Collaborative Testing Services, Inc
FORENSIC TESTING PROGRAM

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DNA Interpretation Test No. 25-5881
Summary Report

Each participant received a digitally downloadable sample pack containing electropherograms and raw data files which they were asked to evaluate using their existing protocols. Data were returned from 40 participants and are compiled into the following tables:

Manufacturer's Information

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

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

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

Amelogenin and STR Results

Results compiled by predistribution laboratories and a consensus of participants.

Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D7S820**
	D8S1179	**D10S1248**	**D12S391**	**D13S317**	**D16S539**	**D18S51**
	D19S433	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**	**FGA**
	Penta D	**Penta E**	**SE33**	**TH01**	**TPOX**	**vWA**
	DYS391	**DYS570**	**DYS576**	**Y Indel**		
1	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
	15,15.2	29,29	15,16	X,Y	11,12	19,26
	*	*	26.2,28.2	8,9.3	8,11	15,17
	11	*	*	2		
2	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
	14,16.2	30.2,31	14,17	X,X	9,12	20,23
	*	*	17,28.2	9,9.3	8,8	16,17
	NM	NM	NM	NM		
3	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
	*	*	17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11	*	*	2		
4	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
	*	*	17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
	NM	NM	NM	NM		

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**
1	36,37	13	15,16	13	30	23	11	14	14
	14	11	12	21	27	15	16	10	24
	38	11	12	17	19	19	22	10	11
3	36,37	13	15,16	13	30	23	11	14	14
	14	11	12	21	27	15	16	10	24
	38	11	12	17	19	19	22	10	11

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

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

Summary Comments

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

Data were returned by 40 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 seven participants.

For YSTR results, all participants reported consistent results.

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

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

DNA Interpretations
For Item 3, all but one participant identified that three (or at least three) individuals contributed to the mixture. The remaining participant identified four contributors. All but one participant included the victim (Item 1) and all but two included the suspect (Item 2) as possible contributors to the stain. Of the two participants who excluded both, one did not provide a response to either conclusion, while the other reported "Inconclusive/Uninterpretable" in regards to the possible contribution of Item 2.

For Item 4, all participants identified that two (or at least two) individuals contributed to the mixture. All participants excluded the victim (Item 1) and included 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)
2LMCUV	75	55	325
2UCZPX	130	60	800
3QVXHT	70	70	345
4NM3CV	130	60	800
6PQHXR	100	70	300
6X648V	75	60	100
7463VP	120	60	360
7DECMP	160	60	630
9RPU8N	75	60	100
ABDFQQ	150	60	400
AECRLQ	[Participant did not provide interpretation guidelines]		
AQ9XFN	130	60	800
AXRZMQ	75	60	100
BJ79CP	75	60	100
CL64AJ	70	70	345
CMJBXL	175	70	175
ETMEXQ		60	200
EUBPBH	75	60	250
GNJ2TH	75	60	100
GYDFTE	70	70	345
JP2ZZB	70	70	345
JTMK6F	130	60	800
K78LZC	180	50	370
KLXLRC	50	65	200
LXR3GD	130	60	800
N2K7XA	130	60	800
NPQP99	[Participant did not provide interpretation guidelines]		
NQL8BA	130	60	800
PGB7PA	130	60	800
Q2UUC7	80	60	250
QJEKB7	120	60	360
RN3K37	50	60	865
RWXPW8	[Participant did not provide interpretation guidelines]		
T3Y2R6	[Participant did not provide interpretation guidelines]		
T7XCN4	100	70	4,290
WHKKY3	130	60	800
XTFDKX	100	60	300

TABLE 1

WebCode	Analytical Threshold (rfu)	Peak Height Ratio (%)	Stochastic Threshold (rfu)
YBTHJV	50	50	900
YDE2PY	75	60	
ZDUK9W	120	60	360

