



DNA Interpretation Test No. 26-5881

Summary Report

Each participant received a digitally downloadable sample pack containing electropherograms and raw data files which they were asked to evaluate using their existing protocols. Data were returned from 31 participants and are compiled into the following tables:

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This report contains the data received from the participants in this test. Since these participants are located in many countries around the world, and it is their option how the samples are to be used (e.g., training exercise, known or blind proficiency testing, research and development of new techniques, etc.), the results compiled in the Summary Report are not intended to be an overview of the quality of work performed in the profession and cannot be interpreted as such. The Summary Comments are included for the benefit of participants to assist with maintaining or enhancing the quality of their results. These comments are not intended to reflect the general state of the art within the profession.

Participant results are reported using a randomly assigned "WebCode". This code maintains participant's anonymity, provides linking of the various report sections, and will change with every report.

Manufacturer's Information

Each sample pack contained digital files consisting of electropherograms from DNA profiles of two reference samples (Items 1 and 2) and two questioned samples (Items 3 and 4). Participants were asked to evaluate the electropherograms and interpret the data using their existing protocols.

SAMPLE PREPARATION: Blood stains from different sources were prepared at separate times and were packaged once they were thoroughly dried into separate envelopes.

VERIFICATION: Predistribution results were consistent with each other and the manufacturer's preparation information. Consistent allelic results were reported for all STR loci, with YSTR allelic results reported by a single participant.

SAMPLE PACK ASSEMBLY: Once sample preparation and verification were completed, digitally downloadable materials were zipped and uploaded to the CTS Portal. The digital upload was then checked to ensure all items were accessible.

Consensus results for each locus were determined when at least 10 participants provide results and 75% or more report the same allele. Additional alleles may be present depending on lab thresholds and/or amplification kit used.

Item	Known/Questioned	Mixture Ratio	Sex	Donor Information
1	Known	--	Female	Victim (African American)
2	Known	--	Male	Suspect (Caucasian)
3	Questioned	3:2	Female/Male	Victim/Suspect
4	Questioned	5:2	Female/Male	Victim/Suspect

Amelogenin and STR Results

Results compiled by predistribution laboratories and a consensus of participants.

Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		
1	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
	13,14	29,30	16,17	X,X	10,13	19,23
	*	*	14,22.2	6,7	8,8	14,17
	NM	NM	NM	NM		
2	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
	*	*	14,16	6,9.3	8,10	15,18
	11	*	*	2		
3	15,15.3,16	15,19,20,24	11,11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
	*	*	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	*	*	2		
4	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
	*	*	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	*	*	2		

YSTR Results

Results compiled from predistribution laboratories and a consensus of at least 10 participants.

Item	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4
2	36,37	14	11,13	13	30	25	11	14	13
	15	12	12	18	30	17	18	11	25
	39	13	12	17	17	24	23	10	13
3	36,37	14	11,13	13	30	25	11	14	13
	15	12	12	18	30	17	18	11	25
	39	13	12	17	17	24	23	10	13
4	36,37	14	11,13	13	30	25	11	14	13
	15	12	12	18	30	17	18	11	25
	39	13	12	17	17	24	23	10	13

NM - Non-Male profile, YSTR results not expected.

*Results were not received from a minimum of 10 participants for the loci indicated.

Summary Comments

This test was designed to allow participants to assess their proficiency in evaluating and interpreting electropherograms (EPGs). Each participant received EPGs (in .pdf and .hid formats) of two reference samples and two questioned samples. The EPG data included were produced from the following amplification kits: GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, YFiler™ Plus, PowerPlex® Y23. Item 1 was created using blood collected from a female donor. Item 2 was created using blood collected from a male donor. Item 3 was created by combining three parts blood from the Item 1 female donor and two parts blood from the Item 2 male donor. Item 4 was created by combining five parts blood from the Item 1 female donor and two parts blood from the Item 2 male donor. Refer to the Manufacturer's Information for preparation details.

Data were returned by 31 participants.

DNA Analysis

All participants that returned results evaluated the provided STR data.

For STR results, all participants reported consistent results with the exception of three participants. For Item 4 locus D21S11, five of the eight participants using the PowerPlex® Fusion 6C kit reported a "29" allele in their STR Results and/or documented an unresolved 29 allele in their Additional Comments.

For YSTR results, all participants reported consistent results.

For Item 3, a consensus was achieved for the full Item 3 profile (unseparated). Two participants attempted the deconvolution of this mixture; however, no consensus was formed for major or minor profiles due to the low reporting population.

For Item 4, a consensus was achieved for the full Item 4 profile (unseparated). Eight participants attempted the deconvolution of this mixture; however, no consensus was formed for major or minor profiles due to the low reporting population.

DNA Interpretations

For Item 3, all but two participants identified that two individuals contributed to the mixture. Of the remaining two participants, one identified three contributors and one did not provide a response. All participants included the victim (Item 1) and the suspect (Item 2) as possible contributors to the stain.

For Item 4, all but one participant identified that two individuals contributed to the mixture. The remaining participant did not provide a response. All but two participants included the victim (Item 1) as a possible contributor to the stain. Of the remaining two participants, one excluded the victim and one reported "Inconclusive/Uninterpretable." All participants included the suspect (Item 2) as a possible contributor to the stain.

STR Interpretation Guidelines

TABLE 1

WebCode	Analytical Threshold (rfu)	Peak Height Ratio (%)	Stochastic Threshold (rfu)
2EPNBF	75	60	250
2P7BJF	120	60	360
2WQB2E	130	60	800
3KQZ7C	130	60	800
A2RF86	[Participant did not provide interpretation guidelines]		
BA24K3	75	60	
BBWPC9	70	70	345
C327B6	75	60	100
C8RGK4	120	60	360
EG9482	70	70	345
FTJULX	130	60	800
GEHKF3	70	70	345
GJNDAX	35	60	250
K8KY2W	75	60	100
M6AV4Q	130	60	800
MPEG4X	75	60	100
MX9J9U	100	60	300
QUW6RQ	75	60	100
QXW4GW	75	60	100
RVMQXL	150	60	400
RY7HAN	100	60	300
TL2MQM	130	60	800
TLZPFQ	160	60	630
TUR9WK	130	60	800
U7FUFK	130	60	800
W9YKFF	130	60	800
WCYVBF	130	60	800
WDUEDH	130	60	800
WFE7NK	70	70	345
WGAPQL	80	60	250
Z88XBE	120	60	360

YSTR Interpretation Guidelines

TABLE 2

WebCode	Analytical Threshold (rfu)	Peak Height Ratio (%)	Stochastic Threshold (rfu)
2EPNBF	[Participant did not provide interpretation guidelines]		
2P7BJF	75	50	75
2WQB2E	50	70	800
3KQZ7C	50	70	800
A2RF86	[Participant did not provide interpretation guidelines]		
BA24K3	75	50	
BBWPC9			550
C327B6	75	50	75
C8RGK4	75	50	75
EG9482			550
FTJULX	50	70	800
GEHKF3			550
GJNDAX	[Participant did not provide interpretation guidelines]		
K8KY2W	75	50	75
M6AV4Q	50	70	800
MPEG4X	75	50	75
MX9J9U	90	40	320
QUW6RQ	75	50	75
QXW4GW	75	50	75
RVMQXL	[Participant did not provide interpretation guidelines]		
RY7HAN	90	40	320
TL2MQM	50	70	800
TLZPFQ	100	60	600
TUR9WK	50	70	800
U7FUFK	50	70	800
W9YKFF	50	70	800
WCYVBF	50	70	800
WDUEDH	50	70	800
WFE7NK			550
WGAPQL	80	50	75
Z88XBE	75	50	75

STR & Amelogenin Results

TABLE 3

WebCode	Amplification Kits	(File Format)	(Probabilistic Genotyping)			
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 1 - STR Results

2EPNBF	GlobalFiler™	(STRmix)				
	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
1	13,14	29,30	16,17	X,X	10,13	19,23
			14,22.2	6,7	8,8	14,17

2P7BJF	GlobalFiler™	(PDF Format)				
	15,16	15,19	11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
1	13,14	29,30	16,17	X,X	10,13	19,23
			14,22.2	6,7	8	14,17
	NM			NM		

2WQB2E	GlobalFiler™	(STRMix)				
	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
1	13,14	29,30	16,17	X,X	10,13	19,23
			14,22.2	6,7	8,8	14,17

3KQZ7C	GlobalFiler™	(HID Format)				
	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
1	13,14	29,30	16,17	X,X	10,13	19,23
	-	-	14,22.2	6,7	8,8	14,17
	-	-	-	-		

A2RF86	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C	(PDF Format), (HID Format)				
	15,16	15,19	11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
1	13,14	29,30	16,17	X	10,13	19,23
	10,12	10,17	14,22.2	6,7	8	14,17

BA24K3	GlobalFiler™	(HID Format) (Lab Retriever)				
	15,16	15,19	11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
1	13,14	29,30	16,17	X	10,13	19,23
			14,22.2	6,7	8	14,17

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 1 - STR Results

BBWPC9	PowerPlex® Fusion 6C (HID Format)					
	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
	13,14	29,30	16,17	X,X	10,13	19,23
	10,12	10,17	14,22.2	6,7	8,8	14,17
	NR	NR	NR			
C327B6	GlobalFiler™, PowerPlex® Fusion 6C (PDF Format), (HID Format)					
	15,16	15,19	11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
	13,14	29,30	16,17	X	10,13	19,23
	10,12	10,17	14,22.2	6,7	8	14,17
	-	-	-	-		
C8RGK4	GlobalFiler™ (PDF Format)					
	15,16	15,19	11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
	13,14	29,30	16,17	X,X	10,13	19,23
			14,22.2	6,7	8	14,17
	NM			NM		
EG9482	PowerPlex® Fusion 6C (HID Format)					
	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
	13,14	29,30	16,17	X,X	10,13	19,23
	10,12	10,17	14,22.2	6,7	8,8	14,17
	NR	NR	NR			
FTJULX	GlobalFiler™ (PDF Format), (HID Format) (STRMix)					
	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
	13,14	29,30	16,17	X,X	10,13	19,23
			14,22.2	6,7	8,8	14,17
GEHKF3	PowerPlex® Fusion 6C (HID Format)					
	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
	13,14	29,30	16,17	X,X	10,13	19,23
	10,12	10,17	14,22.2	6,7	8,8	14,17
	NR	NR	NR			

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 1 - STR Results

GJNDAX	GlobalFiler™					
	15,16	15,19	11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
	13,14	29,30	16,17	X	10,13	19,23
			14,22.2	6,7	8	14,17

K8KY2W	GlobalFiler™ (PDF Format)					
	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
	13,14	29,30	16,17	X,X	10,13	19,23
			14,22.2	6,7	8,8	14,17

M6AV4Q	GlobalFiler™ (HID Format)					
	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
	13,14	29,30	16,17	X,X	10,13	19,23
			14,22.2	6,7	8,8	14,17

MPEG4X	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 6C (PDF Format), (HID Format)					
	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
	13,14	29,30	16,17	X,X	10,13	19,23
	12,12	10,17	14,22.2	6,7	8,8	14,17

MX9J9U	GlobalFiler™ (HID Format)					
	15,16	15,19	11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
	13,14	29,30	16,17	X	10,13	19,23
			14,22.2	6,7	8	14,17

QUW6RQ	GlobalFiler™ (PDF Format)					
	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
	13,14	29,30	16,17	X,X	10,13	19,23
	N/A	N/A	14,22.2	6,7	8,8	14,17
	NSD	N/A	N/A	NSD		

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 1 - STR Results

QXW4GW PowerPlex® Fusion 6C (HID Format)

	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
1	13,14	29,30	16,17	X,X	10,13	19,23
	10,12	10,17	14,22.2	6,7	8,8	14,17

RVMQXL GlobalFiler™ (PDF Format)

	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
1	13,14	29,30	16,17	X,X	10,13	19,23
			14,22.2	6,7	8,8	14,17
	--			--		

RY7HAN GlobalFiler™ (HID Format)

	15,16	15,19	11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
1	13,14	29,30	16,17	X	10,13	19,23
			14,22.2	6,7	8	14,17

TL2MQM GlobalFiler™ (HID Format)

	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
1	13,14	29,30	16,17	X,X	10,13	19,23
			14,22.2	6,7	8,8	14,17

TLZPFQ GlobalFiler™ (HID Format)

	15,16	15,19	11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
1	13,14	29,30	16,17	X	10,13	19,23
			14,22.2	6,7	8	14,17

TUR9WK GlobalFiler™ (HID Format)

	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
1	13,14	29,30	16,17	X,X	10,13	19,23
			14,22.2	6,7	8,8	14,17

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 1 - STR Results

U7FUFK	GlobalFiler™ (HID Format)					
	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
1	13,14	29,30	16,17	X,X	10,13	19,23
			14,22.2	6,7	8,8	14,17

