Converge™ Software 2.2 NGS Data Analysis 1.2

© 2019 Thermo Fisher Scientific. All rights reserved.

TABLE OF CONTENTS

- Products Affected
- Software Overview
- Key Features/Issues addressed in Converge[™] Software 2.2 Software
- System Requirements
- Upgrade of Converge[™] Software 2.2 Software
- Known Issues and Limitations
- Release & Compatibility Summary
- Legal Notices and Disclaimer; Terms and Conditions of Customer's Installation or Use

PRODUCTS AFFECTED

- Converge Software v2.2
 - HID Genotyper Plugin v2.2
 - Next-Generation Sequencing Module for STR, SNPs and Mito Converge-NGS-1.2.zip
 - Upgrade Installer Files upgradecvg (v1.0)

SOFTWARE OVERVIEW

Converge is a multi-phased product suite for Next Generation Software Platform offering upstream data storage and workflow capabilities, genotype calling and tertiary analysis tools. The software supports NGS STR, mtDNA and SNP (ancestry and identity) data analysis as well as Kinship and Paternity testing for global HID customers.

KEY FEATURES IN CONVERGE v2.2

- Mito IGV Lite: Converge user interface now includes a web-based compressed view of IGV read pileup on Mito results page to view the coverage for variants directly in Converge.
 - User can define the % difference value (2% 10%) to determine which base position data is displayed in the user interface. Default value is 2%.
 - Any base position with higher percentage than the value assigned will be shown in IGV Lite.

TO Genotype	r	
	Coverage	Threshold for recording detailed coverage stats 9
	General	Minimum percent of mutation or indel at any position so that the software records and stores the detailed coverage statistics (each base plus indels) in json format, so that this information can then be used later in downstream software (without needing to use the entire barn file)
	Reporting	Minimum:2 Maximum:10
	Thresholds	

• Mito TS plugin output folder : A link from results page that navigates to the Torrent Server folder containing raw files associated with the particular sample.

Bam File: IonCode_0119_rawlib_mvc.bam	Bai File: IonCode_0119_rawlib_mvc.bam.bai	Consensus File: consensus.fasta	Zip file with current data: results.zip
Zip file with images: images.zip	Mito IGV: Mito IGV	Mito IGV JAR: igv.jar	Amplicon Coverage File: Amplicon.xlsx
Results on TS: <u>TS output folder</u>	Variants Excel File (original): variants_colored.xlsx	Original Variants Text File (all positions): coverage_detailed.txt	

• Mito View and search haplogroup : Users can view and search for mtDNA haplogroups.



- Haplogroup information is visible on the profile details page.
- Haplogroups can be searched on the profile dashboard.
- Mito CODIS export: mtDNA profiles can be exported the CODIS .cmf v4.1 file format.
 - Originating Agency Identifier (ORI) was added in Organizational Details screen.
 - Mito CODIS exports will include the ORI number from the Organizational Details.
- Mito profile comparison: If a user performs profile comparison with a sample(s) containing point heteroplasmy (PHP), IUPAC codes are used, and the PHP variants are highlighted in orange.
 - Reference column format is #BASE#POSITION
 - For whole genome sample comparison, the option "Use control region only" is enabled if a user wants to restrict the comparison to only the control regions.

Use control region	ns only 🗌 Use confirmed only	S Reference 🖌	Match Y Partial Match X Not a match C Excluded
Je.			
Reference	007-FBI_1 (I2)	NTC-Mid_1 (I2a1a) 3	007-FBI_4 (12) 🕄
A73	73G	73G	73G
T152	152C	152Y	152C
T199	199C	199Y	199C
T204	204C	204Y	204C
G207	207A	207R	207A
T250	250C	Excluded	250C
A263	263G	Excluded	263G
C309	309c	14 C	309c
C315	315.1C	·	315.1C
T455	455Y	Excluded	-
T460	460C	Excluded	460C
C573	573.CCCC	· ·	573.CCCC
G16129	16129A	16129R	16129A
C16223	16223T	Excluded	16223T

- SNP Ancestry Prediction: Improved ancestry predictions performed by bootstrapping the admixture estimations, and the variability between predictions is used to obtain a likely range in estimates using a user-defined sampling percentage and number of bootstrap replications. In samples where there is uncertainty due to less distinction between the constituent population groups, the results should show larger confidence interval around the predicted means.
 - References:
 - Kidd et. al. Poster: Better SNPs for Better Forensics: Ancestry, Phenotype, and Family Identification. Shown at National Institute of Justice annual meeting, Arlington VA, June 2012.
 - Kosoy R, Nassir R, Tian C, et al. (2009) Ancestry informative marker sets for determining continental origin and admixture proportions in common populations in America. Hum Mutat 30(1) 69–78.
 - In the analysis settings, users select an Ancestry Frequency File v1.1 to display the number of SNPs in the panel and designate (a) Number of Bootstrap Replications, (b) Bootstrap Resampling Size (%) and (c) File Description to perform this tertiary analysis.
 - Note:
 - Admixture analysis between 2.1 and 2.2 are not compatible; any 2.1 admixture analyses should be downloaded before upgrading the software.
 - Profiles generated in 2.1 will remain intact following software upgrade. Users can re-analyze the profiles with the new bootstrap admixture analysis in 2.2.

.



- The Admixture Results displays the following information:
 - Ancestry composition shown as a mean of ethnicity percentages and confidence intervals
 - Probable range of variability of the estimated ethnicity percentages
 - Confidence level of the variability estimate in a percentage
 - Bootstrapping sampling percentage and number of samplings



- Custom SNP panel workflow: The software is now enabled to perform custom SNP genotyping and analysis. This feature allows customers to perform the following options with a custom SNP panel designed by the user:
 - Create, upload and analyze the panel
 - Custom SNP haplotyping and genotyping
 - o Ancestry and identity analysis based off user supplied populations and allele frequency data
 - Custom admixture analysis
- Bulk association of samples : User can link more than 1 sample at a time to a case in sample dashboard and on NGS Batch page.
- Bug fixes:
 - MtDNA primer sequences including fusion products are now removed bringing significant improvement in MVC analysis with fewer false positives which is most evident in NTC and samples with low coverage.



 Image: Contract of the second seco

• MtDNA Consensus fasta file now has as many contigs as there are regions (3 for 3 regions, 5 for 5 regions etc).