YSTR Interpretation Guidelines

TABLE 2

WebCode	Analytical Threshold (rfu)	Peak Height Ratio (%)	Stochastic Threshold (rfu)
2LMCUV	[Participant did not provide interpretation guidelines]		
2UCZPX	50	70	800
3QVXHT			550
4NM3CV	50	70	800
6PQHXR	90		320
6X648V	75	50	75
7463VP	75	50	75
7DECMP	100	60	600
9RPU8N	75	50	75
ABDFQQ	[Participant did not provide interpretation guidelines]		
AECRLQ	[Participant did not provide interpretation guidelines]		
AQ9XFN	50	70	800
AXRZMQ	75	50	75
BJ79CP	75	50	75
CL64AJ			550
CMJBXL	175	70	175
ETMEXQ	75	50	225
EUBPBH	[Participant did not provide interpretation guidelines]		
GNJ2TH	75	50	75
GYDFTE			550
JP2ZZB			550
JTMK6F	50	70	800
K78LZC	[Participant did not provide interpretation guidelines]		
KLXLRC	50	65	175
LXR3GD	50	70	800
N2K7XA	50	70	800
NPQP99	[Participant did not provide interpretation guidelines]		
NQL8BA	50	70	800
PGB7PA	[Participant did not provide interpretation guidelines]		
Q2UUC7	80	50	75
QJEKB7	75	50	75
RN3K37	[Participant did not provide interpretation guidelines]		
RWXPW8	[Participant did not provide interpretation guidelines]		
T3Y2R6	[Participant did not provide interpretation guidelines]		
T7XCN4	[Participant did not provide interpretation guidelines]		
WHKKY3	50	70	800
XTFDKX	90	40	320

TABLE 2

WebCode	Analytical Threshold (rfu)	Peak Height Ratio (%)	Stochastic Threshold (rfu)
YBTHJV	[Participant did not provide interpretation guidelines]		
YDE2PY	75	50	
ZDUK9W	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

2LMCUV	GlobalFiler™ (HID Format)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
2UCZPX	GlobalFiler™ (PDF Format), (HID Format)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11,11			2		
3QVXHT	PowerPlex® Fusion 6C (HID Format)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
	12,13	8,9	26.2,28.2	8,9.3	8,11	15,17
	11	17	19			
4NM3CV	GlobalFiler™ (HID Format) (STRMix)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
6PQHXR	GlobalFiler™ (HID Format)					
	15,17.3	19,21	14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11	14,15
1	15,15.2	29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
6X648V	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format)					
	15,17.3	19,21	14	17,18	11,13	10,12
	14,15	13,14	19,21	10,12	11	14,15
1	15,15.2	29	15,16	X,Y	11,12	19,26
	12,13	8,9	26.2,28.2	8,9.3	8,11	15,17
	11	17	19	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 1 - STR Results			
7463VP	GlobalFiler™ (HID Format)					
	15,17.3	19,21	14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11	14,15
1	15,15.2	29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
7DECMP	GlobalFiler™ (HID Format)					
	15,17.3	19,21	14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11	14,15
1	15,15.2	29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
9RPU8N	GlobalFiler™ (PDF Format)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
ABDFQQ	GlobalFiler™ (PDF Format)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
AECRLQ	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format)					
	15,17.3	19,21	14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11	14,15
1	15,15.2	29	15,16	X,Y	11,12	19,26
	12,13	8,9	26.2,28.2	8,9.3	8,11	15,17
	11	17	19	2		
AQ9XFN	GlobalFiler™ (HID Format)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
	-	-	26.2,28.2	8,9.3	8,11	15,17
	11	-	-	2		

TABLE 3

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

Item 1 - STR Results

AXRZMQ	GlobalFiler™ (HID Format)					
	15,17.3	19,21	14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11	14,15
1	15,15.2	29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
BJ79CP	PowerPlex® Fusion 6C (HID Format)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
	12,13	8,9	26.2,28.2	8,9.3	8,11	15,17
	11	17	19	N/A		
CL64AJ	PowerPlex® Fusion 6C (HID Format) (STRmix)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
	12,13	8,9	26.2,28.2	8,9.3	8,11	15,17
	11	17	19			
CMJBXL	GlobalFiler™ (HID Format)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
ETMEXQ	Investigator® 24plex (HID Format) (GeneMarker V.2.9.5. (SoftGenetics))					
	15,17.3	19,21	14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11	14,15
1	15,15.2	29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11					
EUBPBH	GlobalFiler™ (STRmix)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		