W9YKFF	GlobalFiler™					
	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
1	13,14	29,30	16,17	X,X	10,13	19,23
			14,22.2	6,7	8,8	14,17

WCYVBF	GlobalFiler™ (HID Format) (STRmix)					
	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
1	13,14	29,30	16,17	X,X	10,13	19,23
			14,22.2	6,7	8,8	14,17

WDUEDH	GlobalFiler™ (STRMIX)					
	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
1	13,14	29,30	16,17	X,X	10,13	19,23
			14,22.2	6,7	8,8	14,17

WFE7NK	PowerPlex® Fusion 6C (HID Format) (STRmix)					
	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
1	13,14	29,30	16,17	X,X	10,13	19,23
	10,12	10,17	14,22.2	6,7	8,8	14,17
	NR	NR	NR			

WGAPQL	GlobalFiler™ (PDF Format)					
	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
1	13,14	29,30	16,17	X,X	10,13	19,23
			14,22.2	6,7	8,8	14,17

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 1 - STR Results

Z88XBE	GlobalFiler™ (PDF Format)					
	15,16	15,19	11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
	13,14	29,30	16,17	X,X	10,13	19,23
			14,22.2	6,7	8	14,17
1	NM			NM		

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 2 - STR Results

2EPNBF	GlobalFiler™ (STRmix)					
	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
			14,16	6,9.3	8,10	15,18
	11			2		
2P7BJF	GlobalFiler™ (PDF Format)					
	15,15.3	20,24	11	16,18	12,13	8,11
	10,13	15	19,22	9,12	12	12,17
	13,15.2	28,29.1	16	X,Y	10,13	24
			14,16	6,9.3	8,10	15,18
	11			2		
2WQB2E	GlobalFiler™ (STRmix)					
	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
			14,16	6,9.3	8,10	15,18
	11			2		
3KQZ7C	GlobalFiler™ (HID Format)					
	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
	-	-	14,16	6,9.3	8,10	15,18
	11	-	-	2		
A2RF86	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format)					
	15,15.3	20,24	11	16,18	12,13	8,11
	10,13	15	19,22	9,12	12	12,17
	13,15.2	28,29.1	16	X,Y	10,13	24
	11,12	7,13	14,16	6,9.3	8,10	15,18
	11	17	17	2		
BA24K3	GlobalFiler™ (HID Format) (Lab Retriever)					
	15,15.3	20,24	11	16,18	12,13	8,11
	10,13	15	19,22	9,12	12	12,17
	13,15.2	28,29.1	16	X,Y	10,13	24
			14,16	6,9.3	8,10	15,18
	11			2		

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 2 - STR Results

BBWPC9 PowerPlex® Fusion 6C (HID Format)

	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
2	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
	11,12	7,13	14,16	6,9.3	8,10	15,18
	11	17	17			

C327B6 GlobalFiler™, PowerPlex® Fusion 6C (PDF Format), (HID Format)

	15,15.3	20,24	11	16,18	12,13	8,11
	10,13	15	19,22	9,12	12	12,17
2	13,15.2	28,29.1	16	X,Y	10,13	24
	11,12	7,13	14,16	6,9.3	8,10	15,18
	11	17	17	2		

C8RGK4 GlobalFiler™ (PDF Format)

	15,15.3	20,24	11	16,18	12,13	8,11
	10,13	15	19,22	9,12	12	12,17
2	13,15.2	28,29.1	16	X,Y	10,13	24
			14,16	6,9.3	8,10	15,18
	11			2		

EG9482 PowerPlex® Fusion 6C (HID Format)

	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
2	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
	11,12	7,13	14,16	6,9.3	8,10	15,18
	11	17	17			

FTJULX GlobalFiler™ (PDF Format), (HID Format) (STRMix)

	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
2	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
			14,16	6,9.3	8,10	15,18
	11			2		

GEHKF3 PowerPlex® Fusion 6C (HID Format)

	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
2	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
	11,12	7,13	14,16	6,9.3	8,10	15,18
	11	17	17			

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 2 - STR Results

GJNDAX	GlobalFiler™					
	15,15.3	20,24	11	16,18	12,13	8,11
	10,13	15	19,22	9,12	12	12,17
	13,15.2	28,29.1	16	X,Y	10,13	24
			14,16	6,9.3	8,10	15,18
	11			2		
K8KY2W	GlobalFiler™ (PDF Format)					
	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
			14,16	6,9.3	8,10	15,18
	11			2		
M6AV4Q	GlobalFiler™ (HID Format)					
	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
			14,16	6,9.3	8,10	15,18
	11			2		
MPEG4X	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 6C (PDF Format), (HID Format)					
	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
	11,12	7,13	14,16	6,9.3	8,10	15,18
	11	17	17	2		
MX9J9U	GlobalFiler™ (HID Format)					
	15,15.3	20,24	11	16,18	12,13	8,11
	10,13	15	19,22	9,12	12	12,17
	13,15.2	28,29.1	16	X,Y	10,13	24
			14,16	6,9.3	8,10	15,18
	11			2		
QUW6RQ	GlobalFiler™ (PDF Format)					
	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
	N/A	N/A	14,16	6,9.3	8,10	15,18
	11	N/A	N/A	2		

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 2 - STR Results

QXW4GW PowerPlex® Fusion 6C (HID Format)

	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
2	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
	11,12	7,13	14,16	6,9.3	8,10	15,18
	11	17	17			

RVMQXL GlobalFiler™ (PDF Format)

	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
2	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
			14,16	6,9.3	8,10	15,18
	11			2		

RY7HAN GlobalFiler™ (HID Format)

	15,15.3	20,24	11	16,18	12,13	8,11
	10,13	15	19,22	9,12	12	12,17
2	13,15.2	28,29.1	16	X,Y	10,13	24
			14,16	6,9.3	8,10	15,18
	11			2		

TL2MQM GlobalFiler™ (HID Format)

	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
2	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
			14,16	6,9.3	8,10	15,18
	11			2		

TLZPFQ GlobalFiler™ (HID Format)

	15,15.3	20,24	11	16,18	12,13	8,11
	10,13	15	19,22	9,12	12	12,17
2	13,15.2	28,29.1	16	X,Y	10,13	24
			14,16	6,9.3	8,10	15,18
	11			2		

TUR9WK GlobalFiler™ (HID Format)

	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
2	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
			14,16	6,9.3	8,10	15,18
	11			2		

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
Item	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 2 - STR Results

U7FUFK GlobalFiler™ (HID Format)

2	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
	-	-	14,16	6,9.3	8,10	15,18
	11	-	-	2		

W9YKFF GlobalFiler™

2	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
			14,16	6,9.3	8,10	15,18
	11			2		

WCYVBF GlobalFiler™ (HID Format) (STRmix)

2	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
			14,16	6,9.3	8,10	15,18
	11			2		

WDUEDH GlobalFiler™ (STRMIX)

2	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
			14,16	6,9.3	8,10	15,18
	11			2		

WFE7NK PowerPlex® Fusion 6C (HID Format) (STRmix)

2	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
	11,12	7,13	14,16	6,9.3	8,10	15,18
	11	17	17			

WGAPQL GlobalFiler™ (PDF Format)

2	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
			14,16	6,9.3	8,10	15,18
	11			2		

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 2 - STR Results

Z88XBE	GlobalFiler™ (PDF Format)					
	15,15.3	20,24	11	16,18	12,13	8,11
	10,13	15	19,22	9,12	12	12,17
	13,15.2	28,29.1	16	X,Y	10,13	24
			14,16	6,9.3	8,10	15,18
2	11			2		

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 3 - STR Results

2EPNBF	GlobalFiler™ (STRmix)					
	15,15.3,16	15,19,20,24	11,11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		
2P7BJF	GlobalFiler™ (PDF Format)					
	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		
2WQB2E	GlobalFiler™ (STRMix)					
	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		
3KQZ7C	GlobalFiler™ (HID Format) (STRMix(TM) v 2.10)					
	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
	-	-	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	-	-	2		
A2RF86	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format) (LabRetriever v2.2.1)					
	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
	10,11,12	7,10,13,17	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	17	17	2		
BA24K3	GlobalFiler™ (HID Format) (Lab Retireiver)					
	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 3 - STR Results

BBWPC9 PowerPlex® Fusion 6C (HID Format) (STRmix v2.5.11)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
	10,11,12	7,10,13,17	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	17	17			

C327B6 GlobalFiler™, PowerPlex® Fusion 6C (PDF Format), (HID Format)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
	10,11,12	7,10,13,17	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	17	17	2		

C8RGK4 GlobalFiler™ (PDF Format)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

EG9482 PowerPlex® Fusion 6C (HID Format) (STRmix)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
	10,11,12	7,10,13,17	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	17	17			

FTJULX GlobalFiler™ (PDF Format), (HID Format) (STRMix)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

GEHKF3 PowerPlex® Fusion 6C (HID Format) (STRmix)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
	10,11,12	7,10,13,17	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	17	17			

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 3 - STR Results

GJNDAX	GlobalFiler™					
	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		
K8KY2W	GlobalFiler™ (PDF Format)					
	15,15.3,(16)	15,19,20,24	11,11	14,16,18	(11),12,13	8,10,11,12
	10,12,13	(14),15	15,17.3,19,22	9,11,12,13	(11),12,(13)	(12),17,(18)
	13,(14),15.2	28,29,29.1,30	16,(17)	X,(Y)	10,13	19,23,24
			14,(16,22.2)	6,7,9.3	8,(10)	14,15,17,18
	11			2		
3major	15,15.3	15,19,20,24	11	14,16,18	12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12	17
	13,15.2	28,29,29.1,30	16	X	10,13	19,23,24
			14	6,7,9.3	8	14,15,17,18
	11			2		
3minor	16				11	
		14			11,13	12,18
	14		17	Y		
			16,22.2		10	
M6AV4Q	GlobalFiler™ (HID Format) (STRMix ver. 2.10.0)					
	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		
MPEG4X	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 6C (PDF Format), (HID Format) (Euroformix v4.2.4)					
	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
	10,11,12	7,10,13,17	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	17	17	2		
MX9J9U	GlobalFiler™ (HID Format) (STRmix)					
	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 3 - STR Results

QUW6RQ GlobalFiler™ (PDF Format)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
	N/A	N/A	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	N/A	N/A	2		

QXW4GW PowerPlex® Fusion 6C (HID Format)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
	10,11,12	7,10,13,17	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	17	17			

RVMQXL GlobalFiler™ (PDF Format)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

RY7HAN GlobalFiler™ (HID Format) (STRmix)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

TL2MQM GlobalFiler™ (HID Format) (STRmix)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

TLZPFQ GlobalFiler™ (HID Format)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 3 - STR Results

TUR9WK GlobalFiler™ (HID Format) (STRmix Version 2.10)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

U7FUFK GlobalFiler™ (HID Format) (STRMIX)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
	-	-	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	-	-	2		

	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
3major	13,15.2	28,29.1	16,16		10,13	24,24
			14,16	6,9.3	8,10	15,18

	15,16	15,19	11,11	14,16	11,13	10,12
	12,13	14,15	15,17.3	11,13	11,13	17,18
3minor	13,14	29,30	16,17		10,13	19,23
			14,22.2	6,7	8,8	14,17

W9YKFF GlobalFiler™ (STRMix v. 2.10)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

WCYVBF GlobalFiler™ (HID Format) (STRmix)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

WDUEDH GlobalFiler™ (STRMIX)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 3 - STR Results

WFE7NK PowerPlex® Fusion 6C (HID Format) (STRmix)						
	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
	10,11,12	7,10,13,17	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	17	17			
WGAPQL GlobalFiler™ (PDF Format) (LRmixStudio-2.1.5 CommunityEdition)						
	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		
Z88XBE GlobalFiler™ (PDF Format)						
	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
3	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D25441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 4 - STR Results

2EPNBF	GlobalFiler™ (STRmix)					
	15,15.3	15,19,20,24	11,11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15,15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		
2P7BJF	GlobalFiler™ (PDF Format)					
	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		
4	15,15.3	20,24	11	16,18	12,13	8,11
	10,13	15	19,22	9,12	12	12,17
	13,15.2	28,29.1	16	X,Y	10,13	24
			14,16	6,9.3	8,10	15,18
	11			2		
2WQB2E	GlobalFiler™ (STRMix)					
	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		
3KQZ7C	GlobalFiler™ (HID Format) (STRMix(TM) v 2.10)					
	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
	-	-	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	-	-	2		
A2RF86	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format) (LabRetriever v2.2.1)					
	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
	10,11,12	7,10,13,17	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	17	17	2		

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 4 - STR Results

BA24K3 GlobalFiler™ (HID Format) (Lab Retriever)

	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
4	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

BBWPC9 PowerPlex® Fusion 6C (HID Format) (STRmix v2.5.11)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
4	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
	10,11,12	7,10,13,17	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	17	17			

