



## **DNA Interpretation Test No. 23-5881**

### **Summary Report**

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Each participant received a sample set through the CTS Portal containing electropherograms and raw data files which they were requested to evaluate using their existing protocols. Data were returned from 36 participants and are compiled into the following tables:

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

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

## **Manufacturer's Information**

Each sample set contained digital files consisting of electropherograms from DNA profiles of two reference samples (Items 1 & 2) and two questioned samples (Items 3 & 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 one part of blood from the Item 1 female donor and one part of blood from the Item 2 male donor. Item 4 was created by combining two parts of blood from the Item 2 male donor and one part of blood from a 3rd-party female donor.

**VERIFICATION:** Laboratories that conducted predistribution testing of the electropherograms reported consistent results for all loci, with the exception of one participant who was missing alleles at multiple loci. All associations were consistent amongst the predistribution laboratories.

**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.

### Amelogenin and STR Results

*Results compiled by predistribution laboratories and a consensus of participants.*

Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		
1	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
	13,14	29,31.2	14,15	X,X	12,13	24,25
	*	*	19,29.2	7,9	8,10	15,19
	NM	NM	NM	NM		
2	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15,15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11,11	X,Y	10,13	18,25
	*	*	17,17	7,8	9,11	17,19
	10	*	*	2		
3	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
	*	*	17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10	*	*	2		
4	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
	10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23,2,25
	*	*	16,17,29.2	7,8,9	8,9,11	16,17,18,19
	10	*	*	2		
4Major	12,16	18,19	10,12	15,16	12,13	*
	14,15	15,15	17,20	*	9,12	13,14
	14,15.2	30,31	11,11	*	*	18,25
	*	*	17,17	7,8	9,11	17,19
	*	*	*	*		

### 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	38,40	14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2	10	26
	41	12	12	19	18	20	21	9	10
3	38,40	14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2	10	26
	41	12	12	19	18	20	21	9	10
4	38,40	14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2	10	26
	41	12	12	19	18	20	21	9	10

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

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

## **Summary Comments**

The DNA Interpretation test was designed to allow participants to assess their proficiency in evaluating and interpreting electropherograms (EPGs). Each participant received electropherograms (in .pdf and .hid formats) of two reference items and two questioned items. 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 one part of blood from the Item 1 female donor and one part of blood from the Item 2 male donor. Item 4 was created by combining two parts of blood from the Item 2 male donor and one part of blood from a 3rd-party female 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 36 participants that reported results, 32 participants evaluated the provided STR data.

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

For YSTR results, all participants reported consistent results.

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

For Item 4, eleven participants attempted the deconvolution of this mixture. However, due to the low reporting population, a consensus was formed only for the major profile, but not the minor profile. A consensus was achieved for the full Item 4 profile (unseparated).

### DNA Interpretations

For Item 3, 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.

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

# STR Interpretation Guidelines

TABLE 1

<b>WebCode</b>	<b>Analytical Threshold (rfu)</b>	<b>Peak Height Ratio (%)</b>	<b>Stochastic Threshold (rfu)</b>
23T6MY	120	60	360
2MEWLX	120	60	360
2P447R	[Participant did not provide interpretation guidelines]		
49V6PU	75	60	230
6AECR9	130	60	800
8MJ6FQ	120	60	360
9JCBT6	130	60	800
A7K3RH	[Participant did not provide interpretation guidelines]		
B93GVH	[Participant did not provide interpretation guidelines]		
BHQG6Z	75	60	250
E36763	75	60	
E8XAX8	130	60	800
ER9ZB6	75	60	100
GGGKZX	130	60	800
JXEMQZ	[Participant did not provide interpretation guidelines]		
K79RJ2	130	15	800
L4FHNQ	130	60	800
LBVYJL	75	60	100
LEEDMM	50	70	150
LXQZ9U	50	60	865
MEQ83M	75	60	100
MMKDVN	60	50	
NLNF38	180	50	370
PDDBR3	125	60	600
PEH8UH	75	60	100
PVQXDA	75	60	100
QUEEU6	[Participant did not provide interpretation guidelines]		
QXB9JT	130	60	800
QZJD4A	120	60	360
UTPM3H	130	60	800
VFWKXV	75	60	100
VT4B2N	[Participant did not provide interpretation guidelines]		
WUCZNX	100	65	600
XNMMGH	130	60	800
YU8XCX	80	60	250
ZMRA7V	50	70	150

# YSTR Interpretation Guidelines

TABLE 2

WebCode	Analytical Threshold (rfu)	Peak Height Ratio (%)	Stochastic Threshold (rfu)
23T6MY	75	50	75
2MEWLX	75	50	75
2P447R	[Participant did not provide interpretation guidelines]		
49V6PU	[Participant did not provide interpretation guidelines]		
6AECR9	50	70	725
8MJ6FQ	75	50	75
9JCBT6	50	60	724
A7K3RH	[Participant did not provide interpretation guidelines]		
B93GVH	[Participant did not provide interpretation guidelines]		
BHQG6Z	[Participant did not provide interpretation guidelines]		
E36763	75	50	
E8XAX8	50	60	1,500
ER9ZB6	75	50	75
GGGKZX	50	50	1,500
JXEMQZ	[Participant did not provide interpretation guidelines]		
K79RJ2	50	15	800
L4FHNQ	50	70	725
LBVYJL	75	50	75
LEEDMM	50	70	150
LXQZ9U	[Participant did not provide interpretation guidelines]		
MEQ83M	75	50	75
MMKDVN	60		
NLNF38	[Participant did not provide interpretation guidelines]		
PDDBR3	[Participant did not provide interpretation guidelines]		
PEH8UH	75	50	75
PVQXDA	75	50	75
QUEEU6	[Participant did not provide interpretation guidelines]		
QXB9JT	50	70	725
QZJD4A	75	50	75
UTPM3H	50	70	725
VFWKXV	75	50	75
VT4B2N	[Participant did not provide interpretation guidelines]		
WUCZNX	[Participant did not provide interpretation guidelines]		
XNMMGH	50	70	725
YU8XCX	80	50	75
ZMRA7V	50	60	150

# 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

23T6MY	GlobalFiler™ (HID Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14	17,23	8,12	11	13,17
	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19
	NM		NM			
2MEWLV	GlobalFiler™ (PDF Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14	17,23	8,12	11	13,17
	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19
	NM		NM			
49V6PU	PowerPlex® Fusion 6C (PDF Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14	17,23	8,12	11	13,17
	13,14	29,31.2	14,15	X	12,13	24,25
		9	13,14	19,29.2	7,9	8,10
6AECR9	GlobalFiler™ (HID Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19
8MJ6FQ	GlobalFiler™ (PDF Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14	17,23	8,12	11	13,17
	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19
	NM		NM			
9JCBT6	GlobalFiler™ (HID Format) (STRmix)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	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

BHQG6Z	GlobalFiler™					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19
	F,F		F,F			
E36763	GlobalFiler™, Identifiler™ Plus (HID Format) (Lab Retriever)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14	17,23	8,12	11	13,17
	13,14	29,31.2	14,15	X	12,13	24,25
			19,29.2	7,9.3	8,10	15,19
E8XAX8	GlobalFiler™ (PDF Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19
ER9ZB6	GlobalFiler™, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
	13,14	29,31.2	14,15	X,X	12,13	24,25
		9,9	13,14	19,29.2	7,9	8,10
GGGKZX	GlobalFiler™ (HID Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19
JXEMQZ	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format) (Lab Retriever)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14	17,23	8,12	11	13,17
	13,14	29,31.2	14,15	X	12,13	24,25
		9	13,14	19,29.2	7,9	8,10



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

K79RJ2	GlobalFiler™ (HID Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
1	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19

L4FHNQ	GlobalFiler™					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
1	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19

LBVYJL	GlobalFiler™ (PDF Format) (GeneMapper ID-X v 1.6)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
1	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19

LEEDMM	GlobalFiler™ (STRMix/SMART)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
1	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19

LXQZ9U	GlobalFiler™ (PDF Format) (LRmix Studio 2.1.5 Community Edition)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
1	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19

MEQ83M	GlobalFiler™ (PDF Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
1	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	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

MMKDVN	GlobalFiler™ (PDF Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19
NLNF38	Investigator® 24plex (HID Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
	13,14	29,31.2	14,15	X,X	12,13	24,25
		N/A	N/A	19,29.2	7,9	8,10
	N/A	N/A	N/A	N/A		
PDDBR3	GlobalFiler™ (PDF Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19
	No Results		No Results			
PEH8UH	GlobalFiler™ (PDF Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
	13,14	29,31.2	14,15	X,X	12,13	24,25
		N/A	N/A	19,29.2	7,9	8,10
	NSD	N/A	N/A	NSD		
PVQXDA	GlobalFiler™, PowerPlex® Fusion 6C (PDF Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14	17,23	8,12	11	13,17
	13,14	29,31.2	14,15	X	12,13	24,25
		9	13,14	19,29.2	7,9	8,10
	-	-	-	-		
QXB9JT	GlobalFiler™					
	15,15	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	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

QZJD4A	GlobalFiler™ (PDF Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14	17,23	8,12	11	13,17
1	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19
	NM			NM		

UTPM3H	GlobalFiler™ (STRmix v2.9 (ESR / FSSA))					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
1	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19

VFWKXV	PowerPlex® Fusion 6C (PDF Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14	17,23	8,12	11	13,17
1	13,14	29,31.2	14,15	X	12,13	24,25
	9	13,14	19,29.2	7,9	8,10	15,19

VT4B2N	GlobalFiler™					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
1	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19

WUCZNX	Investigator® 24plex (PDF Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14	17,23	8,12	11	13,17
1	13,14	29,31.2	14,15	X	12,13	24,25
			19,29.2	7,9	8,10	15,19

XNMMGH	GlobalFiler™ (STRmix)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
1	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	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

YU8XCX	GlobalFiler™ (PDF Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
1	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19

ZMRA7V	PowerPlex® Fusion 5C (PDF Format), (HID Format)					
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14	17,23	8,12	11	13,17
1	13,14	29,31.2	14,15	X	12,13	24,25
	9	13,14	-	7,9	8,10	15,19
	-	-	-	-		

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 2 - STR Results

23T6MY	GlobalFiler™ (HID Format)					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11	X,Y	10,13	18,25
	10		17	7,8	9,11	17,19
2			2			
2MEWLV	GlobalFiler™ (PDF Format)					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11	X,Y	10,13	18,25
	10		17	7,8	9,11	17,19
2			2			
49V6PU	PowerPlex® Fusion 6C (PDF Format)					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11	X,Y	10,13	18,25
	10	19	17	7,8	9,11	17,19
2		18				
6AECR9	GlobalFiler™ (HID Format)					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15,15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11,11	X,Y	10,13	18,25
	10		17,17	7,8	9,11	17,19
2			2			
8MJ6FQ	GlobalFiler™ (PDF Format)					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11	X,Y	10,13	18,25
	10		17	7,8	9,11	17,19
2			2			
9JCBT6	GlobalFiler™ (HID Format) (STRmix)					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15,15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11,11	X,Y	10,13	18,25
	10		17,17	7,8	9,11	17,19
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