> 1-576
GATCACAGGGTCTATCACCCCTATTAACCACTCACGGGAGCTCTCCCATGCATTTGGTATTTCGTCTGGGGGGGTGTGCACGCGATAGCATTGCGAGCCGGGGGCCCCATGTCGCAGCACTTTGGTATTTCGTCTTGG
ATTCCTGCCTCATCCCATTATTATCGCACCGTCCACATATTACAGGCGAACATACTTACCAAAGCGTATTAATTA
CAGACATCATAACAAAAAATTTCCACCAAACCCCCCCCCC
GGGGGTATGCACTTTTAACAGTCACCCCCCAACTAACACACTATTTNCCCCCCCCCACTCCCATACTAATCTAATCCAATACAACCCCCGCCCATCCCACCACCACCACCACCACCACCACCACCACCAC
GAACCAACCCAAAGACACCCCCCCCCCCCCCCCA
> 16024-16569
TTCTTTCATGGGGAAGCAGATTTGGGTACCACCCAAGTATTGACTCACCACCACCACCATGAATACTGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA
ATAAAAACCCAATCCACATCCACATCCACATCCCCCCTCCCCATGCTACAAGCCAAGCAAG
CTTAACAGTACATAGTACATAAAGCCATTTACCGTACATAGCACATTACAGTCAAATCCCTTCTCGTCCCCATGGATGACCCCCCCC
AAGAGTGCTACTCTCCGCGCCCCATAACACTTGGGGGTAGCTAAAGTGAACTGTATCCGACATCTGGTTCCTACTTCAGGGCCATAAAGACCACCACGTTCCCCCTTAAATAAGACACTCACGA
TG

• IUPAC codes are now used in Converge UI for profile comparison. Profile comparison now also includes regions analyzed; non overlapping regions are greyed out.

Use control region	ns only 🗌 Use confirmed only	S Reference	✓ Match ✓ Partial Match × Not a match ⊘ Excluded
۶.			
Reference	007-FBI_1 (I2)	NTC-Mid_1 (I2a1a) 🚯	007-FBI_4 (12) 🚯
A73	73G	73G	73G
T152	152C	152Y	152C
T199	199C	199Y	199C
T204	204C	204Y	204C
G207	207A	207R	207A
T250	250C	Excluded	250C
A263	263G	Excluded	263G
C309	309c	÷	309c
C315	315.1C		315.1C
T455	455Y	Excluded	-
T460	460C	Excluded	460C
C573	573.CCCC		573.CCCC
G16129	16129A	16129R	16129A
C16223	16223T	Evoluded	16223T

o In v2.1, excluded regions in Mito IGV were offset by 1 base; this issue is now resolved.

applied biosystems

Hed biosystems reaction			convei	90				
MITO								Select Sample
S-1034.1 (DL8_Mt-CR_HL60_F	🛑 🛑 IGV - Session: h	ttp://10.45.2.22	25/auth/output/Home/Auto	Rexy. S5XL-00324-3	77-377-mtDNA	CR Panel On-market D	L8 Lot1605001 Chi	θ
Sample ID: 51034.1 Median Coverage: 1203 Concordingen Type: N/A	PrecisionID_mt	chrM ᅌ	chrM:590-630	Co 👚 🔹 🕨		🐌 🖪 🗙 🖵 I	🛟 🔝 🥁 🐼 (
Batch ID: Batch-1001 Last Modified Date: Mar-26-2019 12:15:54		_						
Region: 1-610, 10953-16569 Prufile ID(s):				411	æ —			
		10 to 1	600 to	610	•• ,	623 bp	638	Faset Current Data Collepse All
+ Grid	WG primers		•		1 1 1 1 1 1			
- Linear Plot	Sequence -	mt_8				TGTTTAGA	CGGGCTC	
Low coverage threshold: 100 Use to	lonCode_0102_rawlb_mxt.bam (rage	[0-10.00]		C				A
Taxan Taxan Taxan	IonCode_0102_rawlb_mvc.bam							1800
2400 2000 10000 10000	IonCode_0102_rawlb.bam Cover	51-11.08						
14000 19000 10000 8000 8000 4000	IonCode_0102_rawlb.bam							
0								-
	7 tracks loaded chrM:	608	Loading alignments chrM:5	90-630			359M of 1,479M	

o For Y Haplogroup analysis, "Valid genotype data not found" is now displayed when all markers have genotype as "N" for female profiles.

14	Jet .						\odot	Page	× Analysis failed Vali
Sub	ject ID	¥ Name	Ŷ	Gender	¥ Rel	ationship	¥ Ethnici	ity	genotype data not found
				No d	ata found				
_	Analysis								
N	ew Analysis 👻 More	•							
X)et						0	Page	1 of 1 () 10
	Analysis ID 🛛 🕈	Analysis Name * 9	Application Name 9	Analysis Date	Analyzed By	Analysis Result	Original Report	♥ Mod	ified Report 👻 Action
		Y Haplogroup An	Identity 1.1	Jul-12-2019 11:2	converge	N/A			
_	Analysis-4302				converge	N/A			··· .
	 Analysis-4302 Analysis-4067 	Y Haplogroup An	Identity 1.1	Jul-11-2019 9:52:	converge	19/25			•

SYSTEM REQUIREMENTS CONVERGE 2.2:

- TSS v5.10 / Ion GeneStudio S5, Ion Gene Studio Plus, Ion GeneStudio Prime/ Ion S5XLTM
- Converge Software Server & its components \triangleright
 - DellTM PowerEdgeTM T130 Tower Server, motherboard v2 or later
 - Red HatTM Enterprise LinuxTM 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 IntelTM XeonTM 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 Hat[™] Enterprise Linux[™] operating system •
 - Browser Google ChromeTM 66 or later
- Recommended Software (not provided)
 - AdobeTM Acrobat Reader
 - Microsoft Excel
- ➤ Verified Converge 2.2 TM software workflow on Google ChromeTM and MAC Safari browsers.

INSTALLATION / UPGRADE:

applied biosystems

Refer to Converge[™] Software v2.2 SETUP AND REFERENCE GUIDE - Publication Number 100039539, Rev E for following instructions

- ▶ Initial setup and configuration of ConvergeTM Software Server and ConvergeTM 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 2.1 and Converge 2.2 on Dell T110 and T130 Appliance Servers.

Publication Number 100039539, Rev E can be found here.

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.

- 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 contains the following list of files and can be downloaded from <u>S3</u> link.

List of files include (*Note: These files have not changed since Converge 2.1*)

- a. For Mito Panel
 - Mito Reference Precision_ID_mtDNA_rCRS
 - 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. Analysis Parameter File Precision_ID_mtDNA_Panel_AnalysisParams_v1.0.jsonP 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 v2.2 Plugin Download the plugin HIDGenotyper-2.2.zip from <u>S3 link</u> or installation and upload / configure plugin on supported S5/S5XL TM Torrent Suite server. An example of successful configuration of HID Genotyper v2.2 Plugin with TSS and Converge v2.2 software is shown below

Configure Plugin × Converge Account Configuration User Name*: converge@thema.com Password*: TSS Configuration Password*: Market Converge@thema.com Password*: Market Converge@thema.com Password*: Converge@thema.

