



DNA Interpretation Test No. 23-5882

Summary Report

Each participant received a digitally downloadable sample set via the CTS Portal containing electropherograms and raw data files which they were requested to evaluate using their existing protocols. Data were returned from 33 participants and are compiled into the following tables:

Report Contents:	Page:
<u>Manufacturer's Information</u>	<u>2</u>
<u>Summary Comments</u>	<u>4</u>
<u>Table 1: STR Interpretation Guidelines</u>	<u>5</u>
<u>Table 2: YSTR Interpretation Guidelines</u>	<u>6</u>
<u>Table 3: STR & Amelogenin Results</u>	<u>7</u>
<u>Table 4: YSTR Results</u>	<u>29</u>
<u>Table 5: DNA Conclusions</u>	<u>38</u>
<u>Table 6: Statistical Analysis for Item 3</u>	<u>40</u>
<u>Table 7: Statistical Analysis for Item 4</u>	<u>45</u>
<u>Table 8: Amplification Kit Survey</u>	<u>50</u>
<u>Table 9: Additional Comments</u>	<u>51</u>
<u>Appendix: Data Sheet</u>	

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 set 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 requested to evaluate the electropherograms and interpret the data using their existing protocols.

SAMPLE PREPARATION: 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 two parts of blood from the Item 1 female donor, one part of blood from the Item 2 male donor, and one part of blood from an additional male donor whose known reference sample was not provided. Item 4 was created by combining one part of blood from the Item 1 female donor and two parts of blood from the Item 2 male donor.

VERIFICATION: All predistribution participants reported consistent contributor conclusions.

SAMPLE SET ASSEMBLY: Once sample preparation and verification were completed, the digital upload was checked to ensure all items were accessible.

Consensus results on the following pages were determined by ensuring at least 10 participants returned results for the locus. Each allele listed was determined by ensuring that at least 75% of participants that returned data for that specific locus and item reported the same allele. Additional alleles may be present depending on laboratory thresholds and/or amplification kit used.

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	11,12	23,25	10,11	15,15	12,13	8,9
	10,12	14,15	19,3,20	12,13	11,11	15,19
	14,14	30,31	11,12	X,X	12,14	23,23
	10,12	14,17	15,21	8,9,3	8,8	15,19
	NM	NM	NM	NM		
2	17,17.3	17,23	11,14	15,15	11,12	11,11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16,16	X,Y	11,12	20,21
	9,11	7,15	20,31.2	6,9,3	8,9	14,16
	12	18	20	2		
3	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19,3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23,27
	9,10,11,12	7,11,14,15,17,21	15,20,21,24,2,30,2,31.2	6,7,8,9,9,3	8,9	14,15,16,17,18,19
	10,12	16,18	17,20	2		
4	11,12,17,17.3	17,23,25	10,11,14	15,15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19,3,20	9,12,13,14	11,12,13	13,15,16,19
	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
	9,10,11,12	7,14,15,17	15,20,21,31.2	6,8,9,3	8,9	14,15,16,19
	12	18	20	2		

YSTR Results

Results compiled from predistribution laboratories and a consensus of 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	37,38	15	11,15	14	32	24	12	11	13
	15	10	10	20	29	17	18	10	21
	37	12	12	18	20	20	21	13	11
3	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12	12	16,18	17,20	20,21	21	11,13	11
4	37,38	15	11,15	14	32	24	12	11	13
	15	10	10	20	29	17	18	10	21
	37	12	12	18	20	20	21	13	11

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

Summary Comments

The DNA Interpretation 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, Identifiler™ Plus, 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 two parts of blood from the Item 1 female donor, one part of blood from the Item 2 male donor, and one part of blood from an additional male donor whose known reference sample was not provided. Item 4 was created by combining one part of blood from the Item 1 female donor and two parts of blood from the Item 2 male donor. (See Manufacturer's Information for preparation details)

Consensus results for each item were determined per allele for each locus. Allele determinations were identified by ensuring that at least 10 participants reported results for the locus and that of these participants, 75% of them reported the same allele(s). Results that differed from the consensus were further compared to the participant's reported interpretation guidelines.

DNA Analysis

Of the 33 participants that reported results, 29 participants evaluated the provided STR data.

For STR results, all participants reported consistent results with the exception of three participants who reported an inconsistent result for one or more loci.

For YSTR results, all participants reported consistent results with the exception of two participants.

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 3 profile (unseparated). Three 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 three (or at least three) individuals contributed to the mixture. All participants included the victim (Item 1) as a possible contributor, with the exception of four participants which reported "Inconclusive/Uninterpretable." All participants included the suspect (Item 2) as a possible contributor, with the exception of three participants which reported "Inconclusive/Uninterpretable."

For Item 4, all participants identified that two (or at least two) individuals contributed to the mixture. Additionally, all participants included the victim (Item 1) and the suspect (Item 2) as possible contributors.

STR Interpretation Guidelines

TABLE 1

WebCode	Analytical Threshold (rfu)	Peak Height Ratio (%)	Stochastic Threshold (rfu)
33ACQV	75	60	100
3B3PPV	100	65	600
3GAD3W	75	60	250
3QVGBW	[Participant did not provide interpretation guidelines]		
844UTR	37	60	721
9DNKTP	160	60	630
9T3Q6N	[Participant did not provide interpretation guidelines]		
AD8N2P	75	60	100
AQC7CP	120	60	360
BF6NER	75	60	100
BM8XKK	[Participant did not provide interpretation guidelines]		
EPKGHJ	160	60	630
EPZZ3G	[Participant did not provide interpretation guidelines]		
FX9R6J	100	60	150
GF89NM	75	60	100
J48DLC	[Participant did not provide interpretation guidelines]		
KK8PUD	160	60	630
MEA87C	120	60	360
MXPEG9	214	60	347
NHQVBW	50	65	200
QB3NWA	180	60	900
QPN3Y9	75	60	100
T2NJXA	75	60	
TAZY6A	75	60	100
TLDY23	[Participant did not provide interpretation guidelines]		
UHALU4		60	600
UZPXJ9	75	60	100
WKM6Q3	120	60	360
WUX8C4	120	60	360
X6TZXZ	185	60	500
XQ8MK6	75	60	100
XTCFE4	[Participant did not provide interpretation guidelines]		
YRZZK3	150	60	700

YSTR Interpretation Guidelines

TABLE 2

WebCode	Analytical Threshold (rfu)	Peak Height Ratio (%)	Stochastic Threshold (rfu)
33ACQV	75	50	75
3B3PPV	[Participant did not provide interpretation guidelines]		
3GAD3W	75	50	75
3QVGBW	[Participant did not provide interpretation guidelines]		
844UTR	42	60	
9DNKTP	100	60	600
9T3Q6N	[Participant did not provide interpretation guidelines]		
AD8N2P	75	50	75
AQC7CP	75	50	75
BF6NER	75	50	75
BM8XKK	[Participant did not provide interpretation guidelines]		
EPKGHJ	100	60	600
EPZZ3G	[Participant did not provide interpretation guidelines]		
FX9R6J	100	60	200
GF89NM	75	50	75
J48DLC	[Participant did not provide interpretation guidelines]		
KK8PUD	[Participant did not provide interpretation guidelines]		
MEA87C	75	50	75
MXPEG9	75	50	75
NHQVBW	50	65	175
QB3NWA	88	60	455
QPN3Y9	75	50	75
T2NJXA	75	50	
TAZY6A	[Participant did not provide interpretation guidelines]		
TLDY23	[Participant did not provide interpretation guidelines]		
UHALU4		60	600
UZPXJ9	75	50	75
WKM6Q3	75	50	75
WUX8C4	75	50	75
X6TZXZ	90	60	200
XQ8MK6	75	50	75
XTCFE4	[Participant did not provide interpretation guidelines]		
YRZZK3	150	60	450

STR & Amelogenin Results

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 1 - STR Results

33ACQV	GlobalFiler™ (PDF Format), (HID Format)					
	11,12	23,25	10,11	15,15	12,13	8,9
	10,12	14,15	19,3,20	12,13	11,11	15,19
1	14,14	30,31	11,12	X,X	12,14	23,23
			15,21	8,9,3	8,8	15,19

3B3PPV	Investigator® 24plex (PDF Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19,3,20	12,13	11	15,19
1	14	30,31	11,12	X	12,14	23
			15,21	8,9,3	8	15,19

3GAD3W	GlobalFiler™ (HID Format) (STRMix)					
	11,12	23,25	10,11	15,15	12,13	8,9
	10,12	14,15	19,3,20	12,13	11,11	15,19
1	14,14	30,31	11,12	X,X	12,14	23,23
			15,21	8,9,3	8,8	15,19

3QVGBW	GlobalFiler™, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19,3,20	12,13	11	15,19
1	14	30,31	11,12	X	12,14	23
	10,12	14,17	15,21	8,9,3	8	15,19

844UTR	PowerPlex® Fusion 6C (HID Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19,3,20	12,13	11	15,19
1	14	30,31	11,12	X,X	12,14	23
	10,12	14,17	15,21	8,9,3	8	15,19

9DNKTP	GlobalFiler™ (HID Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19,3,20	12,13	11	15,19
1	14	30,31	11,12	X	12,14	23
			15,21	8,9,3	8	15,19

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 1 - STR Results

9T3Q6N	PowerPlex® Fusion 6C (HID Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19.3,20	12,13	11	15,19
	14	30,31	11,12	X	12,14	23
1	10,12	14,17	15,21	8,9.3	8	15,19

AD8N2P	GlobalFiler™					
	11,12	23,25	10,11	15,15	12,13	8,9
	10,12	14,15	19.3,20	12,13	11,11	15,19
	14,14	30,31	11,12	X,X	12,14	23,23
	N/A	N/A	15,21	8,9.3	8,8	15,19
1	NSD	N/A	N/A	NSD		

AQC7CP	GlobalFiler™ (HID Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19.3,20	12,13	11	15,19
	14	30,31	11,12	X,X	12,14	23
			15,21	8,9.3	8	15,19
1	NM		NM			

BF6NER	PowerPlex® Fusion 5C (PDF Format), (HID Format) (LR MIX 2.1.5)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19.3,20	12,13	11	15,19
	14	30,31	11,12	X	12,14	23
1	10,12	14,17		8,9.3	8	15,19

EPKGHJ	GlobalFiler™ (PDF Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19.3,20	12,13	11	15,19
	14	30,31	11,12	X	12,14	23
1		15,21	8,9.3	8	15,19	

FX9R6J	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format) (GENEMAPPER)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19.3,20	12,13	11	15,19
	14	30,31	11,12	X	12,14	23
1	10,12	14,17	15,21	8,9.3	8	15,19