BHQG6Z	GlobalFiler™					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15,15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11,11	X,Y	10,13	18,25
			17,17	7,8	9,11	17,19
	10,F		2,F			
E36763	GlobalFiler™, Identifiler™ Plus (HID Format) (Lab Retriever)					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11	X,Y	10,13	18,25
			17	7,8	9,11	17,19
	10		2			
E8XAX8	GlobalFiler™ (PDF Format)					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15,15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11,11	X,Y	10,13	18,25
			17,17	7,8	9,11	17,19
	10		2			
ER9ZB6	GlobalFiler™, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format)					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15,15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11,11	X,Y	10,13	18,25
	9,13	13,16	17,17	7,8	9,11	17,19
	10	19	18	2		
GGGKZX	GlobalFiler™ (HID Format)					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15,15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11,11	X,Y	10,13	18,25
			17,17	7,8	9,11	17,19
	10		2			
JXEMQZ	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format) (Lab Retriever)					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11	X,Y	10,13	18,25
	9,13	13,16	17	7,8	9,11	17,19
	10	19	18	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

K79RJ2	GlobalFiler™ (HID Format)					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15,15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11,11	X,Y	10,13	18,25
			17,17	7,8	9,11	17,19
	10		2			
L4FHNQ	GlobalFiler™					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15,15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11,11	X,Y	10,13	18,25
			17,17	7,8	9,11	17,19
	10		2			
LBVYJL	GlobalFiler™ (PDF Format) (GeneMapper ID-X v 1.6)					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15,15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11,11	X,Y	10,13	18,25
			17,17	7,8	9,11	17,19
	10		2			
LEEDMM	GlobalFiler™ (STRMix/SMART)					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15,15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11,11	X,Y	10,13	18,25
			17,17	7,8	9,11	17,19
	10		2			
LXQZ9U	GlobalFiler™ (PDF Format) (LRmix Studio 2.1.5 Community Edition)					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15,15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11,11	X,Y	10,13	18,25
			17,17	7,8	9,11	17,19
	10		2			
MEQ83M	GlobalFiler™ (PDF Format)					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15,15	17,20	8,13	9,12	13,14
	14,15.2	30,31	11,11	X,Y	10,13	18,25
			17,17	7,8	9,11	17,19
	10		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

MMKDVN	GlobalFiler™ (PDF Format)						
		12,16	18,19	10,12	15,16	12,13	8,12
		14,15	15,15	17,20	8,13	9,12	13,14
	2	14,15.2	30,31	11,11	X,Y	10,13	18,25
				17,17	7,8	9,11	17,19
	10			2			
NLNF38	Investigator® 24plex (HID Format)						
		12,16	18,19	10,12	15,16	12,13	8,12
		14,15	15,15	17,20	8,13	9,12	13,14
	2	14,15.2	30,31	11,11	X,Y	10,13	18,25
		N/A	N/A	17,17	7,8	9,11	17,19
	10	N/A	N/A	N/A			
PDDBR3	GlobalFiler™ (PDF Format)						
		12,16	18,19	10,12	15,16	12,13	8,12
		14,15	15,15	17,20	8,13	9,12	13,14
	2	14,15.2	30,31	11,11	X,Y	10,13	18,25
				17,17	7,8	9,11	17,19
	10			2			
PEH8UH	GlobalFiler™ (PDF Format)						
		12,16	18,19	10,12	15,16	12,13	8,12
		14,15	15,15	17,20	8,13	9,12	13,14
	2	14,15.2	30,31	11,11	X,Y	10,13	18,25
		N/A	N/A	17,17	7,8	9,11	17,19
	10	N/A	N/A	2			
PVQXDA	GlobalFiler™, PowerPlex® Fusion 6C (PDF Format)						
		12,16	18,19	10,12	15,16	12,13	8,12
		14,15	15	17,20	8,13	9,12	13,14
	2	14,15.2	30,31	11	X,Y	10,13	18,25
		9,13	13,16	17	7,8	9,11	17,19
	10	19	18	2			
QXB9JT	GlobalFiler™						
		12,16	18,19	10,12	15,16	12,13	8,12
		14,15	15,15	17,20	8,13	9,12	13,14
	2	14,15.2	30,31	11,11	X,Y	10,13	18,25
				17,17	7,8	9,11	17,19
	10			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 2 - STR Results

QZJD4A	GlobalFiler™ (PDF Format)						
	12,16	18,19	10,12	15,16	12,13	8,12	
	14,15	15	17,20	8,13	9,12	13,14	
	2	14,15.2	30,31	11	X,Y	10,13	18,25
				17	7,8	9,11	17,19
	10			2			
UTPM3H	GlobalFiler™ (STRmix v2.9 (ESR / FSSA))						
	12,16	18,19	10,12	15,16	12,13	8,12	
	14,15	15,15	17,20	8,13	9,12	13,14	
	2	14,15.2	30,31	11,11	X,Y	10,13	18,25
				17,17	7,8	9,11	17,19
	10			2			
VFWKXV	PowerPlex® Fusion 6C (PDF Format)						
	12,16	18,19	10,12	15,16	12,13	8,12	
	14,15	15	17,20	8,13	9,12	13,14	
	2	14,15.2	30,31	11	X,Y	10,13	18,25
		9,13	13,16	17	7,8	9,11	17,19
	10	19	18				
VT4B2N	GlobalFiler™						
	12,16	18,19	10,12	15,16	12,13	8,12	
	14,15	15,15	17,20	8,13	9,12	13,14	
	2	14,15.2	30,31	11,11	X,Y	10,13	18,25
				17,17	7,8	9,11	17,19
	10			2			
WUCZNX	Investigator® 24plex (PDF Format)						
	12,16	18,19	10,12	15,16	12,13	8,12	
	14,15	15	17,20	8,13	9,12	13,14	
	2	14,15.2	30,31	11	X,Y	10,13	18,25
				17	7,8	9,11	17,19
	10						
XNMMGH	GlobalFiler™ (STRmix)						
	12,16	18,19	10,12	15,16	12,13	8,12	
	14,15	15,15	17,20	8,13	9,12	13,14	
	2	14,15.2	30,31	11,11	X,Y	10,13	18,25
				17,17	7,8	9,11	17,19
	10			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

YU8XCX	GlobalFiler™ (PDF Format)					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15,15	17,20	8,13	9,12	13,14
2	14,15.2	30,31	11	X,Y	10,13	18,25
			17,17	7,8	9,11	17,19
	10			2		
ZMRA7V	PowerPlex® Fusion 5C (PDF Format), (HID Format)					
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15	17,20	8,13	9,12	13,14
2	14,15.2	30,31	11	X,Y	10,13	18,25
	9,13	13,16	-	7,8	9,11	17,19
	10	-	-	-		

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

23T6MY	GlobalFiler™ (HID Format)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10		2			
3	GlobalFiler™ (PDF Format)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10		2			
49V6PU	PowerPlex® Fusion 6C (PDF Format)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
		9,13	13,14,16	17,19,29.2	7,8,9	8,9,10,11
	10	19	18			
6AECR9	GlobalFiler™ (HID Format) (STRmix)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10		2			
8MJ6FQ	GlobalFiler™ (PDF Format)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10		2			
9JCBT6	GlobalFiler™ (HID Format) (STRmix)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10		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

<b>BHQG6Z</b>	GlobalFiler™					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
<b>3</b>	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10,F			2,F		
<b>E36763</b>	GlobalFiler™, Identifiler™ Plus (HID Format) (Lab Retriever)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
<b>3</b>	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10			2		
<b>E8XAX8</b>	GlobalFiler™ (PDF Format) (STRmix)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,16	17,20,23	8,12,13	9,11,12	13,14,17
<b>3</b>	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
	-	-	17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10	-	-	2		
<b>ER9ZB6</b>	GlobalFiler™, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
<b>3</b>	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
	9,13	13,14,16	17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10	19	18	2		
<b>GGGKZX</b>	GlobalFiler™ (HID Format) (STRmix)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
<b>3</b>	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10			2		
<b>JXEMQZ</b>	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format) (Lab Retriever)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
<b>3</b>	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
	9,13	13,14,16	17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10	19	18	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

K79RJ2	GlobalFiler™ (HID Format)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
3	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10			2		

L4FHNQ	GlobalFiler™					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
3	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10			2		

LBVYJL	GlobalFiler™ (PDF Format) (GeneMapper ID-X v 1.6)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
3	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10			2		

LEEDMM	GlobalFiler™ (STRMix/SMART)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
3	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10			2		
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15,15	17,20	8,13	9,12	13,14
3major	14,15.2	30,31	11	X,Y	10,13	18,25
			17,17	7,8	9,11	17,19
	10			2		
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14,14	17,23	8,12	11,11	13,17
3minor	13,14	29,31.2	14,15	X,X	12,13	24,25
			19,29.2	7,9	8,10	15,19

LXQZ9U	GlobalFiler™ (PDF Format) (LRmix Studio 2.1.5 Community Edition)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
3	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10			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

MEQ83M GlobalFiler™ (PDF Format)

	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
3	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10			2		
-----						
			10			8,12
			17,20	8		13,14
3major			11	X	10,13	
			17	7		
-----						
			11,12			7
			23	12,13		17
3minor			14,15	Y	12	
			19,29.2	8,9		

MMKDVN GlobalFiler™ (PDF Format)

	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
3	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10			2		

NLNF38 Investigator® 24plex (HID Format)

	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
3	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
	N/A	N/A	17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10	N/A	N/A	N/A		

PDDBR3 GlobalFiler™ (PDF Format)

	12,(15),16,16.1	(17),18,19,21	10,(11),(12)	15,16	(10),12,13	(7),(8),12
	11,(12),14,15	14,15	17,(20),(23)	8,(12),(13)	9,11,12	13,(14),(17)
3	(13),14,15.2	29,30,31,31.2	11,(14),(15)	X,(Y)	(10),(12),13	(18),(24),25
			17,(19),(29.2)	7,(8),(9)	8,9,10,11	(15),17,19
	10			2		

PEH8UH GlobalFiler™ (PDF Format)

	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
3	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
	N/A	N/A	17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10	N/A	N/A	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

PVQXDA	GlobalFiler™, PowerPlex® Fusion 6C (PDF Format)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
3	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
	9,13	13,14,16	17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10	19	18	2		

QXB9JT	GlobalFiler™ (STRMix)					
	12,15,16	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
3	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10			2		

QZJD4A	GlobalFiler™ (PDF Format)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
3	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10			2		

UTPM3H	GlobalFiler™ (STRmix v2.9 (ESR / FSSA))					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
3	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10			2		

VFWKXV	PowerPlex® Fusion 6C (PDF Format)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
3	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
	9,13	13,14,16	17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10	19	18			

VT4B2N	GlobalFiler™					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
3	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10			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

