Collaborative Testing Services, Inc
FORENSIC TESTING PROGRAM

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DNA Interpretation Test No. 25-5882
Summary Report

Each participant received a digitally downloadable sample pack containing electropherograms and raw data files which they were asked to evaluate using their existing protocols. Data were returned from 51 participants and are compiled into the following tables:

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

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

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

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

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

Item	Known/ Questioned	Mixture Ratio	Sex	Donor Information
1	Known	--	Female	Victim
2	Known	--	Male	Suspect
3	Questioned	1:2	Female/Male	Victim/Additional Male
4	Questioned	2:1	Female/Male	Victim/Suspect

Amelogenin and STR Results

Results compiled by predistribution laboratories and a consensus of at least 10 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	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
	14,14	29,29	11,14	X,X	10,11	20,23
	12,13	7,11	17,20	7,9.3	8,11	14,17
	NM	NM	NM	NM		
2	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
	13,14	28,29	11,15	X,Y	10,11	21,26
	10,13	7,18	20,31.2	9.3,9.3	8,11	16,18
	12	17	18	2		
3	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
	14,14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	10,11,12,13	7,9,11,16	17,18,20,21	7,9.3	8,11	14,17
	10	20	18	2		
4	14,15,16	25,25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	10,12,13	7,11,18	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	17	18	2		

YSTR Results

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

Item	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4
2	35,37	14	11,14	13	29	23	12	13	13
	15	12	12	19	29	17	20	10	22
	40	12	13	17	18	20	23	10	11
3	34,38	13	17,18	13	30	24	10	11	13
	14	10	13	20	33	17	15	9	22
	40	12	12	20	18	21	22	12	12
4	35,37	14	11,14	13	29	23	12	13	13
	15	12	12	19	29	17	20	10	22
	40	12	13	17	18	20	23	10	11

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

Summary Comments

This test was designed to allow participants to assess their proficiency in evaluating and interpreting electropherograms (EPGs). Each participant received EPGs (in .pdf and .hid formats) of two reference samples and two questioned samples. The EPG data included were produced from the following amplification kits: GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C, YFiler™ Plus, PowerPlex® Y23. Item 1 was created using blood collected from a female donor. Item 2 was created using blood collected from a male donor. Item 3 was created by combining one part blood from the Item 1 female donor and two parts blood from an additional male donor whose known standard was not provided. Item 4 was created by combining two parts blood from the Item 1 female donor and one part blood from the Item 2 male donor. Refer to the Manufacturer's Information for preparation details.

Data were returned by 51 participants.

DNA Analysis
All participants that returned results evaluated the provided STR data.

For STR results, all participants reported consistent results with the exception of four participants.

For YSTR results, all but one participant reported consistent results.

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

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

DNA Interpretations
For Item 3, all but two participants identified that two (or at least two) individuals contributed to the mixture. Of the remaining participants, one identified one contributor and the other identified three contributors. All responding participants included the victim (Item 1) and excluded the suspect (Item 2) as possible contributors to the stain.

For Item 4, all but four participants identified that two (or at least two) individuals contributed to the mixture. Of the remaining participants, one identified one contributor, one identified "at least one" contributor, and two identified three contributors. All participants included both the victim (Item 1) and the suspect (Item 2) as possible contributors to the stain.

STR Interpretation Guidelines

TABLE 1

WebCode	Analytical Threshold (rfu)	Peak Height Ratio (%)	Stochastic Threshold (rfu)
36QZJU	70	70	345
3YHFVW	75	60	100
6WK94V	[Participant did not provide interpretation guidelines]		
6X26VV	130	60	800
7DQRET	200	60	1,000
7E6WDQ	75	60	100
7GQ3AR	175	70	175
7MGDKQ	56	30	100
7Y7CBT	130	60	800
8XBUAR	[Participant did not provide interpretation guidelines]		
9DMLDN	70	70	345
9DMP3T	150	60	400
9KJJZR	130	60	800
AGUWHN		60	600
APAF3M	120	60	360
AQ6Y4N	185	60	500
AYN7ZY	[Participant did not provide interpretation guidelines]		
C2G34J	160	60	630
CVNZZJ	100	60	150
CZ747P	150	60	700
D8YVRN	75	60	100
E4GTKJ	120	60	360
E8G4GJ	120	60	360
ELVARH	50	50	900
EPWDHJ	120	60	360
FBV2LK	130	60	800
FF3PYL	75	60	100
GC3ZVJ	130	60	800
GGVZAF	100	70	300
GU2VTG	75	60	250
H8KXNE	100	60	300
H9WUUJ	150	60	300
J8JM7G	130	60	800
JXR8GC	50	60	360
KC7REB	70	70	345
L3XGMC	50	60	840
M2GKUC	[Participant did not provide interpretation guidelines]		

TABLE 1

WebCode	Analytical Threshold (rfu)	Peak Height Ratio (%)	Stochastic Threshold (rfu)
M8P98D	130	60	800
N387Z9	93	60	900
PPGVQ9	75	55	325
PPQEAJ	175	60	500
PXB2KA	75	60	
TL8MC9	130	60	800
UR9LZ3	75	60	100
VQRN93	34	60	721
WFRDD2	60	50	1,200
WRJ6X6	75	60	100
XN22QZ	120	60	360
YMZNJX	70	70	345
YP4J3Z	130	60	800
YWQCDZ	75	60	100

YSTR Interpretation Guidelines

TABLE 2

WebCode	Analytical Threshold (rfu)	Peak Height Ratio (%)	Stochastic Threshold (rfu)
36QZJU			550
3YHFVW	75	50	75
6WK94V	[Participant did not provide interpretation guidelines]		
6X26VV	50	70	800
7DQRET	250	60	1,000
7E6WDQ	75	50	75
7GQ3AR	175	70	175
7MGDKQ	80	30	100
7Y7CBT	50	70	800
8XBUAR	[Participant did not provide interpretation guidelines]		
9DMLDN			550
9DMP3T	[Participant did not provide interpretation guidelines]		
9KJJZR	50	70	800
AGUWHN		60	600
APAF3M	75	50	75
AQ6Y4N	90	60	200
AYN7ZY	75	50	75
C2G34J	100	60	600
CVNZZJ	100	60	200
CZ747P	[Participant did not provide interpretation guidelines]		
D8YVRN	75	50	75
E4GTKJ	75	50	75
E8G4GJ	75	50	75
ELVARH	[Participant did not provide interpretation guidelines]		
EPWDHJ	75	50	75
FBV2LK	50	70	800
FF3PYL	75	50	75
GC3ZVJ	50	70	800
GGVZAF	[Participant did not provide interpretation guidelines]		
GU2VTG	[Participant did not provide interpretation guidelines]		
H8KXNE	90	40	320
H9WUUJ	150	60	300
J8JM7G	50	70	800
JXR8GC	50	60	180
KC7REB			550
L3XGMC	50	0	0
M2GKUC	[Participant did not provide interpretation guidelines]		

TABLE 2

WebCode	Analytical Threshold (rfu)	Peak Height Ratio (%)	Stochastic Threshold (rfu)
M8P98D	50	70	800
N387Z9	86	60	455
PPGVQ9	[Participant did not provide interpretation guidelines]		
PPQEAJ	[Participant did not provide interpretation guidelines]		
PXB2KA	75	50	
TL8MC9	50	70	800
UR9LZ3	75	50	75
VQRN93	49		
WFRDD2	60	50	800
WRJ6X6	75	50	75
XN22QZ	75	50	75
YMZNJX			550
YP4J3Z	50	60	800
YWQCDZ	75	50	75

STR & Amelogenin Results

TABLE 3

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

Item 1 - STR Results

36QZJU	PowerPlex® Fusion 6C (HID Format)						
	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
	12,13	7,11	17,20	7,9.3	8,11	14,17
	NR	NR	NR			
3YHFVW	GlobalFiler™ (PDF Format)						
	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
	N/A	N/A	17,20	7,9.3	8,11	14,17
	NSD	N/A	N/A	NSD		
6WK94V	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format)						
	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X	10,11	20,23
	12,13	7,11	17,20	7,9.3	8,11	14,17
6X26VV	GlobalFiler™ (STR Mix)						
	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17
7DQRET	GlobalFiler™ (HID Format)						
	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17
7E6WDQ	GlobalFiler™ (STRmix)						
	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17

TABLE 3

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

Item 1 - STR Results

7GQ3AR GlobalFiler™ (PDF Format)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17

7MGDKQ GlobalFiler™, PowerPlex® Fusion 6C (HID Format) (GeneMapper ID-X 1.6)

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X	10,11	20,23
	12,13	7,11	17,20	7,9.3	8,11	14,17

7Y7CBT GlobalFiler™ (HID Format)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17

8XBUAR (PDF Format)

	14,16	20,20	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17

9DMLDN PowerPlex® Fusion 6C (HID Format)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
	12,13	7,11	17,20	7,9.3	8,11	14,17
	NR	NR	NR			

9DMP3T GlobalFiler™ (PDF Format)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17
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TABLE 3

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

Item 1 - STR Results

9KJJZR GlobalFiler™ (HID Format) (STRMix)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17

AGUWHN GlobalFiler™ (PDF Format)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17

APAF3M GlobalFiler™ (PDF Format)

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17
	NM			NM		

AQ6Y4N GlobalFiler™ (HID Format) (GeneMapper ID-X 1.5)

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X	10,11	20,23
			17,20	7,9.3	8,11	14,17

C2G34J GlobalFiler™ (HID Format)

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X	10,11	20,23
			17,20	7,9.3	8,11	14,17

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

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X	10,11	20,23
	12,13	7,11	17,20	7,9.3	8,11	14,17

TABLE 3

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

Item 1 - STR Results

CZ747P GlobalFiler™ (PDF Format)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17

D8YVRN PowerPlex® Fusion 5C (PDF Format), (HID Format)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
	12,13	7,11		7,9.3	8,11	14,17
	-					

E4GTKJ GlobalFiler™ (HID Format)

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17
	NM			NM		

E8G4GJ GlobalFiler™ (HID Format)

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17
	NM			NM		

ELVARH GlobalFiler™ (HID Format) (STRmix)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17
	NR			NR		

EPWDHJ GlobalFiler™ (PDF Format)

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17
	NM			NM		

TABLE 3

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

Item 1 - STR Results

FBV2LK GlobalFiler™

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17

FF3PYL GlobalFiler™ (HID Format)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
	N/A	N/A	17,20	7,9.3	8,11	14,17
	NR	N/A	N/A	NR		

GC3ZVJ GlobalFiler™ (STRMix)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17

GGVZAF GlobalFiler™ (HID Format)

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X	10,11	20,23
			17,20	7,9.3	8,11	14,17

GU2VTG GlobalFiler™

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17

H8KXNE GlobalFiler™ (HID Format)

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X	10,11	20,23
			17,20	7,9.3	8,11	14,17

TABLE 3

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

Item 1 - STR Results

H9WUUJ PowerPlex® Fusion 6C

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X	10,11	20,23
	12,13	7,11	17,20	7,9.3	8,11	14,17

J8JM7G GlobalFiler™ (HID Format)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17

JXR8GC GlobalFiler™ (PDF Format)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17

KC7REB PowerPlex® Fusion 6C (HID Format)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
	12,13	7,11	17,20	7,9.3	8,11	14,17
	NR	NR	NR			

L3XGMC GlobalFiler™ (HID Format) (DNAxs, v. 2.8.11)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17

M2GKUC GlobalFiler™, PowerPlex® Fusion 6C (PDF Format), (HID Format)

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X	10,11	20,23
	12,13	7,11	17,20	7,9.3	8,11	14,17

TABLE 3

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

Item 1 - STR Results

M8P98D GlobalFiler™ (HID Format)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
	-	-	17,20	7,9.3	8,11	14,17
	-	-	-	-		

N387Z9 GlobalFiler™, PowerPlex® Fusion 6C (PDF Format)

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X	10,11	20,23
	12,13	7,11	17,20	7,9.3	8,11	14,17

PPGVQ9 GlobalFiler™ (PDF Format)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17

PPQEAJ Investigator® 24plex (HID Format) (STRmix)

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X	10,11	20,23
			17,20	7,9.3	8,11	14,17

PXB2KA PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (HID Format) (Lab Retriever)

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X	10,11	20,23
	12,13	7,11	17,20	7,9.3	8,11	14,17

TL8MC9 GlobalFiler™ (HID Format) (STRMIX v2.10)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
	-	-	17,20	7,9.3	8,11	14,17
	-	-	-	-		

TABLE 3

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

Item 1 - STR Results

UR9LZ3 GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format)

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X	10,11	20,23
	12,13	7,11	17,20	7,9.3	8,11	14,17

VQRN93 PowerPlex® Fusion 6C (HID Format)

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X	10,11	20,23
	12,13	7,11	17,20	7,9.3	8,11	14,17

WFRDD2 GlobalFiler™ (PDF Format)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17

WRJ6X6 PowerPlex® Fusion 6C (PDF Format)

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X	10,11	20,23
	12,13	7,11	17,20	7,9.3	8,11	14,17

XN22QZ GlobalFiler™ (PDF Format)

	14,16	25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14	29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17
	NM			NM		

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

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
	12,13	7,11	17,20	7,9.3	8,11	14,17
	NR	NR	NR			

TABLE 3

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

Item 1 - STR Results

YP4J3Z GlobalFiler™ (PDF Format), (HID Format) (STRMix)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17

YWQCDZ GlobalFiler™ (PDF Format)

	14,16	25,25	12,14	15,16	11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
1	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	7,9.3	8,11	14,17

TABLE 3

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

Item 2 - STR Results

36QZJU PowerPlex® Fusion 6C (HID Format)

	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	10,13	7,18	20,31.2	9.3,9.3	8,11	16,18
	12	17	18			

3YHFVW GlobalFiler™ (PDF Format)

	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	N/A	N/A	20,31.2	9.3,9.3	8,11	16,18
	12	N/A	N/A	2		

6WK94V GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format)

	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	10,13	7,18	20,31.2	9.3	8,11	16,18
	12	17	18	2		

6X26VV GlobalFiler™ (STR Mix)

	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12,12			2		

7DQRET GlobalFiler™ (HID Format)

	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3	8,11	16,18
	12			2		

7E6WDQ GlobalFiler™ (STRmix)

	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12			2		

TABLE 3

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

Item 2 - STR Results

7GQ3AR	GlobalFiler™ (PDF Format)					
	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12			2		
7MGDKQ	GlobalFiler™, PowerPlex® Fusion 6C (HID Format) (GeneMapper ID-X 1.6)					
	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	10,13	7,18	20,31.2	9.3	8,11	16,18
	12	17	18	2		
7Y7CBT	GlobalFiler™ (HID Format)					
	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12			2		
8XBUAR	(PDF Format)					
	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12			2		
9DMLDN	PowerPlex® Fusion 6C (HID Format)					
	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	10,13	7,18	20,31.2	9.3,9.3	8,11	16,18
	12	17	18			
9DMP3T	GlobalFiler™ (PDF Format)					
	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12			2		