C327B6 GlobalFiler™, PowerPlex® Fusion 6C (PDF Format), (HID Format)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
4	13,14,15.2	28,29,29.1,30	16,17	X,Y	10,13	19,23,24
	10,11,12	7,10,13,17	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	17	17	2		

C8RGK4 GlobalFiler™ (PDF Format)

	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
4	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

	15,15.3	20,24	11	16,18	12,13	8,11
	10,13	15	19,22	9,12	12	12,17
4major	13,15.2	28,29.1	16	X,Y	10,13	24
			14,16	6,9.3	8,10	15,18
	11			2		

EG9482 PowerPlex® Fusion 6C (HID Format) (STRmix)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
4	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
	10,11,12	7,10,13,17	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	17	17			

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 4 - STR Results

FTJULX	GlobalFiler™ (PDF Format), (HID Format) (STRMix)					
	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		
GEHKF3	PowerPlex® Fusion 6C (HID Format) (STRmix)					
	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
	10,11,12	7,10,13,17	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	17	17			
GJNDAX	GlobalFiler™					
	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		
	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12,12	12,17
	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
			14,16	6,9.3	8,10	15,18
	11			2		
		15,19	11,any	14,any	11,any	10,12
4major	12,any		15,17.3	11,13	13,any	18,any
	14,any	30,any	17,any	X,X or X,Y		19,23
			22.2,any	7,any		14,17
	11 or N/A			2 or N/A		

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 4 - STR Results

K8KY2W GlobalFiler™ (PDF Format)

4	15,15.3	(15,19),20,24	11,11	(14),16,18	(11),12,13	8,(10),11,(12)
	10,(12),13	15,15	(15,17.3),19,22	9,(11),12,(13)	12,(13)	12,17,(18)
	13,(14),15.2	28,29.1,(30)	16,(17)	X,Y	10,13	(19,23),24
			14,16,(22.2)	6,(7),9.3	8,10	(14),15,(17),18
4major	11			2		
	15,15.3	20,24	11	16,18	12,13	8,11
	10,13	15	19,22	9,12	12	12,17
	13,15.2	28,29.1	16	X,Y	10,13	24
4minor			14,16	6,9.3	8,10	15,18
	11			2		
		15,19		14	11	10,12
	12		15,17.3	11,13	13	18
4minor	14	30	17			19,23
			22.2	7		14,17

M6AV4Q GlobalFiler™ (HID Format) (STRMix ver. 2.10.0)

4	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

MPEG4X GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 6C (PDF Format), (HID Format) (Euroformix v4.2.4)

4	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
	10,11,12	7,10,13,17	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	17	17	2		

MX9J9U GlobalFiler™ (HID Format) (STRmix)

4	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

QUW6RQ GlobalFiler™ (PDF Format)

4	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
	N/A	N/A	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	N/A	N/A	2		

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 4 - STR Results

QXW4GW PowerPlex® Fusion 6C (HID Format)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
4	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
	10,11,12	7,10,13,17	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	17	17			

RVMQXL GlobalFiler™ (PDF Format)

	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
4	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

RY7HAN GlobalFiler™ (HID Format) (STRmix)

	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
4	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

TL2MQM GlobalFiler™ (HID Format) (STRmix)

	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
4	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

TLZPFQ GlobalFiler™ (HID Format)

	15,15.3	20,24	11	16,18	12,13	8,11
	10,13	15	19,22	9,12	12	12,17
4major	13,15.2	28,29.1	16	X,Y	10,13	24
			14,16	6,9.3	8,10	15,18
	11			2		
		15,19		14		12
	12		15,17.3	11,13	13	18
4minor	14	30	17			19
			22.2	7		17

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 4 - STR Results

TUR9WK GlobalFiler™ (HID Format) (STRmix Version 2.10)

	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
4	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

U7FUFK GlobalFiler™ (HID Format) (STRMIX)

	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
4	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
	-	-	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	-	-	2		

	-	20,24	11,11	16,18	12,13	8,11
	10,13	-	19,22	9,12	12,12	12,17
4major	13,15.2	28,29.1	16,16	-	10,13	24,24
			14,16	6,9.3	8,10	15,18
	-			-		

	-	15,19	11,11	14,16	11,13	10,12
	12,13	-	15,17.3	11,13	11,13	17,18
4minor	13,14	29,30	16,17	-	10,13	19,23
			14,22.2	6,7	8,8	14,17
	-			-		

W9YKFF GlobalFiler™ (STRMix v. 2.10)

	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
4	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

WCYVBF GlobalFiler™ (HID Format) (STRmix)

	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
4	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

WDUEDH GlobalFiler™ (STRMIX)

	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
4	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		

Item 4 - STR Results

WFE7NK PowerPlex® Fusion 6C (HID Format) (STRmix)

	15,15.3,16	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	14,15	15,17.3,19,22	9,11,12,13	11,12,13	12,17,18
4	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
	10,11,12	7,10,13,17	14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11	17	17			

WGAPQL GlobalFiler™ (PDF Format) (LRmixStudio-2.1.5 CommunityEdition)

	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,14	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
4	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

	15,15.3	20,24	11,11	16,18	12,13	8,11
	10,13	15,15	19,22	9,12	12	12,17
4major	13,15.2	28,29.1	16,16	X,Y	10,13	24,24
			14,16	6,9.3	8,10	15,18
	11			2		

		15,19		14	11	10,12
	12		15,17.3	11,13	13	18
4minor	14	30	17	X,X		19,23
			22.2	7		14,17

Z88XBE GlobalFiler™ (PDF Format)

	15,15.3	15,19,20,24	11	14,16,18	11,12,13	8,10,11,12
	10,12,13	15	15,17.3,19,22	9,11,12,13	12,13	12,17,18
4	13,14,15.2	28,29.1,30	16,17	X,Y	10,13	19,23,24
			14,16,22.2	6,7,9.3	8,10	14,15,17,18
	11			2		

	15,15.3	20,24	11	16,18	12,13	8,11
	10,13	15	19,22	9,12	12	12,17
4major	13,15.2	28,29.1	16	X,Y	10,13	24
			14,16	6,9.3	8,10	15,18
	11			2		

YSTR Results

TABLE 4

WebCode	Amplification Kits (File Format)								
Item	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4

Item 2 - YSTR Results

2P7BJF	Yfiler™ Plus (PDF Format)								
	36,37	14	11,13	13	30	25	11	14	13
	15	12	12	18	30	17	18	11	25
2	39	13		17	17	24	23		13
	PowerPlex® Y23								
		14	11,13	13	30	25	11	14	13
2	15	12	12	18		17	18		25
		13	12	17	17		23	10	13
3KQZ7C	PowerPlex® Y23 (HID Format)								
	-	14	11,13	13	30	25	11	14	13
	15	12	12	18	-	17	18	-	25
2	-	13	12	17	17	-	23	10	13
A2RF86	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	36,37	14	11,13	13	30	25	11	14	13
	15	12	12	18	30	17	18	11	25
2	39	13	12	17	17	24	23	10	13
BA24K3	Yfiler™ Plus								
	36,37	14	11,13	13	30	25	11	14	13
	15	12	12	18	30	17	18	11	25
2	39	13		17	17	24	23		13
BBWPC9	PowerPlex® Y23 (HID Format)								
		14	11,13	13	30	25	11	14	13
	15	12	12	18		17	18		25
2		13	12	17	17		23	10	13
C327B6	Yfiler™ Plus (PDF Format), (HID Format)								
	36,37	14	11,13	13	30	25	11	14	13
	15	12	12	18	30	17	18	11	25
2	39	13		17	17	24	23		13
C8RGK4	Yfiler™ Plus (PDF Format)								
	36,37	14	11,13	13	30	25	11	14	13
	15	12	12	18	30	17	18	11	25
2	39	13		17	17	24	23		13
EG9482	PowerPlex® Y23 (HID Format)								
		14	11,13	13	30	25	11	14	13
	15	12	12	18		17	18		25
2		13	12	17	17		23	10	13
FTJULX	PowerPlex® Y23 (PDF Format)								
		14	11,13	13	30	25	11	14	13
	15	12	12	18		17	18		25
2		13	12	17	17		23	10	13

TABLE 4

WebCode	Amplification Kits (File Format)								
Item	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4

Item 2 - YSTR Results

GEHKF3	PowerPlex® Y23 (HID Format)								
		14	11,13	13	30	25	11	14	13
	2	15	12	12	18	17	18		25
		13	12	17	17		23	10	13
K8KY2W	Yfiler™ Plus (PDF Format)								
		36,37	14	11,13	13	30	25	11	14
	2	15	12	12	18	30	17	18	11
		39	13		17	17	24	23	
M6AV4Q	PowerPlex® Y23 (PDF Format)								
		14	11,13	13	30	25	11	14	13
	2	15	12	12	18	17	18		25
		13	12	17	17		23	10	13
MPEG4X	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
		36,37	14	11,13	13	30	25	11	14
	2	15	12	12	18	30	17	18	11
		39	13	12	17	17	24	23	10
MX9J9U	Yfiler™ Plus (HID Format)								
		36,37	14	11,13	13	30	25	11	14
	2	15	12	12	18	30	17	18	11
		39	13		17	17	24	23	
QUW6RQ	Yfiler™ Plus (PDF Format)								
		36,37	14	11,13	13	30	25	11	14
	2	15	12	12	18	30	17	18	11
		39	13	N/A	17	17	24	23	N/A
QXW4GW	Yfiler™ Plus (HID Format)								
		36,37	14	11,13	13	30	25	11	14
	2	15	12	12	18	30	17	18	11
		39	13		17	17	24	23	
RY7HAN	Yfiler™ Plus (HID Format)								
		36,37	14	11,13	13	30	25	11	14
	2	15	12	12	18	30	17	18	11
		39	13		17	17	24	23	
TL2MQM	PowerPlex® Y23 (HID Format)								
		14	11,13	13	30	25	11	14	13
	2	15	12	12	18	17	18		25
		13	12	17	17		23	10	13
TLZPFQ	PowerPlex® Y23 (HID Format)								
		14	11,13	13	30	25	11	14	13
	2	15	12	12	18	17	18		25
		13	12	17	17		23	10	13

TABLE 4

WebCode	Amplification Kits (File Format)								
Item	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4

Item 2 - YSTR Results

TUR9WK	PowerPlex® Y23 (HID Format)								
		14	11,13	13	30	25	11	14	13
	2	15	12	12	18	17	18		25
		13	12	17	17		23	10	13
U7FUFK	PowerPlex® Y23 (PDF Format)								
	-	14	11,13	13	30	25	11	14	13
	2	15	12	12	18	-	17	18	-
	-	13	12	17	17	-	23	10	13
W9YKFF	PowerPlex® Y23								
		14	11,13	13	30	25	11	14	13
	2	15	12	12	18	17	18		25
		13	12	17	17		23	10	13
WCYVBF	PowerPlex® Y23 (HID Format)								
		14	11,13	13	30	25	11	14	13
	2	15	12	12	18	17	18		25
		13	12	17	17		23	10	13
WDUEDH	PowerPlex® Y23								
		14	11,13	13	30	25	11	14	13
	2	15	12	12	18	17	18		25
		13	12	17	17		23	10	13
WFE7NK	PowerPlex® Y23 (HID Format)								
		14	11,13	13	30	25	11	14	13
	2	15	12	12	18	17	18		25
		13	12	17	17		23	10	13
WGAPQL	Yfiler™ Plus (PDF Format)								
	36,37	14	11,13	13	30	25	11	14	13
	2	15	12	12	18	30	17	18	11
	39	13		17	17	24	23		13
Z88XBE	Yfiler™ Plus (PDF Format)								
	36,37	14	11,13	13	30	25	11	14	13
	2	15	12	12	18	30	17	18	11
	39	13		17	17	24	23		13

TABLE 4

WebCode	Amplification Kits (File Format)								
Item	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4

Item 3 - YSTR Results

2P7BJF	Yfiler™ Plus (PDF Format)								
	36,37	14	11,13	13	30	25	11	14	13
	15	12	12	18	30	17	18	11	25
3	39	13		17	17	24	23		13
2WQB2E	PowerPlex® Y23								
		14	11,13	13	30	25	11	14	13
	15	12	12	18		17	18		25
3		13	12	17	17		23	10	13
3KQZ7C	PowerPlex® Y23 (HID Format)								
	-	14	11,13	13	30	25	11	14	13
	15	12	12	18	-	17	18	-	25
3	-	13	12	17	17	-	23	10	13
A2RF86	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	36,37	14	11,13	13	30	25	11	14	13
	15	12	12	18	30	17	18	11	25
3	39	13	12	17	17	24	23	10	13
BA24K3	Yfiler™ Plus								
	36,37	14	11,13	13	30	25	11	14	13
	15	12	12	18	30	17	18	11	25
3	39	13		17	17	24	23		13
BBWPC9	PowerPlex® Y23 (HID Format)								
		14	11,13	13	30	25	11	14	13
	15	12	12	18		17	18		25
3		13	12	17	17		23	10	13
C327B6	Yfiler™ Plus (PDF Format), (HID Format)								
	36,37	14	11,13	13	30	25	11	14	13
	15	12	12	18	30	17	18	11	25
3	39	13		17	17	24	23		13
C8RGK4	Yfiler™ Plus (PDF Format)								
	36,37	14	11,13	13	30	25	11	14	13
	15	12	12	18	30	17	18	11	25
3	39	13		17	17	24	23		13
EG9482	PowerPlex® Y23 (HID Format)								
		14	11,13	13	30	25	11	14	13
	15	12	12	18		17	18		25
3		13	12	17	17		23	10	13
FTJULX	PowerPlex® Y23 (PDF Format)								
		14	11,13	13	30	25	11	14	13
	15	12	12	18		17	18		25
3		13	12	17	17		23	10	13