<b>WUCZNX</b>	Investigator® 24plex (PDF Format)					
	12,15,16,16.1	18,19,21**	10,11,12	15,16	12,13**	7,8,12
	11,12,14,15	14,15	17,20,23	8,12**	9,11,12	13,14**
<b>3</b>	13,14**	30,31,31.2**	11,14,15	X**	10,13**	18,24,25
			17**	7,8,9	8,9,11**	15,17,19
	10					
<b>XNMMGH</b>	GlobalFiler™ (STRmix)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
<b>3</b>	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10			2		
<b>YU8XCX</b>	GlobalFiler™ (PDF Format) (Lrmixstudio-2.1.5-CommunityEdition)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
<b>3</b>	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
			17,19,29.2	7,8,9	8,9,10,11	15,17,19
	10			2		
<b>ZMRA7V</b>	PowerPlex® Fusion 5C (PDF Format), (HID Format)					
	12,15,16,16.1	17,18,19,21	10,11,12	15,16	10,12,13	7,8,12
	11,12,14,15	14,15	17,20,23	8,12,13	9,11,12	13,14,17
<b>3</b>	13,14,15.2	29,30,31,31.2	11,14,15	X,Y	10,12,13	18,24,25
	9,13	13,14,16	-	7,8,9	8,9,10,11	15,17,19
	10	-	-	-	-	-
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15	17,20	8,13	9,12	13,14
<b>3major</b>	14,15.2	30,31	11	X,Y	10,13	18,25
	9,13	13,16	-	7,8	9,11	17,19
	10	-	-	-	-	-
	15,16.1	17,21	10,11	15,16	10,13	7,12
	11,12	14	17,23	8,12	11	13,17
<b>3minor</b>	13,14	29,31.2	14,15	X	12,13	24,25
	9	13,14	-	7,9	8,10	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

WebCode	Amplification Kits (File Format)	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
23T6MY	GlobalFiler™ (HID Format)	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
		10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
	4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
				16,17,29.2	7,8,9	8,9,11	16,17,18,19
		10			2		
		12,16	18,19	10,12	15,16	12,13	8,12
		14,15	15	17,20	8,13	9,12	13,14
	4major	14,15.2	30,31	11	X,Y	10,13	18,25
				17	7,8	9,11	17,19
		10			2		
2MEWL	GlobalFiler™ (PDF Format)	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
		10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
	4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
				16,17,29.2	7,8,9	8,9,11	16,17,18,19
		10			2		
		12,16	18,19	10,12	15,16	12,13	8,12
		14,15	15	17,20	8,13	9,12	13,14
	4major	14,15.2	30,31	11	X,Y	10,13	18,25
				17	7,8	9,11	17,19
		10			2		
49V6PU	PowerPlex® Fusion 6C (PDF Format)	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
		10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
	4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
		9,13	7,12,13,16	16,17,29.2	7,8,9	8,9,11	16,17,18,19
		10	19	18			
6AECR9	GlobalFiler™ (HID Format) (STRmix)	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
		10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
	4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
				16,17,29.2	7,8,9	8,9,11	16,17,18,19
		10			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

8MJ6FQ	GlobalFiler™ (PDF Format)							
		12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12	
		10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18	
	4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25	
				16,17,29.2	7,8,9	8,9,11	16,17,18,19	
		10			2			
		12,16	18,19	10,12	15,16	12,13	8,12	
		14,15	15	17,20	8,13	9,12	13,14	
	4major	14,15.2	30,31	11	X,Y	10,13	18,25	
				17	7,8	9,11	17,19	
	10			2				
9JCBT6	GlobalFiler™ (HID Format) (STRmix)							
		12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12	
		10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18	
	4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25	
				16,17,29.2	7,8,9	8,9,11	16,17,18,19	
		10			2			
	BHQG6Z	GlobalFiler™						
			12,14,16	18,19,23	10,11,12	15,16,17,18	11,12,13	8,12
			10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
		4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
				16,17,29.2	7,8,9	8,9,11	16,17,18,19	
		10,F			2,F			
E36763		GlobalFiler™, Identifiler™ Plus (HID Format) (Lab Retriever)						
			12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
			10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
		4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
				16,17,29.2	7,8,9	8,9,11	16,17,18,19	
		10			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

E8XAX8	GlobalFiler™ (PDF Format) (STRmix)					
	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
	10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
	-	-	16,17,29.2	7,8,9	8,9,11	16,17,18,19
	10	-	-	2		
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15,15	17,20	8,13	9,12	13,14
4major	14,15.2	30,31	11,11	-	10,13	18,25
	-	-	17,17	7,8	9,11	17,19
	-	-	-	-	-	-
	12,14	18,23	11,11	16,18	11,13	12,12
	10,13	15,16	18,21	11,11	11,11	13,18
4minor	13,15.2	28,28	11,16	-	12,12	22,23.2
	-	-	16,29.2	7,9	8,11	16,18
	-	-	-	-	-	-

ER9ZB6	GlobalFiler™, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format)					
	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
	10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
	9,13	7,12,13,16	16,17,29.2	7,8,9	8,9,11	16,17,18,19
	10	19	18	2		

GGGKZX	GlobalFiler™ (HID Format) (STRMix)					
	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
	10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
			16,17,29.2	7,8,9	8,9,11	16,17,18,19
	10			2		

JXEMQZ	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, Identifiler™ Plus (PDF Format), (HID Format) (Lab Retriever)					
	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
	10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
	9,13	7,12,13,16	16,17,29.2	7,8,9	8,9,11	16,17,18,19
	10	19	18	2		

K79RJ2	GlobalFiler™ (HID Format)					
	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
	10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
			16,17,29.2	7,8,9	8,9,11	16,17,18,19
	10			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

WebCode	Amplification Kits (File Format)					
L4FHNQ	GlobalFiler™					
	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
	10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
			16,17,29.2	7,8,9	8,9,11	16,17,18,19
	10			2		
LBVYJL	GlobalFiler™ (PDF Format)	(GeneMapper ID-X v 1.6)				
	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
	10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
			16,17,29.2	7,8,9	8,9,11	16,17,18,19
	10			2		
LEEDMM	GlobalFiler™ (STRMix/SMART)					
	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
	10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
			16,17,29.2	7,8,9	8,9,11	16,17,18,19
	10			2		
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15,15	17,20	8,13	9,12	13,14
4major	14,15.2	30,31	11	X,Y	10,13	18,25
			17,17	7,8	9,11	17,19
	10			2		
	12,14	18,23	11,11	18,18	11,13	12,12
	10,13	15,16/16,16	18,21	11,11	9,11	13,18
4minor	13,15.2	28,30/28,28	16,16/11,16	X,X	10,12	22,23.2
			16,29.2	7,9/9,9	8,11/8,8	16,18
LXQZ9U	GlobalFiler™ (PDF Format)	(LRmix Studio 2.1.5 Community Edition)				
	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
	10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
			16,17,29.2	7,8,9	8,9,11	16,17,18,19
	10			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

MEQ83M	GlobalFiler™ (PDF Format)					
	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
	10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
			16,17,29.2	7,8,9	8,9,11	16,17,18,19
	10			2		
	12,16	18,19	10,12	15,16	12,13	
	14,15	15	17,20		9,12	13,14
4major	14,15.2	30,31	11		10,13	18,25
			17	7,8	9,11	17,19
	14	23	11	18	11	
	10,13	16	18,21		11	18
4minor	13	28	16		12	22,23.2
			16,29.2	9	8	16,18

MMKDYN	GlobalFiler™ (PDF Format)					
	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
	10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
			16,17,29.2	7,8,9	8,9,11	16,17,18,19
	10			2		

NLNF38	Investigator® 24plex (HID Format)					
	12,14,16	18,19,23	10,11,12	15,16	11,12,13	8,12
	10,13,14,15	15,16	17,20,21	8,11,13	9,11,12	13,14,18
4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
	N/A	N/A	16,17,29.2	7,8,9	8,9,11	16,17,18,19
	10	N/A	N/A	N/A		
	12,16	18,19	10,12	N/A	12,13	N/A
	14,15	15	17,20	N/A	9,12	13,14
4major	14,15.2	30,31	11	N/A	N/A	18,25
	N/A	N/A	17	7,8	9,11	17,19
	N/A	N/A	N/A	N/A		
	14	23	11	N/A	11	N/A
	10,13	16	21	N/A	11	18
4minor	13	28	16	N/A	N/A	22,23.2
	N/A	N/A	16,29.2	9	8	16,18
	N/A	N/A	N/A	N/A		

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

PDDBR3	GlobalFiler™ (PDF Format)						
		12,(14),16	18,19,(23)	10,(11),12	15,16,(18)	(11),12,13	8,12
		(10),(13),14,15	15,(16)	17,(18),20,(21)	8,11,13	9,(11),12	13,14,(18)
	4	(13),14,15.2	(28),30,31	11,(16)	X,(Y)	10,(12),13	18,(22),(23.2),25
				(16),17,(29.2)	7,8,(9)	(8),9,11	(16),17,(18),19
		10			2		
		12,16	18,19	10,12	15,16	12,13	8,12
		14,15	15,15	17,20	Inc	9,12	13,14
	4major	14,15.2	30,31	11,11	X,Y	10,13	18,25
				17,17	7,8	9,11	17,19
	N/A			N/A			
PEH8UH	GlobalFiler™ (PDF Format)						
		12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
		10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
	4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
		N/A	N/A	16,17,29.2	7,8,9	8,9,11	16,17,18,19
		10	N/A	N/A	2		
PVQXDA	GlobalFiler™, PowerPlex® Fusion 6C (PDF Format)						
		12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
		10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
	4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
		9,13	7,12,13,16	16,17,29.2	7,8,9	8,9,11	16,17,18,19
		10	19	18	2		
QXB9JT	GlobalFiler™ (STRMix)						
		12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
		10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
	4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
				16,17,29.2	7,8,9	8,9,11	16,17,18,19
		10			2		
QZJD4A	GlobalFiler™ (PDF Format)						
		12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
		10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
	4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
				16,17,29.2	7,8,9	8,9,11	16,17,18,19
		10			2		
		12,16	18,19	10,12	15,16	12,13	8,12
		14,15	15	17,20	8,13	9,12	13,14
	4major	14,15.2	30,31	11	X,Y	10,13	18,25
				17	7,8	9,11	17,19
	10			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

UTPM3H	GlobalFiler™ (STRmix v2.9 (ESR / FSSA))					
	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
	10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
			16,17,29.2	7,8,9	8,9,11	16,17,18,19
	10			2		
VFWKXV	PowerPlex® Fusion 6C (PDF Format)					
	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
	10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
	9,13	7,12,13,16	16,17,29.2	7,8,9	8,9,11	16,17,18,19
	10	19	18			
VT4B2N	GlobalFiler™					
	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
	10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
			16,17,29.2	7,8,9	8,9,11	16,17,18,19
	10			2		
WUCZNX	Investigator® 24plex (PDF Format)					
	12,16	18,19	10,12	15,16	–	–
	–	15	17,20	–	9,12	13,14
4major	14,15.2	–	11	X,Y	–	18,25
			17	7,8	9,11	–
	10					
XNMMGH	GlobalFiler™ (STRmix)					
	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
	10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
			16,17,29.2	7,8,9	8,9,11	16,17,18,19
	10			2		
YU8XCX	GlobalFiler™ (PDF Format) (Lrmixstudio-2.1.5-CommunityEdition)					
	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
	10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
			16,17,29.2	7,8,9	8,9,11	16,17,18,19
	10			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

ZMRA7V	PowerPlex® Fusion 5C (PDF Format), (HID Format)					
	12,14,16	18,19,23	10,11,12	15,16,18	11,12,13	8,12
	10,13,14,15	15,16	17,18,20,21	8,11,13	9,11,12	13,14,18
4	13,14,15.2	28,30,31	11,16	X,Y	10,12,13	18,22,23.2,25
	9,13	7,12,13,16	-	7,8,9	8,9,11	16,17,18,19
	10	-	-	-	-	-
	12,16	18,19	10,12	15,16	12,13	8,12
	14,15	15	17,20	8,13	9,12	13,14
4major	14,15.2	30,31	11	-	10,13	18,25
	9,13	13,16	-	7,8	9,11	17,19
	10	-	-	-	-	-
	12,14	18,23	11,12	16,18	-	-
	10,13	15,16	18,21	8,11	11	13,18
4minor	13,14	-	16	-	10,12	22,23.2
	9	7,12	-	7,9	8,11	16,18
	-	-	-	-	-	-