- Upgrade Installer Package Download following two files (Serial Number 4b0cd383b-201908300532) from S3 link for upgrading Converge v2.1 to Converge v2.2 software installed on Dell T110 or T130 Server.
 Refer to ConvergeTM Software v2.2 SETUP AND REFERENCE GUIDE Publication Number 100039539, Rev E (Appendix B) for instructions on upgrading to Converge v2.2 software
 - ConvergeUpgrade-2.2-0.x86_64.rpm S3 link
 - o upgradecvg <u>S3 link</u>
- Download Precision_ID_mtDNA_rCRS File (NCBI reference NC_012920) file from <u>S3 link</u> and upload onto TSS > References page (snapshot below)

Keference Sequences Obsolete Reference Sequences Target Regions	Reference Sequence	ces		imp	ort Preloaded ion R	References Import Custom Re	ference
 Hotspots Test Fragments 	Short Name	Description	Notes	Enabled	Date v	Status	
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> 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-1.2.zip Download Converge-NGS-1.2.zip file from <u>S3 link</u>.
- Post upgrade from Converge v2.1 > Converge 2.2 version, all licenses will be intact, and user need not install it again since its and upgrade from 2v.1, followed by uploading NGS Application Bundle package onto Converge > Admin > Manage Application Software page (snapshot shown below).

applied biosystems

- Admin 0 Manage Applications Kinship and Paternity L Install Application Loci Inclusion List Analysis Parameters Setti Manage Population Datab Installed Applications - Converge-NGS-Bundle 1.2 俞 Global Settings Installed On: Jul-12-2019 4:27:44 PM Installed By: testUser Manage Licenses
 Manage Loci
 Manage Kits
 Manage Templates
 Manage Organizati Ancestry NGS-STR NGS-MH 1.0 Identity ** . *1*] Manage Custom Fields NGS-Mito Manage Case Archive 9 NGS-SNP <u>G</u>JJ Manage Applications > Configure Search Security 龠 Manage User Accounts NGS-Batch 1.2 Manage User Roles Installed On: Jul-12-2019 4:27:37 PM Installed By: testUser Manage User Account Security Policies ▲ Audit NGS-Batch Manage Audit

NOTE:

 \geq

• If earlier version of the Converge [™] Software included the Kinship and Paternity module and/or the NGS module, and the licenses have not expired, the licenses are retained after the upgrade. Licenses need not be reinstalled.

UPDATES TO CONVERGE™ SOFTWARE v2.2 HELP TOPICS

- Refer to Converge[™] Software v2.2 help topics within the application for more information on the following updates:
- > Added the following new features and updated procedures per changes to the UI workflow.
 - Updated Ancestry algorithm workflow
 - Bulk association of samples to a case
 - o Mito IGV light
 - Profile comparison legend
 - Inclusion of Mito regions information in Profile
 - View and search Mito profiles based on Haplogroups
 - New "Reporting" parameter for Mito in HID Genotyper plugin
 - Uploading and analyzing custom panels
 - Troubleshooting section has been enhanced for following sections and recommended actions discussed.
 - o NGS Module workflow, Display Issues, Profile Management, and Kinship & Paternity features.

KNOWN ISSUES AND LIMITATIONS:

General functionality related:

• The profile merge feature will not allow two mtDNA profiles to be combined when selected on Case Details Page > Profile card. See attached screenshot for error message.

ied bi	osystems	CON/Arae	
are sooning		Merge Profile	×
	- Profile(s)		Could not read JSON: Unrecognized field "customAttributes" (Class com.lifetech.converge.dto.Genoteper not marked as ignorable at
	+ New Profile More •		[Source: org.apache.catalina.connector.Covote line: 1, column: 380686] (through reference chain:
	Xr ↓≠ ✓ Profile ID ♀		com lifetech converge dto. Genetroper nested exception is org.codehaus.jackson.map.exc Unrecognized field "customattributes" (class
	✓		Mar com lifetech.converge.dto.GenetypeiP not marked as ignorable at [Source: Mar org.apache.catalina.connector.Coyole
	Profile-1005 Sample	Profile Category*: (*) Required fields Discordant loci are shown in red. Click the allele values to include in the merged profile.	Mar Ung apache Catalina Connector, worke (through reference chain: com.lifetech.converge.dto.Genc Coef
	More -	An allele value of indicates that the corresponding locus is absent in the profile. Cancel	A Merge

• The Control Region panel spans the region from 15,954 – 610. Converge will display only the Control Region sequence (16,026 – 576) when that analysis display is chosen. If users want to view the full sequence, the data must be viewed in IGV by accessing the data from Torrent Server.