TABLE 4

WebCode	Amplification Kits (File Format)								
Item	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4

Item 3 - YSTR Results

GEHKF3	PowerPlex® Y23 (HID Format)								
		14	11,13	13	30	25	11	14	13
	3	15	12	12	18	17	18		25
		13	12	17	17		23	10	13
K8KY2W	Yfiler™ Plus (PDF Format)								
		36,37	14	11,13	13	30	25	11	14
	3	15	12	12	18	30	17	18	11
		39	13		17	17	24	23	
3major		36,37	14	11,13	13	30	25	11	14
		15	12	12	18	30	17	18	11
		39	13		17	17	24	23	
M6AV4Q	PowerPlex® Y23 (PDF Format)								
		14	11,13	13	30	25	11	14	13
	3	15	12	12	18	17	18		25
		13	12	17	17		23	10	13
MPEG4X	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
		36,37	14	11,13	13	30	25	11	14
	3	15	12	12	18	30	17	18	11
		39	13	12	17	17	24	23	10
MX9J9U	Yfiler™ Plus (HID Format)								
		36,37	14	11,13	13	30	25	11	14
	3	15	12	12	18	30	17	18	11
		39	13		17	17	24	23	
QUW6RQ	Yfiler™ Plus (PDF Format)								
		36,37	14	11,13	13	30	25	11	14
	3	15	12	12	18	30	17	18	11
		39	13	N/A	17	17	24	23	N/A
QXW4GW	Yfiler™ Plus (HID Format)								
		36,37	14	11,13	13	30	25	11	14
	3	15	12	12	18	30	17	18	11
		39	13		17	17	24	23	
RY7HAN	Yfiler™ Plus (HID Format)								
		36,37	14	11,13	13	30	25	11	14
	3	15	12	12	18	30	17	18	11
		39	13		17	17	24	23	
TL2MQM	PowerPlex® Y23 (HID Format)								
		14	11,13	13	30	25	11	14	13
	3	15	12	12	18	17	18		25
		13	12	17	17		23	10	13

TABLE 4

WebCode	Amplification Kits (File Format)								
Item	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4

Item 3 - YSTR Results

TLZPFQ	PowerPlex® Y23 (HID Format)								
	14	11,13	13	30	25	11	14	13	
3	15	12	12	18	17	18		25	
	13	12	17	17		23	10	13	
TUR9WK	PowerPlex® Y23								
	14	11,13	13	30	25	11	14	13	
3	15	12	12	18	17	18		25	
	13	12	17	17		23	10	13	
U7FUFK	PowerPlex® Y23 (PDF Format)								
	-	14	11,13	13	30	25	11	14	13
3	15	12	12	18	-	17	18	-	25
	-	13	12	17	17	-	23	10	13
W9YKFF	PowerPlex® Y23								
	14	11,13	13	30	25	11	14	13	
3	15	12	12	18	17	18		25	
	13	12	17	17		23	10	13	
WCYVBF	PowerPlex® Y23 (HID Format)								
	14	11,13	13	30	25	11	14	13	
3	15	12	12	18	17	18		25	
	13	12	17	17		23	10	13	
WDUEDH	PowerPlex® Y23								
	14	11,13	13	30	25	11	14	13	
3	15	12	12	18	17	18		25	
	13	12	17	17		23	10	13	
WFE7NK	PowerPlex® Y23 (HID Format)								
	14	11,13	13	30	25	11	14	13	
3	15	12	12	18	17	18		25	
	13	12	17	17		23	10	13	
WGAPQL	Yfiler™ Plus (PDF Format)								
	36,37	14	11,13	13	30	25	11	14	13
3	15	12	12	18	30	17	18	11	25
	39	13		17	17	24	23		13
Z88XBE	Yfiler™ Plus (PDF Format)								
	36,37	14	11,13	13	30	25	11	14	13
3	15	12	12	18	30	17	18	11	25
	39	13		17	17	24	23		13

TABLE 4

WebCode	Amplification Kits (File Format)								
Item	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4

Item 4 - YSTR Results

2P7BJF	Yfiler™ Plus (PDF Format)								
	36,37	14	11,13	13	30	25	11	14	13
	15	12	12	18	30	17	18	11	25
4	39	13		17	17	24	23		13
2WQB2E	PowerPlex® Y23								
		14	11,13	13	30	25	11	14	13
	15	12	12	18		17	18		25
4		13	12	17	17		23	10	13
3KQZ7C	PowerPlex® Y23 (HID Format)								
	-	14	11,13	13	30	25	11	14	13
	15	12	12	18	-	17	18	-	25
4	-	13	12	17	17	-	23	10	13
A2RF86	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	36,37	14	11,13	13	30	25	11	14	13
	15	12	12	18	30	17	18	11	25
4	39	13	12	17	17	24	23	10	13
BA24K3	Yfiler™ Plus								
	36,37	14	11,13	13	30	25	11	14	13
	15	12	12	18	30	17	18	11	25
4	39	13		17	17	24	23		13
BBWPC9	PowerPlex® Y23 (HID Format)								
		14	11,13	13	30	25	11	14	13
	15	12	12	18		17	18		25
4		13	12	17	17		23	10	13
C327B6	Yfiler™ Plus (PDF Format), (HID Format)								
	36,37	14	11,13	13	30	25	11	14	13
	15	12	12	18	30	17	18	11	25
4	39	13		17	17	24	23		13
C8RGK4	Yfiler™ Plus (PDF Format)								
	36,37	14	11,13	13	30	25	11	14	13
	15	12	12	18	30	17	18	11	25
4	39	13		17	17	24	23		13
EG9482	PowerPlex® Y23 (HID Format)								
		14	11,13	13	30	25	11	14	13
	15	12	12	18		17	18		25
4		13	12	17	17		23	10	13
FTJULX	PowerPlex® Y23 (PDF Format)								
		14	11,13	13	30	25	11	14	13
	15	12	12	18		17	18		25
4		13	12	17	17		23	10	13

TABLE 4

WebCode	Amplification Kits (File Format)								
Item	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4

Item 4 - YSTR Results

GEHKF3	PowerPlex® Y23 (HID Format)								
		14	11,13	13	30	25	11	14	13
	4	15	12	12	18	17	18		25
		13	12	17	17		23	10	13
K8KY2W	Yfiler™ Plus (PDF Format)								
		36,37	14	11,13	13	30	25	11	14
	4	15	12	12	18	30	17	18	11
		39	13		17	17	24	23	
4major		36,37	14	11,13	13	30	25	11	14
		15	12	12	18	30	17	18	11
		39	13		17	17	24	23	
M6AV4Q	PowerPlex® Y23 (PDF Format)								
		14	11,13	13	30	25	11	14	13
	4	15	12	12	18	17	18		25
		13	12	17	17		23	10	13
MPEG4X	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
		36,37	14	11,13	13	30	25	11	14
	4	15	12	12	18	30	17	18	11
		39	13	12	17	17	24	23	10
MX9J9U	Yfiler™ Plus (HID Format)								
		36,37	14	11,13	13	30	25	11	14
	4	15	12	12	18	30	17	18	11
		39	13		17	17	24	23	
QUW6RQ	Yfiler™ Plus (PDF Format)								
		36,37	14	11,13	13	30	25	11	14
	4	15	12	12	18	30	17	18	11
		39	13	N/A	17	17	24	23	N/A
QXW4GW	Yfiler™ Plus (HID Format)								
		36,37	14	11,13	13	30	25	11	14
	4	15	12	12	18	30	17	18	11
		39	13		17	17	24	23	
RY7HAN	Yfiler™ Plus (HID Format)								
		36,37	14	11,13	13	30	25	11	14
	4	15	12	12	18	30	17	18	11
		39	13		17	17	24	23	
TL2MQM	PowerPlex® Y23 (HID Format)								
		14	11,13	13	30	25	11	14	13
	4	15	12	12	18	17	18		25
		13	12	17	17		23	10	13

TABLE 4

WebCode	Amplification Kits (File Format)								
Item	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4

Item 4 - YSTR Results

TLZPFQ	PowerPlex® Y23 (HID Format)								
		14	11,13	13	30	25	11	14	13
	4	15	12	12	18	17	18		25
		13	12	17	17		23	10	13
TUR9WK	PowerPlex® Y23								
		14	11,13	13	30	25	11	14	13
	4	15	12	12	18	17	18		25
		13	12	17	17		23	10	13
U7FUFK	PowerPlex® Y23 (PDF Format)								
		-	14	11,13	13	30	25	11	14
	4	15	12	12	18	-	17	18	-
		-	13	12	17	17	-	23	10
W9YKFF	PowerPlex® Y23								
		14	11,13	13	30	25	11	14	13
	4	15	12	12	18	17	18		25
		13	12	17	17		23	10	13
WCYVBF	PowerPlex® Y23 (HID Format)								
		14	11,13	13	30	25	11	14	13
	4	15	12	12	18	17	18		25
		13	12	17	17		23	10	13
WDUEDH	PowerPlex® Y23								
		14	11,13	13	30	25	11	14	13
	4	15	12	12	18	17	18		25
		13	12	17	17		23	10	13
WFE7NK	PowerPlex® Y23								
		14	11,13	13	30	25	11	14	13
	4	15	12	12	18	17	18		25
		13	12	17	17		23	10	13
WGAPQL	Yfiler™ Plus (PDF Format)								
		36,37	14	11,13	13	30	25	11	14
	4	15	12	12	18	30	17	18	11
		39	13		17	17	24	23	
Z88XBE	Yfiler™ Plus (PDF Format)								
		36,37	14	11,13	13	30	25	11	14
	4	15	12	12	18	30	17	18	11
		39	13		17	17	24	23	

DNA Conclusions

Based on the examination of the DNA profiles provided, could the Victim (Item 1) and/or the Suspect (Item 2) be included as a possible contributor to the questioned Item?

TABLE 5

WebCode	Item 3 Conclusion			Item 4 Conclusion		
	# of Contributors	Item 1	Item 2	# of Contributors	Item 1	Item 2
2EPNBF	3	Included	Included	2	Included	Included
2P7BJF	2	Included	Included	2	Included	Included
2WQB2E	Two (2)	Included	Included	Two (2)	Included	Included
3KQZ7C	2	Included	Included	2	Included	Included
A2RF86	at least 2 (including at least one male)	Included	Included	at least 2 (including at least one male)	Included	Included
BA24K3	2	Included	Included	2	Included	Included
BBWPC9	STR-2; YSTR-1	Included	Included	STR-2; YSTR-1	Included	Included
C327B6	2	Included	Included	2	Included	Included
C8RGK4	2	Included	Included	2	Included	Included
EG9482	2	Included	Included	2	Included	Included
FTJULX	2	Included	Included	2	Included	Included
GEHKF3	2	Included	Included	2	Included	Included
GJNDAX		Included	Included		Included	Included
K8KY2W	2	Included	Included	2	Excluded	Included
M6AV4Q	2	Included	Included	2	Included	Included
MPEG4X	2	Included	Included	2	Included	Included
MX9J9U	2	Included	Included	2	Included	Included
QUW6RQ	2	Included	Included	2	Included	Included
QXW4GW	2	Included	Included	2	Included	Included
RVMQXL	2	Included	Included	2	Included	Included
RY7HAN	2	Included	Included	2	Included	Included
TL2MQM	2	Included	Included	2	Included	Included
TLZPFQ	2, including at least 1 male	Included	Included	2, including at least 1 male	Inconclusive / Uninterpretable	Included
TUR9WK	2	Included	Included	2	Included	Included
U7FUFK	2	Included	Included	2	Included	Included
W9YKFF	2	Included	Included	2	Included	Included
WCYVBF	2	Included	Included	2	Included	Included
WDUEDH	2 contributors including at least one male.	Included	Included	2 Contributors including at least 1 male	Included	Included
WFE7NK	2	Included	Included	2	Included	Included
WGAPQL	2	Included	Included	2	Included	Included

TABLE 5

WebCode	# of Contributors	<u>Item 3 Conclusion</u>		# of Contributors	<u>Item 4 Conclusion</u>	
		<u>Item 1</u>	<u>Item 2</u>		<u>Item 1</u>	<u>Item 2</u>
Z88XBE	2	Included	Included	2	Included	Included