**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

23T6MY	Yfiler™ Plus (PDF Format)								
	38,40	14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2	10	26
2	41	12		19	18	20	21		10
2MEWLX	Yfiler™ Plus (PDF Format)								
	38,40	14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2	10	26
2	41	12		19	18	20	21		10
6AECR9	PowerPlex® Y23 (HID Format)								
		14	16,18	13	29	24	10	13	12
	14	11	10	20		17	16.2		26
2		12	12	19	18		21	9	10
8MJ6FQ	Yfiler™ Plus (PDF Format)								
	38,40	14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2	10	26
2	41	12		19	18	20	21		10
9JCBT6	PowerPlex® Y23								
		14	16,18	13	29	24	10	13	12
	14	11	10	20		17	16.2		26
2		12	12	19	18		21	9	10
E36763	Yfiler™ Plus (HID Format)								
	38,40	14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2	10	26
2	41	12		19	18	20	21		10
E8XAX8	PowerPlex® Y23 (PDF Format)								
	-	14	16,18	13	29	24	10	13	12
	14	11	10	20	-	17	16.2	-	26
2	-	12	12	19	18	-	21	9	10
ER9ZB6	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	38,40	14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2	10	26
2	41	12	12	19	18	20	21	9	10
GGGKZX	PowerPlex® Y23 (HID Format)								
		14	16,18	13	29	24	10	13	12
	14	11	10	20		17	16.2		26
2		12	12	19	18		21	9	10
JXEMQZ	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	38,40	14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2	10	26
2	41	12	12	19	18	20	21	9	10

TABLE 4

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

## Item 2 - YSTR Results

K79RJ2	PowerPlex® Y23 (HID Format)									
		14	16,18	13	29	24	10	13	12	
	2	14	11	10	20	17	16.2	26		
		12	12	19	18		21	9	10	
L4FHNQ	PowerPlex® Y23									
		14	16,18	13	29	24	10	13	12	
	2	14	11	10	20	17	16.2	26		
		12	12	19	18		21	9	10	
LBVYJL	Yfiler™ Plus (PDF Format)									
		38,40	14	16,18	13	29	24	10	13	12
	2	14	11	10	20	28	17	16.2	10	26
		41	12	19	18	20	21		10	
LEEDMM	Yfiler™ Plus									
		38,40	14	16,18	13	29	24	10	13	12
	2	14	11	10	20	28	17	16.2	10	26
		41	12	19	18	20	21		10	
LXQZ9U	Yfiler™ Plus (PDF Format)									
		38,40	14	16,18	13	29	24	10	13	12
	2	14	11	10	20	28	17	16.2	10	26
		41	12	19	18	20	21		10	
MEQ83M	Yfiler™ Plus (PDF Format)									
		38,40	14	16,18	13	29	24	10	13	12
	2	14	11	10	20	28	17	16.2	10	26
		41	12	19	18	20	21		10	
MMKDVN	PowerPlex® Y23 (PDF Format)									
		14	16,18	13	29	24	10	13	12	
	2	14	11	10	20	17	16.2	26		
		12	12	19	18		21	9	10	
PEH8UH	Yfiler™ Plus (PDF Format)									
		38,40	14	16,18	13	29	24	10	13	12
	2	14	11	10	20	28	17	16.2	10	26
		41	12	N/A	19	18	20	21	N/A	10
PVQXDA	Yfiler™ Plus (PDF Format)									
		38,40	14	16,18	13	29	24	10	13	12
	2	14	11	10	20	28	17	16.2	10	26
		41	12	19	18	20	21		10	
QXB9JT	PowerPlex® Y23									
		14	16,18	13	29	24	10	13	12	
	2	14	11	10	20	17	16.2	26		
		12	12	19	18		21	9	10	

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

QZJD4A	Yfiler™ Plus (PDF Format)								
	38,40	14	16,18	13	29	24	10	13	12
2	14	11	10	20	28	17	16.2	10	26
	41	12		19	18	20	21		10
UTPM3H	PowerPlex® Y23 (PDF Format)								
		14	16,18	13	29	24	10	13	12
2	14	11	10	20		17	16.2		26
		12	12	19	18		21	9	10
VFWKXV	(PDF Format)								
		14	16,18	13	29	24	10	13	12
2	14	11	10	20		17	16.2		26
		12	12	19	18		21	9	10
VT4B2N	Yfiler™ Plus								
	38,40	14	16,18	13	29	24	10	13	12
2	14	11	10	20	28	17	16.2	10	26
	41	12		19	18	20	21		10
XNMMGH	PowerPlex® Y23								
		14	16,18	13	29	24	10	13	12
2	14	11	10	20		17	16.2		26
		12	12	19	18		21	9	10
YU8XCX	Yfiler™ Plus (PDF Format)								
	38,40	14	16,18	13	29	24	10	13	12
2	14	11	10	20	28	17	16.2	10	26
	41	12		19	18	20	21		10
ZMRA7V	PowerPlex® Y23 (PDF Format), (HID Format)								
	-	14	16,18	13	29	24	10	13	12
2	14	11	10	20	-	17	16.2	-	26
	-	12	12	19	18	-	21	9	10

TABLE 4

WebCode	Amplification Kits (File Format)								
	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
Item	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4
<b>Item 3 - YSTR Results</b>									
23T6MY	Yfiler™ Plus (PDF Format)								
	38,40	14	16,18	13	29	24	10	13	12
3	14	11	10	20	28	17	16.2	10	26
	41	12		19	18	20	21		10
2MEWLV	Yfiler™ Plus (PDF Format)								
	38,40	14	16,18	13	29	24	10	13	12
3	14	11	10	20	28	17	16.2	10	26
	41	12		19	18	20	21		10
6AECR9	PowerPlex® Y23 (HID Format)								
		14	16,18	13	29	24	10	13	12
3	14	11	10	20		17	16.2		26
		12	12	19	18		21	9	10
8MJ6FQ	Yfiler™ Plus (PDF Format)								
	38,40	14	16,18	13	29	24	10	13	12
3	14	11	10	20	28	17	16.2	10	26
	41	12		19	18	20	21		10
9JCBT6	PowerPlex® Y23 (HID Format)								
		14	16,18	13	29	24	10	13	12
3	14	11	10	20		17	16.2		26
		12	12	19	18		21	9	10
E36763	Yfiler™ Plus (HID Format)								
	38,40	14	16,18	13	29	24	10	13	12
3	14	11	10	20	28	17	16.2	10	26
	41	12		19	18	20	21		10
E8XAX8	PowerPlex® Y23 (PDF Format)								
	-	14	16,18	13	29	24	10	13	12
3	14	11	10	20	-	17	16.2	-	26
	-	12	12	19	18	-	21	9	10
	-	14	16,18	13	29	24	10	13	12
3major	14	11	10	20	-	17	16.2	-	26
	-	12	12	19	18	-	21	9	10
ER9ZB6	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	38,40	14	16,18	13	29	24	10	13	12
3	14	11	10	20	28	17	16.2	10	26
	41	12	12	19	18	20	21	9	10
GGGKZX	PowerPlex® Y23 (HID Format)								
		14	16,18	13	29	24	10	13	12
3	14	11	10	20		17	16.2		26
		12	12	19	18		21	9	10

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

JXEMQZ	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	38,40	14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2	10	26
	41	12	12	19	18	20	21	9	10
K79RJ2	PowerPlex® Y23 (HID Format)								
		14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2		26
	12	12	19	18		21	9	10	
L4FHNQ	PowerPlex® Y23								
		14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2		26
	12	12	19	18		21	9	10	
LBVYJL	Yfiler™ Plus (PDF Format)								
	38,40	14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2	10	26
	41	12		19	18	20	21		10
LEEDMM	Yfiler™ Plus								
	38,40	14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2	10	26
	41	12		19	18	20	21		10
LXQZ9U	Yfiler™ Plus (PDF Format)								
	38,40	14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2	10	26
	41	12		19	18	20	21		10
MEQ83M	Yfiler™ Plus (PDF Format)								
	38,40	14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2	10	26
	41	12		19	18	20	21		10
MMKDVN	PowerPlex® Y23 (PDF Format)								
		14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2		26
	12	12	19	18		21	9	10	
PEH8UH	Yfiler™ Plus (PDF Format)								
	38,40	14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2	10	26
	41	12	N/A	19	18	20	21	N/A	10
PVQXDA	Yfiler™ Plus (PDF Format)								
	38,40	14	16,18	13	29	24	10	13	12
	14	11	10	20	28	17	16.2	10	26
	41	12		19	18	20	21		10

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

QXB9JT	PowerPlex® Y23								
		14	16,18	13	29	24	10	13	12
3	14	11	10	20		17	16.2		26
		12	12	19	18		21	9	10
QZJD4A	Yfiler™ Plus (PDF Format)								
	38,40	14	16,18	13	29	24	10	13	12
3	14	11	10	20	28	17	16.2	10	26
	41	12		19	18	20	21		10
UTPM3H	PowerPlex® Y23 (PDF Format)								
		14	16,18	13	29	24	10	13	12
3	14	11	10	20		17	16.2		26
		12	12	19	18		21	9	10
VFWKXV	PowerPlex® Y23 (PDF Format)								
		14	16,18	13	29	24	10	13	12
3	14	11	10	20		17	16.2		26
		12	12	19	18		21	9	10
VT4B2N	Yfiler™ Plus								
	38,40	14	16,18	13	29	24	10	13	12
3	14	11	10	20	28	17	16.2	10	26
	41	12		19	18	20	21		10
XNMMGH	PowerPlex® Y23								
		14	16,18	13	29	24	10	13	12
3	14	11	10	20		17	16.2		26
		12	12	19	18		21	9	10
YU8XCX	Yfiler™ Plus (PDF Format)								
	38,40	14	16,18	13	29	24	10	13	12
3	14	11	10	20	28	17	16.2	10	26
	41	12		19	18	20	21		10
ZMRA7V	PowerPlex® Y23 (PDF Format), (HID Format)								
	-	14	16,18	13	29	24	10	13	12
3	14	11	10	20	-	17	16.2	-	26
	-	12	12	19	18	-	21	9	10
	-	14	16,18	13	29	24	10	13	12
3major	14	11	10	20	-	17	16.2	-	26
	-	12	12	19	18	-	21	9	10