TABLE 3

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

Item 2 - STR Results

9KJJZR	GlobalFiler™ (HID Format) (STRMix)					
	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12			2		
AGUWHN	GlobalFiler™ (PDF Format)					
	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12			2		
APAF3M	GlobalFiler™ (PDF Format)					
	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3	8,11	16,18
	12			2		
AQ6Y4N	GlobalFiler™ (HID Format)					
	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3	8,11	16,18
	12			2		
C2G34J	GlobalFiler™ (HID Format)					
	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3	8,11	16,18
	12			2		
CVNZZJ	GlobalFiler™, PowerPlex® Fusion 6C (HID Format)					
	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	10,13	7,18	20,31.2	9.3	8,11	16,18
	12	17	18	2		

TABLE 3

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

Item 2 - STR Results

CZ747P GlobalFiler™ (PDF Format)

	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12			2		

D8YVRN PowerPlex® Fusion 5C (PDF Format), (HID Format)

	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	10,13	7,18		9.3,9.3	8,11	16,18
	12					

E4GTKJ GlobalFiler™ (HID Format)

	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3	8,11	16,18
	12			2		

E8G4GJ GlobalFiler™ (HID Format)

	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3	8,11	16,18
	12			2		

ELVARH GlobalFiler™ (HID Format) (STRmix)

	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12			2		

EPWDHJ GlobalFiler™ (PDF Format)

	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3	8,11	16,18
	12			2		

TABLE 3

Item 2 - STR Results

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		
FBV2LK	GlobalFiler™					
	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12			2		
FF3PYL	GlobalFiler™ (HID Format)					
	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	N/A	N/A	20,31.2	9.3,9.3	8,11	16,18
	12	N/A	N/A	2		
GC3ZVJ	GlobalFiler™ (STRMix)					
	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12			2		
GGVZAF	GlobalFiler™ (HID Format)					
	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3	8,11	16,18
	12			2		
GU2VTG	GlobalFiler™					
	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12			2		
H8KXNE	GlobalFiler™ (HID Format)					
	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3	8,11	16,18
	12			2		

TABLE 3

Item 2 - STR Results

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		
H9WUUJ	PowerPlex® Fusion 6C					
	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	10,13	7,18	20,31.2	9.3	8,11	16,18
	12	17	18			
J8JM7G	GlobalFiler™ (HID Format)					
	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12			2		
JXR8GC	GlobalFiler™ (PDF Format)					
	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12			2		
KC7REB	PowerPlex® Fusion 6C (HID Format)					
	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	10,13	7,18	20,31.2	9.3,9.3	8,11	16,18
	12	17	18			
L3XGMC	GlobalFiler™ (HID Format) (DNAxs, v. 2.8.11)					
	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,16
			20,31.2	9.3,9.3	8,11	16,18
	12			2		
M2GKUC	GlobalFiler™, PowerPlex® Fusion 6C (PDF Format), (HID Format)					
	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	10,13	7,18	20,31.2	9.3	8,11	16,18
	12	17	18	2		

TABLE 3

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

Item 2 - STR Results

M8P98D GlobalFiler™ (HID Format)

	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	-	-	20,31.2	9.3,9.3	8,11	16,18
	12	-	-	2		

N387Z9 GlobalFiler™, PowerPlex® Fusion 6C (PDF Format)

	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	10,13	7,18	20,31.2	9.3	8,11	16,18
	12	17	18	2		

PPGVQ9 GlobalFiler™ (PDF Format)

	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12			2		

PPQEAJ Investigator® 24plex (HID Format) (STRmix)

	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3	8,11	16,18
	12					

PXB2KA PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (HID Format) (Lab Retriever)

	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	10,13	7,18	20,31.2	9.3	8,11	16,18
	12	17	18			

TL8MC9 GlobalFiler™ (HID Format) (STRMIX v2.10)

	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	-	-	20,31.2	9.3,9.3	8,11	16,18
	12	-	-	2		

TABLE 3

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

Item 2 - STR Results

UR9LZ3 GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format)

	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	10,13	7,18	20,31.2	9.3	8,11	16,18
	12	17	18	2		

VQRN93 PowerPlex® Fusion 6C (HID Format)

	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	10,13	7,18	20,31.2	9.3	8,11	16,18
	12	17	18			

WFRDD2 GlobalFiler™ (PDF Format)

	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12			2		

WRJ6X6 PowerPlex® Fusion 6C (PDF Format)

	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	10,13	7,18	20,31.2	9.3	8,11	16,18
	12	17	18			

XN22QZ GlobalFiler™ (PDF Format)

	15,16	25	11,14	14	11	8,9
	13,16	14,16	20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3	8,11	16,18
	12			2		

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

	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
	10,13	7,18	20,31.2	9.3,9.3	8,11	16,18
	12	17	18			

TABLE 3

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

Item 2 - STR Results

YP4J3Z	GlobalFiler™ (PDF Format), (HID Format) (STRMix)					
	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12			2		
YWQCDZ	GlobalFiler™ (PDF Format)					
	15,16	25,25	11,14	14,14	11,11	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
2	13,14	28,29	11,15	X,Y	10,11	21,26
			20,31.2	9.3,9.3	8,11	16,18
	12			2		

TABLE 3

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

Item 3 - STR Results

36QZJU PowerPlex® Fusion 6C (HID Format) (STRmix)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	10,11,12,13	7,9,11,16	17,18,20,21	7,9.3	8,11	14,17
	10	20	18			

3YHFVW GlobalFiler™ (PDF Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	N/A	N/A	17,18,20,21	7,9.3	8,11	14,17
	10	N/A	N/A	2		

6WK94V GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format) (LabRetriever v2.2.1)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	10,11,12,13	7,9,11,16	17,18,20,21	7,9.3	8,11	14,17
	10	20	18	2		

6X26VV GlobalFiler™ (STR Mix)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

7DQRET GlobalFiler™ (HID Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

7E6WDQ GlobalFiler™

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14,14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

TABLE 3

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

Item 3 - STR Results

7GQ3AR GlobalFiler™ (PDF Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

7MGDKQ GlobalFiler™, PowerPlex® Fusion 6C (HID Format) (GeneMapper ID-X 1.6, DNAxs 2.8.11, EuroForMix v4.2.5, EuroForMixRep 1.1.0, LRmixStudio 2.1.5)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	10,11,12,13	7,9,11,16	17,18,20,21	7,9.3	8,11	14,17
	10	20	18	2		
	12,16.3	20,25	10,11	14,15	12,13	8,12
	13	13,14	17,19	8,9	11	13,14
3major	14	27,30.2	11,16	X,Y	10,12	23
	10,11	9,16	18,21	7,9.3	8,11	17
	10	20	18	2		

7Y7CBT GlobalFiler™ (HID Format) (STRMix v2.10)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

8XBUAR (PDF Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

9DMLDN PowerPlex® Fusion 6C (HID Format) (STRmix v2.5.11)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	10,11,12,13	7,9,11,16	17,18,20,21	7,9.3	8,11	14,17
	10	20	18			

TABLE 3

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

Item 3 - STR Results

9DMP3T GlobalFiler™ (PDF Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

9KJJZR GlobalFiler™ (HID Format) (STRMix)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

AGUWHN GlobalFiler™ (PDF Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

APAF3M GlobalFiler™ (PDF Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

AQ6Y4N GlobalFiler™ (HID Format) (GeneMapper ID-X 1.5)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

C2G34J GlobalFiler™ (HID Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

TABLE 3

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

Item 3 - STR Results

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

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	10,11,12,13	7,9,11,16	17,18,20,21	7,9.3	8,11	14,17
	10	20	18	2		

CZ747P GlobalFiler™ (PDF Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14,14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		
	12,16.3	20,25	10,11	14,15	12,13	8,12
	13,13	13,14	19,19	8,9	11,11	13,14
3major	14,14	27,30.2		X,Y	10,10	23,23
			18,21	7,9.3	8,11	17,17
	10			2		
	14,16		12,14	15,16	11,13	8,10
	13,16	13,15		11,12	11,13	13,14
3minor		29,29		X,X	10,11	
			17,20		8,11	14,17

D8YVRN PowerPlex® Fusion 5C (PDF Format), (HID Format) (LRmix Studio 2.1.5 Community Edition)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	10,11,12,13	7,9,11,16		7,9.3	8,11	14,17
	10					
	12,16.3	25	10,11	14,15	13	8,12
	13	13,14	17,18,19	8,9	11	13,14
3major	14	27,29,30.2	11	X	10	23
	10,11,12,13	9,16		7,9.3	8,11	17
	10					
	14,16	20	12,14	16	11,12	10
	16	15	-	11,12	13	-
3minor	-	-	14,16	Y	11,12	20
	-	7,11		-	-	14
	-					

TABLE 3

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

Item 3 - STR Results

E4GTKJ GlobalFiler™ (HID Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

E8G4GJ GlobalFiler™ (HID Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

ELVARH GlobalFiler™ (HID Format) (STRmix)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14,14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

EPWDHJ GlobalFiler™ (PDF Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

FBV2LK GlobalFiler™ (STRMix v 2.10)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

FF3PYL GlobalFiler™ (HID Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	N/A	N/A	17,18,20,21	7,9.3	8,11	14,17
	10	N/A	N/A	2		

TABLE 3

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

Item 3 - STR Results

GC3ZVJ GlobalFiler™ (STRMix)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

GGVZAF GlobalFiler™ (HID Format) (STRmix)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

GU2VTG GlobalFiler™

	11,12,13,14,15,15.3, 16,16.3	19,20,24,25	9,10,11,12,13,14	13,14,15,16	10,11,12,13	7,8,9,10,11,12
	12,13,15,16	12,13,14,15	16,17,18,19	7,8,9,10,11,12	10,11,12,13	12,13,14
3	13,14	26,27,28,29,29.2,30.2	10,11,12,13,14,15, 16,17	X,Y	9,10,11,12	19,20,22,23
			16,17,17.2,18,19,19.2,20,20.2,21	6,7,9.3	7,8,10,11	13,14,16,17
	9,10			2		

H8KXNE GlobalFiler™ (HID Format) (STRmix)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

H9WUUJ PowerPlex® Fusion 6C

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	10,11,12,13	7,9,11,16	17,18,20,21	7,9.3	8,11	14,17
	10	20	18			

J8JM7G GlobalFiler™ (HID Format) (STRmix)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

TABLE 3

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

Item 3 - STR Results

JXR8GC GlobalFiler™ (PDF Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

KC7REB PowerPlex® Fusion 6C (HID Format) (STRmix)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	10,11,12,13	7,9,11,16	17,18,20,21	7,9.3	8,11	14,17
	10	20	18			

L3XGMC GlobalFiler™ (HID Format) (DNAxs, v. 2.8.11)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		
	12,16.3	/	10,11	14,15	/	/
	13,13	13,14	/	8,9	11,11	13,14
3major	14,14	/	/	/	10,12	23,23
			18,21	7,9.3	8,11	17,17
	14,16	/	12,14	15,16	/	/
	_,16	13,15	/	11,12	_,13	13,14
3minor	14,14	/	/	/	10,11	20,_
			17,20	7,9.3	8,11	14,_

M2GKUC GlobalFiler™, PowerPlex® Fusion 6C (PDF Format), (HID Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	10,11,12,13	7,9,11,16	17,18,20,21	7,9.3	8,11	14,17
	10	20	18	2		

M8P98D GlobalFiler™ (HID Format) (STRMix(TM))

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	-	-	17,18,20,21	7,9.3	8,11	14,17
	10	-	-	2		

TABLE 3

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

Item 3 - STR Results

N387Z9 GlobalFiler™, PowerPlex® Fusion 6C (PDF Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	10,11,12,13	7,9,11,16	17,18,20,21	7,9.3	8,11	14,17
	10	20	18	2		

PPGVQ9 GlobalFiler™ (PDF Format)

	12,14,[16],16.3	[20],25	10,11,12,14	14,15,[16]	[11],12,13	8,[10],[12]
	13,[16]	13,14,[15]	[17],[18],19	8,9,11,12	11,[13]	13,14
3	14,14	27,29,30.2	11,[14],[16]	X,[Y]	10,[11],12	[20],23
			17,18,20,21	7,9.3	8,11	[14],17
	10			2		

PPQEAJ Investigator® 24plex (STRmix)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10					

PXB2KA PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (HID Format) (Lab Retriever)

	12,14,15,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13,14	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	10,11,12,13	7,9,11,16	17,18,20,21	7,9.3	8,11	14,17
	10	20	18			

TL8MC9 GlobalFiler™ (HID Format) (STRMIX v2.10)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	-	-	17,18,20,21	7,9.3	8,11	14,17
	10	-	-	2		

UR9LZ3 GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	10,11,12,13	7,9,11,16	17,18,20,21	7,9.3	8,11	14,17
	10	20	18	2		

TABLE 3

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

Item 3 - STR Results

VQRN93 PowerPlex® Fusion 6C (HID Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	10,11,12,13	7,9,11,16	17,18,20,21	7,9.3	8,11	14,17
	10	20	18			

WFRDD2 GlobalFiler™ (PDF Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14,14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

WRJ6X6 PowerPlex® Fusion 6C (PDF Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	10,11,12,13	7,9,11,16	17,18,20,21	7,9.3	8,11	14,17
	10	20	18			

XN22QZ GlobalFiler™ (PDF Format)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

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

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
	10,11,12,13	7,9,11,16	17,18,20,21	7,9.3	8,11	14,17
	10	20	18			

YP4J3Z GlobalFiler™ (PDF Format), (HID Format) (STRMix)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

TABLE 3

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

Item 3 - STR Results

YWQCDZ GlobalFiler™ (PDF Format) (LRmix Studio 2.1.5)

	12,14,16,16.3	20,25	10,11,12,14	14,15,16	11,12,13	8,10,12
	13,16	13,14,15	17,18,19	8,9,11,12	11,13	13,14
3	14	27,29,30.2	11,14,16	X,Y	10,11,12	20,23
			17,18,20,21	7,9.3	8,11	14,17
	10			2		

TABLE 3

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

Item 4 - STR Results

36QZJU PowerPlex® Fusion 6C (HID Format) (STRmix)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	10,12,13	7,11,18	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	17	18			

3YHFVW GlobalFiler™ (PDF Format)

	14,15,16	20,25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	N/A	N/A	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	N/A	N/A	2		

6WK94V GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format) (LabRetriever v2.2.1)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	10,12,13	7,11,18	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	17	18	2		

6X26VV GlobalFiler™ (STR Mix)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		

7DQRET GlobalFiler™ (HID Format)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		

7E6WDQ GlobalFiler™ (STRmix)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		

TABLE 3

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

Item 4 - STR Results

7GQ3AR GlobalFiler™ (PDF Format)

	14,15,16	20,25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		

7MGDKQ GlobalFiler™, PowerPlex® Fusion 6C (HID Format) (GeneMapper ID-X 1.6, DNAxs 2.8.11, EuroForMix v4.2.5, EuroForMixRep 1.1.0, LRmixStudio 2.1.5)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	10,12,13	7,11,18	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	17	18	2		

7Y7CBT GlobalFiler™ (HID Format) (STRMix v2.10)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		

8XBUAR (PDF Format)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		

9DMLDN PowerPlex® Fusion 6C (HID Format) (STRmix v2.5.11)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	10,12,13	7,11,18	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	17	18			