TABLE 3

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

Item 1 - STR Results

GNJ2TH	GlobalFiler™ (PDF Format)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
	N/A	N/A	26.2,28.2	8,9.3	8,11	15,17
	11	N/A	N/A	2		
GYDFTE	PowerPlex® Fusion 6C (HID Format)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
	12,13	8,9	26.2,28.2	8,9.3	8,11	15,17
	11	17	19			
JP2ZZB	PowerPlex® Fusion 6C (HID Format)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
	12,13	8,9	26.2,28.2	8,9.3	8,11	15,17
	11	17	19			
JTMK6F	GlobalFiler™ (HID Format) (STRMix)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
K78LZC	Investigator® 24plex					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
	n/a	n/a	26.2,28.2	8,9.3	8,11	15,17
	11	n/a	n/a	n/a		
KLXLRC	PowerPlex® Fusion 5C					
	15,17.3	19,21	14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11	14,15
1	15,15.2	29	15,16	X,Y	11,12	19,26
	12,13	8,9		8,9.3	8,11	15,17
	11					

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

LXR3GD	GlobalFiler™ (HID Format)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
N2K7XA	GlobalFiler™ (HID Format)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
NPQP99	GlobalFiler™ (PDF Format)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
NQL8BA	GlobalFiler™ (STRmix)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
PGB7PA	GlobalFiler™ (PDF Format) (STRMIX)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
Q2UUC7	GlobalFiler™ (PDF Format)					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		

TABLE 3

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

Item 1 - STR Results

QJEKB7	GlobalFiler™ (PDF Format)					
	15,17.3	19,21	14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11	14,15
1	15,15.2	29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
RN3K37	GlobalFiler™ (PDF Format) (LRmix Studio ver. 2.1.5-Community Edition)					
	15,17.3	19,21	14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11	14,15
1	15,15.2	29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
RWXPW8	GlobalFiler™					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
T3Y2R6	GlobalFiler™					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
T7XCN4	PowerPlex® Fusion 5C (HID Format)					
	15,17.3	19,21	14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11	14,15
1	15,15.2	29	15,16	X,Y	11,12	19,26
	12,13	8,9		8,9.3	8,11	15,17
	11					
WHKKY3	GlobalFiler™					
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		

TABLE 3

WebCode	**Amplification Kits**	**(File Format)**	**(Probabilistic Genotyping)**			
	D1S1656	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D7S820**
	D8S1179	**D10S1248**	**D12S391**	**D13S317**	**D16S539**	**D18S51**
Item	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**	**FGA**
	Penta D	**Penta E**	**SE33**	**TH01**	**TPOX**	**vWA**
	DYS391	**DYS570**	**DYS576**	**Y Indel**		
			Item 1 - STR Results			
XTFDKX	GlobalFiler™	(HID Format)				
	15,17.3	19,21	14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11	14,15
1	15,15.2	29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
YBTHJV	GlobalFiler™	(HID Format)	(STRmix)			
	15,17.3	19,21	14,14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11,11	14,15
1	15,15.2	29,29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
YDE2PY	GlobalFiler™	(HID Format)	(Lab Retriever)			
	15,17.3	19,21	14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11	14,15
1	15,15.2	29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		
ZDUK9W	GlobalFiler™	(PDF Format)				
	15,17.3	19,21	14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11	14,15
1	15,15.2	29	15,16	X,Y	11,12	19,26
			26.2,28.2	8,9.3	8,11	15,17
	11			2		

TABLE 3

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		
			Item 2 - STR Results			
2LMCUV	GlobalFiler™ (HID Format)					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8,8	16,17
2UCZPX	GlobalFiler™ (PDF Format), (HID Format)					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8,8	16,17
	-			-		
3QVXHT	PowerPlex® Fusion 6C (HID Format)					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
	9,12	9,11	17,28.2	9,9.3	8,8	16,17
	NR	NR	NR			
4NM3CV	GlobalFiler™ (HID Format) (STRMix)					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8,8	16,17
6PQHXR	GlobalFiler™ (HID Format)					
	16.3,17.3	23,24	10,13	14,15	12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X	9,12	20,23
			17,28.2	9,9.3	8	16,17
6X648V	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format)					
	16.3,17.3	23,24	10,13	14,15	12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X	9,12	20,23
	9,12	9,11	17,28.2	9,9.3	8	16,17