TABLE 4

WebCode	Amplification Kits (File Format)									
	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393	
Item	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481	
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4	
<b>Item 4 - YSTR Results</b>										
23T6MY	Yfiler™ Plus (PDF Format)									
	38,40	14	16,18	13	29	24	10	13	12	
4	14	11	10	20	28	17	16.2	10	26	
	41	12		19	18	20	21		10	
2MEWLV	Yfiler™ Plus (PDF Format)									
	38,40	14	16,18	13	29	24	10	13	12	
4	14	11	10	20	28	17	16.2	10	26	
	41	12		19	18	20	21		10	
6AECR9	PowerPlex® Y23 (HID Format)									
		14	16,18	13	29	24	10	13	12	
4	14	11	10	20		17	16.2		26	
		12	12	19	18		21	9	10	
8MJ6FQ	Yfiler™ Plus (PDF Format)									
	38,40	14	16,18	13	29	24	10	13	12	
4	14	11	10	20	28	17	16.2	10	26	
	41	12		19	18	20	21		10	
9JCBT6	PowerPlex® Y23 (HID Format)									
		14	16,18	13	29	24	10	13	12	
4	14	11	10	20		17	16.2		26	
		12	12	19	18		21	9	10	
E36763	Yfiler™ Plus									
	38,40	14	16,18	13	29	24	10	13	12	
4	14	11	10	20	28	17	16.2	10	26	
	41	12		19	18	20	21		10	
E8XAX8	PowerPlex® Y23 (PDF Format)									
	-	14	16,18	13	29	24	10	13	12	
4	14	11	10	20	-	17	16.2	-	26	
	-	12	12	19	18	-	21	9	10	
	-	14	16,18	13	29	24	10	13	12	
4major	14	11	10	20	-	17	16.2	-	26	
	-	12	12	19	18	-	21	9	10	
ER9ZB6	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)									
	38,40	14	16,18	13	29	24	10	13	12	
4	14	11	10	20	28	17	16.2	10	26	
	41	12	12	19	18	20	21	9	10	
GGGKZX	PowerPlex® Y23 (HID Format)									
		14	16,18	13	29	24	10	13	12	
4	14	11	10	20		17	16.2		26	
		12	12	19	18		21	9	10	

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

JXEMQZ	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	38,40	14	16,18	13	29	24	10	13	12
	41	12	12	19	18	20	21	9	10
4	14	11	10	20	28	17	16.2	10	26
K79RJ2	PowerPlex® Y23 (HID Format)								
4	14	11	10	20	28	17	16.2	10	26
	12	12	19	18	21	9	10		
	14	11	10	20	28	17	16.2	10	26
L4FHNQ	PowerPlex® Y23								
4	14	11	10	20	28	17	16.2	10	26
	12	12	19	18	21	9	10		
	14	11	10	20	28	17	16.2	10	26
LBVYJL	Yfiler™ Plus (PDF Format)								
4	38,40	14	16,18	13	29	24	10	13	12
	41	12	19	18	20	21			
	14	11	10	20	28	17	16.2	10	26
LEEDMM	Yfiler™ Plus								
4	38,40	14	16,18	13	29	24	10	13	12
	41	12	19	18	20	21			
	14	11	10	20	28	17	16.2	10	26
LXQZ9U	Yfiler™ Plus (PDF Format)								
4	38,40	14	16,18	13	29	24	10	13	12
	41	12	19	18	20	21			
	14	11	10	20	28	17	16.2	10	26
MEQ83M	Yfiler™ Plus (PDF Format)								
4	38,40	14	16,18	13	29	24	10	13	12
	41	12	19	18	20	21			
	14	11	10	20	28	17	16.2	10	26
MMKDVN	PowerPlex® Y23 (PDF Format)								
4	14	11	10	20	28	17	16.2	10	26
	12	12	19	18	21	9	10		
	14	11	10	20	28	17	16.2	10	26
PEH8UH	Yfiler™ Plus (PDF Format)								
4	38,40	14	16,18	13	29	24	10	13	12
	41	12	N/A	19	18	20	21	N/A	10
	14	11	10	20	28	17	16.2	10	26
PVQXDA	Yfiler™ Plus (PDF Format)								
4	38,40	14	16,18	13	29	24	10	13	12
	41	12	19	18	20	21			
	14	11	10	20	28	17	16.2	10	26



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

QXB9JT	PowerPlex® Y23								
		14	16,18	13	29	24	10	13	12
4	14	11	10	20		17	16.2		26
		12	12	19	18		21	9	10
QZJD4A	Yfiler™ Plus (PDF Format)								
	38,40	14	16,18	13	29	24	10	13	12
4	14	11	10	20	28	17	16.2	10	26
	41	12		19	18	20	21		10
UTPM3H	PowerPlex® Y23 (PDF Format)								
		14	16,18	13	29	24	10	13	12
4	14	11	10	20		17	16.2		26
		12	12	19	18		21	9	10
VFWKXV	PowerPlex® Y23 (PDF Format)								
		14	16,18	13	29	24	10	13	12
4	14	11	10	20		17	16.2		26
		12	12	19	18		21	9	10
VT4B2N	Yfiler™ Plus								
	38,40	14	16,18	13	29	24	10	13	12
4	14	11	10	20	28	17	16.2	10	26
	41	12		19	18	20	21		10
XNMMGH	PowerPlex® Y23								
		14	16,18	13	29	24	10	13	12
4	14	11	10	20		17	16.2		26
		12	12	19	18		21	9	10
YU8XCX	Yfiler™ Plus (PDF Format)								
	38,40	14	16,18	13	29	24	10	13	12
4	14	11	10	20	28	17	16.2	10	26
	41	12		19	18	20	21		10
ZMRA7V	PowerPlex® Y23 (PDF Format), (HID Format)								
	-	14	16,18	13	29	24	10	13	12
4	14	11	10	20	-	17	16.2	-	26
	-	12	12	19	18	-	21	9	10
	-	14	16,18	13	29	24	10	13	12
4major	14	11	10	20	-	17	16.2	-	26
	-	12	12	19	18	-	21	9	10

# 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
23T6MY	2	Included	Included	2	Excluded	Included
2MEWLV	2	Included	Included	2	Excluded	Included
2P447R	2	Included	Included	2	Excluded	Included
49V6PU	2	Included	Included	2	Excluded	Included
6AECR9	2	Included	Included	2	Excluded	Included
8MJ6FQ	2 individuals	Included	Included	2 individuals	Excluded	Included
9JCBT6	2	Included	Included	2	Excluded	Included
A7K3RH	2	Included	Included	2	Excluded	Included
B93GVH	2	Included	Included	2	Excluded	Included
BHQG6Z	2	Included	Included		Excluded	Included
E36763	2	Included	Included	2	Excluded	Included
E8XAX8	2	Included	Included	2	Excluded	Included
ER9ZB6	2	Included	Included	2	Excluded	Included
GGGKZX	2	Included	Included	2	Excluded	Included
JXEMQZ	At least 2 contributors; including at least one male.	Included	Included	At least 2 contributors; including at least one male.	Excluded	Included
K79RJ2	2	Included	Included	2	Excluded	Included
L4FHNQ	2	Included	Included	2	Excluded	Included
LBVYJL	2	Included	Included	2	Excluded	Included
LEEDMM	2	Included	Included	2	Excluded	Included
LXQZ9U	2	Included	Included	2	Excluded	Included

TABLE 5

WebCode	Item 3 Conclusion			Item 4 Conclusion		
	# of Contributors	Item 1	Item 2	# of Contributors	Item 1	Item 2
MEQ83M	2	Included	Included	2	Excluded	Included
MMKDVN	2	Included	Included	2	Excluded	Included
NLNF38	2	Included	Included	2	Excluded	Included
PDDBR3	2	Included	Included	2	Excluded	Included
PEH8UH	2	Included	Included	2	Excluded	Included
PVQXDA	2	Included	Included	2	Excluded	Included
QUEEU6	2	Included	Included	2	Excluded	Included
QXB9JT	2	Included	Included	2	Excluded	Included
QZJD4A	2	Included	Included	2	Excluded	Included
UTPM3H	2	Included	Included	2	Excluded	Included
VFWKXV		Included	Included		Excluded	Included
VT4B2N	Two (2) contributors	Included	Included	Two (2) contributors	Excluded	Included
WUCZNX	2	Included	Included	2	Excluded	Included
XNMMGH	2	Included	Included	2	Excluded	Included
YU8XCX	2	Included	Included	2	Excluded	Included
ZMRA7V	2	Included	Included	2	Excluded	Included

Conclusions Response Summary			Participants reporting conclusions: 36			
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	36	36	0	36	
	Excluded	0	0	36	0	
	Inconclusive	0	0	0	0	
No Response	0	0	0	0		
	Total	36	36	36	36	

## Statistical Analysis for Item 3

TABLE 6

WebCode	Item 3 Methods & Results
23T6MY	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> The mixed DNA profile is 18 duodecillion (18 x 10e39), 590 duodecillion (590 x 10e39) and 65 undecillion (65 x 10e36) TIMES more likely; IF they originated from "Item 1" (Female Victim) and "Item 2" (Male Suspect) RATHER THAN; IF they originated from two unknown unrelated individuals as calculated based on the [Location Identifying Databases] respectively.</p> <p><b>Database(s):</b> [Location Identifying Databases]</p>
2MEWLV	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> The mixed DNA profile are 18 duodecillion (18 x 10e39), 590 duodecillion (590 x 10e39) and 65 undecillion (65 x 10e36) TIMES more likely; IF they originated from the Female victim (Item 1) and Male suspect (Item 2) RATHER THAN; IF they originated from two unknown unrelated individuals as calculated based on the [Location Identifying Databases] respectively.</p> <p><b>Database(s):</b> [Location Identifying Databases]</p>
49V6PU	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> Reviewing this case, I would expect the analyst to deconvolute this mixture with NOC 2 in STRmix. Then an LRprev would be completed with the following hypotheses, all of which would be reported: (V+U/2U), (POI+U/2U), and (V+POI/2U).</p> <p><b>Database(s):</b> STRmix database</p>
6AECR9	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> LR associated with suspect (Caucasian population) = 9.16e17, LR associated with victim (Hispanic population) = 1.88e17</p> <p><b>Database(s):</b> [Participant did not report database(s).]</p>
8MJ6FQ	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> A mixed DNA profile of two individuals was developed from the DNA profile from the handle of the gun "Item 3". The DNA profile obtained from the reference samples "Item 1" and "Item 2" are consistent with being the contributors to this mixed DNA profile. The mixed DNA profile is 18 duodecillion (18 x 10e39), 590 duodecillion (590 x 10e39) and 65 undecillion (65 x 10e36) times more likely; if they originated from "Item 1" and "Item 2" rather than; if they originated from two unknown unrelated individuals as calculated based on the [Location Identifying Databases] respectively.</p> <p><b>Database(s):</b> [Location Identifying Databases]</p>
9JCBT6	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> Hp-Suspect &amp; Victim vs Hd -Suspect and Unknown = 1.21E29. Hp-Supect &amp; unknown vs Hd - 2 unknowns = 5.95E17. Hp-Victim &amp; unknown vs Hd - 2 unknowns = 1.75E17</p> <p><b>Database(s):</b> Caucasian Expanded 2015 STR Allele Frequency Table, Southeastern Hispanic Expanded 2015 STR Allele Frequency Table</p>
BHQG6Z	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> [Participant did not report statistical analysis.]</p> <p><b>Database(s):</b> NIST-Hispanic, NIST-Caucasian</p>