9DMP3T GlobalFiler™ (PDF Format)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		

TABLE 3

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

Item 4 - STR Results

9KJJZR	GlobalFiler™ (HID Format)					
	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		
AGUWHN	GlobalFiler™ (PDF Format)					
	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		
APAF3M	GlobalFiler™ (PDF Format)					
	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		
AQ6Y4N	GlobalFiler™ (HID Format) (GeneMapper ID-X 1.5)					
	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		
C2G34J	GlobalFiler™ (HID Format)					
	14,15,16			14,15,16	11,13	
		13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4			11,14,15			20,21,23,26
			17,20,31.2	7,9.3		14,16,17,18
		25	12,14			8,10
	13,16					
4major	14	29		X	10,11	
					8,11	
			11			9
4minor	13	28		X,Y		
	12			2		

TABLE 3

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

Item 4 - STR Results

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

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	10,12,13	7,11,18	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	17	18	2		

CZ747P GlobalFiler™ (PDF Format)

	14,15,16	25,25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		
	14,16		12,14			8,10
		13,15	18,19	11,12	11,13	13,14
4major		29,29		X,X		20,23
			17,20			14,17
	15,16		11,14			8,9
		14,16		8,12	13,14	13,18
4minor				X,Y		21,26
			20,31.2			16,18
	12			2		

D8YVRN PowerPlex® Fusion 5C (PDF Format), (HID Format) (LRmix Studio 2.1.5 Community Edition)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	10,12,13	7,11,18		7,9.3	8,11	14,16,17,18
	12					
	14,16	25	14	14,15,16	11	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
4major	14	29	11,14	X	10,11	20,23
	12,13	7,11		7,9.3	8,11	14,17
	12					
	15	-	11,12	-	13	9
	-	14,16	20	8	14	18
4minor	13	28	15	Y	-	21,26
	10	18		-	-	16,18
	-					

TABLE 3

Item 4 - STR Results

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		
E4GTKJ	GlobalFiler™ (HID Format)					
	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		
E8G4GJ	GlobalFiler™ (HID Format)					
	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		
ELVARH	GlobalFiler™ (HID Format) (STRmix)					
	14,15,16	25,25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		
EPWDHJ	GlobalFiler™ (PDF Format)					
	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		
FBV2LK	GlobalFiler™ (STRMix v 2.10)					
	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		
FF3PYL	GlobalFiler™ (HID Format)					
	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	N/A	N/A	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	N/A	N/A	2		

TABLE 3

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

Item 4 - STR Results

GC3ZVJ	GlobalFiler™ (STRMix)					
	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		
GGVZAF	GlobalFiler™ (HID Format) (STRmix)					
	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		
GU2VTG	GlobalFiler™					
	13,OL,14,15,OL,16,17	20,23,24,25	10,11,12,13,14	13,14,15,16	10,11,12,13	7,8,9,10
	12,13,15,16	12,13,14,15,16	17,18,19,20	8,10,11,12	10,11,12,13,14	12,13,14,17,18
4	12,13,14	27,28,29	10,11,13,14,15	X,Y	9,10,11	19,20,21,22,23,25,26
			16,16.2,17,18,19,19.2,20,30.2,31.2	7,8.3,9.3	7,8,10,11	13,14,15,16,17,18
	11,12			2		
H8KXNE	GlobalFiler™ (HID Format) (STRmix)					
	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		

TABLE 3

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

Item 4 - STR Results

H9WUUJ PowerPlex® Fusion 6C

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	10,12,13	7,11,18	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	17	18			
		13,15		11,12		
4major						20,23
		7,11	17,20			14,17
		14,16		8		
4minor						21,26
		18	31.2			16,18

J8JM7G GlobalFiler™ (HID Format) (STRmix)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		

JXR8GC GlobalFiler™ (PDF Format)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		

KC7REB PowerPlex® Fusion 6C (HID Format) (STRmix)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	10,12,13	7,11,18	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	17	18			

TABLE 3

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

Item 4 - STR Results

L3XGMC GlobalFiler™ (HID Format) (DNAxs, v. 2.8.11)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		
	14,16	25,25	12,14	/	/	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
4major	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	/	8,11	14,17
	15,16	25,25	11,14	/	/	8,9
	13,16	14,16	20,20	8,12	13,14	13,18
4minor	13,_	28,_	11,15	X,Y	10,11	21,26
			20,31.2	/	8,11	16,18

M2GKUC GlobalFiler™, PowerPlex® Fusion 6C (PDF Format), (HID Format)

	14,15,16	20*,25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	10,12,13	7,11,18	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	17	18	2		

M8P98D GlobalFiler™ (HID Format) (STRMix(TM))

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	-	-	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	-	-	2		

N387Z9 GlobalFiler™, PowerPlex® Fusion 6C

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	10,12,13	7,11,18	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	17	18	2		

TABLE 3

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

Item 4 - STR Results

PPGVQ9 GlobalFiler™ (PDF Format)

	14,[15],16	[20],25	[11],12,14	14,15,16	11,[13]	8,[9],10
	13,16	13,[14],15,[16]	18,19,20	[8],11,12	11,13,[14]	13,14,[18]
4	[13],14	[28],29	11,14,[15]	X,[Y]	10,11	20,[21],23,[26]
			17,20,[31.2]	[7],9.3	8,11	14,[16],17,[18]
	12			2		
	14,16	25,25	12,14	14,15;14,16;15,16	11,11;11,13	8,10
	13,16	13,15	18,19	11,12	11,13	13,14
4major	14,14	29,29	11,14	X,X	10,11	20,23
			17,20	9.3,9.3;7,9.3	8,11	14,17
	14,15;15,16	25,25	11,12;11,14	14,14;15,15;16,16	11,11;13,13	8,9;9,10
	13,16	14,16	20,20	8,12	11,14;13,14	13,18;14,18
4minor	13,14	28,29	11,15;14,15	X,Y	10,11	21,26
			20,31.2	7,7;9.3,9.3;7,9.3	8,11	16,18
	12			2		

PPQEAJ Investigator® 24plex (HID Format) (STRmix)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12					

PXB2KA PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (HID Format) (Lab Retriever)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	10,12,13	7,11,18	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	17	18			

TL8MC9 GlobalFiler™ (HID Format) (STRMIX v2.10)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	-	-	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	-	-	2		

UR9LZ3 GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	10,12,13	7,11,18	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	17	18	2		

TABLE 3

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

Item 4 - STR Results

VQRN93 PowerPlex® Fusion 6C (HID Format)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	10,12,13	7,11,18	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	17	18			

WFRDD2 GlobalFiler™ (PDF Format)

	14,15,16	20,25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		
		25				
4major						
		20				
4minor						

WRJ6X6 PowerPlex® Fusion 6C (PDF Format)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	10,12,13	7,11,18	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	17	18			

XN22QZ GlobalFiler™ (PDF Format)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		

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

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
	10,12,13	7,11,18	17,20,31.2	7,9.3	8,11	14,16,17,18
	12	17	18			

TABLE 3

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

Item 4 - STR Results

YP4J3Z GlobalFiler™ (PDF Format), (HID Format) (STRMix)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		

YWQCDZ GlobalFiler™ (PDF Format) (LRmix Studio 2.1.5)

	14,15,16	25	11,12,14	14,15,16	11,13	8,9,10
	13,16	13,14,15,16	18,19,20	8,11,12	11,13,14	13,14,18
4	13,14	28,29	11,14,15	X,Y	10,11	20,21,23,26
			17,20,31.2	7,9.3	8,11	14,16,17,18
	12			2		

YSTR Results

TABLE 4

WebCode / Item	Amplification Kits (File Format)								
	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									
36QZJU	PowerPlex® Y23 (HID Format)								
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
3YHFVW	Yfiler™ Plus (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12	N/A	17	18	20	23	N/A	11
6WK94V	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12	13	17	18	20	23	10	11
6X26VV	PowerPlex® Y23								
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
7DQRET	PowerPlex® Y23 (HID Format)								
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
7E6WDQ	Yfiler™ Plus								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
7GQ3AR	Yfiler™ Plus (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
7MGDKQ	Yfiler™ Plus (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
7Y7CBT	PowerPlex® Y23 (PDF Format)								
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
8XBUAR	(PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11

TABLE 4

WebCode / Item	Amplification Kits (File Format)								
	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									
9DMLDN	PowerPlex® Y23 (HID Format)								
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
9KJJZR	PowerPlex® Y23 (HID Format)								
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
AGUWHN	Yfiler™ Plus (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
APAF3M	Yfiler™ Plus (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
AQ6Y4N	Yfiler™ Plus (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
AYN7ZY	Yfiler™ Plus, PowerPlex® Y23 (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12	13	17	18	20	23	10	11
C2G34J	PowerPlex® Y23 (HID Format)								
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
CVNZZJ	Yfiler™ Plus, PowerPlex® Y23 (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12	13	17	18	20	23	10	11
D8YVRN	PowerPlex® Y23 (PDF Format), (HID Format)								
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
E4GTKJ	Yfiler™ Plus (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11

TABLE 4

WebCode / Item	Amplification Kits (File Format)								
	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									
E8G4GJ	Yfiler™ Plus (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
EPWDHJ	Yfiler™ Plus (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
FBV2LK	PowerPlex® Y23								
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
FF3PYL	Yfiler™ Plus (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12	N/A	17	18	20	23	N/A	11
GC3ZVJ	PowerPlex® Y23								
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
H8KXNE	Yfiler™ Plus (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
H9WUUJ									
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
J8JM7G	PowerPlex® Y23 (HID Format)								
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
JXR8GC	Yfiler™ Plus (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
KC7REB	PowerPlex® Y23 (HID Format)								
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11

TABLE 4

WebCode / Item	Amplification Kits (File Format)								
	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									
L3XGMC	Yfiler™ Plus (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
M2GKUC	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12	13	17	18	20	23	10	11
M8P98D	PowerPlex® Y23 (HID Format)								
	-	14	11,14	13	29	23	12	13	13
2	15	12	12	19	-	17	20	-	22
	-	12	13	17	18	-	23	10	11
N387Z9	Yfiler™ Plus, PowerPlex® Y23 (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12	13	17	18	20	23	10	11
PXB2KA	PowerPlex® Y23 (HID Format)								
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
TL8MC9	PowerPlex® Y23 (PDF Format)								
	-	14	11,14	13	29	23	12	13	13
2	15	12	12	19	-	17	20	-	22
	-	12	13	17	18	-	23	10	11
UR9LZ3	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12	13	17	18	20	23	10	11
VQRN93	Yfiler™ Plus (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
WFRDD2	PowerPlex® Y23 (PDF Format)								
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
WRJ6X6	PowerPlex® Y23 (PDF Format)								
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11

TABLE 4

WebCode / Item	Amplification Kits (File Format)								
	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									
XN22QZ	Yfiler™ Plus (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
2	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
YMZNJX	PowerPlex® Y23 (HID Format)								
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
YP4J3Z	PowerPlex® Y23 (PDF Format)								
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
YWQCDZ	PowerPlex® Y23								
		14	11,14	13	29	23	12	13	13
2	15	12	12	19		17	20		22
		12	13	17	18		23	10	11

TABLE 4

Item 3 - YSTR Results

WebCode / Item	Amplification Kits (File Format)								
	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
36QZJU	PowerPlex® Y23 (HID Format)								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12
3YHFVW	Yfiler™ Plus (PDF Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12	N/A	20	18	21	22	N/A	12
6WK94V	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12	12	20	18	21	22	12	12
6X26VV	PowerPlex® Y23								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12
7DQRET	PowerPlex® Y23 (HID Format)								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12
7E6WDQ	Yfiler™ Plus								
	34,38	13	17,18	13	30	24	10	11	13
3major	14	10	13	20	33	17	15	9	22
	40	12		20	18	21	22		12
7GQ3AR	Yfiler™ Plus (PDF Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12		20	18	21	22		12
7MGDKQ	Yfiler™ Plus (HID Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12		20	18	21	22		12
7Y7CBT	PowerPlex® Y23 (PDF Format)								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12
8XBUAR	(PDF Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12		20	18	21	22		12

TABLE 4

WebCode / Item	Amplification Kits (File Format)								
	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									
9DMLDN	PowerPlex® Y23 (HID Format)								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12
9KJJZR	PowerPlex® Y23 (HID Format)								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12
AGUWHN	Yfiler™ Plus (PDF Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12		20	18	21	22		12
APAF3M	Yfiler™ Plus (PDF Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12		20	18	21	22		12
AQ6Y4N	Yfiler™ Plus (HID Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12		20	18	21	22		12
AYN7ZY	Yfiler™ Plus, PowerPlex® Y23 (PDF Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12	12	20	18	21	22	12	12
C2G34J	PowerPlex® Y23 (HID Format)								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12
CVNZZJ	Yfiler™ Plus, PowerPlex® Y23 (HID Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12	12	20	18	21	22	12	12
D8YVRN	PowerPlex® Y23 (PDF Format), (HID Format)								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12
		13	17,18	13	30	24	10	11	13
3major	14	10	13	20		17	15		22
		12	12	20	18		22	12	12

TABLE 4

WebCode / Item	Amplification Kits (File Format)								
	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									
E4GTKJ	Yfiler™ Plus (PDF Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12		20	18	21	22		12
E8G4GJ	Yfiler™ Plus (PDF Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12		20	18	21	22		12
EPWDHJ	Yfiler™ Plus (PDF Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12		20	18	21	22		12
FBV2LK	PowerPlex® Y23								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12
FF3PYL	Yfiler™ Plus (HID Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12	N/A	20	18	21	22	N/A	12
GC3ZVJ	PowerPlex® Y23								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12
H8KXNE	Yfiler™ Plus (HID Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12		20	18	21	22		12
H9WUUJ	PowerPlex® Y23 (PDF Format)								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12
J8JM7G	PowerPlex® Y23 (HID Format)								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12
JXR8GC	Yfiler™ Plus (PDF Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12		20	18	21	22		12

TABLE 4

WebCode / Item	Amplification Kits (File Format)								
	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									
KC7REB	PowerPlex® Y23 (HID Format)								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12
L3XGMC	Yfiler™ Plus (HID Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12		20	18	21	22		12
M2GKUC	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12	12	20	18	21	22	12	12
M8P98D	PowerPlex® Y23 (HID Format)								
	-	13	17,18	13	30	24	10	11	13
3	14	10	13	20	-	17	15	-	22
	-	12	12	20	18	-	22	12	12
N387Z9	Yfiler™ Plus, PowerPlex® Y23 (PDF Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12	12	20	18	21	22	12	12
PXB2KA	PowerPlex® Y23 (HID Format)								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12
TL8MC9	PowerPlex® Y23 (PDF Format)								
	-	13	17,18	13	30	24	10	11	13
3	14	10	13	20	-	17	15	-	22
	-	12	12	20	18	-	22	12	12
UR9LZ3	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12	12	20	18	21	22	12	12
VQRN93	Yfiler™ Plus (HID Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12		20	18	21	22		12
WFRDD2	PowerPlex® Y23 (PDF Format)								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12