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

7463VP	GlobalFiler™ (HID Format)					
	16.3,17.3	23,24	10,13	14,15	12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8	16,17
	NM			NM		
7DECMP	GlobalFiler™ (HID Format)					
	16.3,17.3	23,24	10,13	14,15	12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X	9,12	20,23
			17,28.2	9,9.3	8	16,17
9RPU8N	GlobalFiler™ (PDF Format)					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8,8	16,17
ABDFQQ	GlobalFiler™ (PDF Format)					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8,8	16,17
	--			--		
AECRLQ	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format)					
	16.3,17.3	23,24	10,13	14,15	12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X	9,12	20,23
	9,12	9,11	17,28.2	9,9.3	8	16,17
AQ9XFN	GlobalFiler™ (HID Format)					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
	-	-	17,28.2	9,9.3	8,8	16,17
	-	-	-	-		

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			
AXRZMQ	GlobalFiler™ (HID Format)					
	16.3,17.3	23,24	10,13	14,15	12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X	9,12	20,23
			17,28.2	9,9.3	8	16,17
BJ79CP	PowerPlex® Fusion 6C (HID Format)					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
	9,12	9,11	17,28.2	9,9.3	8,8	16,17
	N/A	N/A	N/A	N/A		
CL64AJ	PowerPlex® Fusion 6C (HID Format) (STRmix)					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
	9,12	9,11	17,28.2	9,9.3	8,8	16,17
	NR	NR	NR			
CMJBXL	GlobalFiler™ (HID Format)					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8,8	16,17
ETMEXQ	Investigator® 24plex (HID Format) (GeneMarker V.2.9.5. (SoftGenetics))					
	16.3,17.3	23,24	10,13	14,15	12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X	9,12	20,23
			17,28.2	9,9.3	8	16,17
	/					
EUBPBH	GlobalFiler™ (STRmix)					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8,8	16,17

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						
GNJ2TH	GlobalFiler™ (PDF Format)					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
	N/A	N/A	17,28.2	9,9.3	8,8	16,17
	NSD	N/A	N/A	NSD		
GYDFTE	PowerPlex® Fusion 6C (HID Format)					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
	9,12	9,11	17,28.2	9,9.3	8,8	16,17
	NR	NR	NR			
JP2ZZB	PowerPlex® Fusion 6C (HID Format)					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
	9,12	9,11	17,28.2	9,9.3	8,8	16,17
	NR	NR	NR			
JTMK6F	GlobalFiler™ (HID Format) (STRMix)					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8,8	16,17
K78LZC	Investigator® 24plex					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
	n/a	n/a	17,28.2	9,9.3	8,8	16,17
	n/a	n/a	n/a	n/a		
KLXLRC	PowerPlex® Fusion 5C					
	16.3,17.3	23,24	10,13	14,15	12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X	9,12	20,23
	9,12	9,11		9,9.3	8	16,17
	-					

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

LXR3GD	GlobalFiler™	(HID Format)				
	19.3,23		14,16.2	14,15	11,13	17,28.2
	10,14	16.3,17.3	23,24	10,12	11,12	15,16
2	9,9.3	30.2,31	12,12	X,X	9,12	14,17
			15,17	20,23	8,8	16,17
	10,13					
N2K7XA	GlobalFiler™	(HID Format)				
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8,8	16,17
NPQP99	GlobalFiler™	(PDF Format)				
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8,8	16,17
NQL8BA	GlobalFiler™	(STRmix)				
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8,8	16,17
PGB7PA	GlobalFiler™	(PDF Format)	(StrMix)			
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8,8	16,17
Q2UUC7	GlobalFiler™	(PDF Format)				
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8,8	16,17