Conclusions Response Summary				Participants reporting conclusions: 31			
Based on the examination of the DNA profiles provided, could the Victim (Item 1) and/or the Suspect (Item 2) be included as a possible contributor to the questioned Item?							
Responses		Item 3			Item 4		
		Item 1	Item 2		Item 1	Item 2	
	Included	31	31		29	31	
	Excluded	0	0		1	0	
	Inconclusive/ Uninterpretable	0	0		1	0	
	No Response	0	0		0	0	
	Total	31	31		31	31	

Statistical Analysis for Item 3

TABLE 6

WebCode	Item 3 Methods & Results
2EPNBF	Method(s): Likelihood Ratio Stats Analysis: The DNA profile obtained from Item 3 was interpreted using STRmix probabilistic genotyping software under a three-contributor model. Likelihood ratios were calculated to evaluate the probability of the observed DNA evidence under the proposition that the person of interest contributed to the mixture versus the alternative proposition that the DNA originated from unknown, unrelated individuals. For Item 1 (victim), the likelihood ratio is on the order of 10^{18} to 10^{19}. For Item 2 (suspect), the likelihood ratio is on the order of 10^{18} to 10^{21}. These results provide extremely strong support for the proposition that both Item 1 and Item 2 contributed to the DNA mixture. Database(s): NIST1036_CAUC, NIST1036_AFAM
2P7BJF	Method(s): Likelihood Ratio Stats Analysis: A mixed DNA profile of two individuals was developed from stain on suspect's shirt "Item 3". The DNA profiles obtained from reference samples "Item 1" and "Item 2" are consistent being the contributors respectively to this mixed DNA profile. The mixed DNA profiles are 490 septillion, 1.3 octillion and 14 octillion TIMES more likely: IF they originated from "Item 1" and "Item 2" RATHER THAN; if they originated from "Item 2" and one unknown unrelated individual as calculated based on the [Location Identifying Database]. Database(s): [Location Identifying Database]
2WQB2E	Method(s): Likelihood Ratio Stats Analysis: The DNA result obtained from Item 3 is consistent with a mixture from at least two (2) contributors. The mixture is approximately 1.89×10^{27} times more likely to occur (very strong support for inclusion) if the complainant (Item 1) and the suspect (Item 2) are contributors, rather than if the suspect and one (1) unknown, unrelated individual are contributors. Database(s): STRMix
3KQZ7C	Method(s): Likelihood Ratio Stats Analysis: The DNA result obtained from the swab (Item 3) allegedly taken from stain on suspect's shirt is consistent with a mixture of at least two (2) contributors, including at least one (1) male. a) This mixture is approximately 3.45×10^{17} times more likely to occur (very strong support for inclusion) if the female victim and one (1) unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. b) This mixture is approximately 7.19×10^{17} times more likely to occur (very strong support for inclusion) if the male suspect and one (1) unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. Database(s): FBI_EXTENDED_AFAM & FBI_EXTENDED_CAUC

TABLE 6

WebCode	Item 3 Methods & Results
A2RF86	Method(s): Likelihood Ratio Stats Analysis: Autosomal Statistical Weight Estimate: Under the assumption that the VICTIM (Item 1) and one unknown unrelated person selected at random from the general population are contributors, the likelihood of observing the mixed source profile developed from the STAIN ON SUSPECT'S SHIRT (Item 3) is $\geq 1,000,000$ times greater (actual LR available upon request) than if it is assumed that two unknown unrelated persons selected at random from the general population are contributors to this mixed-source profile. Under the assumption that the SUSPECT (Item 2) and one unknown unrelated person selected at random from the general population are contributors, the likelihood of observing the mixed source profile developed from the STAIN ON SUSPECT'S SHIRT (Item 3) is $\geq 1,000,000$ times greater (actual LR available upon request) than if it is assumed that two unknown unrelated persons selected at random from the general population are contributors to this mixed-source profile. Under the assumption that the VICTIM (Item 1) and the SUSPECT (Item 2) are contributors, the likelihood of observing the mixed source profile developed from the STAIN ON SUSPECT'S SHIRT (Item 3) is $\geq 1,000,000$ times greater (actual LR available upon request) than if it is assumed that the SUSPECT (Item 2) and one unknown unrelated person selected at random from the general population are contributors to this mixed-source profile. YSTR Statistical Weight Estimate: The SUSPECT (Item 2), his paternally-related male relatives, and an unknown number of males in the general population cannot be excluded as the potential source of the YSTR haplotype developed from the STAIN ON SUSPECT'S SHIRT (Item 3). Given a theta-value of 2.0×10^{-5} and a 95% UCI of the combined Haplotype frequency of 1 in 3,574 (no matches in 10,704 Haplotypes at U.S. subpopulations without Native American), the corrected Match Probability is 1 in 3,336. Database(s): Statistical Calculations employed the following databases: Revised-NIST-1036-Allele Frequencies; ABI ID Allele Frequencies; Promega PowerPlex Fusion Allele Frequencies and YHRD Release R69 valid as per 2024-03-07 20:22:41 UTC
BA24K3	Method(s): Likelihood Ratio Stats Analysis: The genetic profile obtained from Item 3 is interpreted as a mixture of DNA from two contributors. Item 1, (victim) cannot be excluded as a possible contributor to this mixture. Given this genetic profile, assuming two contributors, and assuming the presence of the suspect's profile, it is 394 sextillion times more likely to observe this genetic profile if Item 2 (suspect) and Item 1 (victim) are contributors than if Item 2 (suspect) and one unknown individual are the contributors. Database(s): NIST
BBWPC9	Method(s): Likelihood Ratio Stats Analysis: The DNA profile from this item is at least 1.4 nonillion times more likely if it originated from Suspect and Victim than if it originated from Suspect and an unknown, unrelated individual. Database(s): Most conservative population group statistic is reported. The National Institute of Standards and Technology's published database is utilized in the statistical calculations. Hill, C.R., Duewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. Forensic Sci. Int. Genet. 7: e82-e83. Revised data received on August 10, 2017.
C327B6	Method(s): Likelihood Ratio Stats Analysis: LR=1.0E+17 - The DNA findings provide extremely strong evidence to support the hypothesis that the victim and one unrelated unknown person were the contributors compared to the alternative hypothesis that two unrelated unknown persons were the contributors. LR=1.9E+18 - The DNA findings provide extremely strong evidence to support the hypothesis that the suspect and one unrelated unknown person were the contributors compared to the alternative hypothesis that two unrelated unknown persons were the contributors. Database(s): Local population data

TABLE 6

WebCode	Item 3 Methods & Results
C8RGK4	Method(s): Likelihood Ratio Stats Analysis: A mixed DNA profile of two contributor was developed from "Item 3". The DNA profile obtained from the reference samples "Item 1" and "Item 2" was being the contributors to this mixed DNA profile. The mixed DNA profile are 490 septillion (490x10e24), 1.3 octillion (1.3x10e27) and 14 octillion (14x10e27) TIMES more likely; IF they originated from "Item 1" and "Item 2" RATHER THAN; IF they originated from "Item 2" and one unknown unrelated individual as calculated based on the [Location Identifying Database]. Database(s): [Location Identifying Database]
EG9482	Method(s): Likelihood Ratio Stats Analysis: The STR DNA profile was interpreted as a mixture of two contributors, including male DNA. Suspect was assumed as one of the contributors. The DNA profile from this item is at least 1.3 nonillion times more likely if it originated from Suspect and Victim than if it originated from Suspect and an unknown, unrelated individual. This provides support that Victim is included as a contributor to this DNA profile. A Y-STR DNA profile was obtained. Suspect is consistent with this DNA profile. Database(s): a. Most conservative population group statistic is reported. b. The National Institute of Standards and Technology's published database is utilized in the statistical calculations. Hill, C.R., Duewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. Forensic Sci. Int. Genet. 7: e82-e83. Revised data received on August 10, 2017.
FTJULX	Method(s): Likelihood Ratio Stats Analysis: The DNA result obtained from the sample from stain on the suspect's shirt (Item 3) is consistent with a mixture from at least two (2) contributors, including at least one (1) male. The mixture is approximately 1.30 x 10E28 times more likely to occur (very strong support for inclusion) if the suspect and the victim are contributors, rather than if the suspect and one (1) unknown, unrelated individual are contributors. Database(s): [Location Identifying Database]
GEHKF3	Method(s): Likelihood Ratio Stats Analysis: (STR) The DNA profile from this item is at least 1.3 nonillion times more likely if it originated from Suspect and Victim than if it originated from Suspect and an unknown, unrelated individual. Database(s): Most conservative population group statistic is reported. (STR)The National Institute of Standards and Technology's published database is utilized in the statistical calculations. Hill, C.R., Duewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. Forensic Sci. Int. Genet. 7: e82-e83. Revised data received on August 10, 2017.
GJNDAX	Method(s): Random Match Probability Stats Analysis: Caucasian 1 in 6.85 quadrillion, Black 1 in 231 quadrillion, Hispanic 1 in 21.1 quadrillion. Database(s): From Hill et al. Forensic Science International: Genetics 7 (2013) e82–e83. Supplementary Table 2: Allele frequency values for unrelated U.S. population samples (n=1036) at 29 autosomal STR loci in commercial STR multiplex kits.
K8KY2W	Method(s): Likelihood Ratio Stats Analysis: LRmix Studio used to find Likelihood Ratio (LR). LR, Victim= 3.1095E16. LR, Suspect= 1.9768E15. Database(s): [Location Identifying Database]
M6AV4Q	Method(s): Likelihood Ratio Stats Analysis: The DNA result obtained from the stain on the suspect's shirt (Item 3) is consistent with a mixture from at least two (2) contributors, including at least one (1) male. The mixture is approximately 7.10 x 10²⁷ times more likely to occur (very strong support for inclusion) if the male suspect and the female victim are contributors rather than if the male suspect and an unknown, unrelated individual are contributors. Database(s): LR of the female victim vs an unknown, unrelated individual as a contributor to the mixture was calculated using the FBI Extended African American allele frequencies.

TABLE 6

WebCode	Item 3 Methods & Results
MPEG4X	Method(s): Likelihood Ratio Stats Analysis: The shirt was worn by and recovered from the male subject. The DNA profile obtained from the bloodstain on the shirt of the male subject (item 3) is interpreted as a mixture from two individuals. The results are 4 octillion times more likely if the female and the male are the contributors than if the male and an unknown, unrelated individual are the contributors. The results provide very strong support for the proposition that the female is a contributor to the DNA profile obtained from item 3 rather than the alternative proposition. Database(s): NIST 1036 dataset (2017) for all US population groups
MX9J9U	Method(s): Likelihood Ratio Stats Analysis: STR results: Observing this evidence profile is 66.9 trillion times more likely if the contributors are Item 1 and 1 unknown individual rather than 2 unknown individuals. Observing this evidence profile is 160 trillion times more likely if the contributors are Item 2 and 1 unknown individual rather than 2 unknown individuals. Yfiler Plus results: This DNA profile matches the DNA profile from Item 2. Therefore, Item 2 and any biological, paternal relatives, cannot be excluded as possible contributors. The profile from Item 3 has a frequency of approximately 1 in 4,461 male individuals. Database(s): NIST 1036 (2017) for STR Results
QUW6RQ	Method(s): [Participant did not report a method.] Stats Analysis: Working from the pdf of the electropherogram, it is not possible to perform a thorough evaluation of each locus. As a result it is possible to miss very minor contributions from additional contributors and be incorrect in the possible number of contributors to complex mixture samples. It is also not possible to thoroughly evaluate spikes, pullup, and baseline irregularities which can affect correct allele determinations. I am a forensic consultant that reviews DNA case files submitted to me as evidence. I review the analyst allele calls and evidence to reference sample comparisons so I can understand how the original analyst arrived at their opinions and conclusions. I accept that their population calculations are correct. N/A: Not Applicable. NSD: No Size Data. Database(s): [Participant did not report database(s).]
RVMQXL	Method(s): Random Match Probability Stats Analysis: Item1 RMP 9.66E+29. Item2 RMP 1.27E+32. Database(s): [Location Identifying Database]
RY7HAN	Method(s): Likelihood Ratio, YSTR Profile Probability Stats Analysis: STR Results: The Globalfiler DNA results are consistent with a two-person mixture profile. Observing this evidence profile is 62.3 trillion times more likely if the contributors are Item 1, Female Victim and one unknown individual rather than two unknown individuals. Observing this evidence profile is 162 trillion times more likely if the contributors are Item 2, Male Suspect and one unknown individual rather than two unknown individuals. YSTR Results: The Yfiler Plus DNA results are consistent with a single source profile. This DNA profile matches the DNA profile from Item 2, Male Suspect. Therefore, Item 2, Male Suspect and any biological, paternal relatives cannot be excluded as possible contributors. The profile from Item 3 has a frequency of approximately 1 in 4,461 male individuals. Database(s): NIST 1036 (2017) for STR Results. US National Database in YHRD, R63 for YSTR results.
TL2MQM	Method(s): Likelihood Ratio Stats Analysis: The DNA result obtained from Item 3 is consistent with a mixture from at least two (2) contributors, including at least one (1) male. The mixture is approximately 6.63×10^{27} times more likely to occur (very strong support for inclusion) if Item 2 (suspect) and Item 1 (victim) are contributors, rather than if Item 2 (suspect) and one (1) unknown, unrelated individual are contributors. Database(s): FBI_extended_AfAm
TLZPFQ	Method(s): Combined Probability of Exclusion/Inclusion Stats Analysis: STR Results - The estimated probability of a random, unrelated individual being included as a possible contributor to the profile is rarer than 1 in 330 billion. Database(s): STR population frequency statistics calculated in Popstats using Expanded FBI STR 2015 Caucasian and African American populations as well as [Location Identifying Population]. Only the most common frequency among the five populations or 1 in 330 billion is reported, whichever is more common.