TABLE 4

WebCode / Item	Amplification Kits (File Format)								
	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									
WRJ6X6	PowerPlex® Y23 (PDF Format)								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12
XN22QZ	Yfiler™ Plus (PDF Format)								
	34,38	13	17,18	13	30	24	10	11	13
3	14	10	13	20	33	17	15	9	22
	40	12		20	18	21	22		12
YMZNJX	PowerPlex® Y23 (HID Format)								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12
YP4J3Z	PowerPlex® Y23 (PDF Format)								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12
YWQCDZ	PowerPlex® Y23 (PDF Format)								
		13	17,18	13	30	24	10	11	13
3	14	10	13	20		17	15		22
		12	12	20	18		22	12	12

TABLE 4

WebCode / Item	Amplification Kits (File Format)								
	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									
36QZJU	PowerPlex® Y23 (HID Format)								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
3YHFVW	Yfiler™ Plus (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12	N/A	17	18	20	23	N/A	11
6WK94V	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12	13	17	18	20	23	10	11
6X26VV	PowerPlex® Y23								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
7DQRET	PowerPlex® Y23 (HID Format)								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
7E6WDQ	Yfiler™ Plus								
	35,37	14	11,14	13	29	23	12	13	13
4major	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
7GQ3AR	Yfiler™ Plus (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
7MGDKQ									
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
7Y7CBT	PowerPlex® Y23 (PDF Format)								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
8XBUAR	(PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	20	17	20	10	22
	40	12		17	18	20	23		11

TABLE 4

WebCode / Item	Amplification Kits (File Format)								
	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									
9DMLDN	PowerPlex® Y23 (HID Format)								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
9KJJZR	PowerPlex® Y23 (HID Format)								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
AGUWHN	Yfiler™ Plus (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
APAF3M	Yfiler™ Plus (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
AQ6Y4N	Yfiler™ Plus (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
AYN7ZY	Yfiler™ Plus, PowerPlex® Y23 (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	19,20	10	22
	40	12	13	17	18	20	23	10	11
C2G34J	PowerPlex® Y23 (HID Format)								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
CVNZZJ	Yfiler™ Plus, PowerPlex® Y23 (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12	13	17	18	20	23	10	11
D8YVRN	PowerPlex® Y23 (PDF Format), (HID Format)								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
		14	11,14	13	29	23	12	13	13
4major	15	12	12	19		17	20		22
		12	13	17	18		23	10	11

TABLE 4

WebCode / Item	Amplification Kits (File Format)								
	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									
E4GTKJ	Yfiler™ Plus (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
E8G4GJ	Yfiler™ Plus (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
EPWDHJ	Yfiler™ Plus (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
FBV2LK	PowerPlex® Y23								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
FF3PYL	Yfiler™ Plus (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12	N/A	17	18	20	23	N/A	11
GC3ZVJ	PowerPlex® Y23								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
H8KXNE	Yfiler™ Plus (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
H9WUUJ	PowerPlex® Y23 (PDF Format)								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
J8JM7G	PowerPlex® Y23 (HID Format)								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
JXR8GC	Yfiler™ Plus (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11

TABLE 4

WebCode / Item	Amplification Kits (File Format)								
	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									
KC7REB	PowerPlex® Y23 (HID Format)								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
L3XGMC	Yfiler™ Plus (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
M2GKUC	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12	13	17	18	20	23	10	11
M8P98D	PowerPlex® Y23 (HID Format)								
	-	14	11,14	13	29	23	12	13	13
4	15	12	12	19	-	17	20	-	22
	-	12	13	17	18	-	23	10	11
N387Z9	Yfiler™ Plus, PowerPlex® Y23 (PDF Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12	13	17	18	20	23	10	11
PXB2KA	PowerPlex® Y23 (HID Format)								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
TL8MC9	PowerPlex® Y23 (PDF Format)								
	-	14	11,14	13	29	23	12	13	13
4	15	12	12	19	-	17	20	-	22
	-	12	13	17	18	-	23	10	11
UR9LZ3	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12	13	17	18	20	23	10	11
VQRN93	Yfiler™ Plus (HID Format)								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
WFRDD2	PowerPlex® Y23 (PDF Format)								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	19?,20		22
		12	13	17	18		23	10	11

TABLE 4

WebCode / Item	Amplification Kits (File Format)								
	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									
WRJ6X6	PowerPlex® Y23 (PDF Format)								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	(19),20		22
		12	13	17	18		23	10	11
XN22QZ	Yfiler™ Plus								
	35,37	14	11,14	13	29	23	12	13	13
4	15	12	12	19	29	17	20	10	22
	40	12		17	18	20	23		11
YMZNJX	PowerPlex® Y23 (HID Format)								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
YP4J3Z	PowerPlex® Y23 (PDF Format)								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	20		22
		12	13	17	18		23	10	11
YWQCDZ	PowerPlex® Y23 (PDF Format)								
		14	11,14	13	29	23	12	13	13
4	15	12	12	19		17	19,20		22
		12	13	17	18		23	10	11

DNA Conclusions

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

TABLE 5

WebCode	Item 3 Conclusion			Item 4 Conclusion		
	# of Contributors	Item 1	Item 2	# of Contributors	Item 1	Item 2
36QZJU	2	Included	Excluded	2	Included	Included
3YHFVW	2	Included	Excluded	2	Included	Included
6WK94V	≥2 contributors (including ≥1 male)	Included	Excluded	≥2 contributors (including ≥1 male)	Included	Included
6X26VV	2 Contributors, including at least1 male	Included	Excluded	2 Contributors, including at least one (1) male	Included	Included
7DQRET	2	Included	Excluded	2	Included	Included
7E6WDQ	2	Included	Excluded	2	Included	Included
7GQ3AR	2	Included	Excluded	2	Included	Included
7MGDKQ	2	Included	Excluded	2	Included	Included
7Y7CBT	2	Included	Excluded	2	Included	Included
8XBUAR	2	Included	Excluded	2	Included	Included
9DMLDN	STR-2; YSTR-1	Included	Excluded	STR-2; YSTR-1	Included	Included
9DMP3T	2	Included	Excluded	2	Included	Included
9KJJZR	2	Included	Excluded	2	Included	Included
AGUWHN	2	Included	Excluded	2	Included	Included
APAF3M	2	Included	Excluded	2	Included	Included
AQ6Y4N	2	Included	Excluded	2	Included	Included
AYN7ZY	1		Excluded	1		Included
C2G34J	2, including at least 1 male	Included	Excluded	2, including one male	Included	Included
CVNZZJ	2	Included	Excluded	2	Included	Included
CZ747P	at least 2, including 1 male	Included	Excluded	at least 2, including 1 male	Included	Included
D8YVRN	2	Included	Excluded	2	Included	Included
E4GTKJ	2	Included	Excluded	2	Included	Included
E8G4GJ	2	Included	Excluded	2	Included	Included
ELVARH	2	Included	Excluded	2	Included	Included
EPWDHJ	at least 2	Included	Excluded	at least 2	Included	Included
FBV2LK	2	Included	Excluded	2	Included	Included
FF3PYL	2	Included	Excluded	2	Included	Included
GC3ZVJ	Two (2) persons	Included	Excluded	Two (2) persons	Included	Included
GGVZAF	2	Included	Excluded	2	Included	Included
GU2VTG	2	Included	Excluded	2	Included	Included

TABLE 5

WebCode	Item 3 Conclusion # of Contributors	Item 3 Conclusion Item 1	Item 3 Conclusion Item 2	Item 4 Conclusion # of Contributors	Item 4 Conclusion Item 1	Item 4 Conclusion Item 2
H8KXNE	2	Included	Excluded	2	Included	Included
H9WUUJ	At least 2	Included	Excluded	At least 1	Included	Included
J8JM7G	2	Included	Excluded	2	Included	Included
JXR8GC	2 (1M+1F)	Included	Excluded	2 (1F+1M)	Included	Included
KC7REB	2	Included	Excluded	2	Included	Included
L3XGMC	2	Included	Excluded	2	Included	Included
M2GKUC	2	Included	Excluded	2	Included	Included
M8P98D	2	Included	Excluded	2	Included	Included
N387Z9	2	Included	Excluded	2	Included	Included
PPGVQ9	2	Included	Excluded	3	Included	Included
PPQEAJ	2	Included	Excluded	2	Included	Included
PXB2KA	3	Included	Excluded	2	Included	Included
TL8MC9	2	Included	Excluded	2	Included	Included
UR9LZ3	2	Included	Excluded	2	Included	Included
VQRN93	2	Included	Excluded	2	Included	Included
WFRDD2	2	Included	Excluded	3	Included	Included
WRJ6X6	2	Included	Excluded	2	Included	Included
XN22QZ	2	Included	Excluded	2	Included	Included
YMZNJX	2	Included	Excluded	2	Included	Included
YP4J3Z	2	Included	Excluded	2	Included	Included
YWQCDZ	2	Included	Excluded	2	Included	Included

Conclusions Response Summary

Participants reporting conclusions: 51

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 1	Item 3 Item 2	Item 4 Item 1	Item 4 Item 2
Included	**50**	**0**	**50**	**51**
Excluded	**0**	**51**	**0**	**0**
Inconclusive/ Uninterpretable	**0**	**0**	**0**	**0**
No Response	**1**	**0**	**1**	**0**
Total	**51**	**51**	**51**	**51**

Statistical Analysis for Item 3

TABLE 6

WebCode	Item 3 Methods & Results
36QZJU	**Method(s)**: Likelihood Ratio **Stats Analysis:** (STR): The DNA profile from this item is at least 1.1 octillion times more likely if it originated from Victim and an unknown individual than if it originated from two unknown, unrelated individuals. **Database(s):** Most conservative population group statistic is reported. The National Institute of Standards and Technology's published database is utilized in the statistical calculations. Hill, C.R., Duewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. Forensic Sci. Int. Genet. 7: e82-e83. Revised data received on August 10, 2017. Y-Chromosome Haplotype Reference Database: https://yhrd.org.
3YHFVW	**Method(s)**: [Participant did not report a method.] **Stats Analysis:** Working from the pdf of the electropherogram, it is not possible to perform a thorough evaluation of each locus. As a result it is possible to miss very minor contributions from additional contributors and be incorrect in the possible number of contributors to complex mixture samples. It is also not possible to thoroughly evaluate spikes, pullup, and baseline irregularities which can affect correct allele determinations. I am a forensic consultant that reviews DNA case files submitted to me as evidence. I review the analyst allele calls and evidence to reference sample comparisons so I can understand how the original analyst arrived at their opinions and conclusions. I accept that their population calculations are correct. N/A: Not Applicable. NSD: No Size Data **Database(s):** [Participant did not report database(s).]
6WK94V	**Method(s)**: Likelihood Ratio **Stats Analysis:** Statistical Results (Autosomal): Under the assumption that the VICTIM (Item 1) and one unknown unrelated person selected at random from the general population are contributors, the likelihood of observing the mixed source profile developed from the STAIN ON THE CROSSWALK (Item 3) is ≥1,000,000 times greater (actual LR available upon request) than if it is assumed that two unknown unrelated persons selected at random from the general population are contributors to this mixed-source profile. Under the assumption that two unknown unrelated persons selected at random from the general population are contributors, the likelihood of observing the mixed source profile developed from the STAIN ON THE CROSSWALK (Item 3) is ≥1,000,000 times greater (actual LR available upon request) than if it is assumed that the SUSPECT (Item 2) and one unknown unrelated person selected at random from the general population are contributors to this mixed-source profile. Results (YSTR): The SUSPECT (Item 2), his paternally-related male relatives and and an unknown number of males in the general population are excluded as the potential source of the YSTR haplotype developed from the STAIN ON THE CROSSWALK (Item 3). **Database(s):** Statistical Calculations employed the following databases: Revised-NIST-1036-Allele Frequencies; ABI ID Allele Frequencies; Promega PowePlex Fusion Allele Frequencies
6X26VV	**Method(s)**: Likelihood Ratio **Stats Analysis:** CONCLUSION The DNA result obtained from the stain allegedly taken from crosswalk is consistent with a mixture from at least two (2) contributors, including at least one (1) male: a) The mixture is approximately 4.43 x 10^23 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. b) The suspect has been excluded as being a contributor to this mixture. END OF REPORT **Database(s):** [Participant did not report database(s).]
7DQRET	**Method(s)**: Likelihood Ratio **Stats Analysis:** Hp=V+Un, Hd=Un+Un, LR=9x10^14 **Database(s):** STRider [Location Identifying Database]

TABLE 6

WebCode	Item 3 Methods & Results
7E6WDQ	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile obtained from item 3 is greater than 100 billion times more likely to be obtained if the victim is a contributor, rather than an unknown, unrelated individual from the [Location Identifying Population]. **Database(s):** [Location Identifying Database]
7GQ3AR	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA result from Item 3 is consistent with mixture from at least 2 contributors. The mixture is approximately 5x10^22 times more likely to occur if the victim and one unknown individual are contributors, rather than if the DNA is from two unknown individuals. **Database(s):** EuroFormix: Imported from STRideR [Location Identifying Database]
7MGDKQ	**Method(s)**: Likelihood Ratio **Stats Analysis:** Stutter filter was applied on DNA profiling. Item 3 (crosswalk stain) indicates the presence of a mixture. The number of alleles indicates that the mixture may be a two person mixture. Item 3 (crosswalk stain) could have originated from Victim (Item 1) and one unknown contributor. The unknown male DNA profile can be deconvoluted as the major component of the stain. Common parameters used for statistical analyses: P(dropin) = 0.03; Pmin = 0.001; FST = 0.015. Hp hypothesis: POI + 1 unrelated unknown contributors. Hd hypothesis: 2 unrelated unknown contributors. LRmixStudio v2.1.5 (PowerPlex Fusion 6C and Globalfiler DNA profile replicates): P(dropout) = 0.15; POI: Victim (Item 1) -> LR = 1.7E+15. DNAxs v2.8.11 MLE (PowerPlex Fusion 6C and Globalfiler DNA profile replicates): P(dropout lambda) = 0.01; Backward stutter model was applied. Degradation model was not applied. POI: Victim (Item 1) -> LR = 1.8E+26; Estimated DNA profile mixture ratios: Victim: 41%, Unknown: 59%. DNAxs v2.8.11 MixCal (PPowerPlex Fusion 6C and Globalfiler DNA profile replicates): POI: Victim (Item 1) -> LR = 2.5E+15. EuroForMix v4.2.5 (PowerPlex Fusion 6C DNA profile): P(dropout lambda) = 0.01; Backward stutter model was applied. Degradation model was applied. POI: Victim (Item 1) -> LR = 1.3E+22. EuroForMixRep v1.1.0 (PowerPlex Fusion 6C and Globalfiler DNA profile replicates): EuroForMixRep was used for deconvolution of mixed DNA profiles, too. P(dropout lambda) = 0.01; Backward stutter model was applied. Degradation model was applied. POI: Victim (Item 1) -> LR = 1.9E+26. The LR results of the statistical analyses strongly support the hypothesis that Item 3 (crosswalk stain) contains Victim's and an unknown male contributor's DNA. **Database(s):** STRidER R2 Europe: https://strider.online/frequencies /. Bodner et al. 2016: https://doi.org/10.1016/j.fsigen.2016.06.008.
7Y7CBT	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA result obtained from the stain on crosswalk (Item 3) is consistent with a mixture from at least two (2) contributors, including at least one (1) male: a) The mixture is approximately 5.56 x 10^23 times more likely to occur (very strong support for inclusion) if the female victim and one (1) unknown, unrelated individual are contributors rather than if two (2) unknown, unrelated individuals are contributors. b) The male suspect has been excluded as being a contributor to this mixture. **Database(s):** FBI Extended Caucasian
8XBUAR	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 3 =1,01 x 10^15 (Item 1 + unknown)/(2 unknown) **Database(s):** STRidER
9DMLDN	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile from this item is at least 1.3 octillion times more likely if it originated from Victim and an unknown individual than if it originated from two unknown, unrelated individuals. **Database(s):** Most conservative population group statistic is reported. The National Institute of Standards and Technology's published database is utilized in the statistical calculations. Hill, C.R., Duewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. Forensic Sci. Int. Genet. 7: e82-e83. Revised data received on August 10, 2017.
9DMP3T	**Method(s)**: Random Match Probability **Stats Analysis:** Item 1 RMP(Tri) = 1.73E+26. Item 1RMP(Cau)= 8.27E+26. **Database(s):** [Location Identifying Database]