TABLE 6

WebCode	Item 3 Methods & Results
E36763	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> The genetic profile obtained from Item 3 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 8.34 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 3 is interpreted as a mixture of DNA from two contributors. Item 1 (victim) cannot be excluded as a possible contributor to this mixture. Given this genetic profile, assuming two contributors, it is 31.8 quadrillion times more likely to observe this genetic profile if Item 1 (victim) and one unknown individual are contributors than if 2 unknown individuals are the contributors.</p> <p><b>Database(s):</b> NIST</p>
E8XAX8	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> The DNA result obtained from the handle of the gun (Item 3) is consistent with a mixture from at least two (2) contributors. The mixture is approximately 4.0109E29 times more likely to occur (very strong support for inclusion) if the suspect (Item 2) and the victim (Item 1) are contributors, rather than if the suspect (Item 2) and one (1) unknown, unrelated individual are contributors.</p> <p><b>Database(s):</b> [Participant did not report database(s).]</p>
ER9ZB6	<p><b>Method(s):</b> Likelihood Ratio, YHRD Frequency</p> <p><b>Stats Analysis:</b> The mixed DNA profile obtained from item 3 is 1 billion times more likely if it is a result of contributions from Victim (Item 1) and an unknown person than if it is a result of contributions from two unknown individuals. The mixed DNA profile obtained from item 3 is 1 billion times more likely if it is a result of contributions from Suspect (Item 2) and an unknown person than if it is a result of contributions from two unknown individuals. The mixed DNA profile obtained from item 3 is 1 billion times more likely if it is a result of contributions from Victim (Item 1) and Suspect (Item 2) than if it is a result of contributions from two unknown individuals. The Y-STR DNA profile obtained from item 3 matches the Y-STR profile obtained from Suspect (Item 2) and his paternal relatives. The Y-STR profile obtained from this item is expected to occur approximately 1 match in 289,406 Haplotypes of randomly selected, unrelated males.</p> <p><b>Database(s):</b> NIST 1036 U.S. Population Dataset - 29 autosomal STRs (2013, 2017) (CE-based typing) Genotypes and allele frequencies for 29 autosomal STR loci typed on 1036 samples (AfrAm = 342, Cauc = 361, Hisp = 236, Asian = 97) were originally reported in 2013 in Hill, C. R., et al. YHRD Release 69</p>
GGKZX	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> The mixture is approximately <math>1.99 \times 10^{17}</math> times more likely to occur (very strong support for inclusion) if the female victim and an unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. The mixture is approximately <math>7.30 \times 10^{17}</math> times more likely to occur (very strong support for inclusion) if the male suspect and an unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors.</p> <p><b>Database(s):</b> FBI Extended SE Hispanic, FBI Extended Caucasian</p>

TABLE 6

WebCode	Item 3 Methods & Results
JXEMQZ	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> ITEM 1 compared to ITEM 3_Statistical Weight (Autosomal): Under the assumption that the VICTIM (Item 1) and one unrelated person selected at random from the general population are contributors to the mixture developed from the HANDLE OF THE GUN (Item 3), the likelihood of observing the mixed source profile is <math>\geq 1,000,000</math> 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. ITEM 2 compared to ITEM 3_Statistical Weight (Autosomal): Under the assumption that the SUSPECT (Item 2) and one unrelated person selected at random from the general population are contributors to the mixture developed from the HANDLE OF THE GUN (Item 3), the likelihood of observing the mixed source profile is <math>\geq 1,000,000</math> 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. ITEM 2 compared to ITEM 3_Statistical Weight (YSTR): Neither the suspect (Item 2) nor any of his paternally related male relatives nor an unknown number of males in the general population can be excluded as a possible contributor of the male YSTR profile developed from the HANDLE OF THE GUN (Item 3). Given a theta-value of <math>6.0E-05</math> and a 95% UCI of the combined Haplotype frequency of 1 in 8,568 (no matches in 25,666 Haplotypes at [Country] subpopulations without Native American), the corrected Match Probability is 1 in 5,659.</p> <p><b>Database(s):</b> Revised-NIST-1036-Allele Frequencies, ABI ID Database + Promega PP Fusion. YHRD haplotype frequency database for [Country] subpopulations</p>
K79RJ2	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> LR for Item 1 = <math>2.28E17</math>, LR for Item 2 = <math>6.82E17</math>.</p> <p><b>Database(s):</b> STRMix</p>
L4FHNQ	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> The mixture is approximately <math>1.79 \times 10^{18}</math> times more likely to occur (very strong support for inclusion) if the victim and an unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. The mixture is approximately <math>7.62 \times 10^{18}</math> times more likely to occur (very strong support for inclusion) if the suspect and an unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors.</p> <p><b>Database(s):</b> [Participant did not report database(s).]</p>
LBVYJL	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> LR=<math>1,48E38</math> dropout 0,12</p> <p><b>Database(s):</b> Hill C.R., Duewer D.L., Kline M.C., Coble M.D., Butler J.M., (2013) U.S. population data for 29 autosomal STR loci. Forensic Science Int. Genet. 7: e 82-83, Rev. 2017</p>
LEEDMM	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> LR=<math>1.30 \times 10^{42}</math>(Item1&amp;2 Under HP). LR=<math>4.99 \times 10^{27}</math>(Item1&amp;2 Under HP with Item2 Under HD).</p> <p><b>Database(s):</b> [Location Identifying Population]</p>
LXQZ9U	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> LR = SUSPECT + VICTIM / 2 unknown. LR = <math>1,88354 E40</math>; drop out for SUSPECT = 0.00; drop out for VICTIM = 0.00; drop out for unknown = 0.01.</p> <p><b>Database(s):</b> Global Filer PCR Amplification Kit user guide. Caucastion population base.</p>
MEQ83M	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> LR=<math>1.4677E14</math> through LRmix Studio by Hinda Haned and Jereon de Jong</p> <p><b>Database(s):</b> [Location Identifying Database]</p>

## TABLE 6

WebCode	Item 3 Methods & Results
MMKDVN	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> The autosomal results have not been statistically analysed as, whilst [Laboratory] is accredited to use GlobalFiler, we are not accredited, as yet, to perform statistical evaluations on such results. The Y-STR result has been statistically analysed, however, and, in order to do so I have assumed that the suspect, being Caucasian, is of Western European descent, and I have considered the following propositions: 1. The source of the male DNA is the suspect (or a close paternal-line male relative of his); or 2. The source of the male DNA is not the suspect (or a close paternal-line male relative of his) and this DNA has originated from another male from the Western European population who is unrelated to the suspect. In my opinion, the findings are approximately twenty-eight thousand (28,000) times more likely if the former was true, rather than the latter i.e. if the male DNA had indeed originated from the suspect (or a close paternal-line male relative of his) rather than if it had not. In my opinion, these findings provide very strong support for the proposition that the male DNA detected originated from the suspect (or a close paternal-line male relative of his) rather than the proposition that it had not.</p> <p><b>Database(s):</b> To statistically evaluate this Y-STR result I used a global database of Y-STR profiles (YHRD). The search of the global database was carried out on 26th May 2023 using YHRD Release R69.</p>
NLNF38	<p><b>Method(s):</b> Combined Probability of Exclusion/Inclusion</p> <p><b>Stats Analysis:</b> Item 3 (Handle of the gun) presents a genetic profile of more than one person. Assuming the genetic profile detected on Item 3(Handle of the gun) came from Female Victim, Item 1 and Male suspect, Item 2 we concluded that: The 99.99% of the Caucasian, African-American and Hispanic population are excluded of being the contributors of the genetic profile detected on Item 3. Female victim, Item 1 and Male suspect, Item 2 can not be excluded of being the contributors of the genetic profile detected on Item 3.</p> <p><b>Database(s):</b> The database used for the statistical analysis for item 3 was the NIST's U.S. STR Population Database for Caucasian (Cau), African American (Blk), Hispanic (Hsp), Asian (Asn) and Combined Population Groups (August 2017).</p>
PEH8UH	<p><b>Method(s):</b> [Participant did not report a method.]</p> <p><b>Stats Analysis:</b> Working from the pdf of the electropherogram, it is not possible to perform a thorough evaluation of each locus. As a result it is possible to miss very minor contributions from additional contributors and be incorrect in the possible number of contributors to complex mixture samples. It is also not possible to thoroughly evaluate spikes, pullup, and baseline irregularities which can affect correct allele determinations. I am a forensic consultant that reviews DNA case files submitted to me as evidence. I review the analyst allele calls and evidence to reference sample comparisons so I can understand how the original analyst arrived at their opinions and conclusions. I accept that their population calculations are correct. N/A: Not Applicable. NSD: No Side Data.</p> <p><b>Database(s):</b> [Participant did not report database(s).]</p>
PVQXDA	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> LR=4.3E+16-The DNA findings provide extremely strong evidence to support the hypothesis that the victim and one unrelated unknown person were the contributors compared to the alternative hypothesis that two unrelated unknown persons were the contributors. LR=1.2E+16-The DNA findings provide extremely strong evidence to support the hypothesis that the suspect and one unrelated unknown person were the contributors compared to the alternative hypothesis that two unrelated unknown persons were the contributors.</p> <p><b>Database(s):</b> Item 1 (victim) : NIST U.S. Population Dataset (Hispanic). Item 2 (Suspect) : NIST U.S. Population Dataset (Caucasian).</p>
QXB9JT	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> Item 1 LR= 1.3315x10<sup>11</sup>, Item 2 LR= 2.1000x10<sup>18</sup></p> <p><b>Database(s):</b> Item 1- Hispanic population. Item 2- Caucasian population.</p>

TABLE 6

WebCode	Item 3 Methods & Results
QZJD4A	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> A mixed DNA profile of two (2) contributors was developed from "Item 3". The DNA profile obtained from "Item 1" (victim) and "Item 2" (suspect) are consistent with being the contributors to this mixed DNA profile. The mixed DNA profile are 18 duodecillion (<math>18 \times 10^{e39}</math>), 590 duodecillion (<math>590 \times 10^{e39}</math>) and 65 undecillion (<math>65 \times 10^{e36}</math>) TIMES more likely IF they originated from "Item 1" and "Item 2" RATHER THAN; IF they originated from two unknown unrelated individuals as calculated based on the [Location Identifying Databases] respectively.</p> <p><b>Database(s):</b> [Location Identifying Databases]</p>
UTPM3H	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> The DNA result obtained from the handle of the gun (Item 3) is consistent with a mixture from at least two (2) contributors, including at least one (1) male: a) The mixture is approximately <math>1.20 \times 10^{18}</math> times more likely to occur (very strong support for inclusion) if the female victim and an unknown, unrelated individual, are contributors, rather than if two (2) unknown, unrelated individuals are contributors. b) The mixture is approximately <math>1.00 \times 10^{18}</math> times more likely to occur (very strong support for inclusion) if the male suspect and an unknown, unrelated individual, are contributors, rather than if two (2) unknown, unrelated individuals are contributors.</p> <p><b>Database(s):</b> FBI Caucasian and FBI SW Hispanic</p>
VT4B2N	<p><b>Method(s):</b> Combined Probability of Exclusion/Inclusion</p> <p><b>Stats Analysis:</b> [Participant did not report statistical analysis.]</p> <p><b>Database(s):</b> [Participant did not report database(s).]</p>
WUCZNX	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> The DNA profile obtained from Item 3 is a mixture consistent with the combined DNA profiles from the Female Victim (001-AA) and the Male Suspect (001-AB). This mixed DNA profile is approximately 12.9 trillion (<math>1.29 \times 10^{13}</math>) times more likely to be observed if the Female Victim (001-AA) and the Male Suspect (001-AB) are the contributors than if the Female Victim (001-AA) and a random, unrelated African-American are the contributors; approximately 64.3 trillion (<math>6.43 \times 10^{13}</math>) times more likely than if the Female Victim (001-AA) and a random, unrelated Caucasian are the contributors; and approximately 182 trillion (<math>1.82 \times 10^{14}</math>) times more likely than if the Female Victim (001-AA) and a random, unrelated Southwestern Hispanic are the contributors. This mixed DNA profile is approximately 744 trillion (<math>7.44 \times 10^{14}</math>) times more likely to be observed if the Female Victim (001-AA) and the Male Suspect (001-AB) are the contributors than if the Male Suspect (001-AB) and a random, unrelated African-American are the contributors; approximately 571 trillion (<math>5.71 \times 10^{14}</math>) time more likely than if the Male Suspect (001-AB) and a random, unrelated Caucasian are the contributors; and approximately 778 trillion (<math>7.78 \times 10^{14}</math>) times more likely than if the Male Suspect (001-AB) and a random, unrelated Southwestern Hispanic are the contributors.</p> <p><b>Database(s):</b> Popstats</p>
XNMMGH	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> LR calculated for the victim is 1050800000000000000. LR calculated for the suspect is 5695500000000000000.</p> <p><b>Database(s):</b> FBI_EXTENDED_SW_HISPANIC population was used for the victim. FBI_EXTENDED_CAUCASIAN population was used for the suspect.</p>