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						
QJEKB7	GlobalFiler™ (PDF Format)					
	16.3,17.3	23,24	10,13	14,15	12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8	16,17
	NM			NM		
RN3K37	GlobalFiler™ (PDF Format) (LRmix Studio ver. 2.1.5-Community Edition)					
	16.3,17.3	23,24	10,13	14,15	12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8	16,17
RWXPW8	GlobalFiler™					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8,8	16,17
	---			---		
T3Y2R6	GlobalFiler™					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8,8	16,17
T7XCN4	PowerPlex® Fusion 5C (HID Format)					
	16.3,17.3	23,24	10,13	14,15	12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X	9,12	20,23
	9,12	9,11		9,9.3	8	16,17
	--					
WHKKY3	GlobalFiler™					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8,8	16,17

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

XTFDKX	GlobalFiler™ (HID Format)					
	16.3,17.3	23,24	10,13	14,15	12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X	9,12	20,23
			17,28.2	9,9.3	8	16,17

YBTHJV	GlobalFiler™ (HID Format) (STRmix)					
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8,8	16,17
	NR			NR		

YDE2PY	GlobalFiler™ (HID Format) (Lab Retriever)					
	16.3,17.3	23,24	10,13	14,15	12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X	9,12	20,23
			17,28.2	9,9.3	8	16,17

ZDUK9W	GlobalFiler™ (PDF Format)					
	16.3,17.3	23,24	10,13	14,15	12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
2	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8	16,17
	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 3 - STR Results

2LMCUV	GlobalFiler™ (HID Format)					
	10,14,(15),16.3,17.3	(19),(21),23,(24),(25)	(10),11,(13),14	(14),15,17,(18)	11,12,13	(10),11,(12)
	10,11,14,(15)	(13),(14),15,16,(17)	19,19.3,(21),(23),25	(10),(11),12,13,14	9,11,(12),(13)	(14),15,(16),(18)
3	13,14,(15),(15.2),(16.2)	29,30,30.2,31,32.2	11,14,15,(16),(17)	X,(Y)	(9),(10),(11),12	(19),20,21,23,24,(26)
			17,17.2,18,(26.2),28.2	7,(8),9,9.3	8,(11)	(15),16,17,(18)
	11			2		

2UCZPX	GlobalFiler™ (PDF Format), (HID Format) (STRmix)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		

3QVXHT	PowerPlex® Fusion 6C (HID Format) (STRmix)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
	9,12,13	5,8,9,11,20	17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11	17	19			

4NM3CV	GlobalFiler™ (HID Format) (STRMix)					
	10,14,15,16.3,117.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		

6PQHXR	GlobalFiler™ (HID Format) (STRmix)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		

6X648V	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
	9,12,13	5,8,9,11,20	17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11	17	19	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

7463VP	GlobalFiler™	(HID Format)				
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		
7DECMP	GlobalFiler™	(HID Format)				
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		
9RPU8N	GlobalFiler™	(PDF Format)				
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		
	10,14,16.3,17.3	23,24	10,11,14	14,15,17	11,12,13	10,11
	10,11,14	15,16	19,19.3,23,25	11,12,13,14	9,11	15
3major	13,14	29,30,30.2,31,32.2	11,14,15	X	10,12	19,20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8	16,17
	11			2		
	15	19,21,25	13	18		12
	15	13,14,17	21	10	12,13	14,16,18
3minor	15,15.2,16.2		16,17	Y	9,11	26
			26.2	8	11	15,18
ABDFQQ	GlobalFiler™	(PDF Format)				
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		

TABLE 3

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

Item 3 - STR Results

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

	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
	9,12,13	5,8,9,11,20	17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11	17	19	2		

AQ9XFN GlobalFiler™ (HID Format) (STRMIX)

	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
	-	-	17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11	-	-	2		

AXRZMQ GlobalFiler™ (HID Format)

	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		

BJ79CP PowerPlex® Fusion 6C (HID Format)

	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
	9,12,13	5,8,9,11,20	17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11	17	19	N/A		

CL64AJ PowerPlex® Fusion 6C (HID Format) (STRmix)

	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
	9,12,13	5,8,9,11,20	17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11	17	19			

CMJBXL GlobalFiler™ (HID Format)