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 1 - STR Results

GF89NM	PowerPlex® Fusion 6C					
	11,12	23,25	10,11	15,15	12,13	8,9
	10,12	14,15	19,3,20	12,13	11,11	15,19
1	14,14	30,31	11,12	X,X	12,14	23,23
	10,12	14,17	15,21	8,9,3	8,8	15,19

KK8PUD	GlobalFiler™ (HID Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19,3,20	12,13	11	15,19
1	14	30,31	11,12	X	12,14	23
			15,21	8,9,3	8	15,19

MEA87C	GlobalFiler™ (HID Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19,3,20	12,13	11	15,19
1	14	30,31	11,12	X,X	12,14	23
			15,21	8,9,3	8	15,19
	NM			NM		

MXPEG9	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19,3,20	12,13	11	15,19
1	14	30,31	11,12	X	12,14	23
	10,12	14,17	15,21	8,9,3	8	15,19

NHQVBW	PowerPlex® Fusion 5C (PDF Format), (HID Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19,3,20	12,13	11	15,19
1	14	30,31	11,12	X	12,14	23
	10,12	14,17		8,9,3	8	15,19

QB3NWA	PowerPlex® Fusion 6C (PDF Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19,3,20	12,13	11	15,19
1	14	30,31	11,12	X	12,14	23
	10,12	14,17	15,21	8,9,3	8	15,19

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 1 - STR Results

QPN3Y9	GlobalFiler™ (PDF Format)					
	11,12	23,25	10,11	15,15	12,13	8,9
	10,12	14,15	19.3,20	12,13	11,11	15,19
	14,14	30,31	11,12	X,X	12,14	23,23
			15,21	8,9.3	8,8	15,19

T2NJXA	PowerPlex® Fusion 6C (HID Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19.3,20	12,13	11	15,19
	14	30,31	11,12	X	12,14	23
	10,12	14,17	15,21	8,9.3	8	15,19

TAZY6A	PowerPlex® Fusion 6C (PDF Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19.3,20	12,13	11	15,19
	14	30,31	11,12	X	12,14	23
	10,12	14,17	15,21	8,9.3	8	15,19

UHALU4	GlobalFiler™ (HID Format) (GeneMapper ID-X 1.5)					
	11,12	23,25	10,11	15,15	12,13	8,9
	10,12	14,15	19.3,20	12,13	11,11	15,19
	14,14	30,31	11,12	X,X	12,14	23,23
			15,21	8,9.3	8,8	15,19

UZPXJ9	GlobalFiler™ (PDF Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19.3,20	12,13	11	15,19
	14	30,31	11,12	X	12,14	23
			15,21	8,9.3	8	15,19

WKM6Q3	GlobalFiler™ (HID Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19.3,20	12,13	11	15,19
	14	30,31	11,12	X,X	12,14	23
			15,21	8,9.3	8	15,19

NM

NM

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 1 - STR Results

WUX8C4	GlobalFiler™ (PDF Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19,3,20	12,13	11	15,19
	14	30,31	11,12	X,X	12,14	23
			15,21	8,9,3	8	15,19
	NM		NM			

X6TZXZ	(HID Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19,3,20	12,13	11	15,19
	14	30,31	11,12	X	12,14	23
			15,21	8,9,3	8	15,19

XQ8MK6	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19,3,20	12,13	11	15,19
	14	30,31	11,12	X	12,14	23
		10,12	14,17	15,21	8,9,3	8

XTCFE4	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format) (Lab Retriever)					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19,3,20	12,13	11	15,19
	14	30,31	11,12	X	12,14	23
		10,12	14,17	15,21	8,9,3	8

YRZZK3	GlobalFiler™ (PDF Format)					
	11,12	23,25	10,11	15,15	12,13	8,9
	10,12	14,15	19,3,20	12,13	11,11	15,19
	14,14	30,31	11,12	X,X	12,14	23,23
			15,21	8,9,3	8,8	15,19

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

33ACQV	GlobalFiler™ (PDF Format)					
	17,17.3	17,23	11,14	15,15	11,12	11,11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16,16	X,Y	11,12	20,21
			20,31.2	6,9.3	8,9	14,16
	12		2			
3B3PPV	Investigator® 24plex (PDF Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
			20,31.2	6,9.3	8,9	14,16
	12					
3GAD3W	GlobalFiler™ (HID Format) (STRMix)					
	17,17.3	17,23	11,14	15,15	11,12	11,11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16,16	X,Y	11,12	20,21
			20,31.2	6,9.3	8,9	14,16
	12		2			
3QVGBW	GlobalFiler™, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
		9,11	7,15	20,31.2	6,9.3	8,9
	12	18	20	2		
844UTR	PowerPlex® Fusion 6C (HID Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
		9,11	7,15	20,31.2	6,9.3	8,9
	12	18	20			
9DNKTP	GlobalFiler™ (HID Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
			20,31.2	6,9.3	8,9	14,16
	12		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

9T3Q6N	PowerPlex® Fusion 6C (HID Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
	9,11	7,15	20,31.2	6,9.3	8,9	14,16
2	12	18	20			
AD8N2P	GlobalFiler™					
	17,17.3	17,23	11,14	15,15	11,12	11,11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16,16	X,Y	11,12	20,21
	N/A	N/A	20,31.2	6,9.3	8,9	14,16
2	12	N/A	N/A	2		
AQC7CP	GlobalFiler™ (HID Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
			20,31.2	6,9.3	8,9	14,16
2	12		2			
BF6NER	PowerPlex® Fusion 5C (PDF Format), (HID Format) (LR MIX 2.1.5)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
	9,11	7,15		6,9.3	8,9	14,16
2	12					
EPKGHJ	GlobalFiler™ (PDF Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
			20,31.2	6,9.3	8,9	14,16
2	12		2			
FX9R6J	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format) (GENEMAPPER)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
	9,11	7,15	20,31.2	6,9.3	8,9	14,16
2			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

GF89NM	PowerPlex® Fusion 6C					
	17,17.3	17,23	11,14	15,15	11,12	11,11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16,16	X,Y	11,12	20,21
	9,11	7,15	20,31.2	6,9.3	8,9	14,16
	12	18	20			
KK8PUD	GlobalFiler™ (HID Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
			20,31.2	6,9.3	8,9	14,16
	12		2			
MEA87C	GlobalFiler™ (HID Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
			20,31.2	6,9.3	8,9	14,16
	12		2			
MXPEG9	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
	9,11	7,15	20,31.2	6,9.3	8,9	14,16
	12	18	20	2		
NHQVBW	PowerPlex® Fusion 5C (PDF Format), (HID Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
	9,11	7,15		6,9.3	8,9	14,16
	12					
QB3NWA	PowerPlex® Fusion 6C (PDF Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
	9,11	7,15	20,31.2	6,9.3	8,9	14,16
	12	18	20			

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

QPN3Y9	GlobalFiler™ (PDF Format)					
	17,17.3	17,23	11,14	15,15	11,12	11,11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16,16	X,Y	11,12	20,21
			20,31.2	6,9.3	8,9	14,16
	12		2			
T2NJXA	PowerPlex® Fusion 6C (HID Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
		9,11	7,15	20,31.2	6,9.3	8,9
	12	18	20			
TAZY6A	PowerPlex® Fusion 6C (PDF Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
		9,11	7,15	20,31.2	6,9.3	8,9
	12	18	20			
UHALU4	GlobalFiler™ (HID Format) (GeneMapper ID-X 1.5)					
	17,17.3	17,23	11,14	15,15	11,12	11,11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16,16	X,Y	11,12	20,21
			20,31.2	6,9.3	8,9	14,16
	12		2			
UZPXJ9	GlobalFiler™ (PDF Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
			20,31.2	6,9.3	8,9	14,16
	12		2			
WKM6Q3	GlobalFiler™ (HID Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
			20,31.2	6,9.3	8,9	14,16
	12		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

WUX8C4	GlobalFiler™ (PDF Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
			20,31.2	6,9.3	8,9	14,16
	12		2			
X6TZXZ	(HID Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
			20,31.2	6,9.3	8,9	14,16
	12		2			
XQ8MK6	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
	9,11	7,15	20,31.2	6,9.3	8,9	14,16
	12	18	20	2		
XTCFE4	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format) (Lab Retriever)					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16	X,Y	11,12	20,21
	9,11	7,15	20,31.2	6,9.3	8,9	14,16
	12	18	20	2		
YRZZK3	GlobalFiler™ (PDF Format)					
	17,17.3	17,23	11,14	15,15	11,12	11,11
	12,14	13,16	17,18	9,14	12,13	13,16
	14,15	27,32.2	16,16	X,Y	11,12	20,21
			20,31.2	6,9.3	8,9	14,16
	12		2			

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D25441	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 3 - STR Results

33ACQV	GlobalFiler™ (PDF Format), (HID Format) (STRmix)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15,15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23,27
			15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,8,9	14,15,16,17,18,19
	10,12			2		
3B3PPV	Investigator® 24plex (PDF Format)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23,27
			15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12					
3GAD3W	GlobalFiler™ (HID Format) (STRMix)					
	11,12,16,17,17.3	17,21,23,25	10,11,14,15	15,16	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,17,19
3	13,14,15,16.2	27,28,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23,25,26,27
			15,19,20,21,22,24.2,29.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12			2		
3QVGBW	GlobalFiler™, PowerPlex® Fusion 6C, Identifier™ Plus (PDF Format), (HID Format)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23,27
	9,10,11,12	7,11,14,15,17,21	15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12	16,18	17,20			
844UTR	PowerPlex® Fusion 6C (HID Format) (CASESOLVER, LRMIX, LABRETRIEVER, EUROFORMIX, YHRD)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,13,14	20,21,23,26,27
	9,10,11,12	7,11,14,15,17,21	15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12	16,18	17,20			
9DNKTP	GlobalFiler™ (HID Format)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23,27
			15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12			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 3 - STR Results

9T3Q6N	PowerPlex® Fusion 6C (HID Format) (STRmix)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,13,14	20,21,23,27
	9,10,11,12	7,11,14,15,17,21	15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12	16,18	17,20			
AD8N2P	GlobalFiler™					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,17,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23,26,27
	N/A	N/A	15,19,20,21,24.2,29.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12	N/A	N/A	2		
AQC7CP	GlobalFiler™ (HID Format)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23,27
			15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12			2		
BF6NER	PowerPlex® Fusion 5C (PDF Format), (HID Format) (LR MIX 2.1.5)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23,27
	9,10,11,12	7,11,14,15,17,21		6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12					
	11,12	23	10,11	15	12	8,10
	10,12	13,14	19.3,20	13	11	15
3major	14	32.2	16	X	12,14	23
	10,12	14,17		8,9.3	8	15,19
	10					
	16 17,17.3	17,25	14,15		11,13	9,11
	11,13,14	12,15,16	17,18,22	9,12,14	9,12,13	13,16,19
3minor	13,15	27,28,30,31	11,12	Y	11	20,21,27
	9,11	7,11,15,21		6,7,9	9	14,16,17,18
	12					