TABLE 6

WebCode	Item 3 Methods & Results
9KJJZR	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA result is approximately 6.80E23 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 suspect has been excluded as being a contributor to this mixture. **Database(s):** FBI extended caucasian
AGUWHN	**Method(s)**: Likelihood Ratio **Stats Analysis:** LRmix Studio v.2.1.3. Item 1. LR = 1,06824E013 (drop out probability 0,26). **Database(s):** STRidER 2.0 [Location Identifying Database]
APAF3M	**Method(s)**: Likelihood Ratio **Stats Analysis:** The mixed DNA profile is 16 quadrillion (16e15), 480 quadrillion (480e15) and 13 quadrillion (13e15) TIMES more likely if they originated from the victim (Item 1) and one unknown unrelated individual RATHER THAN; IF they originated from two unknown unrelated individuals as calculated based on the [Location Identifying Population] databases respectively. **Database(s):** [Location Identifying Database]
AQ6Y4N	**Method(s)**: Likelihood Ratio **Stats Analysis:** The obtained DNA result is approximately 1,08792 x 10e13 times more likely to occur if originated from Victim and 1 Unknown individual than from 2 unknown individuals in [Location Identifying Population]. Victim + 1 Unknown / 2 Unknown **Database(s):** STRidER
C2G34J	**Method(s)**: Combined Probability of Exclusion/Inclusion **Stats Analysis:** STR Results: Number of contributors: 2, including at least one male. INCLUDED as a possible contributor: Female Victim, Unknown Contributor 1. EXCLUDED as a possible contributor: Male Suspect. The estimated probability of a random, unrelated individual being included as a possible contributor to the profile is rarer than 1 in 330 billion. Y-STR Results: Number of contributors: 1 male. INCLUDED as a possible contributor: Unknown Contributor 1. Assuming no mutations in the Y chromosome, all paternal male relatives of this individual(s) are also included. EXCLUDED as a possible contributor: Male Suspect. Assuming no mutations in the Y chromosome, all paternal male relatives of this individual(s) are also excluded. **Database(s):** STR population frequency statistics calculated in Popstats using Expanded FBI STR 2015 Caucasian and African American populations as well as [Location Identifying Database]. Only the most common frequency among the five populations or 1 in 330 billion is reported, whichever is more common.
CVNZZJ	**Method(s)**: Likelihood Ratio **Stats Analysis:** INTERPRETATION: The genetic profiles obtained in each sample analyzed are presented in the results table. In the blood stain found on the crosswalk (ITEM 3), more than two alleles were found in several of the genetic systems analyzed, which indicates the presence of cells from more than one individual. The profiles of the victim and an unknown individual are included in the mixture. The probability of the discovery was then calculated assuming two hypotheses (H): H1: The mixture comes from the victim and an unknown individual. H2: The mixture comes from at least 2 unknown individuals from the reference population not genetically related. It was found that the genetic finding is 10.083.398.616.370.700.000 times more probable under the first hypothesis than under the second. CONCLUSION: The victim and an unknown individual are not excluded as contributors to the mixture of blood found on the crosswalk (ITEM 3). The discovery is 1,0 x 10^19 times more likely if the mixture comes from the victim and an unknown individual as to comes from at least 2 unknown individuals taken at random in the reference population. **Database(s):** [Location Identifying Database]
CZ747P	**Method(s)**: Random Match Probability **Stats Analysis:** For the minor contributor, which matches Item 1, the probability of randomly selecting an unrelated individual is greater than the current world population. **Database(s):** Allele frequencies were obtained from NIST 1036 Revised US Population Database (July 2017) located at https://strbase.nist.gov/NISTpop.htm.

TABLE 6

WebCode	Item 3 Methods & Results
D8YVRN	**Method(s)**: Likelihood Ratio **Stats Analysis:** LR = 2,252*e+14. ITEM 1 + 1 NN / 2 NN. **Database(s):** STRidER_2019-08-02
E4GTKJ	**Method(s)**: Likelihood Ratio **Stats Analysis:** The mixed DNA profile is 16 quadrillion, 480 quadrillion and 13 quadrillion TIMES more likely; IF it originated from Item 1 and one unknown, unrelated individual RATHER THAN; IF it originated from two unknowns, unrelated individual as calculated based on the [Location Identifying Population] databases respectively. **Database(s):** [Location Identifying Database]
E8G4GJ	**Method(s)**: Likelihood Ratio **Stats Analysis:** The mixed DNA profile are 16 quadrillion, 480 quadrillion and 13 quadrillion TIMES more likely; IF they originated from "Item 1" and one unknown individual RATHER THAN; IF they originated from two unknown unrelated individual as calculated based on the [Location Identifying Population] databases respectively. **Database(s):** [Location Identifying Database]
ELVARH	**Method(s)**: Likelihood Ratio **Stats Analysis:** The evidence is 10 sextillion times more likely if the Female Victim is a contributor to the DNA mixture than if she is not a contributor. Further comparison may be done for the remaining component of the mixture upon the submission of additional relevant reference standards. **Database(s):** FBI Expanded
EPWDHJ	**Method(s)**: Likelihood Ratio **Stats Analysis:** The mixed DNA profile are 16 quadrillion (16e15), 480 quadrillion (480e15) and 13 quadrillion (13e15) TIMES more likely; IF they originated from the source represented by Item 1 and one unknown unrelated individual RATHER THAN; IF they originated from two unknown unrelated individuals as calculated based on the [Location Identifying Population] databases, respectively. **Database(s):** [Location Identifying Database]
FBV2LK	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA result obtained from stain (Item 3) on crosswalk is consistent with a mixture from at least two (2) contributors: a) The mixture is approximately 4.46 x 10^23 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. b) The suspect has been excluded as being a contributor to this mixture. **Database(s):** FBI_extended_Cauc population.
GC3ZVJ	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA result obtained from Item 3 is consistent with a mixture from at least two (2) contributors, including at least one (1) male: a) The mixture is approximately 3.88 x 10^23 times more likely to occur (very strong support for inclusion) if the Female victim and one (1) unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. b) The Male suspect has been excluded as being a contributor to this mixture. **Database(s):** STRMix
GGVZAF	**Method(s)**: Likelihood Ratio **Stats Analysis:** This DNA result is approximately 6.76 quadrillion times more likely if Item 1 and 1 unknown individual were the sources of the mixture DNA profile than if 2 unknown individuals were the sources. (STRmix LR): This favors support that Item 1 is included as a contributor to the DNA profile from Item 3. The DNA profile from Item 2 was compared to Item 3. Item 2 is excluded as a contributor to the DNA profile from Item 3. **Database(s):** NIST 1036 (2017)
GU2VTG	**Method(s)**: Likelihood Ratio **Stats Analysis:** [Participant did not report statistical analysis.] **Database(s):** NIST1036_CAUC

TABLE 6

WebCode	Item 3 Methods & Results
H8KXNE	**Method(s)**: Likelihood Ratio **Stats Analysis:** STR Results: This DNA result is approximately 6.80 quadrillion times more likely if Item 1 (Female Victim) and 1 unknown individual were the sources of the mixture DNA profile than if 2 unknown individuals were the sources. Item 2 (Male Suspect) is excluded as a contributor to the DNA profile from Item 3. (The exclusion of an individual with a listed LR of zero). YSTR Results: The Yfiler Plus DNA profile obtained from Item 3 is a single source profile and does not match the DNA profile from Item 2 (Male Suspect). **Database(s):** NIST 1036 (2017) for STR Results.
J8JM7G	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA result obtained from Item 3 is consistent with a mixture from at least two (2) contributors, including at least one (1) male: (a) The mixture is approximately 3.70 x 10 ^23 times more likely to occur (very strong support for inclusion) if Item 1 (victim) and one (1) unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. (b) Item 2 (suspect) has been excluded as being a contributor to this mixture. **Database(s):** FBI_extended_Cauc
JXR8GC	**Method(s)**: Likelihood Ratio **Stats Analysis:** It is exceedingly more probable, by 1,17601E013 times, to observe the DNA profile if the mixed stain originated from Item 1 and one unknown persons than if it originated from two unknown persons. No full DNA from Item 2 was detected in Item 3. A full Y-chromosome DNA profile was identified in ITEM 3. A full Y-chromosome DNA profile consistent with Item 2 was not identified in the stain. **Database(s):** GlobalFiler calculations were performed using LRmix Studio version 2.1.5 and the STRidER allele frequency database.
KC7REB	**Method(s)**: Likelihood Ratio **Stats Analysis:** (STR): The DNA profile from this item is at least 1.3 octillion times more likely if it originated from Victim and an unknown individual than if it originated from two unknown, unrelated individuals. **Database(s):** Most conservative population group statistic is reported. (STR): The National Institute of Standards and Technology's published database is utilized in the statistical calculations. Hill, C.R., Duewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. Forensic Sci. Int. Genet. 7: e82-e83. Revised data received on August 10, 2017.
L3XGMC	**Method(s)**: Likelihood Ratio **Stats Analysis:** H0: The donors of the biological traces identified on the crosswalk (ITEM 3) are the victim and one unknown, with the victim unrelated individual from our population. H1: The donors of the biological traces identified on crosswalk (ITEM 3) are two unknown, with the victim unrelated individuals from our population. It is 8,4e21 times more likely to observe the DNA profile if the mixed stain on crosswalk (ITEM 3) originates from ITEM 1 (Victim) and one unknown individual unrelated to the victim, than if it originated from two unknown individuals, unrelated to the ITEM 1 (Victim). Theta is 0.01 and probability of drop in is 0.05. **Database(s):** Rare allele frequency 0,0007. We used frequencies based on [Location Identifying Population] (available at http://strider.online/frequencies). At STRiDER there are frequencies combined from GlobalFiler and NGM, in test we used only frequencies from GlobalFiler (population of 700 people).
M2GKUC	**Method(s)**: [Participant did not report a method.] **Stats Analysis:** Probabilistic genotyping performed upon request in order to determine LR **Database(s):** [Participant did not report database(s).]

TABLE 6

WebCode	Item 3 Methods & Results
M8P98D	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA result obtained from the stain (Item 3) allegedly taken from crosswalk at the scene of crime is consistent with a mixture from at least two (2) contributors, including at least one (1) male. This mixture is approximately 3.00 x 10^23 times more likely to occur if the female complainant and one (1) unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. The male suspect has been excluded as being a contributor to this mixture. **Database(s):** FBI_EXTENDED_CAUC
N387Z9	**Method(s)**: Likelihood Ratio **Stats Analysis:** 10.083.398.616.370.700.000 **Database(s):** [Location Identifying Database]
PPGVQ9	**Method(s)**: Random Match Probability **Stats Analysis:** The probability of selecting an unrelated individual at random who could be included as a possible contributor to the mixture DNA profile is approximately 1 in 4.5 quadrillion (10^15) **Database(s):** NIST 1036 (2017 revision)
PPQEAJ	**Method(s)**: Likelihood Ratio **Stats Analysis:** It is 100 sextillion times more likely that the DNA profile obtained from this item originates from Item 1 (victim) and an unknown, unrelated individual rather than two unknown, unrelated individuals. Item 2 (suspect) can be excluded as a possible contributor to the DNA profile due to an LR of 0. **Database(s):** NIST 1036 combined
PXB2KA	**Method(s)**: Likelihood Ratio **Stats Analysis:** The genetic profile obtained from Item 3 is interpreted as a mixture of DNA from three contributors. Item 1 (victim) cannot be excluded as a possible contributor to this mixture. Given this genetic profile, assuming three contributors, it is 19.8 trillion times more likely to observe this genetic profile if Item 1 (victim) and two unknown individuals are contributors than if 3 unknown individuals are the contributors. Item 2 (suspect) is excluded as a possible contributor to this mixture. **Database(s):** NIST
TL8MC9	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA result obtained from stain on crosswalk (Item 3) is consistent with a mixture from at least two (2) contributors, including at least one (1) male: a) The mixture is approximately 5.60 x 10^23 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 male suspect has been excluded as being a contributor to this mixture. **Database(s):** [Participant did not report database(s).]
UR9LZ3	**Method(s)**: Likelihood Ratio **Stats Analysis:** The victim and one unknown person are not excluded as contributors of the mixed cells found in the Item 3. Is 1,01E+19 times more probable this finding if the mixture comes from the victim and one unknown person than if the mixture come from the two unknown persons from the reference population. **Database(s):** [Location Identifying Database]
VQRN93	**Method(s)**: Likelihood Ratio **Stats Analysis:** Log10LR ITEM 3 (2 persons mixture). - CASESOLVER: item1+1unkn vs 2 unkn = 1.6E+01, item2+1unkn vs 2 unkn = -6.0+00. - LRMIX STUDIO: item1+1unkn vs 2 unkn = 1.4E+01. - LAB RETRIEVER: item1+1unkn vs 2 unkn = 1.3E+01 (afr. pop), 1.3E+01 (cauc. pop), 1.4E+01 (hisp. pop). - EUROFORMIX: item1+1unkn vs 2 unkn = 2.5E+01. **Database(s):** NIST All population

TABLE 6

WebCode	Item 3 Methods & Results
XN22QZ	**Method(s)**: Likelihood Ratio **Stats Analysis:** A mixed DNA profile of two contributors was developed from "Item 3". The DNA profile obtained from the reference sample of "Item 1" is one of the contributors to this mixed profile. The mixed DNA profile is 16 quadrillion (16 x 10e15), 480 quadrillion (480 x 10e15) and 13 quadrillion (13 x 10e15) TIMES more likely; IF they originated from "Item 1" and one unknown unrelated individual RATHER THAN; IF they originated from two unknown unrelated individual as calculated based on the [Location Identifying Population] databases respectively. **Database(s):** [Location Identifying Database]
YMZNJX	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile from this item is at least 1.2 octillion times more likely if it originated from Item 1 (victim) and an unknown individual than if it originated from two unknown, unrelated individuals. **Database(s):** The most conservative statistic is reported. The National Institute of Standards and Technology's published database is utilized in the statistical calculations. Hill, C.R., Duewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. Forensic Sci. Int. Genet. 7: e82-e83. Revised data received on August 10, 2017.
YP4J3Z	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA result obtained from the stain on crosswalk (Item 3) is consistent with a mixture from at least two (2) contributors, including one (1) male. The mixture is approximately 2.07E23 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 suspect has been excluded as being a contributor to this mixture **Database(s):** FBI_EXTENDED_CAUC
YWQCDZ	**Method(s)**: Likelihood Ratio **Stats Analysis:** Prosecution Hypothesis: ITEM1 + unknow. Defense Hypothesis: 2 unknow. LR= 8,9959E14 dropout= 0. **Database(s):** STRidER_ [Location Identifying Database]