am file ample lose hapl	D:/da Samp		D /IonC	E	F	G	н	1	1	K				0	0	0		S	Т	U	V
am file ample lose hapl	D:/da Samp	ta/rob	/IonC						9	N	L	M	N	0	Р	Q	R	5	1	0	V
ample lose hapl	Samp		/lonC																		
lose hapl		MOKY		ode_0185	_Manual_U	INT_mtWG_	results/Ion	Code_0185	_Manual_U	UNT_n	ntWG_	_mvc.l	bam								
		NUQKI	Q.lon	Code_018	5																
	C1																				
egions	1-574	16024	1-1656	9																	
osition	Ref	Samp	Varia	Var Freq	Туре	Read Cove	Read Cove	Allele Cov	Allele Cov	Allele	G%	A%	т%	C%	N%	ins%	del%	Polymorp	Control Re	State	Frequ
3	Α	G	G	99.9	SNP	3824	4375	8193	3823	4370	99.9	0.1	0	0	0	0.1	0	73G	73G	confirmed	99.9
53	Α	G	G	99.6	SNP	697	563	-			99.6	0.2	0.2	0	0	0.2	0	263G	263G	confirmed	99.6
90	Α	_	_	94.1	DEL	669	607	1201		_	0	5.9	0	0	0		94.1	290del	290del	likely	94.1
91	Α	_	_	97.9	DEL		607				0	0.8	1.3	0.1	0		97.9	291del	291del	confirmed	97.9
09	Т	+	C	23.9	INS	757	1113			359	0	0	0	0		25.3	0	309.1C	309.1C	likely	23.9
15	G	+	C	57.8	INS	747	1128	1083				0	0	0	0	60.7	0	315.1C	315.1C	possible	57.8
89	Т	С	C	99.5	SNP	1352				989	0	0		99.5	0	0.6	0	489C	489C	confirmed	99.5
5169	C	Т	Т	98.4	SNP	876	1382	2222	853	1369	0	0.1	98.4	1.1	0	0.3	0.4	16169T	16169T	confirmed	98.4
5223	С	Т	Т	99	SNP	1260	1926					0	99	0.8	0		0.2	16223T	16223T	confirmed	99
5298	Т	C	C	99.5	SNP	718	824	1535				-	0.5	99.5			0	16298C	16298C	confirmed	99.5
5325	Т	С	С	99	SNP	706	824	1515	697			0.2	0.8	99	0	0.2	0	16325C	16325C	confirmed	99
5327	С	Т	Т	99.6	SNP	706	_				0	0	99.6	0.4	0	0.5	0	16327T	16327T	confirmed	99.6
5642	Α	G	G	99.9	SNP	2103	2220	4318	2100	2218	99.9	0.1	0	0	0	0.1	0	73G	73G	confirmed	99.9
	3 0 1 9 5 5 9 169 223 298 325 327	A 3 A 0 A 1 A 9 T 5 G 9 T 169 C 223 C 298 T 325 T 327 C	A G 3 A G 0 A _ 1 A _ 9 T + 5 G + 9 T C 169 C T 223 C T 298 T C 325 T C 327 C T	A G G 3 A G G 0 A _ _ _ 1 A _ _ _ 9 T + C S 9 T C C C 9 T C C Z 9 T C C Z 9 T C C Z 92 T C C Z 928 T C C Z 325 T C C 32 327 C T T T	$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	A G G 99.9 SNP 3 A G G 99.6 SNP 3 A G G 99.6 SNP 3 A _ _ 94.1 DEL 1 A _ _ 97.9 DEL 9 T + C 23.9 INS 5 G + C 57.8 INS 9 T C C 99.5 SNP 169 C T T 98.4 SNP 223 C T T 99.5 SNP 235 T C C 99.5 SNP 325 T C C 99.6 SNP	A G G 99.9 SNP 3824 3 A G G 99.6 SNP 697 3 A G G 99.6 SNP 697 0 A _ _ 94.1 DEL 669 1 A _ _ 97.9 DEL 669 9 T + C 23.9 INS 757 5 G + C 57.8 INS 747 9 T C C 99.5 SNP 1352 169 C T T 98.4 SNP 876 223 C T T 99.5 SNP 1260 298 T C C 99.5 SNP 718 325 T C T 99.6 SNP 706	$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	A G G 99.9 SNP 3824 4375 8193 3 A G G 99.6 SNP 697 563 1255 0 A _ _ 94.1 DEL 669 607 1201 1 A _ _ 97.9 DEL 669 607 1249 9 T + C 23.9 INS 757 1113 446 5 G + C 57.8 INS 747 1128 1083 9 T C C 99.5 SNP 1352 992 233 169 C T T 98.4 SNP 876 1382 2222 223 C T T 99.5 SNP 1260 1926 3153 298 T C C 99.5 SNP 706 824 1515 325	$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	A G G 99.9 SNP 3824 4375 8193 3823 4370 3 A G G 99.6 SNP 697 563 1255 693 552 0 A _ _ 94.1 DEL 669 607 1201 603 598 11 A _ _ 97.9 DEL 669 607 1249 651 598 9 T + C 23.9 INS 757 1113 446 87 359 5 G + C 57.8 INS 747 1128 1083 69 1014 9 T C C 99.5 SNP 1352 292 2333 1344 989 169 C T T 98.4 SNP 716 1382 2222 853 1369 2232 C T T	$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	A G G 99.9 SNP 3824 4375 8193 3823 4370 99.9 0.1 3 A G G 99.6 SNP 697 563 1255 693 562 99.6 0.2 0 A _ '94.1 DEL 669 607 1201 603 598 0 0.8 1 A _ '97.9 DEL 669 607 1249 651 598 0 0.8 99 T + C '23.9 INS '757 1113 '446 '87 '359<'0	A G G 99.9 SNP 3824 4375 8193 3823 4370 99.9 0.1 0 3 A G G 99.6 SNP 697 563 1255 693 562 99.6 0.2 0.4 1.3 0 603 598 0 0.8 1.3 0.2 <t< td=""><td>$\begin{array}{c ccccccccccccccccccccccccccccccccccc$</td><td>$\begin{array}{cccccccccccccccccccccccccccccccccccc$</td><td>$\begin{array}{c ccccccccccccccccccccccccccccccccccc$</td><td>A G G 99.9 SNP 3824 4375 8193 3823 4370 99.9 0.1 0 0 0.1 0 0.1 0 0.1 0 0.1 0 0 0.1 0 0 0.1 0 0 0.1 0 0 0.1 0 0 0.1 0 0 0.1 0 0 0.1 0 0 0.1 0 0 0.1 0 0 0 0.1 0 0 0 0.1 0</td><td>A G G 99.9 SNP 3824 4375 8193 3823 4370 99.9 0.1 0 0 0.1 0 736 3 A G G 99.6 SNP 563 1255 693 562 99.6 0.2 0.2 0 0.2 0 263G 0 A _ _94.1 DEL 669 607 1201 603 598 0 0.2 0 0 94.1 290del 1 A _ _97.9 DEL 669 607 1249 651 598 0 0.8 1.3 0.1 0 97.9 291del 9 T + C 23.9 INS 757 1113 446 87 359 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</td><td>A G G 99.9 SNP 3824 4375 8193 3823 4370 99.9 0.1 0 0 0.1 0 736 736 736 3 A G G 99.9 SNP 697 563 1255 693 562 99.6 0.2 0 0.2 0 2636 2636 0 A _ 94.1 DEL 669 607 1201 603 598 0 0.8 0 0 9.7 291del 290del 1 A _ 97.9 DEL 669 607 1249 651 598 0 0.8 1.3 0.1 0 0 9.7 291del 291del 291del 291del 291del 291del 291del 291del 291del 135.1 135.1 135.1 135.1 135.1 135.1 135.1 135.1 135.1 135.1 135.1 135.1 135.1<td>A G G 99.9 SNP 3824 4375 8193 3823 4370 99.9 0.1 0 0 0.1 0 73G 73G confirmed 3 A G G 99.6 SNP 697 563 1255 693 562 99.6 0.2 0.2 0 0 0.4 2 0 263G 263G confirmed 0 A _ 94.1 DEL 669 607 1201 603 598 0 0.8 0 0 9.4 1200del 290del 1414 290del 290del 1414 290del 290del 1414 290del 290del 1414 290del 290del 1414 0 0 0 0 0 9.7 291del 290del 1414 290del 290del 1414 290del 290del 1414 290del 1200del 290del 1414 0 0 0 0 0 0 0 0 0 0 0 0 0 0<</td></td></t<>	$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	A G G 99.9 SNP 3824 4375 8193 3823 4370 99.9 0.1 0 0 0.1 0 0.1 0 0.1 0 0.1 0 0 0.1 0 0 0.1 0 0 0.1 0 0 0.1 0 0 0.1 0 0 0.1 0 0 0.1 0 0 0.1 0 0 0.1 0 0 0 0.1 0 0 0 0.1 0	A G G 99.9 SNP 3824 4375 8193 3823 4370 99.9 0.1 0 0 0.1 0 736 3 A G G 99.6 SNP 563 1255 693 562 99.6 0.2 0.2 0 0.2 0 263G 0 A _ _94.1 DEL 669 607 1201 603 598 0 0.2 0 0 94.1 290del 1 A _ _97.9 DEL 669 607 1249 651 598 0 0.8 1.3 0.1 0 97.9 291del 9 T + C 23.9 INS 757 1113 446 87 359 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	A G G 99.9 SNP 3824 4375 8193 3823 4370 99.9 0.1 0 0 0.1 0 736 736 736 3 A G G 99.9 SNP 697 563 1255 693 562 99.6 0.2 0 0.2 0 2636 2636 0 A _ 94.1 DEL 669 607 1201 603 598 0 0.8 0 0 9.7 291del 290del 1 A _ 97.9 DEL 669 607 1249 651 598 0 0.8 1.3 0.1 0 0 9.7 291del 291del 291del 291del 291del 291del 291del 291del 291del 135.1 135.1 135.1 135.1 135.1 135.1 135.1 135.1 135.1 135.1 135.1 135.1 135.1 <td>A G G 99.9 SNP 3824 4375 8193 3823 4370 99.9 0.1 0 0 0.1 0 73G 73G confirmed 3 A G G 99.6 SNP 697 563 1255 693 562 99.6 0.2 0.2 0 0 0.4 2 0 263G 263G confirmed 0 A _ 94.1 DEL 669 607 1201 603 598 0 0.8 0 0 9.4 1200del 290del 1414 290del 290del 1414 290del 290del 1414 290del 290del 1414 290del 290del 1414 0 0 0 0 0 9.7 291del 290del 1414 290del 290del 1414 290del 290del 1414 290del 1200del 290del 1414 0 0 0 0 0 0 0 0 0 0 0 0 0 0<</td>	A G G 99.9 SNP 3824 4375 8193 3823 4370 99.9 0.1 0 0 0.1 0 73G 73G confirmed 3 A G G 99.6 SNP 697 563 1255 693 562 99.6 0.2 0.2 0 0 0.4 2 0 263G 263G confirmed 0 A _ 94.1 DEL 669 607 1201 603 598 0 0.8 0 0 9.4 1200del 290del 1414 290del 290del 1414 290del 290del 1414 290del 290del 1414 290del 290del 1414 0 0 0 0 0 9.7 291del 290del 1414 290del 290del 1414 290del 290del 1414 290del 1200del 290del 1414 0 0 0 0 0 0 0 0 0 0 0 0 0 0<