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 3 - STR Results

EPKGHJ	GlobalFiler™ (PDF Format)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
	3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14
			15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12		2			
FX9R6J	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format) (GENEMAPPER)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
	3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14
		9,10,11,12	7,11,14,15,17,21		6,7,8,9,9.3	8,9
			2			
GF89NM	PowerPlex® Fusion 6C					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
	3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14
		9,10,11,12	7,11,14,15,17,21	15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9
	10,12	16,18	17,20			
KK8PUD	GlobalFiler™ (HID Format)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
	3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14
			15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12		2			
MEA87C	GlobalFiler™ (HID Format)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
	3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14
			15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12		2			
MXPEG9	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
	3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14
		9,10,11,12	7,11,14,15,17,21	15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9
	10,12	16,18	17,20	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 3 - STR Results

NHQVBW PowerPlex® Fusion 5C (PDF Format), (HID Format)

	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,29,30,31,32.2	11,12,16	X,Y	11,12,14,15	20,21,23,27
	9,10,11,12	7,11,14,15,17,21		6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19.3,20	12,13	11	15,19
3major	14	30,31	11,12	X	12,14	23
	10,12	14,17		8,9.3	8	15,19
	16,17,17.3	17	14,15	15	11	10,11
	11,13,14	12,13,16	17,18,22	9,14	9,12,13	13,16
3minor	13,15	27,28,29,32.2	16	X,Y	11,15	20,21,27
	9,11	7,11,15,21		6,7,9	9	14,16,17,18
	10,12					

QB3NWA PowerPlex® Fusion 6C (PDF Format)

	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,13,14	
	9,10,11,12	7,11,14,15,17,21	15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12	16,18	17,20			

QPN3Y9 GlobalFiler™ (PDF Format) (LRmix Studio 2.1.3)

	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23,26,27
			15,19,20,21,24.2,29.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12			2		

T2NJXA PowerPlex® Fusion 6C (HID Format) (Lab Retriever)

	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,13,14	20,21,23,26,27
	9,10,11,12	7,11,14,15,17,21	15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12	16,18	17,20			

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 3 - STR Results

TAZY6A	PowerPlex® Fusion 6C (PDF Format)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,13,14	20,21,23,27
	9,10,11,12	7,11,14,15,17,21	15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12	16,18	17,20			
UHALU4	GlobalFiler™ (HID Format) (GeneMapper ID-X 1.5)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23,27
			15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12			2		
UZPXJ9	GlobalFiler™ (PDF Format)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23,27
			15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12			2		
WKM6Q3	GlobalFiler™ (HID Format)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23,27
			15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12			2		
WUX8C4	GlobalFiler™ (PDF Format)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23,27
			15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12			2		
X6TZXZ	(HID Format) (LRmix Studio)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,17,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23,27
			15,19,20,21,24.2,29.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12			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 3 - STR Results

XQ8MK6	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,13,14	20,21,23,26,27
	9,10,11,12	7,11,14,15,17,21	15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12	16,18	17,20	2		
XTCFE4	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format) (Lab Retriever)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23,27
	9,10,11,12	7,11,14,15,17,21	15,20,21,24.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12	16,18	17,20	2		
YRZZK3	GlobalFiler™ (PDF Format)					
	11,12,16,17,17.3	17,23,25	10,11,14,15	15,15	11,12,13	8,9,10,11
	10,11,12,13,14	12,13,14,15,16	17,18,19.3,20,22	9,12,13,14	9,11,12,13	13,15,16,17,19
3	13,14,15	27,28,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23,26,27
			15,19,20,21,24.2,29.2,30.2,31.2	6,7,8,9,9.3	8,9	14,15,16,17,18,19
	10,12			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 4 - STR Results

33ACQV	GlobalFiler™ (PDF Format), (HID Format) (STRmix)					
	11,12,17,17.3	17,23,25	10,11,14	15,15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
			15,20,21,31.2	6,8,9,3	8,8,9	14,15,16,19
	12			2		

3B3PPV	Investigator® 24plex (PDF Format)					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
			15,20,21,31.2	6,8,9,3	8,9	14,15,16,19
	12					

	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
4major	14,15	27,32.2	16	X,Y	11,12	20,21
			20,31.2	6,9,3	8,9	14,6
	12					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19.3,20	12,13	11	15,19
4minor	14	30,31	11,12	X	12,14	23
			15,21	8,9,3	8	15,19

3GAD3W	GlobalFiler™ (HID Format) (STRMix)					
	11,12,17,17.3	17,23,25	10,11,14	15,15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
			15,20,21,31.2	6,8,9,3	8,9	14,15,16,19
	12			2		

3QVGBW	GlobalFiler™, PowerPlex® Fusion 6C, Identifier™ Plus (PDF Format), (HID Format)					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
	9,10,11,12	7,14,15,17	15,20,21,31.2	6,8,9,3	8,9	14,15,16,19
	12	18	20			

844UTR	PowerPlex® Fusion 6C (HID Format) (CASESOLVER, LRMIX, LABRETRIEVER, EUROFORMIX)					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,13,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,13,14	20,21,23
	9,10,11,12	7,14,15,17	15,20,21,31.2	6,8,9,3	8,9	14,15,16,19
	12	18	20			

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 4 - STR Results

9DNKTP	GlobalFiler™ (HID Format)					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
			15,20,21,31.2	6,8,9,3	8,9	14,15,16,19
	12			2		

9T3Q6N	PowerPlex® Fusion 6C (HID Format) (STRmix)					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
	9,10,11,12	7,14,15,17	15,20,21,31.2	6,8,9,3	8,9	14,15,16,19
	12	18	20			

AD8N2P	GlobalFiler™					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
	N/A	N/A	15,20,21,31.2	6,8,9,3	8,9	14,15,16,19
	12	N/A	N/A	2		

AQC7CP	GlobalFiler™ (HID Format)					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
			15,20,21,31.2	6,8,9,3	8,9	14,15,16,19
	12			2		

BF6NER	PowerPlex® Fusion 5C (PDF Format), (HID Format) (LR MIX 2.1.5)					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
	9,10,11,12	7,14,15,17		6,8,9,3	8,9	14,15,16,19
	12					

	17,17.3	23	11	15	12	11
	12	13	17,18	9,13	11	13,16
4major	14	32.2	16	X	12	20,23
	9	7,15		9.3	8	14,16
	12					

	11,12	17,25	10,14		11,13	8,9
	10,14	14,15,16	19.3,20	12,14	12,13	15,19
4minor	15	27,30 31	11,12	Y	11,14	21
	10,11,12	14,17		6,8	9	15,19

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 4 - STR Results

EPKGHJ	GlobalFiler™ (PDF Format)					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
			15,20,21,31.2	6,8,9.3	8,9	14,15,16,19
	12			2		

FX9R6J	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format)					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
	9,10,11,12	7,14,15,17	15,20,21,31.2	6,8,9.3	8,9	14,15,16,19

GF89NM	PowerPlex® Fusion 6C					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
	9,10,11,12	7,14,15,17	15,20,21,31.2	6,8,9.3	8,9	14,15,16,19
	12	18	20			

KK8PUD	GlobalFiler™ (HID Format)					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
			15,20,21,31.2	6,8,9.3	8,9	14,15,16,19
	12			2		

MEA87C	GlobalFiler™ (HID Format)					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
			15,20,21,31.2	6,8,9.3	8,9	14,15,16,19
	12			2		

MXPEG9	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format)					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
	9,10,11,12	7,14,15,17	15,20,21,31.2	6,8,9.3	8,9	14,15,16,19
	12	18	20	2		

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D25441	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 4 - STR Results

NHQVBW PowerPlex® Fusion 5C (PDF Format), (HID Format)

	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
	9,10,11,12	7,14,15,17		6,8,9.3	8,9	14,15,16,19
	12					
	17,17.3	17,23	11,14	15	11,12	11
	12,14	13,16	17,18	9,14	12,13	13,16
4major	14,15	27,32.2	16	X,Y	11,12	20,21
	9,11	7,15		6,9.3	8,9	14,16
	12					
	11,12	23,25	10,11	15	12,13	8,9
	10,12	14,15	19.3,20	12,13	11	15,19
4minor	14	30,31	11,12	X	12,14	23
	10,12	14,17		8,9.3	8	15,19

QB3NWA PowerPlex® Fusion 6C (PDF Format)

	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
	9,10,11,12	7,14,15,17	15,20,21,31.2	6,8,9.3	8,9	14,15,16,19
	12	18	20			

QPN3Y9 GlobalFiler™ (PDF Format) (LRmix Studio 2.1.3)

	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
			15,20,21,31.2	6,8,9.3	8,9	14,15,16,19
	12			2		

T2NJXA PowerPlex® Fusion 6C (HID Format) (Lab Retriever)

	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,13,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,13,14	20,21,23
	9,10,11,12	7,14,15,17	15,20,21,31.2	6,8,9.3	8,9	14,15,16,19
	12	18	20			

TAZY6A PowerPlex® Fusion 6C (PDF Format)

	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
	9,10,11,12	7,14,15,17	15,20,21,31.2	6,8,9.3	8,9	14,15,16,19
	12	18	20			

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 4 - STR Results

UHALU4	GlobalFiler™ (HID Format) (GeneMapper ID-X 1.5)					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
			15,20,21,31.2	6,8,9,3	8,9	14,15,16,19
	12			2		
UZPXJ9	GlobalFiler™ (PDF Format)					
	11,12,17,17.3	17,23,25	10,11,14	15	12,13,14	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
			15,20,21,31.2	6,8,9,3	8,9	14,15,16,19
	12			2		
WKM6Q3	GlobalFiler™ (HID Format)					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
			15,20,21,31.2	6,8,9,3	8,9	14,15,16,19
	12			2		
WUX8C4	GlobalFiler™ (PDF Format)					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
			15,20,21,31.2	6,8,9,3	8,9	14,15,16,19
	12			2		
X6TZXZ	(HID Format) (LRmix Studio)					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
			15,20,21,31.2	6,8,9,3	8,9	14,15,16,19
	12			2		
XQ8MK6	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format)					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
	9,10,11,12	7,14,15,17	15,20,21,31.2	6,8,9,3	8,9	14,15,16,19
	12	18	20	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 4 - STR Results