	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		

TABLE 3

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

Item 3 - STR Results

ETMEXQ	Investigator® 24plex (HID Format) (GeneMarker V.2.9.5. (SoftGenetics))					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11					
EUBPBH	GlobalFiler™ (STRmix)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		
GNJ2TH	GlobalFiler™ (PDF Format)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
	N/A	N/A	17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11	N/A	N/A	2		
GYDFTE	PowerPlex® Fusion 6C (HID Format) (STRmix)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
	9,12,13	5,8,9,11,20	17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11	17	19			
JP2ZZB	PowerPlex® Fusion 6C (HID Format) (STRmix v2.5.11)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
	9,12,13	5,8,9,11,20	17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11	17	19			
JTMK6F	GlobalFiler™ (HID Format) (STRMix)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		

TABLE 3

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

Item 3 - STR Results

K78LZC Investigator® 24plex

	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
	n/a	n/a	17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11	n/a	n/a	n/a		

KLXLRC PowerPlex® Fusion 5C

	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,25
	9,12,13	5,8,9,11,20		7,8,9,9.3	8,11	15,16,17,18
	11					
	16.3,17.3	23,24	10,13	14,15	12	10,11
	10,14	15,17	19.3,23	11,13	11,12	15,16
3major	14,16.2	30.2,31	14,17	X	9,12	20,23
	9,12	9,11		9,9.3	8	16,17
	-					
	15,17.3	19,21	14	17,18	11,13	10,11
	14,15	13,14	19,21	10,12	11	14,15
3minor	15,15.2	29	15,16	X,Y	11,12	19,26
	12,13	8,9		8,9.3	8,11	15,17
	11					

LXR3GD GlobalFiler™ (HID Format)

	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		

N2K7XA GlobalFiler™ (HID Format) (STRmix 2.10.0)

	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		

NPQP99 GlobalFiler™ (PDF Format)

	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		

TABLE 3

WebCode	**Amplification Kits (File Format) (Probabilistic Genotyping)**					
	D1S1656	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D7S820**
	D8S1179	**D10S1248**	**D12S391**	**D13S317**	**D16S539**	**D18S51**
Item	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**	**FGA**
	Penta D	**Penta E**	**SE33**	**TH01**	**TPOX**	**vWA**
	DYS391	**DYS570**	**DYS576**	**Y Indel**		
			Item 3 - STR Results			
NQL8BA	GlobalFiler™ (STRmix)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
PGB7PA	GlobalFiler™ (PDF Format) (STRMix)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		
Q2UUC7	GlobalFiler™ (PDF Format) (LRmixStudio-2.1.5 CommunityEdition)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		
QJEKB7	GlobalFiler™ (PDF Format)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		
RN3K37	GlobalFiler™ (PDF Format) (LRmix Studio ver. 2.1.5-Community Edition)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		
RWXPW8	GlobalFiler™					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		

TABLE 3

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

Item 3 - STR Results

T3Y2R6	GlobalFiler™					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		
T7XCN4	PowerPlex® Fusion 5C (HID Format)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
	9,12,13	5,8,9,11,20		7,8,9,9.3	8,11	15,16,17,18
	11					
WHKKY3	GlobalFiler™ (STRMix v 2.10)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		
XTFDKX	GlobalFiler™ (HID Format) (STRmix)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		
YBTHJV	GlobalFiler™ (HID Format) (STRmix)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	16,17,18
	11			2		
YDE2PY	GlobalFiler™ (HID Format) (Lab Retriever)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		

TABLE 3

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

Item 3 - STR Results

ZDUK9W	GlobalFiler™ (PDF Format)					
	10,14,15,16.3,17.3	19,21,23,24,25	10,11,13,14	14,15,17,18	11,12,13	10,11,12
	10,11,14,15	13,14,15,16,17	19,19.3,21,23,25	10,11,12,13,14	9,11,12,13	14,15,16,18
3	13,14,15,15.2,16.2	29,30,30.2,31,32.2	11,14,15,16,17	X,Y	9,10,11,12	19,20,21,23,24,26
			17,17.2,18,26.2,28.2	7,8,9,9.3	8,11	15,16,17,18
	11			2		