applied biosystems

rCRS_plus_80.fasta 👻	Tracks Re		264	Go	a 4				¶ ×× □			- @ %					
rCRS_plus_80.fasta 💌	chrM	• cnrw:1-1	,304	GO	-	Image: A state of the state	7 6	"## E	1 A (V		<u> </u>) 🎫 🔌	Em		
	pp			200 bp					400 bp					600 bp		1'359 bp	
	-	1					1		1				_				
mers	ntDNA_1	RV_mtDNA_16				< >				>	<			< R) (
quence 🗕				mmmi								ĨŬIJIJŨŬĨ			in in the second		
Code_0185_Manual_UNT_m [.] s.mito		730			:	2836	309.1C				489 C						
mito						291d	el										
																	S.
																	20
	0.40707																
	[0 - 10725]																
	[0 - 10725]						[4]							\$ 1 77 . 1	and the second		
	[0 - 10725]								- -							10	
	0 - 10725)			-										6 77			
	(0 - 10725)							-:									
⊧_mvc.bam Coverage	(0 - 10725)							<u> </u>									
s_mvc.bam Coverage Code_0185_Manual_UNT_m	(0 - 10725)														100 C		
mvc.bam Coverage Code_0185_Manual_UNT_m	[0 - 10725]														2		
mvc.bam Coverage Code_0185_Manual_UNT_m	[0-10725]														1000		
nCode_D185_Manual_UNT_m G_mvc.bam Coverage nCode_D185_Manual_UNT_m 9_mvc.bam	0 - 107253														N WE WANT		

• Exported multi EMPOP file generated for Mito "Export Results" on the result card does have entries for all samples. This occurs when selected samples have more than 3 discrete regions as highlighted in the image below.

Ibiosy	stems				CC	on∨	#! 1-480 526-543 16024- IonCode 0123 rawlib 207A 250C 263G #! 1-480 526-533 16024- IonCode 0105 rawlib	16129A 16223T 16569 12	1 736 16519C 1 736			284C 284C	
-	Mito Results C	ard					207A 250C 263G	16129A 16519C					
Ex	port Results More	-) (
N	Je												50
In	Result ID Y	Sample Name Y	Barcode 🖤	Sample Type Y	Batch Prodes Y	Haplo							Actio
103	Result-S-1677.1	007-pos_10	IonCode_0118	Unknown	Complete	121	Centrol Region	1-576,16024-16569			2842	-	
	Result-S-1654.1	007-pos_2	ionCode_0102	Unknown	Complete	12	Control Region	1-576,16024-16569			4279		
121	. Result-S-1657.1	007-pos_1	ionCode_0101	Unknown	Complete	12	Control Region	1-576,16024-16569			5162		
	. Result-S-1659.1	007-pos_8	IonCode_0112	Unknown	Complete	12	Control Region	1-576,16024-16569			3863		
101	Result-S-1660.1	007-pos_4	IonCode_0104	Unknown	Complete	12	Control Region	1-576,16024-16569			48578		***
0	Result-S-1662.1	007-pos_3	IonCode_0103	Unknown	Complete	12	Control Region	1-576,16024-16569			57634		
13	Result-S-1664.1	007-pos_12	IonCode_0120	Unknown	Complete	12	Control Region	1-576,16024-16569			46532		
103	Result-S-1666.1	007-pos_7	lonCode_0111	Unknown	Complete .	12	Control Region	1-576,16024-16569			2964		
-01	. Result-S-1668.1	007-pos_6	IonCode_0110	Unkoown	Complete	12	Control Region	1-576,16024-16569			8494		***
11	. Result-S-1669.1	007-pos_5	lonCode_0109	Unknown	Complete	12	Control Region	1-576,16024-16569			6994		
0	. Result-S-1671.1	007-pos_9	IonCode_0117	Unknown	Complete	12	Control Region	1-576,16024-16569			3704		
	Result-S-1674.1	007-pos_11	lonCode_0119	Unknown	Complete	12	Control Region	1-576,16024-16569			29007		
03	Result-S-1676.1	nte.,3	ionCode_0107	Unknown	Complete	12	Partial	1-480,526-535,1602	4-16131,16222-165	69	74		
G	Result-S-1655.1	ntc.,12	IonCode_0124	Unknown	Complete .	ItoTa	Partial	1-248,385-411,1602	4-16069,16076-161	31,16219-16269,	21		***
0	Result-S-1656.1	ntc_5	ionCode_0113	Unknown	Complete	12	Partial	1-446,460-480,526-5	43,16024-16131,10	222-16569	5-6		+++
(2)	Result-S-1658.1	ntc_11	lonCode_0123	Unknown	Complete	12	Partial	1-480,526-543,1602	4-16569		123		
181	Result-S-1661.1	nte_7	IonCode_0115	Unknown	Complete	12	Partial	1-248,299-411,1602	4-16131,16222-164	58,16542-16569	38		
0	Result-5-1663.1	ntc_6	lonCode_0114	Unknown	Complete	CZ	Partial	1-200.000-411.1002			23		
0	Result-S-1665.1	ntc_10	lonCode_0122	Unknown	Complete	licia	Partial	1-268,299-411,1602	4-16131,16222-165	69	40		
G	Result-S-1667.1	ntc_9	IonCode_0121	Unknown	Complete	62	Partial	1-79,119-248,303-32	9,385-411,460-543	16024-16131,16	33		•••
	Result-S-1670.1	ntc_2	lonCode_0106	Unknown	Complete	12c	Partial	1-248,299-480,1602	4-16131,16222-165	69	42		
3	Result-S-1672.1	rite_1	IonCode_0105	Unknown	Complete	12;	Partial	1-480,526-533,1602	4-16569		78		
127	. Result-S-1673.1	nto.8	IonCode_0116	Unknown	Complete		Partial	1-119.16024-16131.	16220-16450 1654	1.145560	3.4		***