XTCFE4	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format) (Lab Retriever)					
	11,12,17,17.3	17,23,25	10,11,14	15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
	9,10,11,12	7,14,15,17	15,20,21,31.2	6,8,9.3	8,9	14,15,16,19
	12	18	20	2		
YRZZK3	GlobalFiler™ (PDF Format)					
	11,12,17,17.3	17,23,25	10,11,14	15,15	11,12,13	8,9,11
	10,12,14	13,14,15,16	17,18,19.3,20	9,12,13,14	11,12,13	13,15,16,19
4	14,15	27,30,31,32.2	11,12,16	X,Y	11,12,14	20,21,23
			15,20,21,31.2	6,8,9.3	8,9	14,15,16,19
	12			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

33ACQV	Yfiler™ Plus (PDF Format)								
	37,38	15	11,15	14	32	24	12	11	13
	15	10	10	20	29	17	18	10	21
2	37	12		18	20	20	21		11
3GAD3W	Yfiler™ Plus (PDF Format)								
	37,38	15	11,15	14	32	24	12	11	13
	15	10	10	20	29	17	18	10	21
2	37	12		18	20	20	21		11
3QVGBW	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	37,38	15	11,15	14	32	24	12	11	13
	15	10	10	20	29	17	18	10	21
2	37	12	12	18	20	20	21	13	11
844UTR	Yfiler™ Plus (HID Format)								
	37,38	15	11,15	14	32	24	12	11	13
	15	10	10	20	29	17	18	10	21
2	37	12		18	20	20	21		11
9DNKTP	PowerPlex® Y23 (HID Format)								
		15	11,15	14	32	24	12	11	13
	15	10	10	20		17	18		21
2		12	12	18	20		21	13	11
AD8N2P	Yfiler™ Plus								
	37,38	15	11,15	14	32	24	12	11	13
	15	10	10	20	29	17	18	10	21
2	37	12	N/A	18	20	INC	21	N/A	11
AQC7CP	Yfiler™ Plus (PDF Format)								
	37,38	15	11,15	14	32	24	12	11	13
	15	10	10	20	29	17	18	10	21
2	37	12		18	20	20	21		11
BF6NER	PowerPlex® Y23 (PDF Format), (HID Format)								
		15	11,15	14	32	24	12	11	13
	15	10	10	20		17	18		21
2		12	12	18	20		21	13	11
EPKGHJ	PowerPlex® Y23 (PDF Format)								
		15	11,15	14	32	24	12	11	13
	15	10	10	20		17	18		21
2		12	12	18	20		21	13	11
FX9R6J	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	37,38	15	11,15	14	32	24	12	11	13
	15	10	10	20	29	17	18	10	21
2	37	12	12	18	20	20	21	13	11

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

GF89NM	Yfiler™ Plus	37,38	15	11,15	14	32	24	12	11	13
	2	15	10	10	20	29	17	18	10	21
		37	12		18	20	20	21		11
MEA87C	Yfiler™ Plus (PDF Format)	37,38	15	11,15	14	32	24	12	11	13
	2	15	10	10	20	29	17	18	10	21
		37	12		18	20	20	21		11
MXPEG9	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)	37,38	15	11,15	14	32	24	12	11	13
	2	15	10	10	20	29	17	18	10	21
		37	12	12	18	20	20	21	13	11
NHQVBW	PowerPlex® Y23 (PDF Format), (HID Format)		15	11,15	14	32	24	12	11	13
	2		15	10	10	20	17	18		21
			12	12	18	20		21	13	11
QB3NWA	PowerPlex® Y23 (PDF Format)		15	11,15	14	32	24	12	11	13
	2		15	10	10	20	17	18		21
			12	12	18	20		21	13	11
QPN3Y9	Yfiler™ Plus (PDF Format)	37,38	15	11,15	14	32	24	12	11	13
	2	15	10	10	20	29	17	18	10	21
		37	12		18	20	20	21		11
T2NJXA	PowerPlex® Y23 (HID Format)		15	11,15	14	32	24	12	11	13
	2		15	10	10	20	17	18		21
			12	12	18	20		21	13	11
UHALU4	Yfiler™ Plus (HID Format)	37,38	15	11,15	14	32	24	12	11	13
	2	15	10	10	20	29	17	18	10	21
		37	12		18	20	20	21		11
UZPXJ9	Yfiler™ Plus (PDF Format)	37,38	15	11,15	14	32	24	12	11	13
	2	15	10	10	20	29	17	18	10	21
		37	12		18	20	20	21		11
WKM6Q3	Yfiler™ Plus (PDF Format)	37,38	15	11,15	14	32	24	12	11	13
	2	15	10	10	20	29	17	18	10	21
		37	12		18	20	20	21		11

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

WUX8C4	Yfiler™ Plus (PDF Format)								
	37,38	15	11,15	14	32	24	12	11	13
	15	10	10	20	29	17	18	10	21
2	37	12		18	20	20	21		11
X6TZXZ	(HID Format)								
	37,38	15	11,15	14	32	24	12	11	13
	15	10	10	20	29	17	18	10	21
2	37	12		18	20	20	21		11
XQ8MK6	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	37,38	15	11,15	14	32	24	12	11	13
	15	10	10	20	29	17	18	10	21
2	37	12	12	18	20	20	21	13	11
XTCFE4	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	37,38	15	11,15	14	32	24	12	11	13
	15	10	10	20	29	17	18	10	21
2	37	12	12	18	20	20	21	13	11
YRZZK3	Yfiler™ Plus								
	37,28	15	11,15	14	32	24	12	11	13
	15	10	10	20	29	17	18	10	21
2	37	12		18	20	19.2,20	21		11

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

33ACQV	Yfiler™ Plus (PDF Format)								
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
3	15,16	10,10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12		16,18	17,20	20,21	21,21		11,11
3GAD3W	Yfiler™ Plus (PDF Format)								
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
3	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12		16,18	17,20	20,21	21		11
3QVGBW	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
3	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12	12	16,18	17,20	20,21	21	11,13	11
844UTR	Yfiler™ Plus (HID Format)								
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
3	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12		16,18	17,20	20,21	21		11
9DNKTP	PowerPlex® Y23 (HID Format)								
		15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
3		15,16	10	10,12	20,21	14,17	18		21,23
		10,12	12	16,18	17,20		21	11,13	11
AD8N2P	Yfiler™ Plus								
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
3	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12	N/A	16,18	17,20	20,21	21	N/A	11
AQC7CP	Yfiler™ Plus (PDF Format)								
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
3	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12		16,18	17,20	20,21	21		11
BF6NER	PowerPlex® Y23 (PDF Format), (HID Format)								
		15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
3		15,16	10	10,12	20,21	14,17	18		21,23
		10,12	12	16,18	17,20		21	11,13	11
		16	15	12	29	22	10	10	14
3major		16	10	12	21	14	18		23
		10	12	16	17		21	11	11
		15	11	14	32	24	12	11	13
3minor		15	10	20		17			21
		12		18	20			13	
EPKGHJ	PowerPlex® Y23 (PDF Format)								
		15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
3		15,16	10	10,12	20,21	14,17	18		21,23
		10,12	12	16,18	17,20		21	11,13	11

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

FX9R6J	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12	12	16,18	17,20	20,21	21	11,13	11
GF89NM	Yfiler™ Plus								
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12		16,18	17,20	20,21	21		11
MEA87C	Yfiler™ Plus (PDF Format)								
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12		16,18	17,20	20,21	21		11
MXPEG9	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12	12	16,18	17,20	20,21	21	11,13	11
NHQVBW	PowerPlex® Y23 (PDF Format), (HID Format)								
		15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
	15,16	10	10,12	20,21		14,17	18		21,23
		10,12	12	16,18	17,20		21	11,13	11
3major		16	15	12	29	22	10	10	14
	16	10	12	21		14	18		23
		10	12	16	17		21	11	11
3minor		15	11,15	14	32	24	12	11	13
	15	10	10	20		17	18		21
		12	12	18	20		21	13	11
QB3NWA	PowerPlex® Y23 (PDF Format)								
		15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
	15,16	10	10,12	20,21		14,17	18		21,23
		10,12	12	16,18	17,20		21	11,13	11
QPN3Y9	Yfiler™ Plus (PDF Format)								
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12		16,18	17,20	20,21	21		11
T2NJXA	PowerPlex® Y23 (HID Format)								
		15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
	15,16	10	10,12	20,21		14,17	18		21,23
		10,12	12	16,18	17,20		21	11,13	11
UHALU4	Yfiler™ Plus (HID Format)								
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12		16,18	17,20	20,21	21		11

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

UZPXJ9	Yfiler™ Plus (PDF Format)								
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
3	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,28	10,12		16,18	17,20	20,21	21		11
WKM6Q3	Yfiler™ Plus (PDF Format)								
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
3	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12		16,18	17,20	20,21	21		11
WUX8C4	Yfiler™ Plus (PDF Format)								
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
3	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12		16,18	17,20	20,21	21		11
X6TZXZ	(HID Format)								
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
3	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12		16,18	17,20	20,21	21		11
XQ8MK6									
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
3	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12	12	16,18	17,20	20,21	21	11,13	11
XTCFE4	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
3	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12	12	16,18	17,20	20,21	21	11,13	11
YRZZK3	Yfiler™ Plus (PDF Format)								
	37,38	15,16	11,15	12,14	29,32	22,24	10,12	10,11	13,14
3	15,16	10	10,12	20,21	27,29	14,17	18	10	21,23
	37,38	10,12		16,18	17,20	20,21	21		11

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

33ACQV	Yfiler™ Plus (PDF Format)								
	37,38	15	11,15	14	32	24	12	11	13
4	15	10	10	20	29	17	18	10	21
	37	12		18	20	20	21		11
3GAD3W	Yfiler™ Plus (PDF Format)								
	37,38	15	11,15	14	32	24	12	11	13
4	15	10	10	20	29	17	18	10	21
	37	12		18	20	19.2,20	21		11
3QVGBW	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	37,38	15	11,15	14	32	24	12	11	13
4	15	10	10	20	29	17	18	10	21
	37	12	12	18	20	20	21	13	11
844UTR	Yfiler™ Plus (HID Format)								
	37,38	15	11,15	14	32	24	12	11	13
4	15	10	10	20	29	17	18	10	21
	37	12		18	20	20	21		11
9DNKTP	PowerPlex® Y23 (HID Format)								
		15	11,15	14	32	24	12	11	13
4		15	10	20		17	18		21
		12	12	18	20		21	13	11
AD8N2P	Yfiler™ Plus								
	37,38	15	11,15	14	32	24	12	11	13
4	15	10	10	20	29	17	18	10	21
	37	12	N/A	18	20	INC	21	N/A	11
AQC7CP	Yfiler™ Plus (PDF Format)								
	37,38	15	11,15	14	32	24	12	11	13
4	15	10	10	20	29	17	18	10	21
	37	12		18	20	20	21		11
BF6NER	PowerPlex® Y23 (PDF Format), (HID Format)								
		15	11,15	14	32	24	12	11	13
4		15	10	20		17	18		21
		12	12	18	20		21	13	11
EPKGHJ	PowerPlex® Y23 (PDF Format)								
		15	11,15	14	32	24	12	11	13
4		15	10	20		17	18		21
		12	12	18	20		21	13	11
FX9R6J	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	37,38	15	11,15	14	32	24	12	11	13
4	15	10	10	20	29	17	18	10	21
	37	12	12	18	20	20	21	13	11