TABLE 6

WebCode	Item 3 Methods & Results
TUR9WK	Method(s): Likelihood Ratio Stats Analysis: The DNA result obtained from the stain on the suspect's shirt (26-5881 Item 3) is consistent with a mixture from at least two (2) contributors, including at least one (1) male. The mixture is approximately 1.33×10^{28} times more likely to occur (very strong support for inclusion) if the suspect and the victim are contributors, rather than if the suspect and an unknown, unrelated individual are contributors. Database(s): African American 2015 Expanded FBI STR Loci Allele Frequencies T.R. Moretti, et al, Forensic Sci. Int. Genet. 25 (2016) 175-181.
U7FUFK	Method(s): Likelihood Ratio Stats Analysis: The DNA result obtained from stain on suspect's shirt (Item 3) is consistent with a mixture from at least two (2) contributors, including at least one (1) male. The mixture is approximately 1.71×10^{27} times more likely to occur (very strong support for inclusion) if the male suspect and the female victim are contributors, rather than if the complainant male suspect and one (1) unknown, unrelated individual are contributors. Database(s): [Location Identifying Database], FBI_EXTENDED_CAUC
W9YKFF	Method(s): Likelihood Ratio Stats Analysis: The DNA result obtained from stain on suspect's shirt (Item 3) is consistent with a mixture from at least two (2) contributors, including at least one (1) male individual. The mixture is approximately 1.71×10^{27} (Stratified) times (7.78×10^{27} in the African American Population and 8.65×10^{26} in the Caucasian Population) more likely to occur (very strong support for inclusion) if the suspect and the victim are contributors, rather than if the suspect and one (1) unknown, unrelated individual are contributors. Database(s): FBI_EXTENDED_AFAM FBI_EXTENDED_CAUC
WCYVBF	Method(s): Likelihood Ratio Stats Analysis: The mixture is approximately $1.34E28$ times more likely to occur (very strong support for inclusion) if the suspect and the victim are contributors, rather than if the suspect and an unknown, unrelated individual are contributors. Database(s): FBI Extended African American, [Location Identifying Database]
WDUEDH	Method(s): Likelihood Ratio Stats Analysis: CONCLUSION: The DNA result obtained from the stain (FL 25-3473_1A) allegedly taken from suspect shirt is consistent with a mixture from at least two (2) contributors, including at least one (1) male. The mixture is approximately 1.30×10^{28} times more likely to occur (very strong support for inclusion) if the victim and the suspect are contributors, rather than if the victim and one (1) unknown, unrelated individual are contributors. END OF REPORT. Database(s): [Participant did not report database(s).]
WFE7NK	Method(s): Likelihood Ratio Stats Analysis: STR: The DNA profile from this item is at least 1.4 quintillion times more likely if it originated from Item 1 (victim) and an unknown individual than if it originated from two unknown, unrelated individuals. The DNA profile from this item is at least 7.7 quintillion times more likely if it originated from Item 2 (suspect) and an unknown individual than if it originated from two unknown, unrelated individuals. YSTR: The DNA profile is at least 1,030 times more likely if the profile originated from Item 2 (suspect) (or a patrilineal relative) than if it originated from a randomly selected individual. Database(s): The most conservative statistic is reported. The National Institute of Standards and Technology's published database is utilized in the statistical calculations. Hill, C.R., Duewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. Forensic Sci. Int. Genet. 7: e82-e83. Revised data received on August 10, 2017. Y-Chromosome Haplotype Reference Database: https://yhrd.org.

TABLE 6

WebCode	Item 3 Methods & Results
WGAPQL	Method(s): Likelihood Ratio Stats Analysis: H1 : the mixture is made up of the victim's genetic profile (item 1) and the genetic profile of one unknown unrelated person. H2 : the mixture is made up of the genetic profiles of two unknown unrelated people. LR= 2.51E15 (drop-out=0.1, drop-in=0.05, Theta=0.01). H1 : the mixture is made up of the suspect's genetic profile (item 2) and the genetic profile of one unknown unrelated person. H2 : the mixture is made up of the genetic profiles of two unknown unrelated people. LR= 9.64E14 (drop-out=0.1, drop-in=0.05, Theta=0.01). Database(s): https://strider.online/frequencies
Z88XBE	Method(s): Random Match Probability Stats Analysis: A mixed DNA profile of two individuals was developed from the stain on suspect's shirt "ITEM 3". The DNA profile obtained from the reference blood "ITEM 2" and "ITEM 1" is being the male and female contributors respectively to this mixed DNA profile. The probability of a randomly selected unrelated individual having a matching DNA profile of the female contributor, "ITEM 1" is approximately: a) 1 in 4.5 nonillion (4.5×10^{30}) as calculated based on the [Location Identifying Database]. b) 1 in 2.4 nonillion (2.4×10^{30}) as calculated based on the [Location Identifying Database]. c) 1 in 79 nonillion (79×10^{30}) as calculated based on the [Location Identifying Database]. Database(s): [Location Identifying Database]

Statistical Analysis for Item 4

TABLE 7

WebCode	Item 4 Methods & Results
2EPNBF	Method(s): Likelihood Ratio Stats Analysis: The DNA profile obtained from Item 4 was interpreted using STRmix probabilistic genotyping software under a two-contributor model. Likelihood ratios were calculated to evaluate the probability of the observed DNA evidence under the proposition that the person of interest contributed to the mixture versus the alternative proposition that the DNA originated from unknown, unrelated individuals. For Item 2 (suspect), the likelihood ratio is on the order of 10^{27} to 10^{30}, providing extremely strong support for the proposition that Item 2 contributed to the DNA mixture. For Item 1 (victim), the likelihood ratio is on the order of 10^2 to 10^3, providing limited to moderate support for the proposition that Item 1 contributed to the DNA mixture. The mixture proportions are consistent with a major contributor comprising approximately 90% of the DNA and a minor contributor comprising approximately 10%, supporting the interpretation that Item 2 is the major contributor and Item 1 is the minor contributor. Database(s): NIST1036_CAUC, NIST1036_AFAM
2P7BJF	Method(s): Random Match Probability Stats Analysis: A mixed DNA profile of two individuals was developed from stain on victim's shirt "Item 4". The DNA profiles obtained from the reference blood "Item 2" and "Item 1" are being the major (male) and minor (female) contributors respectively to this mixed DNA profile. The probability of a randomly selected unrelated individual having a matching DNA profile of the major contributor, "Item 2" is approximately: a) 1 in 220 nonillion (220×10^{30}) as calculated based on the [Location Identifying Database]. b) 1 in 11 decillion (11×10^{33}) as calculated based on the [Location Identifying Database]. c) 1 in 97 nonillion (97×10^{30}) as calculated based on the [Location Identifying Database] Database(s): [Location Identifying Database]
2WQB2E	Method(s): Likelihood Ratio Stats Analysis: The DNA result obtained from Item 4 is consistent with a mixture from at least two (2) contributors. The mixture is approximately 2.93×10^{28} times more likely to occur (very strong support for inclusion) if the complainant (Item 1) and the suspect (Item 2) are contributors, rather than if the complainant and one (1) unknown, unrelated individual are contributors. Database(s): STRMix
3KQZ7C	Method(s): Likelihood Ratio Stats Analysis: The DNA result obtained from the swab (Item 4) allegedly taken from stain on victim's shirt is consistent with a mixture from at least two (2) contributors, including at least one (1) male. a) This mixture is approximately 2.69×10^{19} times more likely to occur (very strong support for inclusion) if the female victim and one (1) unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. b) This mixture is approximately 5.85×10^{27} times more likely to occur (very strong support for inclusion) if the male suspect and one (1) unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. Database(s): FBI_EXTENDED_AFAM & FBI_EXTENDED_CAUC

TABLE 7

WebCode	Item 4 Methods & Results
A2RF86	Method(s): Likelihood Ratio Stats Analysis: Autosomal Statistical Weight Estimate: Under the assumption that the VICTIM (Item 1) and one unknown unrelated person selected at random from the general population are contributors, the likelihood of observing the mixed source profile developed from the STAIN ON VICTIM'S SHIRT (Item 4) is $\geq 1,000,000$ times greater (actual LR available upon request) than if it is assumed that two unknown unrelated persons selected at random from the general population are contributors to this mixed-source profile. Under the assumption that the SUSPECT (Item 2) and one unknown unrelated person selected at random from the general population are contributors, the likelihood of observing the mixed source profile developed from the STAIN ON VICTIM'S SHIRT (Item 4) is $\geq 1,000,000$ times greater (actual LR available upon request) than if it is assumed that two unknown unrelated persons selected at random from the general population are contributors to this mixed-source profile. Under the assumption that the VICTIM (Item 1) and the SUSPECT (Item 2) are contributors, the likelihood of observing the mixed source profile developed from the STAIN ON VICTIM'S SHIRT (Item 4) is $\geq 1,000,000$ times greater (actual LR available upon request) than if it is assumed that the VICTIM (Item 1) and one unknown unrelated person selected at random from the general population are contributors to this mixed-source profile. YSTR Statistical Weight Estimate: The SUSPECT (Item 2), his paternally-related male relatives, and an unknown number of males in the general population cannot be excluded as the potential source of the YSTR haplotype developed from the STAIN ON VICTIM'S SHIRT (Item 4). Given a theta-value of 2.0×10^{-5} and a 95% UCI of the combined Haplotype frequency of 1 in 3,574 (no matches in 10,704 Haplotypes at U.S. subpopulations without Native American), the corrected Match Probability is 1 in 3,336. Database(s): Statistical Calculations employed the following databases: Revised-NIST-1036-Allele Frequencies; ABI ID Allele Frequencies; Promega PowerPlex Fusion Allele Frequencies and YHRD Release R69 valid as per 2024-03-07 20:22:41 UTC
BA24K3	Method(s): Likelihood Ratio Stats Analysis: The genetic profile obtained from Item 4 is interpreted as a mixture of DNA from two contributors. Item 2, (suspect) cannot be excluded as a possible contributor to this mixture. Given this genetic profile, assuming two contributors, and assuming the presence of the victim's profile, it is 2.1 septillion times more likely to observe this genetic profile if Item 2 (suspect) and Item 1 (victim) are contributors than if Item 1 (victim) and one unknown individual are the contributors. Database(s): NIST
BBWPC9	Method(s): Likelihood Ratio Stats Analysis: The DNA profile from this item is at least 20 octillion times more likely if it originated from Victim and Suspect than if it originated from Victim and an unknown, unrelated individual. The YSTR DNA profile is at least 1,030 times more likely if the profile originated from Suspect (or a patrilineal relative) than if it originated from a randomly selected individual. Database(s): Most conservative population group statistic is reported. The National Institute of Standards and Technology's published database is utilized in the statistical calculations. Hill, C.R., Duewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. Forensic Sci. Int. Genet. 7: e82-e83. Revised data received on August 10, 2017. Match probability and profile probability are approximate and derived from queries against the Y-Chromosome Haplotype Reference Database: https://yhrd.org.
C327B6	Method(s): Likelihood Ratio Stats Analysis: $LR = 1.0E+17$ - The DNA findings provide extremely strong evidence to support the hypothesis that the victim and one unrelated unknown person were the contributors compared to the alternative hypothesis that two unrelated unknown persons were the contributors. $LR = 1.9E+18$ - The DNA findings provide extremely strong evidence to support the hypothesis that the suspect and one unrelated unknown person were the contributors compared to the alternative hypothesis that two unrelated unknown persons were the contributors. Database(s): Local population data