• In Mito IGV "Excluded regions" are incorrectly highlighted when variant is loaded on first instance. A second click on the variant is required to view the correct excluded region highlight in IGV.

In the example below, the excluded region begins from position 577 but in IGV its highlighted from 578. A second click on the variant will highlight the excluded region from 577.

First variant click instance:

•••	🗲 Со	nverge		😑 😑 🕒 IGV - Session: h																						
		Not Secure	10	PrecisionID_mt ᅌ	chrM	0	chrM:556-596		Go 👚	◄ ▶		۰,	۰ 🤿	¢,		×Ţ		🛟		2	~ () 🗉) V	Em [- 1	
		Not Secure	10.4			_		_			_	_	_	_	_	_	_	_	_	_		_	_	_	_	_
applied biosy	/stems																									
	_																									
міто													- 4	41 bp												
5-17	12.1 ((007-Mid_2)	^				560 bp	1		570 bp			1			5	80 bp 			I			590 bp			
	ple ID: S	1712.1		CR primers	< <	<		<	< .							ition: 5										
\sim		rage: 2889					mt_6			c c		~				and d			с т		~ ~					
		Type: N/A		Sequence -	~ ~			, ,	C A C			–	? .	^					6 1	^			^		1.0	- · ·
4		ch-1044 d Date: Jun-20-2019		results.mito							57	73.0000	с													
		5, 16024-16569	12:30																							
		Profile-1118		IonCode_0126_rawlib_mvc.bam ((0 - 10.00)																					
				rage											-											
				IonCode 0126 rawlib mvc.bam																						
-	Grid																									
	onu		-																							
Va	ariants	Uncalled Varian	Its																							
*)e																									
		ariant 🗸	Frequ	IonCode_0126_rawlib.bam Cover	(0 - 10.00)																					
		73G	99.8												+											
		152C	98.2	IonCode_0126_rawlib.bam																						
		199C	99.1																							
		204C	99.7																							
		207A	98.2																							
		250C	99.8																							
		263G	99.9																							
		309c	36.2																							
		315.10	75.1																							_
		460C	93.0																							
		4000 573 CCCC		Reads loaded: 10000 chrM:	576		Loading alignment	s chrMd	56-596						_		_								602M	of 1.658M

Second variant click instance:

••		Cor	nverge		🔵 🌑 🗶 IGV - Session: h	ttp://10.4	3.6.39/a	auth/output/H	lome/Reana	lysis_Re	(y_S5XI	-003	324-380	-380-m	tDNA	_WG_	Panel_	OnMa	irket_L	ot180	7005	_Bas	eline2	_Chip2	_fore	ign_55	0_Dot	263/
					PrecisionID_mt 0	chrM	٥	chrM:556-5	96	Go 🕤	•			•	ŵ		×		📢	> 🗉	1	S 🖂	C		*	Em[- 1	
← →	C	A	Not Secure	10.		_	_				_	_				_	_		_		_				_	_	_	_
applied	biosys	sterns				-																						_
	міто					-									41 bр	. —												
U	S-171	12.1 (007-Mid_2	^			5	60 bp	1		57	10 bp				_		580 bp			I			5	90 bp 			
æ	Sample		1712.1 rage: 2889		CR primers	× ×	•	• • • • • • • • • • • • • • • • • • •	< <	¢																		
~			Type: N/A		Sequence 🗕	A C	сс	CAA/	A G A	C A	c c	c c	; c c	A C	Α	G '	гт	т	A T	G	T A	G	C 1	т	A (c c	тс	СТ
2		lodified	Date: Jun-20-20	19 12:3	Converge S-1712.1 (007-Mid_2)								573.C	200														
2	-		, 16024-16569 Profile-1118		lonCode_0126_rawlb_mvc.bam (rage	(0 - 10.00)																						
.																												
	-	Grid			IonCode_0126_rawlb_mvc.bam																							
	Vari	riants	Uncalled Varia	ints																								
	Ж)c				[0 - 10.00]																						_
		Va	ariant ~	Freq	IonCode_0126_rawlb.bam Cover	1																						
	,	•	73G	99.8																								
	•	•	152C	98.2	lonCode_0126_rawlib.bam																							
	•	•	199C	99.1																								
	•	•	204C	99.7																								
	,		207A	98.2																								
	•	•	250C	99.8																								
	,	•	263G	99.9																								
	•	• •	309c	36.2			_				_	_		_	_			_	_	_		_		_	_			

• Genotype errors may be observed in homopolymer regions with a continuous string of A bases. For example rs7722456 (aiSNP), which lies near a homopolymer region (6As; A bases incorrectly align with rs7722456 position & hence, "A" genotype overcall is added). Approximately 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.