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

GF89NM	Yfiler™ Plus	37,38	15	11,15	14	32	24	12	11	13
	4	15	10	10	20	29	17	18	10	21
		37	12		18	20	20	21		11
MEA87C	Yfiler™ Plus (PDF Format)	37,38	15	11,15	14	32	24	12	11	13
	4	15	10	10	20	29	17	18	10	21
		37	12		18	20	20	21		11
MXPEG9	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)	37,38	15	11,15	14	32	24	12	11	13
	4	15	10	10	20	29	17	18	10	21
		37	12	12	18	20	20	21	13	11
NHQVBW	PowerPlex® Y23 (PDF Format), (HID Format)		15	11,15	14	32	24	12	11	13
	4		15	10	10	20		17	18	21
			12	12	18	20		21	13	11
QB3NWA	PowerPlex® Y23 (PDF Format)		15	11,15	14	32	24	12	11	13
	4		15	10	10	20		17	18	21
			12	12	18	20		21	13	11
QPN3Y9	Yfiler™ Plus (PDF Format)	37,38	15	11,15	14	32	24	12	11	13
	4	15	10	10	20	29	17	18	10	21
		37	12		18	20	20	21		11
T2NJXA	PowerPlex® Y23 (HID Format)		15	11,15	14	32	24	12	11	13
	4		15	10	10	20		17	18	21
			12	12	18	20		21	13	11
UHALU4	Yfiler™ Plus (HID Format)	37,38	15	11,15	14	32	24	12	11	13
	4	15	10	10	20	29	17	18	10	21
		37	12		18	20	20	21		11
UZPXJ9	Yfiler™ Plus	37,38	15	11,15	14	32	24	12	11	13
	4	15	10	10	20	29	17	18	10	21
		37	12		18	20	20	21		11
WKM6Q3	Yfiler™ Plus (PDF Format)	37,38	15	11,15	14	32	24	12	11	13
	4	15	10	10	20	29	17	18	10	21
		37	12		18	20	20	21		11

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

WUX8C4	Yfiler™ Plus (PDF Format)								
	37,38	15	11,15	14	32	24	12	11	13
4	15	10	10	20	29	17	18	10	21
	37	12		18	20	20	21		11
X6TZXZ	(HID Format)								
	37,38	15	11,15	14	32	24	12	11	13
4	15	10	10	20	29	17	18	10	21
	37	12		18	20	20	21		11
XQ8MK6									
	37,38	15	11,15	14	32	24	12	11	13
4	15	10	10	20	29	17	18	10	21
	37	12	12	18	20	20	21	13	11
XTCFE4	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	37,38	15	11,15	14	32	24	12	11	13
4	15	10	10	20	29	17	18	10	21
	37	12	12	18	20	20	21	13	11

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
33ACQV	3	Included	Included	2	Included	Included
3B3PPV	3	Included	Included	2	Included	Included
3GAD3W	3	Included	Included	2	Included	Included
3QVGBW	3 (auto) / 2 (YSTR)	Included	Included	2 (auto) / 1 (YSTR)	Included	Included
844UTR	3	Included	Included	2	Included	Included
9DNKTP	at least 3	Inconclusive / Uninterpretable	Inconclusive / Uninterpretable	2	Included	Included
9T3Q6N	3	Included	Included	2	Included	Included
AD8N2P	3 or more	Included	Included	2	Included	Included
AQC7CP	3	Included	Included	2	Included	Included
BF6NER	3	Included	Included	2	Included	Included
BM8XKK	3	Included	Included	2	Included	Included
EPKGHJ	at least 3 individuals, 2 males	Inconclusive / Uninterpretable	Inconclusive / Uninterpretable	two individuals, one male	Included	Included
EPZZ3G	3	Included	Included	2	Included	Included
FX9R6J	3	Included	Included	2	Included	Included
GF89NM	3	Included	Included	2	Included	Included
J48DLC	3	Included	Included	2	Included	Included
KK8PUD	At least three sources with at least two males.	Inconclusive / Uninterpretable	Inconclusive / Uninterpretable	Two source mixture with one male.	Included	Included
MEA87C	3	Included	Included	2	Included	Included
MXPEG9	3	Included	Included	2	Included	Included
NHQVBW	3	Included	Included	2	Included	Included

TABLE 5

WebCode	Item 3 Conclusion			Item 4 Conclusion		
	# of Contributors	Item 1	Item 2	# of Contributors	Item 1	Item 2
QB3NWA	3	Included	Included	2	Included	Included
QPN3Y9	3	Included	Included	2	Included	Included
T2NJXA	3	Included	Included	2	Included	Included
TAZY6A	Mix of at least 3	Included	Included	Mix of at least 2	Included	Included
TLDY23	3	Included	Included	2	Included	Included
UHALU4	3	Included	Included	2	Included	Included
UZPXJ9		Included	Included		Included	Included
WKM6Q3	at least 3	Included	Included	at least 2	Included	Included
WUX8C4	3	Included	Included	2	Included	Included
X6TZXZ	3	Included	Included	2	Included	Included
XQ8MK6	4	Included	Included	2	Included	Included
XTCFE4	≥3 contributors (including ≥2 unrelated males)	Included	Included	≥2 contributors (including ≥1 male)	Included	Included
YRZZK3	at least 4	Inconclusive / Uninterpretable	Included	at least 2	Included	Included

Conclusions Response Summary			Participants reporting conclusions: 33		
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	29	30	33	33
	Excluded	0	0	0	0
	Inconclusive	4	3	0	0
No Response	0	0	0	0	
Total	33	33	33	33	

Statistical Analysis for Item 3

TABLE 6

WebCode	Item 3 Methods & Results
33ACQV	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: autosomal DNA profile is greater than 100 billion times more likely if it originates from the victim and two unknown individuals than if it originates from three unknown unrelated individuals. autosomal DNA profile is greater than 100 billion times more likely if it originates from the suspect and two unknown individuals than if it originates from three unknown unrelated individuals. No statistics for the Y STR profile. Not suitable due to mixture</p> <p>Database(s): FBI_extended_cauc</p>
3B3PPV	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: The DNA profile obtained from this item is a mixture consistent with the combined DNA profiles from the Victim (001-AA Item 1), the Suspect (001-AB Item 2), and an unidentified individual. This mixed DNA profile is approximately 332 quadrillion (3.32×10^{17}) times more likely to be observed if the Victim (001-AA Item 1), the Suspect (001-AB Item 2), and an unidentified individual are the contributors than if the Victim (001-AA Item 1), and two random, unrelated African Americans are the contributors; approximately 65.6 trillion (6.56×10^{13}) times more likely than if the Victim (001-AA Item 1), and two random, unrelated Caucasians are the contributors; and approximately 584 trillion (5.84×10^{14}) times more likely than if the Victim (001-AA Item 1), and two random, unrelated Southwestern Hispanics are the contributors. This mixed DNA profile is approximately 803 quadrillion (8.03×10^{17}) times more likely to be observed if the Victim (001-AA Item 1), the Suspect (001-AB Item 2), and an unidentified individual are the contributors than if the Suspect (001-AB Item 2) and two random, unrelated African Americans are the contributors; approximately 74.8 quadrillion (7.48×10^{16}) times more likely than if the Suspect (001-AB Item 2) and two random, unrelated Caucasians are the contributors; and approximately 3.25 quintillion (3.25×10^{18}) times more likely than if the Suspect (001-AB Item 2), and two random, unrelated Southwestern Hispanics are the contributors.</p> <p>Database(s): PopStats Expanded FBI STR 2015</p>
3GAD3W	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: Item 1 LR: 4.5954E21. Item 2 LR: 2.6308E15.</p> <p>Database(s): NIST1036_CAUC</p>
3QVGBW	<p>Method(s): Counting Method</p> <p>Stats Analysis: The autosomal DNA profile from Item #3 (DNA profile from the passenger side seat of victim's car) is a mixture of at least 3 individuals. Item #1 (Female Victim - Caucasian) and Item #2 (Male Suspect - Caucasian) are included as contributors to the DNA profile from item #3. Probabilistic Genotyping will be used to aid in the statistical correlations of the autosomal STR results upon request. The YSTR profile from Item #3 is a mixture of at least two males. Given the YSTR mixture profile, the likelihood of observing the given profile under the hypothesis of the donorship of the suspect is approx. 31,000 times more likely than observing the given profile under the hypothesis of the non-donorship.</p> <p>Database(s): YSTR: YHRD Online Database</p>
844UTR	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: Autosomal STRs. Propositions tested: Item 1 + 2 unkn vs. 3 unkn. Propositions tested: Item 2 + 2 unkn vs. 3 unkn. Data reported as LogLR. CaseSolver: 1.4E+01, 1.1E+01. Propositions tested: Item 1 + Item 2 + 1 unkn vs. 3 unkn. Data reported as LogLR. LRmix: 2.6E+01. Labretriever: 2.2E+01. EuroForMix: 4.6E+01. Given the DNA profile obtained, it is at least 10^{22} times more probable if it derives from the suspect and the victim together with a third subject instead of 3 unknown persons. Y-STRs. Propositions tested: Item 2 + 1 unkn vs. 2 unkn. Given the aplotype obtained, it is 30,000 times more probable if it derives from the suspect (or a male from the same paternal germline) together with a second male instead of 2 unknown males.</p> <p>Database(s): Autosomal STRs: Nist-caucasian (NIST 1036 U.S. Population Dataset, 2017). Y-STR: Worldwide population dataset</p>