TABLE 6

WebCode	Item 3 Methods & Results
YU8XCX	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> H1 :the mixture is made up of the victim's genetic profile (item 1) and the suspect's genetic profile (item 2). H2:the mixture is made up of the genetic profiles of two unknown unrelated people. LR= 4.10E37 (drop-out = 0.1, drop-in = 0.05, Theta = 0.01). H1:the mixture is made up of the victim's genetic profile (item 1) and the genetic profile of an unknown unrelated person. H2:the mixture is made up of the genetic profiles of two unknown unrelated people. LR=8.51E15 (drop-out = 0.1, drop-in = 0.05, Theta = 0.01). H1:the mixture is made up of the suspect's genetic profile (item 2) and the genetic profile of an unknown unrelated person. H2:the mixture is made up of the genetic profiles of two unknown unrelated people. LR=5.26E14 (drop-out = 0.1, drop-in = 0.05, Theta = 0.01)</p> <p><b>Database(s):</b> Personal Databases</p>
ZMRA7V	<p><b>Method(s):</b> Random Match Probability</p> <p><b>Stats Analysis:</b> A mixed DNA profile (PowerPlex™ Fusion 5C) consisting of DNA from at least two contributors was obtained from the handle of the gun (item CTS-23-5881-3). The DNA profile from CTS-23-5881-3 is consistent with the DNA profile of CTS-23-5881-1. CTS-23-5881-1 can not be excluded as the contributor of CTS-23-5881-3 (major) at the above mentioned loci. The probability of selecting a random unrelated individual having a DNA profile identical to CTS-23-5881-1 at the loci observed is 1 in 1.03x10<sup>34</sup> for African Americans, 1 in 1.51x10<sup>32</sup> for Caucasian Americans, 1 in 1.21x10<sup>33</sup> for Hispanic Americans, and 1 in 2.21x10<sup>34</sup> for Asian Americans. The DNA profile from CTS-23-5881-3 is consistent with the DNA profile of CTS-23-5881-2. CTS-23-5881-2 can not be excluded as the contributor of CTS-23-5881-3 (major) at the above mentioned loci. The probability of selecting a random unrelated individual having a DNA profile identical to CTS-23-5881-2 at the loci observed is 1 in 2.59x10<sup>34</sup> for African Americans, 1 in 1.66x10<sup>32</sup> for Caucasian Americans, 1 in 4.93x10<sup>32</sup> for Hispanic Americans, and 1 in 3.53x10<sup>29</sup> for Asian Americans. A single source DNA profile (PowerPlex Y23) was obtained from the lobby floor. The individual represented by the reference sample, item CTS-23-5881-2 (suspect), cannot be excluded as a contributor of the DNA profile obtained from the lobby floor (item CTS-23-5881-4). 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><b>Database(s):</b> Promega, YHRD</p>

# Statistical Analysis for Item 4

## TABLE 7

WebCode	Item 4 Methods & Results
23T6MY	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> The mixed DNA profile is 22 quadrillion (22 x 10e15), 100 quadrillion (100 x 10e15) and 900 trillion (900 x 10e12) TIMES more likely; IF they originated from "Item 2" (Male Suspect) and one unknown individual RATHER THAN; IF they originated from two unknown unrelated individuals as calculated based on the [Location Identifying Databases] respectively.</p> <p><b>Database(s):</b> [Location Identifying Databases]</p>
2MEWLV	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> The mixed DNA profile are 22 quadrillion (22 x 10e15), 100 quadrillion (100 x 10e15) and 900 trillion (900 x 10e12) TIMES more likely; IF they originated from the Male suspect (Item 2) and one unknown unrelated individual RATHER THAN; IF they originated from two unknown unrelated individuals as calculated based on the [Location Identifying Databases] respectively.</p> <p><b>Database(s):</b> [Location Identifying Databases]</p>
49V6PU	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> Upon reviewing this case, I would expect the analyst to do a deconvolution NOC 2 in STRmix and then LRprev using the references. (V+U/2U) = which would be an exclusion, (POI+U/2U) which could potentially generate a major contributor profile to be entered into CODIS. I would not expect the analyst to attempt to determine the minor contributor because based on the scenario that would be an alternate victim that attempted to subdue him.</p> <p><b>Database(s):</b> STRmix database</p>
6AECR9	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> Suspect LR (Caucasian population)= 3.14e29, Victim LR (Hispanic Population) = 0</p> <p><b>Database(s):</b> [Participant did not report database(s).]</p>
8MJ6FQ	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> A mixed DNA profile of two individuals was developed from the DNA profile from the lobby floor "Item 4". The DNA profile obtained from the reference sample "Item 2" is being one of the contributor to this mixed DNA profile. However, reference sample "Item 1" is excluded from being one of the contributor to this mixed DNA profile. The mixed DNA profile is 22 quadrillion (22 x 10e15), 100 quadrillion (100 x 10e15) and 900 trillion (900 x 10e12) times more likely; if they originated from "Item 2" and "Unknown" rather than; if they originated from two unknown unrelated individuals as calculated based on the [Location Identifying Databases] respectively.</p> <p><b>Database(s):</b> [Location Identifying Databases]</p>
9JCBT6	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> Hp - Suspect &amp; 1 unknown vs Hd- 2 unknowns = 3.13E29. Hp - Victim &amp; 1 unknown vs Hd - 2 unknowns = 0.</p> <p><b>Database(s):</b> Caucasian Expanded 2015 STR Allele Frequency Table, Southeastern Hispanic Expanded 2015 STR Allele Frequency Table</p>
BHQG6Z	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> [Participant did not report statistical analysis.]</p> <p><b>Database(s):</b> NIST-Hispanic, NIST-Caucasian</p>
E36763	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> 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 51.7 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.</p> <p><b>Database(s):</b> NIST</p>

## TABLE 7

WebCode	Item 4 Methods & Results
E8XAX8	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> The DNA result obtained from the lobby floor (Item 4) is consistent with a mixture from at least two (2) contributors. The mixture is approximately 3.1231E29 times more likely to occur (very strong support for inclusion) if the suspect (Item 2) and an unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. The DNA result obtained from the lobby floor (Item 4) is consistent with a mixture from at least two (2) contributors. The victim (Item 1) has been excluded as being a contributor to this mixture.</p> <p><b>Database(s):</b> [Participant did not report database(s).]</p>
ER9ZB6	<p><b>Method(s):</b> Likelihood Ratio, YHRD Frequency</p> <p><b>Stats Analysis:</b> The mixed DNA profile obtained from item 4 is 1 billion times more likely if it is a result of contributions from Suspect (Item 2) and an unknown person than if it is a result of contributions from two unknown individuals. Victim (Item 1) is excluded as a contributor to the mixed DNA profile obtained from item 4. The DNA profile obtained from item 3 is 1 billion times more likely if it is a result of contributions from Victim (Item 1) and Suspect (Item 2) than if it is a result of contributions from two unknown individuals. The Y-STR DNA profile obtained from item 4 matches the Y-STR profile obtained from Suspect (Item 2) and his paternal relatives. The Y-STR profile obtained from this item is expected to occur approximately 1 match in 289,406 Haplotypes of randomly selected, unrelated males.</p> <p><b>Database(s):</b> NIST 1036 U.S. Population Dataset - 29 autosomal STRs (2013, 2017) (CE-based typing) Genotypes and allele frequencies for 29 autosomal STR loci typed on 1036 samples (AfrAm = 342, Cauc = 361, Hisp = 236, Asian = 97) were originally reported in 2013 in Hill, C. R., et al. YHRD Release 69</p>
GGGKZX	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> The female victim has been excluded as a contributor to this mixture. The mixture is approximately <math>2.79 \times 10^{29}</math> times more likely to occur (very strong support for inclusion) if the male suspect and an unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors.</p> <p><b>Database(s):</b> FBI Extended SE Hispanic, FBI Extended Caucasian</p>
JXEMQZ	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> ITEM 1 compared to ITEM 4_Statistical Weight (Autosomal): Under the assumption two unrelated persons selected at random from the general population are contributors to the mixture developed from the LOBBY FLOOR (Item 4), the likelihood of observing the mixed source profile is <math>\geq 1,000,000</math> times greater (actual LR available upon request) than if it is assumed that the VICTIM (Item 1) and one unrelated person selected at random from the general population are contributors to this mixed-source sample. ITEM 2 compared to ITEM 4_Statistical Weight (Autosomal): Under the assumption that the SUSPECT (Item 2) and one unrelated person selected at random from the general population are contributors to the mixture developed from the LOBBY FLOOR (Item 4), the likelihood of observing the mixed source profile is <math>\geq 1,000,000</math> 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. ITEM 2 compared to ITEM 4_Statistical Weight (YSTR): Neither the suspect (Item 2) nor any of his paternally related male relatives nor an unknown number of males in the general population can be excluded as a possible contributor of the male YSTR profile developed from the HANDLE OF LOBBY FLOOR (Item 4). Given a theta-value of 6.0E-05 and a 95% UCI of the combined Haplotype frequency of 1 in 8,568 (no matches in 25,666 Haplotypes at [Country] subpopulations without Native American), the corrected Match Probability is 1 in 5,659.</p> <p><b>Database(s):</b> Revised-NIST-1036-Allele Frequencies, ABI ID Database + Promega PP Fusion; YHRD haplotype frequency database for [Country] subpopulations</p>
K79RJ2	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> LR for Item 1 = 0, LR for Item 2 = 4.90E29.</p> <p><b>Database(s):</b> STRMix</p>