TABLE 3

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

Item 4 - STR Results

2LMCUV	GlobalFiler™ (HID Format)					
	10,14,16.3,17.3	23,(24),(25)	10,11,13,14	14,15,(17)	11,12,(13)	(10),11,(12)
	10,(11),(14)	15,(16),(17)	19,19.3,23,25	11,12,13,14	9,11,12,13	15,(16),(18)
4	13,14,(16.2)	30,30.2,31,32.2	11,14,15,17	X,X	9,(10),12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,(11)	16,(17),(18)
2UCZPX	GlobalFiler™ (PDF Format), (HID Format) (STRmix)					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
	-			-		
3QVXHT	PowerPlex® Fusion 6C (HID Format) (STRmix)					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,12	20,21,23,24
	9,12,13	5,9,11,20	17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
	NR	NR	NR			
4NM3CV	GlobalFiler™ (HID Format) (STRMix)					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
6PQHXR	GlobalFiler™ (HID Format) (STRmix)					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
6X648V	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format)					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,12	20,21,23,24
	9,12,13	5,9,11,20	17,17.2,18,28.2	7,9,9.3	8,11	16,17,18

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

7463VP	GlobalFiler™ (HID Format)					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
	NM			NM		
7DECMP	GlobalFiler™ (HID Format)					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
9RPU8N	GlobalFiler™ (PDF Format)					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
	10,14,16.3,17.3	23	10,11,13,14	14,15,17	11,12	10,11
	10,11	15	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16
4major	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8	16,17,18
		24,25			13	12
	14	16,17				18
4minor						
					11	
ABDFQQ	GlobalFiler™ (PDF Format)					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
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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 4 - STR Results

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

	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,12	20,21,23,24
	9,12,13	5,9,11,20	17,17.2,18,28.2	7,9,9.3	8,11	16,17,18

AQ9XFN GlobalFiler™ (HID Format) (STRMIX)

	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
	-	-	17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
	-	-	-	-		

AXRZMQ GlobalFiler™ (HID Format)

	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18

BJ79CP PowerPlex® Fusion 6C (HID Format)

	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,12	20,21,23,24
	9,12,13	5,9,11,20	17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
	N/A	N/A	N/A	N/A		

CL64AJ PowerPlex® Fusion 6C (HID Format) (STRmix)

	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,12	20,21,23,24
	9,12,13	5,9,11,20	17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
	NR	NR	NR			

CMJBXL GlobalFiler™ (HID Format)

	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18

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

ETMEXQ Investigator® 24plex (HID Format) (GeneMarker V.2.9.5. (SoftGenetics))

	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18

EUBPBH GlobalFiler™

	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18

GNJ2TH GlobalFiler™ (PDF Format)

	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,12	20,21,23,24
	N/A	N/A	17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
	NSD	N/A	N/A	NSD		

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

	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,12	20,21,23,24
	9,12,13	5,9,11,20	17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
	NR	NR	NR			

JP2ZZB PowerPlex® Fusion 6C (HID Format) (STRmix v2.5.11)

	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,12	20,21,23,24
	9,12,13	5,9,11,20	17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
	NR	NR	NR			

JTMK6F GlobalFiler™ (HID Format) (STRMix)

	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18

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

K78LZC	Investigator® 24plex					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,12	20,21,23,24
	n/a	n/a	17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
	n/a	n/a	n/a	n/a		
KLXLRC	PowerPlex® Fusion 5C					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,11,12	20,21,23,24
	9,12,13	5,9,11,20		7,9,9.3	8,11	16,17,18
	-					
	16.3,17.3	23,24	10,13	14,15	12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
4major	14,16.2	30.2,31	14,17	X	9,12	20,23
	9,12	9,11		9,9.3	8	16,17
	10,14	25	11,14	17	11,13	11
	11	16	19,25	12,14	9,13	18
4minor	13	30,32.2	11,15	X	10,11	21,24
	12,13	5,20		7	8,11	18
LXR3GD	GlobalFiler™ (HID Format)					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
N2K7XA	GlobalFiler™ (HID Format) (STRmix 2.10.0)					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
NPQP99	GlobalFiler™ (PDF Format)					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18