TABLE 6

WebCode	Item 3 Methods & Results
9T3Q6N	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: The LR value calculated for the possible involvement of the Victim in this DNA mixture was 3.56×10^{26} to 1, which means it is about 3.56×10^{26} times more likely that the observed DNA profile being a mixture originating from the Victim and two unrelated individuals than if it originating from three unrelated individuals selected at random from the local [Location Identifying] population. The LR value calculated for the possible involvement of the Suspect in this DNA mixture was 3.40×10^{21} to 1, which means it is about 3.40×10^{21} times more likely that the observed DNA profile being a mixture originating from the Suspect and two unrelated individuals than if it originating from three unrelated individuals selected at random from the local [Location Identifying] population.</p> <p>Database(s): [Location Identifying Database]</p>
AD8N2P	<p>Method(s): [Participant did not report a method.]</p> <p>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. INC: Inconclusive. N/A: Not Applicable. NSD: No Size Data.</p> <p>Database(s): [Participant did not report database(s).]</p>
AQC7CP	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: The mixed DNA profile is 18 quadrillion, 52 quadrillion and 1.3 quadrillion TIMES more likely if it originated from "Item 1", "Item 2" and one unknown RATHER THAN; IF it originated from "Item 1" and two unknown, unrelated individuals as calculated based on the [Location Identifying Database].</p> <p>Database(s): [Location Identifying Database]</p>
BF6NER	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: LR = $1,141 \times 10^{20}$. ITEM 1 + ITEM 2 + 1 NN / 3 NN</p> <p>Database(s): [Location Identifying Database]</p>
FX9R6J	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: 1. Interpretation. The genetic profiles obtained for each analyzed sample are presented in the findings table. In the DNA profile recovered from the passenger seat of the victim's car, more than two alleles were found in several of the genetic systems analyzed, indicating the presence of cells from more than one individual. The victim and suspect profiles are included in the mix, and additional alleles are observed. The probability of these findings was then calculated assuming two hypotheses (H): H1: The mixture comes from the victim, the suspect and an unknown individual. H2: The mixture comes from at least three unknown individuals not genetically related from the reference population. It was found that the genetic finding is 205,565,912,274,750,000,000,000 times more likely under the first hypothesis than under the second one. Conclusion. The victim, the suspect and at least one unknown individual are not excluded as contributors to the mixture of cells found in the DNA profile recovered from the passenger seat of the victim's car. The finding is 205 quadrillion times more likely if the mixture comes from the victim, the suspect and at least one unknown individual, than if it comes from at least three unknown individuals randomly taken from the reference population.</p> <p>Database(s): [Location Identifying Database]</p>
MEA87C	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: The mixed DNA profile is 18 quadrillion ($18e15$), 52 quadrillion ($52e15$) and 1.3 quadrillion ($1.3e15$) TIMES more likely if they originated from "Item 1", "Item 2" and and unknown unrelated individual RATHER THAN; if they originated from "Item 1" and two unknown unrelated individual as calculated based on the [Location Identifying Database].</p> <p>Database(s): [Location Identifying Database]</p>

TABLE 6

WebCode	Item 3 Methods & Results
MXPEG9	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: LR= 183.731.997.503.817.000.000.000.000.000.000. Item 1, Item 2 and at least an unknown individual cannot be excluded as possible contributors to the DNA obtained from Item 3.</p> <p>Database(s): [Location Identifying Database]</p>
NHQVBW	<p>Method(s): Random Match Probability, Lab Retriever</p> <p>Stats Analysis: A mixed DNA profile (PowerPlex™ Fusion 5C) consisting of DNA from at least three contributors was obtained from the passenger side seat of the victim's car (item CTS-23-5882-3). The DNA profile for the major contributor is consistent with the DNA profile of CTS-23-5882-1 (victim). Therefore, the individual represented by the reference sample, item CTS-23-5882-1 (victim), cannot be excluded as a contributor of the three-person mixture obtained from the passenger side seat of the victim's car (item CTS-23-5882-3). The probability of selecting a random, unrelated individual having a DNA profile identical to CTS-23-5882-1 at the loci observed is 1 in 3.24×10^{32} for Caucasian Americans. The suspect (CTS-23-5882-2) cannot be excluded as a contributor to the three-person mixture obtained from the passenger side seat of the victim's car (item CTS-23-5882-3). The observed mixture profile is approximately 6.16×10^{15} times more likely to occur under the scenario that it is a mixture of DNA from the victim, the suspect, and an unknown individual, as opposed to the scenario that it originated from a mixture of DNA from the victim, and two unrelated unknown individuals in the African American population. The observed mixture profile is approximately 6.10×10^{12} times more likely to occur under the scenario that it is a mixture of DNA from the victim, the suspect, and an unknown individual, as opposed to the scenario that it originated from a mixture of DNA from the victim, and two unrelated unknown individuals in the Caucasian population. The observed mixture profile is approximately 6.83×10^{12} times more likely to occur under the scenario that it is a mixture of DNA from the victim, the suspect, and an unknown individual, as opposed to the scenario that it originated from a mixture of DNA from the victim, and two unrelated unknown individuals in the Hispanic population. A mixed DNA profile (PowerPlex® Y23) consisting of two male individuals was obtained from the passenger side seat of the victim's car (item CTS-23-5882-3). The DNA profile for the minor contributor is consistent with the DNA profile of CTS-23-5882-2 (suspect). Therefore, the individual represented by the reference sample, item CTS-23-5882-2 (suspect) cannot be excluded as a contributor to the two male DNA mixture obtained from the passenger side seat of the victim's car (item CTS-23-5882-3). The selected haplotype is found 0 times out of 3, 625 haplotypes in the [Country] for the Caucasian American population. Applying the 95% upper confidence interval results in 1, in 1, 211 haplotypes in the [Country] for the Caucasian American population.</p> <p>Database(s): Promega, Lab Retriever</p>
QB3NWA	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: 756.640.797.722.511.000.000.000.000.000</p> <p>Database(s): [Location Identifying Database]</p>
QPN3Y9	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: LR 2,71623E010 for Item 1, dropout: 0,1. LR 1,42250E008 for Item 2, dropout: 0,1.</p> <p>Database(s): [Location Identifying Database]</p>
T2NJXA	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: The genetic profile obtained from Item 3 is interpreted as a mixture of DNA from three contributors. Item 2 (suspect) cannot be excluded as a possible contributor to this mixture. Given this genetic profile, assuming three contributors, it is 152.8 billion times more likely to observe this genetic profile if Item 2 (suspect) and two unknown individuals are contributors than if 3 unknown individuals are the contributors. The genetic profile obtained from Item 3 is interpreted as a mixture of DNA from three contributors. Item 1 (victim) cannot be excluded as a possible contributor to this mixture. Given this genetic profile, assuming three contributors, it is 2.5 billion times more likely to observe this genetic profile if Item 1 (victim) and two unknown individuals are contributors than if 3 unknown individuals are the contributors.</p> <p>Database(s): NIST</p>

TABLE 6

WebCode	Item 3 Methods & Results
UHALU4	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: LRmix Studio v.1.2.3: Item 1: LR =8,18E010 (Drop out probability: 0.12). Item 2 LR =2,69E008 (Drop out probability: 0.12).</p> <p>Database(s): [Location Identifying Database]</p>
WKM6Q3	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: The mixed DNA profile are 18 quadrillion (18e15), 52 quadrillion (52e15) and 1.3 quadrillion (1.3e15) TIMES more likely; IF they originated from the sources represented by Item 1 and Item 2, and one unknown unrelated individual RATHER THAN; IF they originated from the source represented by Item 1 and two unknown unrelated individuals as calculated based on the [Location Identifying Database].</p> <p>Database(s): [Location Identifying Database]</p>
WUX8C4	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: The mixed DNA profiles are 18 quadrillion (18 x 10e15), 52 quadrillion (52 x 10e15) and 1.3 quadrillion (1.3 x 10e15) TIMES more likely; if they originated from reference samples "Item 1" (Female Victim – Caucasian) and "Item 2" (Male Suspect – Caucasian) and one unknown individual RATHER THAN; if they originated from reference sample "Item 1" (Female Victim – Caucasian) and two unknown unrelated individuals as calculated based on the [Location Identifying Database].</p> <p>Database(s): [Location Identifying Database]</p>
X6TZXZ	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: LR 8,2479E10 Hp (victim + 2 unknown) vs. Hd (3 unknown). LR 2,4771E08 Hp (suspect + 2 unknown) vs. Hd (3 unknown).</p> <p>Database(s): Applied Biosystems Global Filer Caucasian Population Database</p>
XQ8MK6	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: The DNA profile evidence is 1 billion times more likely if victim 1, suspect 2 and two unknown individuals are contributors to the profile than if four random, unrelated persons are contributors to the profile.</p> <p>Database(s): Hill CR, Duewer DL, Kline MC, Coble MD, Butler JM. U.S. population data for 29 autosomal STR loci. Forensic Sci Int Genet. 2013 May;7(3):e82-3. doi: 10.1016/j.fsigen.2012.12.004. Epub 2013 Jan 11. Erratum in: Forensic Sci Int Genet. 2017 Nov;31:e36-e40. PMID: 23317915.</p>
XTCFE4	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: Under the assumption that the VICTIM (Item 1) and two unrelated persons selected at random from the general population are contributors to this mixture, the likelihood of observing the mixed source profile on Item 3 is $\geq 1,000,000$ times greater (actual LR available upon request) than if it is assumed that three unrelated persons selected at random from the general population are contributors to this mixed-source sample. Under the assumption that the SUSPECT (Item 2) and two unrelated persons selected at random from the general population are contributors to this mixture, the likelihood of observing the mixed source profile on Item 3 is $\geq 1,000,000$ times greater (actual LR available upon request) than if it is assumed that three unrelated persons selected at random from the general population are contributors to this mixed-source sample. YSTR Conclusion: The YSTR haplotype developed from Item 3 is an irresolvable/indistinguishable mixture of at least 2 unrelated males. This haplotype is currently uninterpretable given that statistical subject matter experts have not yet reached consensus on a statistical approach for estimating the occurrence of a combination of haplotypes in a population.</p> <p>Database(s): Revised-NIST-1036-Allele Frequencies, ABI ID Database + Promega PP Fusion</p>

TABLE 6

WebCode	Item 3 Methods & Results
YRZZK3	<p>Method(s): Counting method</p> <p>Stats Analysis: GlobalFiler: The DNA profile obtained is a mixture of at least four (4) contributors, including at least two (2) male individuals. Due to the complex nature of this mixture, this profile is inconclusive for comparison purposes. YFiler Plus: The DNA profile obtained is a mixture of two (2) male individuals. The profile is consistent with being a mixture of Item 2 (suspect) and an unknown male individual. Therefore, Item 2 (suspect) can not be excluded as a contributor to this male DNA profile, and, barring a mutation, neither can any of his male relatives.</p> <p>Database(s): YHRD: Found no match in 289,405 Haplotypes (95% CI: 1 in Infinity — 1 in 78,454) (10/16/23)</p>