TABLE 7

WebCode	Item 4 Methods & Results
C8RGK4	Method(s): Random Match Probability Stats Analysis: A mixed DNA profile of two individuals was developed from the stain on victim's shirt "Item 4". The DNA profile obtained from the reference blood "Item 2" and "Item 1" is being the major (male) and minor (female) contributors respectively to this mixed DNA profile. The probability a randomly selected unrelated individual having a matching DNA profile of the major contributor, "item 2" is approximately: a) 1 in 220 nonillion (220×10^{30}) as calculated based on the [Location Identifying Database]. b) 1 in 11 decillion (11×10^{33}) as calculated based on the [Location Identifying Database]. c) 1 in 97 nonillion (97×10^{30}) as calculated based on the [Location Identifying Database] Database(s): [Location Identifying Database]
EG9482	Method(s): Likelihood Ratio Stats Analysis: The STR DNA profile was interpreted as a mixture of two contributors, including male DNA. Victim was assumed as one of the contributors. The DNA profile from this item is at least 6.8 nonillion times more likely if it originated from Victim and Suspect than if it originated from Victim and an unknown, unrelated individual. This provides support that Suspect is included as a contributor to this DNA profile. A Y-STR DNA profile was obtained. The DNA profile is at least 1,030 times more likely if the profile originated from Suspect (or a patrilineal relative) than if it originated from a randomly selected individual. This provides support that Suspect is included as a contributor to this DNA profile. Database(s): a. Most conservative population group statistic is reported. b. The National Institute of Standards and Technology's published database is utilized in the statistical calculations. Hill, C.R., Duewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. Forensic Sci. Int. Genet. 7: e82-e83. Revised data received on August 10, 2017. c. Y-Chromosome Haplotype Reference Database: https://yhrd.org.
FTJULX	Method(s): Likelihood Ratio Stats Analysis: The DNA result obtained from the sample from stain on the victim's shirt (Item 4) is consistent with a mixture from at least two (2) contributors, including at least one (1) male. The mixture is approximately 1.45×10^{28} times more likely to occur (very strong support for inclusion) if the victim and the suspect are contributors, rather than if the victim and one (1) unknown, unrelated individual are contributors. Database(s): FBI_EXTENDED_CAUC
GEHKF3	Method(s): Likelihood Ratio Stats Analysis: (STR) The DNA profile from this item is at least 7.4 nonillion times more likely if it originated from Victim and Suspect than if it originated from Victim and an unknown, unrelated individual. (YSTR) The DNA profile is at least 1,030 times more likely if the profile originated from Suspect (or a patrilineal relative) than if it originated from a randomly selected individual. Database(s): Most conservative population group statistic is reported. (STR) The National Institute of Standards and Technology's published database is utilized in the statistical calculations. Hill, C.R., Duewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. Forensic Sci. Int. Genet. 7: e82-e83. Revised data received on August 10, 2017. (YSTR)Y-Chromosome Haplotype Reference Database: https://yhrd.org.
GJNDAX	Method(s): Random Match Probability Stats Analysis: Major: Caucasian 1 in 1.09 nonillion, Black 1 in 609 nonillion, Hispanic 1 in 2.92 nonillion. Minor: Caucasian 1 in 29.0 quadrillion, Black 1 in 189 quadrillion, Hispanic 1 in 34.3 quadrillion. Database(s): From Hill et al. Forensic Science International: Genetics 7 (2013) e82–e83. Supplementary Table 2: Allele frequency values for unrelated U.S. population samples (n=1036) at 29 autosomal STR loci in commercial STR multiplex kits.
K8KY2W	Method(s): Likelihood Ratio Stats Analysis: LRMix Studio used to find Likelihood Ratio (LR). LR, Suspect= 5.6134×10^{16}. Database(s): [Location Identifying Database]

TABLE 7

WebCode	Item 4 Methods & Results
M6AV4Q	Method(s): Likelihood Ratio Stats Analysis: The DNA result obtained from the stain on the victim's shirt (Item 4) is consistent with a mixture from at least two (2) contributors, including at least one (1) male. The mixture is approximately 1.53×10^{28} times more likely to occur (very strong support for inclusion) if the female victim and the male suspect are contributors rather than if the female victim and an unknown, unrelated individual are contributors. Database(s): LR of the male suspect vs an unknown, unrelated individual as a contributor to the mixture was calculated using the FBI Extended Caucasian allele frequencies.
MPEG4X	Method(s): Likelihood Ratio Stats Analysis: The shirt was worn by and recovered from the female subject. The DNA profile obtained from the bloodstain on the shirt (item 4) of the female subject is interpreted as a mixture from two individuals. The results are 190 octillion times more likely if the female and the male are the contributors than if the female and an unknown, unrelated individual are the contributors. The results provide very strong support for the proposition that the male subject is a contributor to the DNA profile obtained from item 4 rather than the alternative proposition. Database(s): NIST 1036 dataset (2017) for all US population groups
MX9J9U	Method(s): Likelihood Ratio Stats Analysis: STR results: Observing this evidence profile is 208 million times more likely if the contributors are Item 1 and 1 unknown individual rather than 2 unknown individuals. Observing this evidence profile is 30.1 quadrillion times more likely if the contributors are Item 2 and 1 unknown individual rather than 2 unknown individuals. Yfiler Plus Results: This DNA profile matches the DNA profile from Item 2. Therefore, Item 2 and any biological, paternal relatives, cannot be excluded as possible contributors. The profile from Item 4 has a frequency of approximately 1 in 4,461 male individuals Database(s): NIST 1036 (2017) for STR Results
QUW6RQ	Method(s): [Participant did not report a method.] Stats Analysis: Working from the pdf of the electropherogram, it is not possible to perform a thorough evaluation of each locus. As a result it is possible to miss very minor contributions from additional contributors and be incorrect in the possible number of contributors to complex mixture samples. It is also not possible to thoroughly evaluate spikes, pullup, and baseline irregularities which can affect correct allele determinations. I am a forensic consultant that reviews DNA case files submitted to me as evidence. I review the analyst allele calls and evidence to reference sample comparisons so I can understand how the original analyst arrived at their opinions and conclusions. I accept that their population calculations are correct. N/A: Not Applicable. NSD: No Size Data. Database(s): [Participant did not report database(s).]
RVMQXL	Method(s): Random Match Probability Stats Analysis: Item1 RMP $2.75E+25$. Item2 RMP $1.27E+32$. Database(s): [Location Identifying Database]
RY7HAN	Method(s): Likelihood Ratio, YSTR Profile Probability Stats Analysis: STR Results: The Globalfiler DNA results are consistent with a two-person mixture profile. Observing this evidence profile is 1.19 billion times more likely if the contributors are Item 1, Female Victim and one unknown individual rather than two unknown individuals. Observing this evidence profile is 30.0 quadrillion times more likely if the contributors are Item 2, Male Suspect and one unknown individual rather than two unknown individuals. YSTR Results: The Yfiler Plus DNA results are consistent with a single source profile. This DNA profile matches the DNA profile from item 2, Male Suspect. Therefore, Item 2, Male Suspect and any biological, paternal relatives cannot be excluded as possible contributors. The profile from Item 4 has a frequency of approximately 1 in 4,461 male individuals Database(s): NIST 1036 (2017) for STR Results. US National Database in YHRD, R63 for YSTR results.

TABLE 7

WebCode	Item 4 Methods & Results
TL2MQM	Method(s): Likelihood Ratio Stats Analysis: The DNA result obtained from Item 4 is consistent with a mixture from at least two (2) contributors, including at least one (1) male. The mixture is approximately 1.23×10^{28} times more likely to occur (very strong support for inclusion) Item 1 (victim) and Item 2 (suspect) are contributors, rather than if Item 1 (victim) and one (1) unknown, unrelated individual are contributors. Database(s): FBI_extended_Cauc
TLZPFQ	Method(s): Random Match Probability, YHRD Stats Analysis: STR - Major component: The estimated frequency of this profile is rarer than 1 in 330 billion. Y-STR: This Y-STR profile is not expected to occur more frequently than 1 in 140 male individuals. Database(s): STR population frequency statistics calculated in Popstats using Expanded FBI STR 2015 Caucasian and African American populations as well as [Location Identifying Population]. Only the most common frequency among the five populations or 1 in 330 billion is reported, whichever is more common. Y-STR population frequency statistics calculated in YHRD.org using the Y17 dataset with the National Database (with Subpopulations, 2014 SWGDAM compliant) - [Location Identifying Population]. Only the most common frequency is reported, using the 95% confidence interval.
TUR9WK	Method(s): Likelihood Ratio Stats Analysis: The DNA result obtained from the stain on the victim's shirt (26-5881 Item 4) is consistent with a mixture from at least two (2) contributors, including at least one (1) male. The mixture is approximately 1.42×10^{28} times more likely to occur (very strong support for inclusion) if the victim and the suspect are contributors, rather than if the victim and an unknown, unrelated individual are contributors. Database(s): Caucasian 2015 Expanded FBI STR Loci Allele Frequencies T.R. Moretti, et al, Forensic Sci. Int. Genet. 25 (2016) 175-181.
U7FUFK	Method(s): Likelihood Ratio Stats Analysis: The DNA result obtained from stain on victim's shirt is consistent with a mixture from at least two (2) contributors, including at least one (1) male. The mixture is approximately 2.96×10^{28} times more likely to occur (very strong support for inclusion) if the female victim and the male suspect are contributors, rather than if the complainant female victim and one (1) unknown, unrelated individual are contributors. Database(s): [Location Identifying Database], FBI_EXTENDED_CAUC
W9YKFF	Method(s): Likelihood Ratio Stats Analysis: The DNA result obtained from stain on victim's shirt (Item 4) is consistent with a mixture from at least two (2) contributors, including at least one (1) male individual. The mixture is approximately 2.63×10^{28} (Stratified) times (1.79×10^{30} in the African American Population and 1.32×10^{28} in the Caucasian Population) more likely to occur (very strong support for inclusion) if the victim and the suspect are contributors, rather than if the victim and one (1) unknown, unrelated individual are contributors. Database(s): FBI_EXTENDED_AFAM FBI_EXTENDED_CAUC
WCYVBF	Method(s): Likelihood Ratio Stats Analysis: The mixture is approximately $1.45E28$ times more likely to occur (very strong support for inclusion) if the victim and the suspect are contributors, rather than if the victim and an unknown, unrelated individual are contributors. Database(s): FBI Extended Caucasian
WDUEDH	Method(s): Likelihood Ratio Stats Analysis: CONCLUSION: The DNA result obtained from the stain (FL 25-3473_2A) allegedly taken from victims' shirt is consistent with a mixture from at least two (2) contributors, including at least one (1) male. The mixture is approximately 1.55×10^{28} times more likely to occur (very strong support for inclusion) if the victim and the suspect are contributors, rather than if the victim and one (1) unknown, unrelated individual are contributors. END OF REPORT. Database(s): [Participant did not report database(s).]

TABLE 7

WebCode	Item 4 Methods & Results
WFE7NK	Method(s): Likelihood Ratio Stats Analysis: STR: The DNA profile from this item is at least 69 septillion times more likely if it originated from Item 1 (victim) and an unknown individual than if it originated from two unknown, unrelated individuals. The DNA profile from this item is at least 12 octillion times more likely if it originated from Item 2 (suspect) and an unknown individual than if it originated from two unknown, unrelated individuals. YSTR: The DNA profile is at least 1,030 times more likely if the profile originated from Item 2 (suspect) (or a patrilineal relative) than if it originated from a randomly selected individual. Database(s): The most conservative statistic is reported. The National Institute of Standards and Technology's published database is utilized in the statistical calculations. Hill, C.R., Duwewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. Forensic Sci. Int. Genet. 7: e82-e83. Revised data received on August 10, 2017. Y-Chromosome Haplotype Reference Database: https://yhrd.org.
WGAPQL	Method(s): Likelihood Ratio Stats Analysis: H1 : the mixture is made up of the victim's genetic profile (item 1) and the genetic profile of one unknown unrelated person. H2 : the mixture is made up of the genetic profiles of two unknown unrelated people. LR= 9.35E11 (drop-out=0.1, drop-in=0.05, Theta=0.01). H1 : the mixture is made up of the suspect's genetic profile (item 2) and the genetic profile of one unknown unrelated person. H2 : the mixture is made up of the genetic profiles of two unknown unrelated people. LR= 2.33E16 (drop-out=0.1, drop-in=0.05, Theta=0.01). Database(s): https://strider.online/frequencies
Z88XBE	Method(s): Random Match Probability Stats Analysis: A mixed DNA profile of two individuals was developed from the stain on victim's shirt "ITEM 4". The DNA profile obtained from the reference blood "ITEM 2" and "ITEM 1" is being the major (male) and minor (female) contributors respectively to this mixed DNA profile. The probability of a randomly selected unrelated individual having a matching DNA profile of the major contributor, "ITEM 2" is approximately: a) 1 in 220 nonillion (220×10^{30}) as calculated based on the [Location Identifying Database]. b) 1 in 11 decillion (11×10^{33}) as calculated based on the [Location Identifying Database]. c) 1 in 97 nonillion (97×10^{30}) as calculated based on the [Location Identifying Database] Database(s): [Location Identifying Database]