## TABLE 7

WebCode	Item 4 Methods & Results
L4FHNQ	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> The victim has been excluded as being a contributor to this mixture. LR = 0 The mixture is approximately <math>2.89 \times 10^{29}</math> times more likely to occur (very strong support for inclusion) if the suspect and an unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors.</p> <p><b>Database(s):</b> [Participant did not report database(s).]</p>
LBVYJL	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> LR=3,34E15 dropout 0,16</p> <p><b>Database(s):</b> Hill C.R., Duewer D.L., Kline M.C., Coble M.D., Butler J.M., (2013) U.S. population data for 29 autosomal STR loci. Forensic Science Int. Genet. 7: e 82-83, Rev. 2017</p>
LEEDMM	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> LR=3.26<math>\times 10^{25}</math>(Item2 Under HP)</p> <p><b>Database(s):</b> [Location Identifying Population]</p>
LXQZ9U	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> LR = SUSPECT + unknown / 2 unknown. LR = 1,09323 E17; drop out for SUSPECT = 0.00; drop out for unknown = 0.01.</p> <p><b>Database(s):</b> Global Filer PCR Amplification Kit user guide. Caucastion population base.</p>
MEQ83M	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> LR=9.5730E14 through LRmix Studio by Hinda Haned and Jereon de Jong</p> <p><b>Database(s):</b> [Location Identifying Database]</p>
MMKDVN	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> The autosomal results have not been statistically analysed as, whilst [Laboratory] is accredited to use GlobalFiler, we are not accredited, as yet, to perform statistical evaluations on such results. The Y-STR result has been statistically analysed, however, and, in order to do so I have assumed that the suspect, being Caucasian, is of Western European descent, and I have considered the following propositions: 1. The source of the male DNA is the suspect (or a close paternal-line male relative of his); or 2. The source of the male DNA is not the suspect (or a close paternal-line male relative of his) and this DNA has originated from another male from the Western European population who is unrelated to the suspect. In my opinion, the findings are approximately twenty-eight thousand (28,000) times more likely if the former was true, rather than the latter i.e. if the male DNA had indeed originated from the suspect (or a close paternal-line male relative of his) rather than if it had not. In my opinion, these findings provide very strong support for the proposition that the male DNA detected originated from the suspect (or a close paternal-line male relative of his) rather than the proposition that it had not.</p> <p><b>Database(s):</b> To statistically evaluate this Y-STR result I used a global database of Y-STR profiles (YHRD). The search of the global database was carried out on 26th May 2023 using YHRD Release R69.</p>

## TABLE 7

WebCode	Item 4 Methods & Results
NLNF38	<p><b>Method(s):</b> Random Match Probability</p> <p><b>Stats Analysis:</b> Item 4 (lobby floor), presents a genetic profile from more than one person. Assuming that the genetic profile on Item 4 (lobby floor) comes from at least two contributors and that Male suspect, Item 2 is one of the contributors we conclude that: Male suspect, Item 2 is the major contributor to the genetic profile on Item 4. The genetic profile of the major contributor is: 172 Septillions times more likely using the Caucasian Population database 182 Septillions times more likely using the African-American Population database 266 Septillions times more likely using the Hispanic Population database to have come from Male suspect, Item 2 than from any other unrelated person chosen randomly, using the following genetic Markers THO1, vWA, D21S11, TPOX, D1S1656, D12S391, SE33, D10S1248, D22S1045, D19S433, D8S1179, D2S1338, D2S441, D18S51, FGA, D16S539 and D5S818. Male suspect can not be excluded from being the major contributor of the genetic profile detected on Item 4. No inclusion statement can be done for the minor's contributor's genetic profile on Item 4, due to that there is no reference available for comparison. Female Victim Item 1 is excluded from being the minor contributors of the genetic profile detected on Item 4.</p> <p><b>Database(s):</b> The database used for the statistical analysis for item 3 was the NIST's U.S. STR Population Database for Caucasian (Cau), African American (Blk), Hispanic (Hsp), Asian (Asn) and Combined Population Groups (August 2017).</p>
PEH8UH	<p><b>Method(s):</b> [Participant did not report a method.]</p> <p><b>Stats Analysis:</b> Working from the pdf of the electropherogram, it is not possible to perform a thorough evaluation of each locus. As a result it is possible to miss very minor contributions from additional contributors and be incorrect in the possible number of contributors to complex mixture samples. It is also not possible to thoroughly evaluate spikes, pullup, and baseline irregularities which can affect correct allele determinations. I am a forensic consultant that reviews DNA case files submitted to me as evidence. I review the analyst allele calls and evidence to reference sample comparisons so I can understand how the original analyst arrived at their opinions and conclusions. I accept that their population calculations are correct. N/A: Not Applicable. NSD: No Side Data.</p> <p><b>Database(s):</b> [Participant did not report database(s).]</p>
QXB9JT	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> Item 1 LR= 0, Item 2 LR= 3.044x10<sup>29</sup></p> <p><b>Database(s):</b> Item 1- Hispanic population. Item 2- Caucasian population.</p>
QZJD4A	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> A mixed DNA profile of two (2) contributors was developed from "Item 4". The DNA profile obtained from "Item 2" is consistent with being one of the contributor to this mixed DNA profile. The DNA profile obtained from "Item 1" is excluded from being the other contributor to the mixed DNA profile. The mixed DNA profile are 22 quadrillion (22 x 10<sup>15</sup>), 100 quadrillion (100 x 10<sup>15</sup>) and 900 trillion (900 x 10<sup>12</sup>) TIMES more likely IF they originated from "Item 2" and one unknown individual RATHER THAN; IF they originated from two unknown unrelated individuals as calculated based on the [Location Identifying Databases] respectively.</p> <p><b>Database(s):</b> [Location Identifying Databases]</p>
UTPM3H	<p><b>Method(s):</b> Likelihood Ratio</p> <p><b>Stats Analysis:</b> The DNA result obtained from the lobby floor (Item 4) is consistent with a mixture from at least two (2) contributors, including at least one (1) male: a) The mixture is approximately 2.55 x10<sup>29</sup> times more likely to occur (very strong support for inclusion) if the male suspect and an unknown, unrelated individual, are contributors, rather than if two (2) unknown, unrelated individuals are contributors. b) The female victim has been excluded as being a contributor to this mixture.</p> <p><b>Database(s):</b> FBI Caucasian and FBI SW Hispanic</p>
VT4B2N	<p><b>Method(s):</b> Combined Probability of Exclusion/Inclusion</p> <p><b>Stats Analysis:</b> [Participant did not report statistical analysis.]</p> <p><b>Database(s):</b> [Participant did not report database(s).]</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
23T6MY	1. GlobalFiler PCR Amplification Kit. 2. GlobalFiler Express PCR Amplification Kit. 3. AmpFLSTR Yfiler PCR Amplification Kit. 4. AmpFLSTR Minifiler PCR Amplification Kit.
2MEWLX	(1) Applied Biosystem GlobalFiler PCR Amplification Kit. (2) Applied Biosystem GlobalFiler Express PCR Amplification Kit. (3) Applied Biosystem AmpFLSTR Yfiler PCR Amplification Kit. (4) Applied Biosystem AmpFLSTR Minifiler PCR Amplification Kit.
8MJ6FQ	GlobalFiler PCR Amplification Kit. GlobalFiler Express PCR Amplification Kit. AmpFLSTR Y-filer PCR Amplification Kit. AmpFLSTR Minifiler PCR Amplification Kit.
9JCBT6	GlobalFiler and PowerPlex Y23
MMKDVN	NGM Select. GlobalFiler. PPY-23. ForenSeq DNA Signature Prep Kit (MPS)
UTPM3H	GlobalFiler, Fusion 6C and Powerplex Y23. In the future Y Filer Plus.
WUCZNX	Qiagen Investigator 24 plex. QS Qiagen Investigator 24 plex GO!.

## Additional Comments

TABLE 9

WebCode	Additional Comments
23T6MY	NM: Non-male. The statistical calculations were carried out using DNA View Software.
2MEWLX	The statistical evaluation were performed on the DNA.VIEW Statistical Software version 37.63.
8MJ6FQ	NM: Non-male. The statistical calculations were carried out using DNA View Software.
GGGKZX	For items 1 and 3 an off ladder peak was observed at the D1S1656 locus. The sizes of the peaks were reported as 189.31 bp and 189.21 bp respectively. By comparison to the allelic ladder, the peaks were estimated to be the 16.1 allele. This allele was also reported on strbase.nist.gov using the GlobalFiler Express kit on the ABI 3500 with a size of 189.29 bp.
LXQZ9U	DNA analysis for ITEM 3: LR = SUSPECT + VICTIM / 2 unknown LR = 1,88354E40 drop out for SUSPECT = 0.00 drop out for VICTIM = 0.00 drop out for unknown = 0.01 The probability of the evidence is 1,88354E40 times more likely if a gun swab came from SUSPECT and VICTIM, than if it came from two unknown, unrelated individuals. DNA analysis for ITEM 4: LR = SUSPECT + unknown / 2 unknown LR = 1,09323E17 drop out for SUSPECT = 0.00 drop out for unknown = 0.01 The probability of the evidence is 1,09323E17 times more likely if a floor swab came from SUSPECT and unknown, unrelated individuals, than if it came from two unknown, unrelated individuals. The Female Victim (ITEM 1) is excluded as a possible contributor to the DNA obtained from ITEM 4. [Participant submitted data in a format that could not be reproduced in this report. Data is presented as is.]
MEQ83M	Though we have our interpretation guidelines,we used the guidelines supplied by CTS.
MMKDVN	[Laboratory] does not employ a specific stochastic threshold for GlobalFiler, whilst being aware that for quantities of DNA below 0.125ng, there is an increased chance of allelic and/or locus drop-out. For PPY-23, the peak height ratio would only be appropriate for DYS385, as it is the only multiple copy marker contained within the multiplex. No peak height ratio has been determined in validation at [Laboratory] and the interpretation of whether a single peak at this locus should be treated as N,N or N,F is at the discretion of the reporting scientist based on their experience. No specific stochastic threshold is employed for PPY-23 at [Laboratory].
PDDBR3	( ) = minor allele(s)
QZJD4A	NM - Non-male profile. The statistical calculations were carried out using DNA View Software.
WUCZNX	**notations for item 3 indicate alleles less than STH - Locus not used for LR statistics. Minor component of item 4 is inconclusive due to insufficient DNA (per our procedure).

-End of Report-  
(Appendix may follow)



Collaborative Testing Services ~ Forensic Testing Program

**Test No. 23-5881: DNA Interpretation**

DATA MUST BE SUBMITTED BY **June 05, 2023, 11:59 p.m. EDT** TO BE INCLUDED IN THE REPORT

Participant Code: U1234A

WebCode: RUQV6N

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 an attempted bank robbery. The victim, a bank teller, reported to police that the suspect entered the lobby of the business and immediately began demanding money. The victim told the suspect to leave and threatened to call the police. The suspect then displayed a gun and fired at the ceiling. The suspect hit the victim in the face with the handle of the gun, causing the victim to heavily bleed. Several patrons attempted to subdue the suspect, and were injured during the incident. The suspect escaped the business without any money. Police were able to apprehend the suspect later that day based on imaging captured by security cameras. While processing the scene, police located a gun in a bush outside the business matching the description of the one used by the suspect. The handle of the gun was swabbed and confirmed as blood by the Serology unit and submitted for DNA analysis (Item 3). A reddish-brown stain from the lobby floor was also swabbed and confirmed as blood and submitted for DNA analysis (Item 4).

*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 INT1):**

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

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

Item 3: DNA profile from the handle of the gun

Item 4: DNA profile from the lobby floor

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

23-5881 Data For Participants.zip MD5 hash value: 47412f02fa4d66027ce0df1b48ff4739

23-5881 Data For Participants.zip SHA1 hash value: 4f65b9e717320b4a8579e0542a7ea021ff920a91

**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:

- |                                                                                 |                                                |
|---------------------------------------------------------------------------------|------------------------------------------------|
| <input type="checkbox"/> Combined Probability of Exclusion/Inclusions (CPE/CPI) | <input type="checkbox"/> Likelihood Ratio (LR) |
| <input type="checkbox"/> Random Match Probability (RMP)                         | Other: <input type="text"/>                    |

*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)