Statistical Analysis for Item 4

TABLE 7

WebCode	Item 4 Methods & Results
33ACQV	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: The autosomal DNA profile is greater than 100 billion times more likely if it originates from the victim and an unknown individual than if it originates from two unknown unrelated individuals from the Caucasian population. The autosomal DNA profile is greater than 100 billion times more likely if it originates from the suspect and an unknown individual than if it originates from two unknown unrelated individuals from the Caucasian population. The autosomal DNA profile is greater than 100 billion times more likely if it originates from the victim and suspect than if it originates from suspect and an unknown unrelated individual from the Caucasian population. No statistical analysis for Y STR DNA profile. DNA profile matches the suspect on his shirt.</p> <p>Database(s): FBI_extended_Cauc</p>
3B3PPV	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: The DNA profile obtained from this item is a mixture consistent with the combined DNA profiles from the Victim (001-AA Item 1) and the Suspect (001-AB Item 2). This mixed DNA profile is approximately 70.2 octillion (7.02×10^{28}) times more likely to be observed if the Suspect (001-AB Item 2) and the Victim (001-AA Item 1) are the contributors than if the Suspect (001-AB Item 2) and a random, unrelated African American are the contributors; approximately 5.69 octillion (5.69×10^{27}) times more likely than if Suspect (001-AB Item 2) and a random, unrelated Caucasian are the contributors; and approximately 352 octillion (3.52×10^{29}) times more likely than if the Suspect (001-AB Item 2) and a random, unrelated Southwestern Hispanic are the contributors.</p> <p>Database(s): PopStats Expanded FBI STR 2015</p>
3GAD3W	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: Item 1 LR: 4.1470E25. Item 2 LR: 1.7232E22.</p> <p>Database(s): NIST1036_CAUC</p>
3QVGBW	<p>Method(s): Counting Method</p> <p>Stats Analysis: The autosomal DNA profile from Item #4 (DNA profile from the suspect's shirt) is a mixture of at least 2 individuals. Item #1 (Female Victim - Caucasian) and Item #2 (Male Suspect - Caucasian) are included as contributors to the DNA profile from item #4. Probabilistic Genotyping will be used to aid in the statistical correlations of the autosomal STR results upon request. The YSTR profile from Item #3 is consistent with being single source. The expected frequency of males who could be a contributor to the YSTR DNA profile from item #4 is approximately 1 in 9,700 males.</p> <p>Database(s): YSTR: YHRD Online National [Country] Database with Subpopulations</p>
844UTR	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: Autosomal STRs. Propositions tested: Item 1 + 1 unkn vs. 2 unkn. Propositions tested: Item 2 + 1 unkn vs. 2 unkn. Data reported as LogLR CaseSolver: 1.9E+01, 1.5E+01. Propositions tested: Item 1 + Item 2 unkn vs. 2 unkn. Data reported as LogLR. LRmix: 4.0E+01. Labretriever: 3.4E+01. EuroForMix: 5.9E+01. Given the DNA profile obtained, it is at least 10^{34} times more probable if it derives from the suspect and the victim instead of 2 unknown persons.</p> <p>Database(s): Autosomal STRs: Nist-caucasian (NIST 1036 U.S. Population Dataset, 2017)</p>
9DNKTP	<p>Method(s): Combined Probability of Exclusion/Inclusion</p> <p>Stats Analysis: The estimated probability of selecting an unrelated individual at random that can be included as one of the possible contributors to the DNA profile obtained from this sample is rarer than 1 in 330 billion.</p> <p>Database(s): STR population frequency statistics calculated in Popstats using Expanded FBI STR 2015 Caucasian and African American populations as well as [Location] expanded core 2017 (includes [Location Identifying Population]). Only the most common frequency among the five populations or 1 in 330 billion is reported, whichever is more common.</p>

TABLE 7

WebCode	Item 4 Methods & Results
9T3Q6N	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: The LR value calculated for the possible involvement of the Victim in this DNA mixture was 1.66×10^{29} to 1, which means it is about 1.66×10^{29} times more likely that the observed DNA profile being a mixture originating from the Victim and an unrelated individual than if it originating from two unrelated individuals selected at random from the local [Location Identifying] population. The LR value calculated for the possible involvement of the Suspect in this DNA mixture was 3.62×10^{26} to 1, which means it is about 3.62×10^{26} times more likely that the observed DNA profile being a mixture originating from the Suspect and an unrelated individual than if it originating from two unrelated individuals selected at random from the local [Location Identifying] population.</p> <p>Database(s): [Location Identifying Database]</p>
AD8N2P	<p>Method(s): [Participant did not report a method.]</p> <p>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. INC: Inconclusive. N/A: Not Applicable. NSD: No Size Data.</p> <p>Database(s): [Participant did not report database(s).]</p>
AQC7CP	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: The mixed DNA profile is 2.2 nonillion, 10 nonillion and 2.8 octillion TIMES more likely if it originated from "Item 1" and "Item 2" RATHER THAN; IF it originated from "Item 2" and one unknown, unrelated individual as calculated based on the [Location Identifying Database].</p> <p>Database(s): [Location Identifying Database]</p>
BF6NER	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: LR = $9,243 \times 10^{33}$. ITEM 1 + ITEM 2 / 2 NN</p> <p>Database(s): [Location Identifying Database]</p>
EPKGHJ	<p>Method(s): Combined Probability of Exclusion/Inclusion, YHRD</p> <p>Stats Analysis: The estimated probability of selecting an unrelated individual at random that can be included as one of the possible contributors to the STR DNA profile obtained from this sample is rarer than 1 in 330 billion. This Y-STR profile is not expected to occur more frequently than 1 in 140 male individuals.</p> <p>Database(s): STR population frequencies statistics calculated in Popstats using Expanded FBI STR 2015 Caucasian and African American populations ($\theta = 0.01$) as well as [Location] expanded core 2017 (includes [Location Identifying Population], $\theta = 0.03$). 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.</p>

TABLE 7

WebCode	Item 4 Methods & Results
FX9R6J	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: The genetic profiles obtained for each sample analyzed are presented in the findings table. In the DNA profile recovered from the suspect's shirt, more than two alleles were found in several of the genetic systems analyzed, indicating the presence of cells from more than one individual. The profiles of the victim and the suspect are included in the mix. The probability of these findings was then calculated assuming two hypotheses (H): H1: The mixture comes from the suspect and the victim. H2: The mixture comes from two unknown individuals not genetically related from the reference population. It was found that the genetic finding is 21,187,713,365,461,900,000,000,000,000,000,000,000,000,000,000,000 times more likely under the first hypothesis than under the second one. Conclusion. The victim and the suspect are not excluded as contributors to the mixture of cells found in the DNA profile recovered from the suspect's shirt. The finding is 21 octillion times more likely if the mixture comes from the victim and the suspect than if it comes from at least two unknown individuals, randomly taken from the reference population.</p> <p>Database(s): [Location Identifying Database]</p>
KK8PUD	<p>Method(s): Combined Probability of Exclusion/Inclusion</p> <p>Stats Analysis: The estimated probability (21 loci) of selecting an unrelated individual at random that can be included as one of the possible contributors to the DNA profile obtained from this sample is rarer than 1 in 330 billion.</p> <p>Database(s): STR population frequency statistics calculated in Popstats using Expanded FBI STR 2015 Caucasian and African American populations as well as [Location] expanded core 2017 (includes [Location Identifying Population]). Only the most common frequency among the five populations or 1 in 330 billion is reported, whichever is more common.</p>
MEA87C	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: The mixed DNA profile is 2.2 nonillion (2.2e30), 10 nonillion (10e30) and 2.8 octillion (2.8e27) TIMES more likely if they originated from "Item 1" and "Item 2" RATHER THAN; if they originated from "Item 2" and an unknown unrelated individual as calculated based on [Location Identifying Database]</p> <p>Database(s): [Location Identifying Database]</p>
MXPEG9	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: LR= 853.441.518.585.702.000.000.000.000.000.000. Item 1 and Item 2 cannot be excluded as possible contributors to the DNA obtained from Item 4.</p> <p>Database(s): [Location Identifying Database]</p>
NHQVBW	<p>Method(s): Random Match Probability, Lab Retriever</p> <p>Stats Analysis: A mixed DNA profile (PowerPlex™ Fusion 5C) consisting of DNA from at least two contributors was obtained from the suspect's shirt (CTS23-5882-4). The DNA profile for the major contributor is consistent with the DNA profile of CTS-23-5882-2 (suspect). Therefore, the individual represented by the reference sample, item CTS-23-5882-2 (suspect), cannot be excluded as a contributor to the two-person mixture obtained from the suspect's shirt (item CTS-23-5882-4). The probability of selecting a random unrelated individual having a DNA profile identical to CTS-23-5882-2 at the loci observed is 1 in 6.29×10^{27} for Caucasian Americans. The DNA profile for the minor contributor is consistent with the DNA profile of CTS-23-5882-1 (victim). Therefore, the individual represented by the reference sample, item CTS-23-5882-1 (victim), cannot be excluded as a contributor to the two-person mixture obtained from the suspect's shirt (item CTS-23-5882-4). The probability of selecting a random unrelated individual having a DNA profile identical to CTS-23-5882-1 at the loci observed is 1 in 3.24×10^{32} for Caucasian Americans. A single source DNA profile (PowerPlex Y23) was obtained from the suspect's shirt (CTS-23-5882-4). The individual represented by the reference sample, item CTS-23-5882-2 (suspect), cannot be excluded as the contributor of the DNA profile obtained from the suspect's shirt (item CTS-23-5882-4). The selected haplotype is found 0 times out of 3,625 haplotypes in the [Country] for the Caucasian American population. Applying the 95% upper confidence interval results in 1, in 1,211 haplotypes in the [Country] for the Caucasian American population.</p> <p>Database(s): Promega, Lab Retriever</p>

