 2018 July 19th 2017

Precision_ID_mtDNA_rCRS.fasta File (NCBI reference NC_012920)

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