Additional SNP id's with similar sequence artifacts follow: a. rs772262 – C is added to this SNP position because of poly Cs (5Cs) b. rs13400937 T is added to this SNP position because of poly Ts (4 Ts) c. rs7997709 A & G is added due to polyA region in the vicinity (snapshot below)



						1
rs7722456						
\rightarrow \rightarrow \rightarrow \rightarrow	:el targets deepti		\rightarrow \rightarrow \rightarrow \rightarrow \rightarrow	>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>	> > > > > > > > >	\rightarrow \rightarrow \rightarrow
				121 221 102		
	eI hotspots deep			rs7997709		
	1		_			
				TAT	G	Ŧ
			ŤÄ	TAL		
GATTAAAAATAA						
GATTAAAAAAA				GT		
GATTAAAAA			T A T A			
GATTAAAAA		с	1.0	T		
GATTAAAAAATA			ТА	G T T A F	ŧ	
GATTAAAAATA			1 A	GT		
GATAAAAAA TA		F		т		
GATTAAAAA AA			ТА	TAE		
GATTAAAAATA				T		G
GATTAAAAAATA			T A T A			
GATTAAAAATA			T Å			
GATTAAAAAAAAA				GT		
GATTAAAAATA			_	Ţ		
GATTAAAAAAAA	→	C A A A T A G T G C	ΤΑΑΑΑΤΑΑ		C C A C T G A G G	GAAACA
GATTAAAAATA		T N S A		N R	P L R	ÊÎÎ
			LK		т — Н т — С	
GATCAAAAAATA				<u> </u>		

• For admixture analysis inputs, "Bootstrap Resampling Size (%)" parameter value 50.25 is automatically converted to 50.2499999999999 after analysis is complete.



• The limitation for report generation for admixture analysis is 9999 bootstrapping replications and 99.99 resampling size.







- In "Manage Kit" section while importing a kit with \sim 50 or more loci, there is a delay in response when the • order of loci is changed.
- Export of STR Results grid in pdf format shows SNPs in Flank (SIF) indicator (red dot) across markers that do • not have SIFs.

applied biosystems

	Locus		Genotype	AN	OL	PHR	BST	ME	IGV
•	•	AMELX	1	۲	۲	۲			۲
,	•	AMELY		۲					۲
•	•	CSF1P0	6, 10, 11	۲	٠	٠		~	۲
•	•	D10S1248	13, 14, 15	۲	٠	٠			۲
•	•	D12ATA63	13, 14, 15, 15, 16					~	۲
•	•	D12S391	19, 20, 20, 20, 21, 21.1		٠				۲
•	•	D13S317	9, 10, 12, 13		٠			1	۲
•	•	D14S1434	13, 14	۲	٠				۲
•	•	D16S539	8, 9, 11, 12		٠			~	۲
•	•	D18S51	16, 17, 18, 19	۲	٠	٠			۲
•	•	D19S433	9, 10, 11	٠	٠	۲		~	٩
•	•	D1S1656	13, 14, 16.3, 17.3	٠	٠	٠			٢
•	•	D1S1677	14, 15	٠	٠	٠		~	۲
•	•	D21S11	27, 28, 29, 30	٠	٠				٢
•	•	D22S1045	10, 11, 15, 16, 17		٠				۲
•	•	D2S1338	17, 18, 18, 19		٠				٢
•	•	D2S1776	11, 12	۲	٠				۲
•	•	D2S441	9, 10, 11		٠				٢
•	•	D3S1358	14, 15	۲	٠	۲		~	۲
•	•	D3S4529	14, 16	٠		٠			۲
•	•	D4S2408	10, 11	٠	٠			1	۲
•	•	D5S2800	13, 14, 19, 20	٠	٠	٠			۲
•	•	D5S818	10, 11, 12	٠	٠	٠		~	٢
•	•	D6S1043	10, 11, 12	٠	٠				٢
•	•	D6S474	13, 14, 15	٠	٠	٠		~	٢
•	•	D7S820	7, 8, 9	۲	٠	۲			۲
•	•	D8S1179	13, 14	٠	٠	۲		~	٢
•	•	DYS391		٠					۲
	-		22.22.21						-

• Altered version of STR target.bed file is downloaded from HID Genotyper Result page.

Target file download button downloads the "Processed" version of the STR target.bed file. This version has all the motif and insert coordinate information stripped from the file and cannot be re-uploaded and used by the user. The application does not deliver the "original" uploaded target.bed file.

• On the Admixture summary page "Universal Kit" is displayed though a different kit is associated with Ancestry template.

erno Fisher Scientific	osystems		COr	iverge			4
Ad	lmixture Resul	ts					
Sum	nmary						
	Profile ID: Profile-10		 ForAnalysis_test	Sample Name: Set-A		Kit Name: Universal_Kit	
	SNPs Used in Analy Analysed By: testUs		tstrap Replications: 40 0-2019 3:25:41 PM	Bootstrap Resampli	ng Size (%): 50 Result: Result-PC-1002	Confidence Interval(%): 95 Description:	
	– Admixture						
11	- Admixture	result					Generate Report
	Admixture	Profile					Generate Report
			Ar	cestry Prediction			
	Europe	ŀ					
	Africa	-				H	1
	America	-					
	East Asia	-					
	Southwest Asia						
	Oceania	1 .					

 A warning message is displayed on launching IGV for SNP loci. IGV will be launched when user clicks on "OK"



dbiosystems					C	conve	rge									
alSNP															Sele	ct Sampl
S-1167.1 (HG0042	21_D1) ^															0
Sample ID: S-1167.1			Case ID:	Case 1002			Sample Name: HO	00421_01			Sample Type: Un	known				
Profile CGQ:				CGQ: IIII			Profile Gender: N				Sample Gender:					
Concordance Type: N/A				oncordance:			Sample Concorda				Secondary Analy					
Batch ID: Batch-1008				rocessed			Created Date: Aug	-5-2019 2:27:10 PM			Last Modified Da	te: Aug-6-	2019 1:04	21 PM		
Created By: converge Profile ID(s): Profile-1050			Modified	By: converge												
Prome mgd): Prome-1050												-				
								🟵 Upload 🗸 A	oprove	X Reject	Pl Apply Changes	13 R	set Ouriert	Data	C Sector	And in case of the local division of the loc
- Grid																
More -																
Nr Jer													Page 1	of1		10 •
	Ŷ	Position	۷	Genstype	Ŷ	Coverage	۷	Allele Freq	1	Coverage	r\.	Y	QC Y	Exclude Locus	IGV	Analys
Locus *																
						No	issaga							212	-	0
Locus * 197722456	• Igv	I was not able to I						665'plugin_out/HIDGenoty						(D)	Ð	0

The locus order in audit is incorrect when locus in the kit is deleted. •

For example: If there are 7 loci while uploading the kit, all except 4th and 7th loci are deleted then the remaining 2 loci should have 1 and 2 order respectively. Presently the initial loci order is created during uploading the kit is retained and not reindexed.