Statistical Analysis for Item 4

TABLE 7

WebCode	Item 4 Methods & Results
36QZJU	**Method(s)**: Likelihood Ratio **Stats Analysis**: (STR): The DNA profile from this item is at least 1.2 octillion times more likely if it originated from Victim and an unknown individual than if it originated from two unknown, unrelated individuals. The DNA profile from this item is at least 320 octillion times more likely if it originated from Suspect and an unknown individual than if it originated from two unknown, unrelated individuals. (Y-STR): The DNA profile is at least 1,030 times more likely if the profile originated from Suspect (or a patrilineal relative) than if it originated from a randomly selected individual. **Database(s):** Most conservative population group statistic is reported. The National Institute of Standards and Technology's published database is utilized in the statistical calculations. Hill, C.R., Duewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. Forensic Sci. Int. Genet. 7: e82-e83. Revised data received on August 10, 2017. Y-Chromosome Haplotype Reference Database: https://yhrd.org.
3YHFVW	**Method(s)**: [Participant did not report a method.] **Stats Analysis**: Working from the pdf of the electropherogram, it is not possible to perform a thorough evaluation of each locus. As a result it is possible to miss very minor contributions from additional contributors and be incorrect in the possible number of contributors to complex mixture samples. It is also not possible to thoroughly evaluate spikes, pullup, and baseline irregularities which can affect correct allele determinations. I am a forensic consultant that reviews DNA case files submitted to me as evidence. I review the analyst allele calls and evidence to reference sample comparisons so I can understand how the original analyst arrived at their opinions and conclusions. I accept that their population calculations are correct. N/A: Not Applicable. NSD: No Size Data **Database(s):** [Participant did not report database(s).]
6WK94V	**Method(s)**: Likelihood Ratio **Stats Analysis**: Statistical Results (Autosomal): Under the assumption that the VICTIM (Item 1) and one unknown unrelated person selected at random from the general population are contributors, the likelihood of observing the mixed source profile developed from the STAIN ON SUSPECT'S CAR (Item 4) is ≥1,000,000 times greater (actual LR available upon request) than if it is assumed that two unknown unrelated persons selected at random from the general population are contributors to this mixed-source profile. Under the assumption that the SUSPECT (Item 2) and one unknown unrelated person selected at random from the general population are contributors, the likelihood of observing the mixed source profile developed from the STAIN ON SUSPECT'S CAR (Item 4) is ≥1,000,000 times greater (actual LR available upon request) than if it is assumed that two unknown unrelated persons selected at random from the general population are contributors to this mixed-source profile. Statistical Results (YSTR): The SUSPECT (Item 2), his paternally-related male relatives, and an unknown number of males in the general population cannot be excluded as the potential source of the YSTR haplotype developed from the STAIN ON SUSPECT'S CAR (Item 4). Given a theta-value of 6.0 × 10-05 and a 95% UCI of the combined Haplotype frequency of 1 in 8,568 (0 matches in 25,666 Haplotypes at [Location Identifying Population] without Native American), the corrected Match Probability is 1 in 5,659. **Database(s):** Statistical Calculations employed the following databases: Revised-NIST-1036-Allele Frequencies; ABI ID Allele Frequencies; Promega PowePlex Fusion Allele Frequencies and YHRD Release R69 valid as per 2024-03-07 20:22:41 UTC
6X26VV	**Method(s)**: Likelihood Ratio **Stats Analysis**: CONCLUSION The DNA result obtained from the stain allegedly taken from the exterior of the suspect car is consistent with a mixture from at least two (2) contributors, including at least one (1) male: a) The mixture is approximately 4.88 x 10^ 24 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. b) The mixture is approximately 2.66 x 10^ 26 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. END OF REPORT **Database(s):** [Participant did not report database(s).]

TABLE 7

WebCode	Item 4 Methods & Results
7DQRET	**Method(s)**: Likelihood Ratio **Stats Analysis**: Hp=V+Un, Hd=Un+Un, LR=1,4x10^15. Hp=S+Un, Hd=Un+Un, LR=2,4x10^15. **Database(s):** STRider [Location Identifying Database]
7E6WDQ	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA profile obtained from Item 4 is greater than 100 billion times more likely to be obtained if the victim and the suspect have contributed rather than two unknown, unrelated, individuals. **Database(s):** [Location Identifying Database]
7GQ3AR	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result from Item 4 is consistent with mixture from at least 2 contributors. The mixture is approximately 1x10^26 times more likely to occur if the victim and one unknown individual are contributors, rather than if the DNA is from two unknown individuals. The DNA result from Item 4 is consistent with mixture from at least 2 contributors. The mixture is approximately 1x10^27 times more likely to occur if the suspect and one unknown individual are contributors, rather than if the DNA is from two unknown individuals. **Database(s):** EuroForMix: Imported from STRideR [Location Identifying Database]
7MGDKQ	**Method(s)**: Likelihood Ratio **Stats Analysis**: Stutter filter was applied on DNA profiling. Item 4 (car stain) indicates the presence of a mixture. The number of alleles indicates that the mixture may be a two person mixture. Item 4 (car stain) could have originated from Victim (Item 1) and Suspect (Item 2). Common parameters used for statistical analyses: P(dropin) = 0.03; Pmin = 0.001; FST = 0.015. Hp hypothesis: POI + 1 unrelated unknown contributor. Hd hypothesis: 2 unrelated unknown contributors. LRmixStudio v2.1.5 (PowerPlex Fusion 6C and Globalfiler DNA profile replicates): P(dropout) = 0.2; POI: Victim (Item 1) -> LR = 3.6E+15; POI: Suspect (Item 2) -> LR = 2.9E+16 / DNAxs v2.8.11 MLE (PowerPlex Fusion 6C and Globalfiler DNA profile replicates): P(dropout lambda) = 0.01; Backward stutter model was applied. Degradation model was not applied. POI: Victim (Item 1) -> LR = 4.4E+26; POI: Suspect (Item 2) -> LR = 7.0E+28; Estimated DNA profile mixture ratios: Victim: 71%, Suspect: 29% / DNAxs v2.8.11 MixCal (PowerPlex Fusion 6C and Globalfiler DNA profile replicates): POI: Victim (Item 1) -> LR = 1.0E+16; POI: Suspect (Item 2) -> LR = 7.7E+16 / EuroForMix v4.2.5 (PowerPlex Fusion 6C DNA profile): P(dropout lambda) = 0.01; Backward stutter model was applied. Degradation model was applied. POI: Victim (Item 1) -> LR = 3.0E+26; POI: Suspect (Item 2) -> LR = 8.6E+27 / EuroForMixRep v1.1.0 (PowerPlex Fusion 6C and Globalfiler DNA profile replicates): P(dropout lambda) = 0.01; Backward stutter model was applied. Degradation model was applied. POI: Victim (Item 1) -> LR = 3.8E+26; POI: Suspect (Item 2) -> LR = 9.6E+28 / The LR results of the statistical analyses strongly support the hypothesis that Item 4 (car stain) contains Victim's and Suspect's DNA. **Database(s):** STRidER R2 Europe: https://strider.online/frequencies / Bodner et al. 2016: https://doi.org/10.1016/j.fsigen.2016.06.008.
7Y7CBT	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result obtained from the stain on suspect's car (Item 4) is consistent with a mixture from at least two (2) contributors, including at least one (1) male: a) The mixture is approximately 4.86 x 10^23 times more likely to occur (very strong support for inclusion) if the female victim and one (1) unknown, unrelated individual are contributors rather than if two (2) unknown, unrelated individuals are contributors. b) The mixture is approximately 2.34 x 10^26 times more likely to occur (very strong support for inclusion) if the male suspect and one (1) unknown, unrelated individual are contributors rather than if two (2) unknown, unrelated individuals are contributors. **Database(s):** FBI Extended Caucasian
8XBUAR	**Method(s)**: Likelihood Ratio **Stats Analysis**: Item 1: 1,51 x 10^15 (Item 1 + unknown/2 unknown). Item 2: 2,38 x 10^15 (Item 2 + unknown/2 unknown). Item 1 + Item 2 : 6,52 x 10^34 (Item 1 + Item 2/2 unknown). **Database(s):** STRidER

TABLE 7

WebCode	Item 4 Methods & Results
9DMLDN	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA profile from this item is at least 1.4 octillion times more likely if it originated from Victim and an unknown individual than if it originated from two unknown, unrelated individuals. The DNA profile from this item is at least 340 octillion times more likely if it originated from Suspect and an unknown individual than if it originated from two unknown, unrelated individuals. The YSTR DNA profile is at least 1,030 times more likely if the profile originated from Suspect (or a patrilineal relative) than if it originated from a randomly selected individual. **Database(s):** Most conservative population group statistic is reported. The National Institute of Standards and Technology's published database is utilized in the statistical calculations. Hill, C.R., Duewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. Forensic Sci. Int. Genet. 7: e82-e83. Revised data received on August 10, 2017. Match probability and profile probability are approximate and derived from queries against the Y-Chromosome Haplotype Reference Database: https://yhrd.org.
9DMP3T	**Method(s)**: Random Match Probability **Stats Analysis**: Item 1 RMP(Tri) = 1.73E+26. Item 1 RMP(Cau)= 8.27E+26. Item 2 RMP(Tri) = 5.80E+30. Item 2 RMP(Cau)= 1.03E+29. **Database(s):** [Location Identifying Database]
9KJJZR	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA results is approximately 4.65E24 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 DNA results is approximately 2.35E26 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. **Database(s):** FBI extended caucasian
AGUWHN	**Method(s)**: Likelihood Ratio **Stats Analysis**: LRmix Studio v.2.1.3. Item 1: LR =1,35683E013 (drop out probability 0,26). Item 2: LR =1,56850E013 (drop out probability 0,26). **Database(s):** STRidER 2.0 [Location Identifying Database]
APAF3M	**Method(s)**: Likelihood Ratio **Stats Analysis**: The mixed DNA profile is 910 quintillion (910e18), 7.5 sextillion (7.5e21) and 750 quintillion (750e18) TIMES more likely if they originated from the victim (Item 1) and suspect (Item 2) RATHER THAN; IF they originated from suspect (Item 2) and one unknown unrelated individual as calculated based on the [Location Identifying Population] databases respectively. **Database(s):** [Location Identifying Database]
AQ6Y4N	**Method(s)**: Likelihood Ratio **Stats Analysis**: The obtained DNA result is approximately 1,37139 x 10e13 times more likely to occur if originated from Victim and 1 Unknown individual than from 2 unknown individuals in [Location Identifying Population]. Victim + 1 Unknown / 2 Unknown. The obtained DNA result is approximately 1,86757 x 10e13 times more likely to occur if originated from Suspect and 1 Unknown individual than from 2 unknown individuals in [Location Identifying Population]. Suspect + 1 Unknown / 2 Unknown. **Database(s):** STRidER

TABLE 7

WebCode	Item 4 Methods & Results
C2G34J	**Method(s)**: Combined Probability of Exclusion/Inclusion, Random Match Probability, YHRD **Stats Analysis**: STR Results: Number of contributors: 2, including at least one male. INCLUDED as a possible contributor (17 loci used): Female Victim, Male Suspect. The estimated probability of a random, unrelated individual being included as a possible contributor to the profile is rarer than 1 in 330 billion. Major Component: Number of contributors: 1 female. INCLUDED as a possible contributor (8 loci used): Female Victim. The estimated frequency of this profile is rarer than 1 in 26 billion. Y-STR Results: Number of contributors: 1 male. INCLUDED as a possible contributor: Male Suspect. Assuming no mutations in the Y chromosome, all paternal male relatives of this individual(s) are also included. This Y-STR profile is not expected to occur more frequently than 1 in 140 male individuals. **Database(s):** STR population frequency statistics calculated in Popstats using Expanded FBI STR 2015 Caucasian and African American populations as well as [Location Identifying Database]. Only the most common frequency among the five populations or 1 in 330 billion is reported, whichever is more common. Y-STR population frequency statistics calculated in YHRD.org using the Y17 dataset with the National Database (with Subpopulations, 2014 SWGDAM compliant) - [Location Identifying Population]. Only the most common frequency is reported, using the 95% confidence interval.
CVNZZJ	**Method(s)**: Likelihood Ratio **Stats Analysis**: INTERPRETATION: The genetic profiles obtained in each sample analyzed are presented in the results table. In the blood stain found on the suspect's car (ITEM 4), more than two alleles were found in several of the genetic systems analyzed, which indicates the presence of cells from more than one individual. The profiles of the victim and the suspect are included in the mixture. The probability of the discovery was then calculated assuming two hypotheses (H): H1: The mixture comes from the suspect and the victim. H2: The mixture comes from at least 2 unknown individuals from the reference population who are not genetically related. It was found that the genetic finding is 481.280.414.224.782.000.000.000.000.000.000.000.000.000.000 times more probable under the first hypothesis than under the second. CONCLUSION: The victim and the suspect are not excluded as contributors to the mixture of blood found on the suspect's car (ITEM 4). The discovery is 4,81 x 10^44 times more likely if the mixture comes from the victim and the suspect as to comes from at least 2 unknown individuals taken at random in the reference population. **Database(s):** [Location Identifying Database]
CZ747P	**Method(s)**: Random Match Probability **Stats Analysis**: For the major contributor, which matches Item 1, the probability of randomly selecting an unrelated individual is greater than the current world population. For the minor contributor, which matches Item 2, the probability of randomly selecting an unrelated individual is greater than the current world population. **Database(s):** Allele frequencies were obtained from NIST 1036 Revised US Population Database (July 2017) located at https://strbase.nist.gov/NISTpop.htm.
D8YVRN	**Method(s)**: Likelihood Ratio **Stats Analysis**: LR = 3,5149*e+35. ITEM 1 + ITEM 2 / 2 NN. **Database(s):** STRidER_2019-08-02
E4GTKJ	**Method(s)**: Likelihood Ratio **Stats Analysis**: The mixed DNA profile are 910 quintillion, 7.5 sextillion and 750 quintillion TIMES more likely; IF it originated from Item 1 and Item 2 RATHER THAN; IF it originated from Item 2 and one unknown, unrelated individual as calculated based on the [Location Identifying Population] databases respectively. **Database(s):** [Location Identifying Database]
E8G4GJ	**Method(s)**: Likelihood Ratio **Stats Analysis**: The mixed DNA profile are 910 quintillion, 7.5 sextillion and 750 quintillion TIMES more likely; IF they originated from “Item 1” and “Item 2” RATHER THAN; IF they originated from “Item 2” and one unknown unrelated individual as calculated based on the [Location Identifying Population] databases respectively. **Database(s):** [Location Identifying Database]