TABLE 7

WebCode	Item 4 Methods & Results
QB3NWA	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: 11.319.463.304.835.800.000.000.000.000.000.000.000.000.000.000.000</p> <p>Database(s): [Location Identifying Database]</p>
QPN3Y9	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: LR 2,06837E015 for Item 1, dropout:0,1. LR 4,41128E012 for Item 2, dropout:0,1.</p> <p>Database(s): [Location Identifying Database]</p>
T2NJXA	<p>Method(s): Likelihood Ratio</p> <p>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, it is 5.05 quadrillion times more likely to observe this genetic profile if Item 2 (suspect) and one unknown individual are contributors than if 2 unknown individuals are the contributors. The genetic profile obtained from Item 4 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 Item 2 (suspect) is a contributor, it is 46.4 quintillion times more likely to observe this genetic profile if Item 1 (victim) and Item 2 (suspect) are contributors than if Item 2 (suspect) and one unknown individual are the contributors.</p> <p>Database(s): NIST</p>
UHALU4	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: LRmix Studio v.1.2.3: Item 1: LR = 1,41E015 (Drop out probability: 0.1). Item 2: LR = 3,42E012 (Drop out probability: 0.08).</p> <p>Database(s): [Location Identifying Database]</p>
WKM6Q3	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: The mixed DNA profile are 2.2 nonillion (2.2e30), 10 nonillion (10e30) and 2.8 octillion (2.8e27) TIMES more likely; IF they originated from the sources represented by Item 1 and Item 2 RATHER THAN; IF they originated from the source represented by Item 2 and one unknown unrelated individual as calculated based on the [Location Identifying Database].</p> <p>Database(s): [Location Identifying Database]</p>
WUX8C4	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: The mixed DNA profiles are 2.2 nonillion (2.2 x 10e30), 10 nonillion (10 x 10e30) and 2.8 octillion (2.8 x 10e27) TIMES more likely; if they originated from reference samples "Item 1" (Female Victim – Caucasian) and "Item 2" (Male Suspect – Caucasian) RATHER THAN; if they originated from reference sample "Item 2" (Male Suspect – Caucasian) and one unknown unrelated individual as calculated based on the [Location Identifying Database].</p> <p>Database(s): [Location Identifying Database]</p>
X6TZXZ	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: LR 3,3229E15 Hp (victim + unknown) vs. Hd (2 unknown). LR 7,5213E12 Hp (suspect + unknown) vs. Hd (2 unknown).</p> <p>Database(s): Applied Biosystems Global Filer Caucasian Population Database</p>
XQ8MK6	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: The DNA profile evidence is 1 billion times more likely if victim 1 and suspect 2 are contributors to the profile than if random, unrelated persons are contributors to the profile.</p> <p>Database(s): Hill CR, Duewer DL, Kline MC, Coble MD, Butler JM. U.S. population data for 29 autosomal STR loci. Forensic Sci Int Genet. 2013 May;7(3):e82-3. doi: 10.1016/j.fsigen.2012.12.004. Epub 2013 Jan 11. Erratum in: Forensic Sci Int Genet. 2017 Nov;31:e36-e40. PMID: 23317915.</p>

TABLE 7

WebCode	Item 4 Methods & Results
XTCFE4	<p>Method(s): Likelihood Ratio</p> <p>Stats Analysis: Under the assumption that the VICTIM (Item 1) and one unrelated person selected at random from the general population are contributors to this mixture, the likelihood of observing the mixed source profile on Item 4 is $\geq 1,000,000$ times greater (actual LR available upon request) than if it is assumed that two unrelated persons selected at random from the general population are contributors to this mixed-source sample. Under the assumption that the SUSPECT (Item 2) and one unrelated person selected at random from the general population are contributors to this mixture, the likelihood of observing the mixed source profile on Item 4 is $\geq 1,000,000$ times greater (actual LR available upon request) than if it is assumed that two unrelated persons selected at random from the general population are contributors to this mixed-source sample. YSTR Conclusion: 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 Item 4. On 21 August 2023, this DNA haplotype was searched against the YHRD database (Release 69). Given a theta-value of 2.0×10^{-5} and a 95% UCI of the combined Haplotype frequency of 1 in 3,131 (no matches in 9,379 Haplotypes at [Country] subpopulations without [Population]), the corrected Match Probability is 1 in 2,947.</p> <p>Database(s): Revised-NIST-1036-Allele Frequencies, ABI ID Database + Promega PP Fusion YHRD database (Release 69)</p>
YRZZK3	<p>Method(s): Random Match Probability</p> <p>Stats Analysis: The DNA profile obtained is a mixture of at least 2 individuals, including a male. Assuming the presence of Item 2 (suspect), Item 1 (victim) is a contributor to this mixture profile. The probability of randomly selecting an unrelated individual who would be included as a contributor to this DNA profile is approximately 1 in 429 trillion for the African American population, 1 in 407 billion for the Caucasian population, 1 in 21.4 trillion for the Hispanic population, and 1 in 548 trillion for the Asian population.</p> <p>Database(s): NIST 1036 Revised US Population Database (July 2017) located at https://strbase.nist.gov/NISTpop.htm.</p>

Amplification Kit Survey

Please list all PCR amplification kits (Autosomal and YSTR) utilized as well as any future kits yet to be implemented in your laboratory.

TABLE 8

WebCode	Amplification Kit
3B3PPV	Qiagen Investigator 24plex QS Qiagen Investigator 24plex GO!
AQC7CP	1. GlobalFiler PCR Amplification Kit. 2. GlobalFiler Express PCR Amplification Kit. 3. AmpFLSTR Yfiler PCR Amplification Kit.
EPKGHJ	GlobalFiler, GlobalFiler Express, and PowerPlex Y23.
MEA87C	1. GlobalFiler PCR Amplification Kit. 2. GlobalFiler Express PCR Amplification Kit. 3. AmpFLSTR Yfiler PCR Amplification Kit.
WKM6Q3	(1) Applied Biosystems™ Globalfiler™ PCR Amplification Kit. (2) Applied Biosystems™ Globalfiler™ Express PCR Amplification Kit. (3) Applied Biosystems™ AmpFLSTR™ Yfiler™ PCR Amplification Kit. (4) Applied Biosystems™ AmpFLSTR™ Minifiler™ PCR Amplification Kit.
X6TZXZ	Global Filer. Yfiler Plus. Fusion 6C.

Additional Comments

TABLE 9

WebCode	Additional Comments
3QVGBW	GeneMarker HID Analysis Software used. Peak height difference may be accounted for by the different analysis programs. PG analysis outsourced and performed upon request.
9DNKTP	The YSTR profile obtained from item 3 is consistent with being from two male individuals, and would (in our lab) be suitable for exclusions only. No conclusions are reported as to whether the suspect (Item 2) could be a contributor to this sample due to insufficient DNA. DNA from at least 3 individuals was observed in the STR profile obtained from item 3. Due to the complexity of the genetic profile obtained from this sample, no meaningful comparisons can be made to known reference samples. The following are not included in the STR table for item 3 (once stutter was removed they were less than the analytical threshold and were determined to be A/TA): 17 at D18, 26 at FGA, 19 and 29.2 at SE33
AQC7CP	1. Statistical calculations were carried out using DNAView software. 2. NM represents non-male profile.
BF6NER	Item 3 - 2 man (NN + Item 2) and 1 women (Item 1). The suspect (Item 2) does not dominate the Y profile.
EPKGHJ	All control data was reviewed by creating a GMID-X project; test item profiles were used from PDFs. After stutter is subtracted, the following peaks in the item 3 GlobalFiler profile may be artifacts or true alleles and are therefore not included in the GF allele table for Item 3: 17 at D18S51, 26 at FGA, and 19 and 29.2 at SE33.
KK8PUD	Item 3 had the following called peaks that were A/TA (unable to distinguish between artifact or true allele) after removing stutter: 17 at D18S51, 26 at FGA, 19 and 29.2 at SE33.
MEA87C	1. Statistical calculations were carried out using DNAView Software. 2. NM represents non-male profile.
WKM6Q3	Statistical Evaluation: The statistical evaluations were performed on the DNA.View Statistical Software version 37.42. Remark: 'NM' denotes non-male profile.
WUX8C4	Statistical calculation was carried out using DNAVIEW software version 37.56 and calculated at 21 loci.

-End of Report-
(Appendix may follow)

Collaborative Testing Services ~ Forensic Testing Program

Test No. 23-5882: DNA Interpretation

DATA MUST BE SUBMITTED BY **Dec. 04, 2023, 11:59 p.m. EST** TO BE INCLUDED IN THE REPORT

Participant Code: U1234A

WebCode: GPBJXX

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 homicide involving a female victim and male suspect. The victim's body was found in the driver's seat of her car. Security footage reviewed by police shows a male and the victim fighting inside the car and the male frantically leaving the scene. The male has been apprehended by police. A reddish-brown stain was identified on the passenger's seat of the victim's car and confirmed as blood by the Serology Unit (Item 3). A reddish-brown stain from the shirt the suspect was wearing was also confirmed as blood (Item 4). Both Items were submitted for DNA analysis.

Note: Minor low level peaks present in the Negative and/or Reagent Blank samples have been confirmed with the Supplier to be artifacts of the analysis process. Please continue performing interpretation of the associated samples.

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

The Identifiler™ Plus files that are included are utilizing the following amplification thresholds - Blue: 32 rfu, Green: 41 rfu, Yellow: 71 rfu, Red: 76 rfu, Internal Lane Standard (ILS): 500 rfu.

Items Submitted (Sample Pack INT2):

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

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

Item 3: DNA profile from the passenger side seat of victim's car

Item 4: DNA profile from the suspect's shirt

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

23-5882 Data For Participants.zip MD5 hash value: 53030f282c584e8758a5d66b976de40b

23-5882 Data For Participants.zip SHA1 hash value: cb2b2edfd92566d3e7fdfb7379c53226f721917b

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:

- | | | | |
|--|---|---|---|
| <input type="checkbox"/> GlobalFiler™ | <input type="checkbox"/> Investigator® 24plex | <input type="checkbox"/> PowerPlex® Fusion 5C | <input type="checkbox"/> PowerPlex® Fusion 6C |
| <input type="checkbox"/> Identifiler® Plus | <input type="checkbox"/> HID format | <input type="checkbox"/> PDF format | |

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

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:

Please note: Any additional formatting applied in the free form space below will not transfer to the Summary Report and may cause your information to be illegible. This includes additional spacing and returns that present your responses in lists and tabular formats.

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:

Please note: Any additional formatting applied in the free form space below will not transfer to the Summary Report and may cause your information to be illegible. This includes additional spacing and returns that present your responses in lists and tabular formats.

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.

Please note: Any additional formatting applied in the free form space below will not transfer to the Summary Report and may cause your information to be illegible. This includes additional spacing and returns that present your responses in lists and tabular formats.

Part III: AMPLIFICATION KIT SURVEY (optional)

To accommodate your laboratory's future needs, please list all PCR amplification kits (Autosomal and YSTR) utilized as well as any future kits to be implemented in your laboratory.

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

A2LA Certificate No.

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

Authorized Contact Person and Title

Laboratory Name

Location (City/State)