Additional Comments

TABLE 8

WebCode	Additional Comments
2EPNBF	The DNA profile from Item 3 is consistent with a mixture of at least three contributors, and the DNA profile from Item 4 is consistent with a mixture of at least two contributors. Both profiles were interpreted using STRmix probabilistic genotyping software. Likelihood ratios were calculated to evaluate the probability of the observed DNA evidence under competing propositions. The results provide extremely strong support for the proposition that Item 2 (suspect) contributed to both DNA mixtures, and strong support for the proposition that Item 1 (victim) contributed to the DNA mixtures, with relatively lower support observed for Item 1 in Item 4 consistent with a minor contribution. Some expected alleles are not observed at all loci, which may be due to allelic dropout and/or stochastic effects in mixed DNA samples.
2P7BJF	NM - Non male.
A2RF86	This proficiency test included one particularly challenging interpretation issue at the D21S11 locus in Item 4 (stain from the victim's shirt). The PowerPlex Fusion 5C profile supported calling a 29 allele and if this profile had been evaluated in isolation the interpretation would have been relatively straightforward. However, I routinely employ a comprehensive review strategy when multiple kit systems are available. While the 29 allele was not called in the GlobalFiler, PowerPlex Fusion 6C or Investigator profiles, close examination revealed a distinct but unresolved shoulder adjacent to the much larger 29.1 peak in the Fusion 6C profile and a similar, less-resolved feature in the GlobalFiler profile. The corresponding feature was not clearly apparent to me in the Investigator data, even upon review of the .hid files. Considering all available data collectively, I elected to include the 29 allele in my final interpretation of this profile. Nevertheless, I believe analysts or laboratories relying solely on a single kit system (particularly GlobalFiler, Investigator, or Fusion 6C in this case) might reasonably reach a different conclusion regarding this allele call. I commend the inclusion of this more challenging interpretation scenario and will be interested to see the responses generated by participants.
BBWPC9	NR=No Results. No Peak Height Ratio is applicable to YSTR Analysis. Analytical Thresholds for YSTR Analysis: Blue - 45rfu, Green - 70rfu, Yellow - 65rfu, Red - 75rfu. For Item #4(1-4), an unresolved 29 allele peak can be observed at locus D21S11, but is not called by the GeneMapper ID-X software. This locus was ignored during STRmix assessment. Data will be reported per laboratory protocols, to include only alleles labeled in the electropherogram.
C8RGK4	1. Statistical calculation were carried out using DNA View Software. 2. NM represents non-male profile.
EG9482	NR=No Results. Y-STR Analytical Threshold: Blue= 45; Green= 70; Yellow= 65; Red= 75; Orange= 50; No Peak Height Ratio (%) for Y-STR data utilized.
GEHKF3	NR = No Results. Y-STR AT: Blue=45, Green=70, Yellow=65, Red=75, No PHR threshold for Y-STR data utilized.
GJNDAX	Since there is no ability to examine peak height data to evaluate peaks filtered out or to turn the stutter filters off, in order to best approximate laboratory interpretation guidelines, the following approach was used with respect to the minor contributor: 1. 2 minor peaks, the full genotype was reported; 2. 1 minor peak, the genotype was reported as any individual which has that allele is a possible contributor; 3. 0 minor peaks, the genotype was not predicted.
MX9J9U	For items 3 and 4, probabilistic genotyping software was used to aid in the interpretation and statistical analysis of the DNA profiles generated. The results listed in the CTS report reflect DNA profiles with stutter filters on.
QXW4GW	Unresolved 29 allele present at D21S11 for Item 4.
RY7HAN	For items 3 and 4, probabilistic genotyping software was used to aid in the interpretation and statistical analysis of the DNA profiles generated. The results listed in the CTS report reflect DNA profiles with stutter filters on.

TABLE 8

WebCode	Additional Comments
TLZPFQ	In the INT-item 4 profile, the minor component was not suitable for comparison due to insufficient DNA. In that minor component, the following were assessed as either artifact or true alleles (could not be determined): 14 at vWA, 11 and D5S818, and 10 at D7S820.
WFE7NK	NR = No results. Y-STR Analytical Threshold (RFU): Blue = 45, Green = 70, Yellow = 65, Red = 75. No PHR threshold utilized for Y-STR. Note for Item 4: Unresolved 29 peak noted at D21S11.
Z88XBE	1. Statistical calculations were carried out using DNView software 2. NM represents non-male profile.

-End of Report-
(Appendix may follow)

Collaborative Testing Services ~ Forensic Testing Program

Test No. 26-5881: DNA Interpretation

DATA MUST BE SUBMITTED BY **June 08, 2026, 11:59 p.m. EDT** TO BE INCLUDED IN THE REPORT

Participant Code: U1234A

WebCode: X4JEG

The Accreditation Release section can be accessed by using the "Continue to Final Submission" button above. This information can be entered at any time prior to submitting to CTS.

Scenario:

Police are investigating a reported shooting involving a female victim and a male suspect. The victim stated that during a physical altercation, the suspect shot her in the arm. No weapon has been recovered. The suspect was apprehended the same day. Investigators have identified a reddish-brown stain on the shirt the suspect was wearing at the time of arrest, which the Serology Unit indicated as blood (Item 3). Additionally, a reddish-brown stain was identified on the shirt the victim was wearing at the time of the assault and was also indicated as blood (Item 4).

HID and PDF file formats are provided for use in this test, choose any or all formats for evaluation.

Items Submitted (Sample Pack INT1):

Item 1: DNA profile from reference sample (Female Victim - African American)

Item 2: DNA profile from reference sample (Male Suspect - Caucasian)

Item 3: DNA profile from stain on suspect's shirt

Item 4: DNA profile from stain on victim's shirt

To verify a complete and accurate download, the hash value for the downloaded .ZIP file is as follows:

26-5881 Data.zip MD5 hash value: ef0a6dab8eb64f4051463a7afbab190c

26-5881 Data.zip SHA1 hash value: 281865d17a657648167a90c9ad36feef83b19188

Part I: DNA ANALYSIS INSTRUCTIONS

- Use your laboratory's Interpretation guidelines for evaluation of this test.
- Only numerical values can be entered into the fields below. If other values are needed, add this information to the Additional Comments section.
- Please report Laboratory Specific Interpretation Guidelines below per amplification kit.
- If interpretation guidelines are not reported, the consensus information will be utilized in the review of results.

STR Analysis Thresholds

Analytical Threshold (RFU):

Peak Height Ratio (%):

Stochastic Threshold (RFU) (Peak Amplitude):

YSTR Analysis Thresholds

Analytical Threshold (RFU):

Peak Height Ratio (%):

Stochastic Threshold (RFU) (Peak Amplitude):

If you do not have Interpretation guidelines, please use the following guidelines and report these values above:

For STR Analysis: Analytical Threshold: 75 rfu, Peak Height Ratio: 60%, Stochastic Threshold (Peak Amplitude): 100 rfu

For YSTR Analysis: Analytical Threshold: 75 rfu, Peak Height Ratio: 50%, Stochastic Threshold (Peak Amplitude): 75 rfu

- Report the allelic results for each Item in the appropriate response boxes.
- If major and minor contributor(s) can be distinguished and your laboratory normally reports this distinction, report the results of the major profile and the minor profile in the appropriately labeled boxes; otherwise, list the alleles in numerical order in the remaining row of boxes labeled with the Item number.
- Please Note: Samples were completely consumed during extraction.

Part I: DNA ANALYSIS

STR & Amelogenin Results for Known Item 1

- Report alleles in numerical order, separated by a comma.
- Follow your laboratory procedures for reporting homozygotes (i.e. X,X or X) and null responses.

STR Amplification Kit Used For Item 1:

Please indicate the electropherogram(s) reviewed for this test.

☐ GlobalFiler™ ☐ Investigator® 24plex ☐ PowerPlex® Fusion 5C ☐ PowerPlex® Fusion 6C
☐ HID format ☐ PDF format

Report the Probabilistic Genotyping Software Used (if applicable):

Alleles below are sorted in Default order.

ITEM	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
1						
ITEM	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
1						
ITEM	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
1						
ITEM	Penta D	Penta E	SE33	TH01	TPOX	vWA
1						
ITEM	DYS391	DYS570	DYS576	Y Indel		
1						

Part I: DNA ANALYSIS (continued)

Item 3 DNA Analysis Questions

1) Record the number of contributors found in the Item 3 DNA profile:

2) Choose the conclusion statement that best describes the results of the analysis for Item 3 based on comparisons with the Known Items (If the wording below differs from the normal wording of your conclusions, adapt these conclusions as best you can and use your preferred wording in the Additional Comments section.):

Item 1 Conclusion

- ☐ Item 1 (victim) is included (cannot be excluded) as a possible contributor to the DNA obtained from Item 3.
- ☐ Item 1 (victim) is excluded as a possible contributor to the DNA obtained from Item 3.
- ☐ The DNA typing results for Item 3 in comparison with Item 1 are inconclusive/uninterpretable.

Item 2 Conclusion

- ☐ Item 2 (suspect) is included (cannot be excluded) as a possible contributor to the DNA obtained from Item 3.
- ☐ Item 2 (suspect) is excluded as a possible contributor to the DNA obtained from Item 3.
- ☐ The DNA typing results for Item 3 in comparison with Item 2 are inconclusive/uninterpretable.

3) Statistical Analysis of Item 3 DNA Typing Results:

Select the statistical method(s) used by marking the associated box and report these results in the space below:

☐ Combined Probability of Exclusion/Inclusions (CPE/CPI)

☐ Likelihood Ratio (LR)

☐ Random Match Probability (RMP)

Other:

Note: Please use appropriate punctuation to indicate the end of sentences, sections, and statements in the free-form space below. Extra spacing and returns used for separation within your text will not transfer and may cause your information to be illegible in the Summary Report. The use of lists and tabular formats to deliver information is also cautioned against, as these do not transfer.

4) Please list any databases used in the statistical analyses of Item 3 below.

Part I: DNA ANALYSIS (continued)

Item 4 DNA Analysis Questions

1) Record the number of contributors found in the Item 4 DNA profile:

2) Choose the conclusion statement that best describes the results of the analysis for Item 4 based on comparisons with the Known Items (If the wording below differs from the normal wording of your conclusions, adapt these conclusions as best you can and use your preferred wording in the Additional Comments section.):

Item 1 Conclusion

- ☐ Item 1 (victim) is included (cannot be excluded) as a possible contributor to the DNA obtained from Item 4.
- ☐ Item 1 (victim) is excluded as a possible contributor to the DNA obtained from Item 4.
- ☐ The DNA typing results for Item 4 in comparison with Item 1 are inconclusive/uninterpretable.

Item 2 Conclusion

- ☐ Item 2 (suspect) is included (cannot be excluded) as a possible contributor to the DNA obtained from Item 4.
- ☐ Item 2 (suspect) is excluded as a possible contributor to the DNA obtained from Item 4.
- ☐ The DNA typing results for Item 4 in comparison with Item 2 are inconclusive/uninterpretable.

3) Statistical Analysis of Item 4 DNA Typing Results:

Select the statistical method(s) used by marking the associated box and report these results in the space below:

☐ Combined Probability of Exclusion/Inclusions (CPE/CPI)

☐ Likelihood Ratio (LR)

☐ Random Match Probability (RMP)

Other:

Note: Please use appropriate punctuation to indicate the end of sentences, sections, and statements in the free-form space below. Extra spacing and returns used for separation within your text will not transfer and may cause your information to be illegible in the Summary Report. The use of lists and tabular formats to deliver information is also cautioned against, as these do not transfer.

4) Please list any databases used in the statistical analyses of Item 4 below.

Part II: ADDITIONAL COMMENTS
Comments regarding any part of this Test.

Note: Please use appropriate punctuation to indicate the end of sentences, sections, and statements in the free-form space below. Extra spacing and returns used for separation within your text will not transfer and may cause your information to be illegible in the Summary Report. The use of lists and tabular formats to deliver information is also cautioned against, as these do not transfer.

RELEASE OF DATA TO ACCREDITATION BODIES

The Accreditation Release is accessed by pressing the "Continue to Final Submission" button online and can be completed at any time prior to submission to CTS.

CTS submits external proficiency test data directly to ANAB and/or A2LA. Please select one of the following statements to ensure your data is handled appropriately.

- ☐ This participant's data is intended for submission to ANAB and/or A2LA. (Accreditation Release section below must be completed.)
- ☐ This participant's data is **not** intended for submission to ANAB and/or A2LA.

Have the laboratory's designated individual complete the following steps
only if your laboratory is accredited in this testing/calibration discipline
by one or more of the following Accreditation Bodies.

Step 1: Provide the applicable Accreditation Certificate Number(s) for your laboratory.

ANAB Certificate No.

A2LA Certificate No.

Step 2: Complete the Laboratory Identifying Information in its entirety.

Authorized Contact Person and Title

Laboratory Name

Location (City/State)