biosystems			CO	nverge					
Data Operation: Edit K	it	Data ID: superUs	erAudit	Data Type: K	üt		Created B	y: superUser	
User Name: superUser	r@hid.com	Creation Date: M	lay-3-2019 3:07:00 PM						
 Reason for Change: No reason available 	able								
– Audit Details									
- Audit Details							()	Page 1 of 1	(>) 10
More 👻	Ŷ	Data Operation	♥ Data Field		Ŷ	Old Value	<u>ج</u>	Page 1 of 1 New Value	> 10
More •		Data Operation Update		me: Locus Order	Ŷ	Old Value testLocus::7			> 10
More ▼ Xr ↓= Data Type			Locus Na		Ŷ			New Value	> 10

> Upgrade related:

Audit Search with creation date "Equal to" operand in Converge 2.2 does not return any result. •

appli	edbiosystems			CONVE	erge			
Ē	Audit Dashboard							0
Ū	Views Search							
&	Search Context: Audit	÷						
	Condition:		Attribute:		Operand:		Value:	۲
2			User Action	٥	= Equal To	\$	Change Password	
2	AND	¢	Created Date	\$	= Equal To	\$	June-12-2019	Θ
_							× Clear	Q Search + Views
*	More 👻							
	Nr						Page 0	of 0 🕟 10 🔻
	User Action	♥ Data ID	♥ Data Type	♥ First Name	♀ Last Name	♥ User Name	Y Creation Date	♀ Action
				No data fo	und			

• Admixture analysis results generated with Converge 2.1 version cannot be viewed on Converge 2.2 and results will be empty, as Converge 2.2 has Bootstrap method and related UI elements.

Admixture Results			erge	
Aumixture Results				
Summary				
Profile ID: Profile-1006 SNPs Used in Analysis: 144 Analysed By: converge	Frequency File: / Number of Boots Run Date: Jul-12		Sample Name: Set-A_IB-0615 Bootstrap Resampling Size (%): NaN Secondary Analysis Result: Result:S-1036.1	Kit Name: Universal_Kit Confidence Interval(%): NaN Description:
 Admixture Result 				
Admiture Profile 12 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0				Generatio Report
02				Update Results
× *				Page 0 of 0 > 10 +
Population	♥ Mean %	♥ Confidence Rang	e % Ÿ Likelihood	♥ Likelihood Ratio ♥
		No	o data found	

• Ancestry and Identity templates of Converge 2.1 will not be visible as the older versions (e.g. Converge 2.1, Ancestry 1.0 templates) are uninstalled during the upgrade process.

SYSTEM	ТҮРЕ	DESCRIPTION	VERSION / DATE STAMP
	Software	TSS Compatibility	v5.10
		Control_Samples	v1.01
	Publisher	Precision_ID_GlobalFiler_NGS_STR_Control_Sample_male007	v1.1
TSS	STR Control	Precision_ID_GlobalFiler_NGS_STR_Control_Sample_9947A	v1.1
	Files	Precision_ID_GlobalFiler_NGS_STR_Control_Sample_NegCtrl	v1.1
		Precision_ID_GlobalFiler_NGS_STR_Control_Sample_9947A_an d_male007_and_NegCtrl	v1.1
	NGS mtDNA Module	$Precision_ID_mtDNA_Whole_Genome_Panel_Targets_v1.0.bed$	v1.0
TSS		Precision_ID_mtDNA_Control_Region_Panel_Targets_v1.0.bed	v1.0
Control	STR Control Files	Precision_ID_mtDNA_Panel_AnalysisParams_v1.0.json	v1.0
Publisher	NGS SNP	Precision_ID_Ancestry_Panel_Targets_v1.0.bed	v1.0
	Module	Precision_ID_Ancestry_Panel_Hotspot_v1.0.bed	v1.0
	NGS mtDNA	Precision_ID_Identity_Panel_Target_v1.0.bed	v1.0
	Module NGS STR	Precision_ID_Identity_Panel_Hotspot_v1.0.bed	v1.0
	Module	Precision_ID_GlobalFiler_NGS_STR_Panel_Target	v1.1
		Precision_ID_GlobalFiler_NGS_STR_Panel_Hotspot	v1.1
BED/	NGS SNP	Precision_ID_GlobalFiler_NGS_STR_Panel_AnalysisParams	v1.1
JSON File	Module Plugin	HIDGenotyper-2.2 (Serial No.)	2.2_4b0cd383b
	Software	About (Serial No.)	4b0cd383b- 201908300532
	Module	Platform	v2.2
	License	Case Management	v2.2
	Module	Kinship and Paternity Analysis	v1.0
HID Genotyper	License	Converge Kinship	v1.0
<i></i>	Module	NGS Application	v1.2
	License	Converge NGS	v1.2
	Upgrade Installer Components	ConvergeUpgrade-2.2-0.x86_64.rpm (Serial No.)	4b0cd383b- 201908300532
Converge	Module	upgradecvg (Serial No.)	v1.0
Software	Supplemental Files	Converge-NGS-1.2.zip	v1.2
	Module	Precision_ID_Panel_Definitions.zip	Oct 15th 2018
	License	Precision_ID_mtDNA_rCRS File (NCBI reference NC_012920)	July 19th 2017

LEGAL NOTICES AND DISCLAIMER

For Research Forensic or Paternity Use Only. Not for use in diagnostic procedures. For licensing and limited use restrictions visit <u>thermofisher.com/HIDlicensing</u>

Information in this document is subject to change without notice.

DISCLAIMER: THERMO FISHER SCIENTIFIC AND/OR ITS AFFILIATE (S) DISCLAIM ALL WARRANTIES WITH RESPECT TO THIS DOCUMENT, EXPRESSED OR IMPLIED, INCLUDING BUT NOT LIMITED TO THOSE OF MERCHANTABILITY, FITNESS FOR A PARTICULAR PURPOSE, OR NONINFRINGEMENT.TO THE EXTENT ALLOWED BY LAW, IN NO EVENT SHALL LIFE TECHNOLOGIES AND/OR ITS AFFILIATE(S) BE LIABLE, WHETHER INCONTRACT, TORT, WARRANTY, OR UNDER ANY STATUTE OR ON ANY OTHER BASIS FOR SPECIAL, INCIDENTAL, INDIRECT, PUNITIVE, MULTIPLE OR CONSEQUENTIAL DAMAGES IN CONNECTION WITH OR ARISING FROM THIS DOCUMENT, INCLUDING BUT NOT LIMITED TO THE USE THEREOF.

TRADEMARKS

© 2019 Thermo Fisher Scientific Inc. All rights reserved. All trademarks are the property of Thermo Fisher Scientific and its subsidiaries unless otherwise specified.