TABLE 7

WebCode	Item 4 Methods & Results
ELVARH	**Method(s)**: Likelihood Ratio **Stats Analysis**: The evidence is 76 sextillion times more likely if the Female Victim is a contributor to the DNA mixture than if she is not a contributor. The evidence is 1.2 septillion times more likely if the Male Suspect is a contributor to the DNA mixture than if he is not a contributor. **Database(s):** FBI Expanded
EPWDHJ	**Method(s)**: Likelihood Ratio **Stats Analysis**: The mixed DNA profile are 910 quintillion (910e18), 7.5 sextillion (7.5e21) and 750 quintillion (750e18) TIMES more likely; IF they originated from the sources represented by Item 1 and Item 2 RATHER THAN; IF they originated from the source represented by Item 2 and one unknown unrelated individual as calculated based on the [Location Identifying Population] databases, respectively. **Database(s):** [Location Identifying Database]
FBV2LK	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result obtained from stain (Item 4) on suspect's car is consistent with a mixture from at least two (2) contributors: a) The mixture is approximately 2.20 x 10^25 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. b) The mixture is approximately 2.58 x 10^26 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. **Database(s):** FBI_extended_Cauc population.
GC3ZVJ	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result obtained from Item 4 is consistent with a mixture from at least two (2) contributors, including at least one (1) male: a) The mixture is approximately 5.44 x 10^24 times more likely to occur (very strong support for inclusion) if the Female victim and one (1) unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. b) The mixture is approximately 1.98 x 10^26 times more likely to occur (very strong support for inclusion) if the Male suspect and one (1) unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. **Database(s):** STRMix
GGVZAF	**Method(s)**: Likelihood Ratio **Stats Analysis**: This DNA result is approximately 15.4 quadrillion times more likely if Item 1 and 1 unknown individual were the sources of the mixture DNA profile than if 2 unknown individuals were the sources. (STRmix LR): This favors support that Item 1 is included as a contributor to the DNA profile from Item 4. This DNA result is approximately 22.1 quadrillion times more likely if Item 2 and 1 unknown individual were the sources of the mixture DNA profile than if 2 unknown individuals were the sources. (STRmix LR): This favors support that Item 2 is included as a contributor to the DNA profile from Item 4. **Database(s):** NIST 1036 (2017)
GU2VTG	**Method(s)**: Likelihood Ratio **Stats Analysis**: [Participant did not report statistical analysis.] **Database(s):** NIST1036_CAUC

TABLE 7

WebCode	Item 4 Methods & Results
H8KXNE	**Method(s)**: Likelihood Ratio, YSTR Profile Probability **Stats Analysis**: STR Results: This DNA result is approximately 14.7 quadrillion times more likely if Item 1 (Female Victim) and 1 unknown individual were the sources of the mixture DNA profile than if 2 unknown individuals were the sources. This DNA result is approximately 21.6 quadrillion times more likely if Item 2 (Male Suspect) and 1 unknown individual were the sources of the mixture DNA profile than if 2 unknown individuals were the sources. YSTR Results: The Yfiler Plus DNA profile obtained from Item 4 is a single source profile and matches the DNA profile from Item 2 (Male Suspect). Therefore, Item 2 and any of his biological paternal relatives cannot be excluded as possible contributors to this DNA profile. The profile from Item 4 has a frequency of approximately 1 in 2,829 male individuals. **Database(s):** NIST 1036 (2017) for STR Results. US National Database in YHRD, R63 for YSTR results.
J8JM7G	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result obtained from Item 4 is consistent with a mixture from at least two (2) contributors, including at least one (1) male: (a) The mixture is approximately 4.97 x 10 ^24 times more likely to occur (very strong support for inclusion) if Item 1 (victim) and one (1) unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. (b) The mixture is approximately 2.32 x 10 ^26 times more likely to occur (very strong support for inclusion) if Item 2 (suspect) and one (1) unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. **Database(s):** FBI_extended_Cauc
JXR8GC	**Method(s)**: Likelihood Ratio **Stats Analysis**: It is exceedingly more probable, by 1,11674E013 times, to observe the DNA profile if the mixted stain originated from Item 1 and one uknown person than of it originated from two unknown persons. It is exceedingly more probable, by 1,39060E013 times, to observe the DNA profile if the mixted stain originated from Item 2 and one uknown person than of it originated from two unknown persons. It is exceedingly more probable, by 4,63307E028 times, to observe the DNA profile if the mixted stain originated from Item 1 and Item 2 than of it originated from two unknown persons. A full Y-chromosome DNA profile consistent with Item 2 was identified in the stain. During the analysis, no identical Y-chromosome DNA profile matching Item 2 was found among 103 280 Y-chromosome profiles in the global population database, nor among 34,890 Y-chromosome profiles in the [Location Identifying Database], nor among 56 Y-chromosome profiles in the [Location Identifying Database]. The Y-chromosome DNA profile is inherited through the paternal line, meaning that biological relatives such as a father, son, grandfather, and brothers will share the same Y-chromosome DNA profile. The calculations were performed using the Yfiler Plus kit and the Y23 dataset. **Database(s):** GlobalFiler calculations were performed using LRmix Studio version 2.1.5 and the STRidER allele frequency database. Yfiler Plus calculations utilized the Y-Chromosome STR Haplotype Reference Database.
KC7REB	**Method(s)**: Likelihood Ratio **Stats Analysis**: (STR): The DNA profile from this item is at least 1.4 octillion times more likely if it originated from Victim and an unknown individual than if it originated from two unknown, unrelated individuals. The DNA profile from this item is at least 320 octillion times more likely if it originated from Suspect and an unknown individual than if it originated from two unknown, unrelated individuals. (YSTR): The DNA profile is at least 1,030 times more likely if the profile originated from Suspect (or a patrilineal relative) than if it originated from a randomly selected individual. **Database(s):** Most conservative population group statistic is reported. (STR): The National Institute of Standards and Technology's published database is utilized in the statistical calculations. Hill, C.R., Duewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. Forensic Sci. Int. Genet. 7: e82-e83. Revised data received on August 10, 2017. (YSTR): Y-Chromosome Haplotype Reference Database: https://yhrd.org.

TABLE 7

WebCode	Item 4 Methods & Results
L3XGMC	**Method(s)**: Likelihood Ratio **Stats Analysis**: H0: The donors of the biological traces identified on the exterior of the suspect`s car are the victim and one unknown, with the victim unrelated individual from our population. H1: The donors of the biological traces identified on the exterior of the suspect`s car are two unknown, with the victim unrelated individuals from our population. It is 1,1e25 times more likely to observe the DNA profile if the mixed stain on the exterior of the suspect's car (ITEM 4) originates from ITEM 1 (Victim) and one unknown individual unrelated to the victim, than if it originated from two unknown individuals, unrelated to the ITEM 1 (Victim). Theta os 0.01 and probability of drop in is 0.05. H0: The donors of the biological traces identified on the exterior of the suspect`s car are the suspect and one unknown, with the suspect unrelated individual from our population. H1: The donors of the biological traces identified on the exterior of the suspect`s car are two unknown, with the suspect unrelated individuals from our population. It is 4,4e25 times more likely to observe the DNA profile if the mixed stain on the exterior of the suspect`s car (ITEM 4) originates from ITEM 2 (Suspect) and one unknown individual unrelated to the suspect, than if it originated from two unknown individuals, unrelated to the ITEM 2 (Suspect). Theta is 0.01 and probability of drop in is 0.05. H0: The donors of the biological traces identified on the exterior of the suspect`s car are the suspect and the victim. H1: The donors of the biological traces identified on the exterior of the suspect`s car are two unknown, with the victim and the suspect unrelated individuals from our population. It is 1,0e51 times more likely to observe the DNA profile if the mixed stain on the exterior of the suspect`s car (ITEM 4) originates from ITEM 1 (Victim) and ITEM 2 (Suspect), than if it originated from two unknown individuals, unrelated to the ITEM 1 (Victim) and ITEM 2 (Suspect). Theta is 0.01 and probability of drop in is 0.05. **Database(s):** Rare allele frequency 0,0007. We used frequencies based on [Location Identifying Population] (available at http://strider.online/frequencies). At STRiDER there are frequencies combined from GlobalFiler and NGM, in test we used only frequencies from GlobalFiler (population of 700 people).
M2GKUC	**Method(s)**: [Participant did not report a method.] **Stats Analysis**: 20* allele at D2 only detected in Globalfiler - can neither confirm nor deny the presence of the minor 20(a) at D2. Probabilistic Genotyping performed upon request. **Database(s):** [Participant did not report database(s).]
M8P98D	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result obtained from the stain (Item 4) allegedly taken from suspect's car at the scene of crime is consistent with a mixture from at least two (2) contributors, including at least one (1) male: a) The mixture is approximately 5.39 x 10^24 times more likely to occur if the female complainant and one (1) unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. b) The mixture is approximately 2.24 x 10^26 times more likely to occur if the male suspect and one (1) unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. **Database(s):** FBI_EXTENDED_CAUC
N387Z9	**Method(s)**: Likelihood Ratio **Stats Analysis**: 481.280.414.224.782.000.000.000.000.000.000.000.000.000.000 **Database(s):** [Location Identifying Database]
PPGVQ9	**Method(s)**: Random Match Probability **Stats Analysis**: The probability of selecting an unrelated individual at random who could be included as a possible major contributor to the mixture DNA profile is approximately 1 in 55 septillion (10^24). The probability of selecting an unrelated individual at random who could be included as a possible minor contributor to the mixture DNA profile is approximately 1 in 46 septillion (10^24). **Database(s):** NIST 1036 (2017 revision)
PPQEAJ	**Method(s)**: Likelihood Ratio **Stats Analysis**: It is 400 quindecillion times more likely that the DNA profile obtained from this item originates from Item 1 (victim) and Item 2 (suspect) rather than two unknown, unrelated individuals. **Database(s):** NIST 1036

TABLE 7

WebCode	Item 4 Methods & Results
PXB2KA	**Method(s)**: Likelihood Ratio **Stats Analysis**: The genetic profile obtained from Item 4 is interpreted as a mixture of DNA from two contributors. Item 1 (victim) cannot be excluded as a possible contributor to this mixture. Given this genetic profile, assuming two contributors, it is 236.6 trillion 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. Item 2 (suspect) cannot be excluded as a possible contributor to this mixture. Given this genetic profile, assuming two contributors, it is 103.8 million times more likely to observe this genetic profile if Item 2 (suspect) and one unknown individual are contributors than if two unknown individuals are the contributors. Given this genetic profile, assuming two contributors, it is 3.2 decillion times more likely to observe this genetic profile if Item 1 (victim) and Item 2 (suspect) are both contributors than if two unknown individuals are the contributors. **Database(s):** NIST
TL8MC9	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result obtained from stain on suspect's car (Item 4) is consistent with a mixture from at least two (2) contributors, including at least one (1) male: a) The mixture is approximately 5.02 x 10^24 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 2.11 x 10^26 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. **Database(s):** [Participant did not report database(s).]
UR9LZ3	**Method(s)**: Likelihood Ratio **Stats Analysis**: The victim and the suspect are not excluded as contributors of the mixed cells found in the Item 4. Is 4,81E+44 times more probable this finding if the mixture comes from the two unknown persons from the reference population. **Database(s):** [Location Identifying Database]
VQRN93	**Method(s)**: Likelihood Ratio **Stats Analysis**: Log10LR ITEM 4 (2 persons mixture). - CASESOLVER: item1+1unkn vs 2 unkn = 1.7E+01, item2+1unkn vs 2 unkn = 1.8E+01. - LRMIX STUDIO: item1+1unkn vs 2 unkn = 1.4E+01, item2+1unkn vs 2 unkn = 1.6E+01, item1+item2 vs 2unkn = 3.4E+01. - LABRETRIEVER: item1+1unkn vs 2 unkn = 1.3E+01 (afr. pop), 1.3E+01 (cauc pop), 1.4E+01 (hisp pop), item2+1unkn vs 2 unkn = 1.5E+01 (afr. pop), 1.3E+01 (cauc pop), 1.5E+01 (hisp pop), item1+item2 vs 2unkn = 3.0E+01 (afr. pop), 2.9E+01 (cauc pop), 3.1E+01 (hisp pop). - EUROFORMIX: item1+1unkn vs 2 unkn = 2.8E+01, item2+1unkn vs 2 unkn = 2.9E+01, item1+item2 vs 2unkn = 5.7E+01. **Database(s):** NIST All population
WFRDD2	**Method(s)**: Likelihood Ratio **Stats Analysis**: I have statistically analysed this Y-STR result by considering two alternative hypotheses: (1) The source of the male DNA is "Male Suspect" and (2) The source of the male DNA is a random male from the admixed - [Location Identifying Population]. The Y-STR profile detected in Item 4 is approximately 8,400 (eight thousand and four hundred) times more likely to be obtained under hypothesis 1, rather than under hypothesis 2. NB. This statistical evaluation will also apply to other males who have the same Y-STR profile as "Male Suspect". Close paternal-line male relatives of "Male Suspect" (such as his father, brothers, sons) have a higher probability of having the same Y-STR profile as him, compared to random males in the population. However, it should be noted that a small number of close paternal-line male relatives may have different Y-STR profiles. 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 15th October 2025 using YHRD Release R69. **Database(s):** YHRD Database - https://yhrd.org

TABLE 7

WebCode	Item 4 Methods & Results
XN22QZ	**Method(s)**: Likelihood Ratio **Stats Analysis**: A mixed DNA profile of two contributors was developed from "Item 4". The DNA profile obtained from the reference sample of "Item 1" and "Item 2" are the major and minor contributors respectively to this mixed DNA profile. The mixed DNA profile is 910 quintillion (910 x 10e18), 7.5 sextillion (7.5 x 10e21) and 750 quintillion (750 x 10e18) TIMES more likely; IF they originated from "Item 2" and "Item1" RATHER THAN; IF they originated from "Item 2" and one unknown unrelated individual as calculated based on the [Location Identifying Population] databases respectively. **Database(s):** [Location Identifying Database]
YMZNJX	**Method(s)**: Likelihood Ratio **Stats Analysis**: STR: The DNA profile from this item is at least 1.4 octillion times more likely if it originated from Item 1 (victim) and an unknown individual than if it originated from two unknown, unrelated individuals. The DNA profile from this item is at least 330 octillion times more likely if it originated from Item 2 (suspect) and an unknown individual than if it originated from two unknown, unrelated individuals. YSTR: The DNA profile is at least 1,030 times more likely if the profile originated from Item 2 (suspect) (or a patrilineal relative) than if it originated from a randomly selected individual. **Database(s):** Most conservative statistic is reported. The National Institute of Standards and Technology's published database is utilized in the statistical calculations. Hill, C.R., Duewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. Forensic Sci. Int. Genet. 7: e82-e83. Revised data received on August 10, 2017. Y-Chromosome Haplotype Reference Database: https://yhrd.org.
YP4J3Z	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result obtained from the stain on suspect's car (Item 4) is consistent with a mixture from at least two (2) contributors, including one (1) male: a) The mixture is approximately 4.70E24 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. b)The mixture is approximately 2.39E26 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. **Database(s):** FBI_EXTENDED_CAUC
YWQCDZ	**Method(s)**: Likelihood Ratio **Stats Analysis**: Prosecution Hypothesis: ITEM1 + UNKWON. Defence Hypothesis: 2 UNKOWN. LR= 3,2438E14 dropout=0. Prosecution Hypothesis: ITEM2 + UNKWON. Defence Hypothesis: 2 UNKOWN. LR= 5,7382E14 dropout=0. Prosecution Hypothesis: ITEM1 + ITEM2. Defence Hypothesis: 2 UNKOWN. LR= 4, 2025E31 dropout=0. **Database(s):** STRidER_[Location Identifying Database]

Additional Comments

TABLE 8

WebCode	Additional Comments
36QZJU	NR=No Results; Y-STR AT: Blue =45, Green=70, Yellow=65, Red=75; No PHR threshold for Y-STR data utilized.
6WK94V	First the negative and reagent blank controls were quite clean in these runs with little if any indication of capillary crosstalk or spectral pull up. The analysts who generated the profiles are to be commended for the quality of their work. Second, given that the scenaro for this round indicated a presumptive blood stain recovered from a crosswalk (item 3), it was somewhat surprising that the DNA profile from the victim (item 1) would show up as a minor contributor. This is based on the fact that blood is generally a rich source of DNA and studies of environmental samples in urban environments do not typically yield strong profiles. This would not impact the reporting of the ultimate reporting of the test resulsts but it was somewhat "unexpected".
7E6WDQ	Note that in this case, I would not have used YSTR analysis as the Autosomal results are reportable - the YSTR analysis does not add any value. However, for the purposes of the proficiency test I reviewed the Y STR results. The YSTR results are single source, and support the conclusions formed in the Autosomal DNA analysis. The number of contributors assigned relates to the Autosomal testing, representing the minimum, and would be reported as such. There is an apparent elevated stutter in the suspects YFP profile at DYS458. I would re-amplify the sample to confirm this, but have assumed it to be an elevated stutter for the purpose of the CTS. Item 4 - possible artefact (316.75 bp). I would investigate this further through re-amplification.
7Y7CBT	For Item 3, the 200 RFU peak observed at D21S11 was initially called a pull up of allele 7 at TH01 by Genemapper ID-X 1.7. Upon inspection of the peak, the analyst made the decision to rename this peak as allele 26, the expected stutter peak of allele 27 (RFU 3507), for the no-stutter filter project. Under current laboratory procedures Y-STR analysis would normally not be carried out for this case as it is non-sexual in nature.
9DMLDN	NR=No Results. No Peak Height Ratio is applicable to YSTR Analysis. Analytical Thresholds for YSTR Analysis: Blue - 45rfu, Green - 70rfu, Yellow - 65rfu, Red - 75rfu.
AGUWHN	Analytical treshold: GlobalFiler -B:100rfu, G:100rfu, Y:70rfu, R:70rfu, P:70rfu, O:100rfu. Analytical treshold: YFiler Plus -B:50rfu, G:50rfu, Y:100rfu, R:150rfu, P:100rfu, O:100rfu
APAF3M	Statistical calculation was carried out using DNAview software version 37.56 and calculated at 21 genetic loci.
AYN7ZY	Our lab does not have analysis parameters for Y-STR and will be interpreting only. Item 4 DYS458 amped with PowerPlex 23 has a 19,20. The peak height ratio is 16%. Item 2 (Standard) matches at all loci except DYS458 where it is missing the 19. It is believed the 19 allele at DYS458 for item 4 is stutter. I reported it in the allele table since it was not removed from the PDF, but I believe it is stutter.
C2G34J	On Item 4, PowerPlex Y23 data at DYS458 included a low-level19 peak likely attributable to elevated stutter. There was no other indication of a possible additional contributor.
CZ747P	The statistical results obtained mean that the results are greater than 9 billion. Data interpretation for Globalfiler was performed using the PDF files. The conclusions reached were included in this submission. Data interpretation for PowerPlex Fusion was performed using the .hid files. The conclusions were consistent with the conclusions reached for GlobalFiler.
D8YVRN	Item 3: 1 women (Item 1) and NN man.
E4GTKJ	Data Analysis: 1. The HID data was analyzed with GeneMapper ID-X v1.5 software. 2. YFiler Plus was reviewed using PDF format. 3. Statistical evaluation was performed on DNAVIEW ver 37.56.
E8G4GJ	Data Analysis: 1. The HID data was analyzed with GeneMapper ID-X v1.5 software. 2. YFiler Plus was reviewed using PDF format. 3. Statistical evaluation was performed on DNA-view ver 37.56.

TABLE 8

WebCode	Additional Comments
ELVARH	Please note, my lab uses the FaSTR software rather than Genemapper ID-X, at 50RFU. This has been validated within our laboratory, with our instrumentation. This PT utilizes our validated FaSTR software using data obtained from an instrument outside our laboratory. Artifacts and stutter presentation may vary given this internal software vs external instrumentation situation. Thank you.
EPWDHJ	Statistical Evaluation: The statistical evaluations were performed on the DNA.View Statistical Software version 37.42. Remark: 'NM' denotes non-male profile.
FF3PYL	NR = No Results.
GGVZAF	For items 3 and 4, probabilistic genotyping software was used to aid in the interpretation and statistical analysis of the DNA profiles generated. The results listed in the CTS report reflect DNA profiles with stutter filters on
H8KXNE	Item 4 is determined to be an assumed 2 person mixture. At D2S1338, allele 20 appears to be an extraneous drop-in peak. The RFU for this peak is 106 and just above the labs' analytical threshold (AT) and below the drop-in cap for STRmix. Additionally, peaks consistent with a minor contributor to this assumed 2 person mixture are approximately 1000 to 2000 RFUs. The lab does not report allele tables for casework. The deconvoluted genotype for contributors 1 and 2 do not include allele 20 at D2S1338. Therefore, for the purpose of reporting the profile from item 4, allele 20 will not be included.
KC7REB	NR = No Results, Y-STR AT: Blue=45, Green=70, Yellow=65, Red=75, No PHR threshold for Y-STR data utilized.
L3XGMC	In our internal validation study of Y STR analysis (YFilerTM Plus) we didn`t do the peak height ratio and stochastic threshold for the two loci DYS385 and DY387S1.
PPGVQ9	For the interpretation of item 4, questioned sample from stain on suspect's car: Based on the zoom-in profile, the 20 allele at D2S1338 appears to be a bit wide; likewise, it is the only indication of a third contributor to this profile, as such, the peak could be artifactual; with that in mind, I will still process the 20 allele as a true peak and my interpretation will indicate that
PPQEAJ	During DNA analysis in Genemapper, the size quality had to be overridden and edited for items 1B (Known Female Reference standard) and the two positive controls (Known and Questioned). Some of the peaks for the internal size standard were not above the [Laboratory] analytical threshold of 175 RFU which caused the size quality to be lowered and incorrectly sized. For Item 1B and the Known Positive Control, 160 peak was skipped which in turn caused the 180 peak to be labeled as 160. The 240 peak was skipped and the 250 peak was then labeled as "240". To resolve the discrepancy, all incorrectly labeled peaks were edited and were able to be correctly labeled. For the Questioned Positive Control, many of the peaks were below the analytical threshold of 175 causing many of the peaks to be incorrectly labeled. Instead of the internal size standard starting at 60 bp, the size standard began at 300 bp and many peaks were skipped until the 500 peak was reached. To resolve this discrepancy, all peaks over 175 RFU were edited. Peaks 140, 160, 200, 220, 240, 260, 280, 450, and 475 were under 175 RFU and unable to be corrected. All troubleshooting steps were confirmed with the technical leader at the [Laboratory] before execution.
VQRN93	Based on DNA profile obteined from item 3, the proposition of inclusion of the Victim is at least 10^13 times more probable. Based on DNA profile obteined from item 4, the proposition of inclusion of the Victim is at least 10^13 times more probable. Based on DNA profile obteined from item 4, the proposition of inclusion of the Suspect is at least 10^13 times more probable.
XN22QZ	The statistical calculation was carried out using DNAView Statistical Software version 37.63.
YMZNJX	NR = No results. Y-STR Analytical Threshold (RFU): Blue = 45, Green = 70, Yellow = 65, Red = 75. No PHR threshold utilized for Y-STR.

-End of Report-
(Appendix may follow)

Collaborative Testing Services ~ Forensic Testing Program

Test No. 25-5882: DNA Interpretation

DATA MUST BE SUBMITTED BY **Dec. 08, 2025, 11:59 p.m. EST** TO BE INCLUDED IN THE REPORT

Participant Code: U1234A WebCode: JANDBB

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

Scenario:
Police are investigating a hit and run involving a female victim and male suspect. The victim told police that the suspect hit her with his vehicle while she was in the crosswalk and that she has several injuries from the incident. The suspect has been apprehended due to an eyewitness account. Investigators have identified a reddish-brown stain on the crosswalk where the victim was struck, which the Serology Unit indicated as blood (Item 3). Additionally, a reddish-brown stain was identified on the exterior of the suspect's car and was also indicated as blood (Item 4).

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

Items Submitted (Sample Pack INT2):
Item 1: DNA profile from reference sample (Female Victim - Caucasian)
Item 2: DNA profile from reference sample (Male Suspect - Caucasian)
Item 3: DNA profile from stain on crosswalk
Item 4: DNA profile from stain on suspect's car

To verify a complete and accurate download, the hash value for the downloaded .ZIP file is as follows:
25-5882 DNA Interpretation.zip MD5 hash value: 35a4882485b8d8e1fd3d51902c1e3c38
25-5882 DNA Interpretation.zip SHA1 hash value: 431eb9983bfc58220e6b821affc5d38e964dcd23

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:

☐ GlobalFiler™ ☐ Investigator® 24plex
☐ HID format ☐ PDF format

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

☐ PowerPlex® Fusion 5C ☐ PowerPlex® Fusion 6C

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)

STR & Amelogenin Results for Known Item 2

- 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 2:

☐ GlobalFiler™ ☐ Investigator® 24plex

☐ HID format ☐ PDF format

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

☐ PowerPlex® Fusion 5C ☐ PowerPlex® Fusion 6C

Report the Probabilistic Genotyping Software Used (if applicable):

Alleles below are sorted in **Default** *order.*

ITEM	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
2						
ITEM	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
2						
ITEM	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
2						
ITEM	Penta D	Penta E	SE33	TH01	TPOX	vWA
2						
ITEM	DYS391	DYS570	DYS576	Y Indel		
2						

YSTR Results for Known Item 2

YSTR Amplification Kit Used For Item 2:

☐ YFiler® Plus ☐ PowerPlex® Y23

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

☐ HID format ☐ PDF format

Alleles below are sorted in **Default** *order.*

ITEM	DYF387S1	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
2									
ITEM	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
2									
ITEM	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	Y GATA H4
2									

Part I: DNA ANALYSIS (continued)

STR & Amelogenin Results for Questioned Item 3

- 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.
- For each locus, if a major and minor contributor can be distinguished and your laboratory normally reports this distinction, record the results in the appropriately labeled response boxes.

STR Amplification Kit Used For Item 3:

☐ GlobalFiler™ ☐ Investigator® 24plex ☐ HID format ☐ PDF format

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

☐ PowerPlex® Fusion 5C ☐ PowerPlex® Fusion 6C

Report the Probabilistic Genotyping Software Used (if applicable):

Alleles below are sorted in **Default** *order.*

ITEM	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
3						
3 major						
3 minor						
ITEM	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**	**D18S51**
3						
3 major						
3 minor						
ITEM	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**	**FGA**
3						
3 major						
3 minor						
ITEM	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**	**vWA**
3						
3 major						
3 minor						
ITEM	**DYS391**	**DYS570**	**DYS576**	**Y Indel**		
3						
3 major						
3 minor						

YSTR Results for Questioned Item 3

YSTR Amplification Kit Used For Item 3:

☐ YFiler® Plus ☐ PowerPlex® Y23

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

☐ HID format ☐ PDF format

Alleles below are sorted in **Default** *order.*

ITEM	DYF387S1	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
3									
3 major									
3 minor									
ITEM	**DYS437**	**DYS438**	**DYS439**	**DYS448**	**DYS449**	**DYS456**	**DYS458**	**DYS460**	**DYS481**
3									
3 major									
3 minor									
ITEM	**DYS518**	**DYS533**	**DYS549**	**DYS570**	**DYS576**	**DYS627**	**DYS635**	**DYS643**	**Y GATA H4**
3									
3 major									
3 minor									

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 inconconclusive/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 inconconclusive/uninterpretable.

3) **Statistical Analysis of Item 3 DNA Typing Results:**

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

- ☐ Combined Probability of Exclusion/Inclusions (CPE/CPI)
- ☐ Likelihood Ratio (LR)
- ☐ Random Match Probability (RMP)
- Other:

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

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

Part I: DNA ANALYSIS (continued)

STR & Amelogenin Results for Questioned Item 4

- 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.
- For each locus, if a major and minor contributor can be distinguished and your laboratory normally reports this distinction, record the results in the appropriately labeled response boxes.

STR Amplification Kit Used For Item 4:

☐ GlobalFiler™ ☐ Investigator® 24plex ☐ HID format ☐ PDF format

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

☐ PowerPlex® Fusion 5C ☐ PowerPlex® Fusion 6C

Report the Probabilistic Genotyping Software Used (if applicable):

Alleles below are sorted in **Default** *order.*

ITEM	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
4						
4 major						
4 minor						
ITEM	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
4						
4 major						
4 minor						
ITEM	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
4						
4 major						
4 minor						
ITEM	Penta D	Penta E	SE33	TH01	TPOX	vWA
4						
4 major						
4 minor						
ITEM	DYS391	DYS570	DYS576	Y Indel		
4						
4 major						
4 minor						

YSTR Results for Questioned Item 4

YSTR Amplification Kit Used For Item 4:

☐ YFiler® Plus ☐ PowerPlex® Y23

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

☐ HID format ☐ PDF format

Alleles below are sorted in **Default** *order.*

ITEM	DYF387S1	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
4									
4 major									
4 minor									
ITEM	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
4									
4 major									
4 minor									
ITEM	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	Y GATA H4
4									
4 major									
4 minor									

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 inconconclusive/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 inconconclusive/uninterpretable.

3) **Statistical Analysis of Item 4 DNA Typing Results:**

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

- Combined Probability of Exclusion/Inclusions (CPE/CPI)
- Likelihood Ratio (LR)
- Random Match Probability (RMP)
- Other:

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

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

Part II: ADDITIONAL COMMENTS

Comments regarding any part of this Test.

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

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 ANAB and/or A2LA. Please select one of the following statements to ensure your data is handled appropriately.

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

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

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

ANAB Certificate No.

A2LA Certificate No.

Step 2: Complete the Laboratory Identifying Information in its entirety

Authorized Contact Person and Title

Laboratory Name

Location (City/State)