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

NQL8BA	GlobalFiler™	(STRmix)				
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
PGB7PA	GlobalFiler™	(PDF Format)	(STRMix)			
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
Q2UUC7	GlobalFiler™	(LRmixStudio-2.1.5 CommunityEdition)				
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
	16.3,17.3	23,24	10,13	14,15	12,12	10,12
	10,14	15,17	19.3,23	11,13	11,12	15,16
4major	14,16.2	30.2,31	14,17	X,X	9,12	20,23
			17,28.2	9,9.3	8,8	16,17
	10,14	23,25	11,14	15,17	11,13	11,11
	10,11	15,16	19,25	12,14	9,13	15,18
4minor	13,14	30,32.2	11,15	X,X	10,12	21,24
			17.2,18	7,9	8,11	16,18
QJEKB7	GlobalFiler™	(PDF Format)				
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
	NM			NM		
RN3K37	GlobalFiler™	(PDF Format)	(LRmix Studio ver. 2.1.5-Community Edition)			
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18

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

RWXPW8	GlobalFiler™					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
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T3Y2R6	GlobalFiler™					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
T7XCN4	PowerPlex® Fusion 5C (HID Format)					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,12	20,21,23,24
	9,12,13	5,9,11,20		7,9,9.3	8,11	16,17,18
	--					
WHKKY3	GlobalFiler™ (STRMix v 2.10)					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
XTFDKX	GlobalFiler™ (HID Format) (STRmix)					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
YBTHJV	GlobalFiler™ (HID Format) (STRmix)					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
	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 4 - STR Results

YDE2PY	GlobalFiler™ (HID Format) (Lab Retriever)					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
ZDUK9W	GlobalFiler™ (PDF Format)					
	10,14,16.3,17.3	23,24,25	10,11,13,14	14,15,17	11,12,13	10,11,12
	10,11,14	15,16,17	19,19.3,23,25	11,12,13,14	9,11,12,13	15,16,18
4	13,14,16.2	30,30.2,31,32.2	11,14,15,17	X,X	9,10,12	20,21,23,24
			17,17.2,18,28.2	7,9,9.3	8,11	16,17,18
	NM			NM		

YSTR Results

TABLE 4

WebCode	Amplification Kits (File Format)								
	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
Item	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4
	Item 1 - YSTR Results								
2UCZPX	PowerPlex® Y23 (PDF Format), (HID Format)								
		13	15,16	13	30	23	11	14	14
1	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
3QVXHT	PowerPlex® Y23 (HID Format)								
		13	15,16	13	30	23	11	14	14
1	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
4NM3CV	(HID Format)								
		13	15,16	13	30	23	11	14	14
1	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
6PQHXR	Yfiler™ Plus (HID Format)								
	36,37	13	15,16	13	30	23	11	14	14
1	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
6X648V									
	36,37	13	15,16	13	30	23	11	14	14
1	14	11	12	21	27	15	16	10	24
	38	11	12	17	19	19	22	10	11
7463VP	Yfiler™ Plus (PDF Format)								
	36,37	13	15,16	13	30	23	11	14	14
1	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
7DECMP	PowerPlex® Y23 (HID Format)								
		13	15,16	13	30	23	11	14	14
1	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
9RPU8N	Yfiler™ Plus (PDF Format)								
	36,37	13	15,16	13	30	23	11	14	14
1	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
AECRLQ	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	36,37	13	15,16	13	30	23	11	14	14
1	14	11	12	21	27	15	16	10	24
	38	11	12	17	19	19	22	10	11
AQ9XFN	PowerPlex® Y23 (PDF Format)								
	-	13	15,16	13	30	23	11	14	14
1	14	11	12	21	-	15	16	-	24
	-	11	12	17	19	-	22	10	11

TABLE 4

WebCode	Amplification Kits (File Format)								
	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
Item	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4
	Item 1 - YSTR Results								
AXRZMQ	Yfiler™ Plus (PDF Format)								
	36,37	13	15,16	13	30	23	11	14	14
1	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
BJ79CP	Yfiler™ Plus (HID Format)								
	36,37	13	15,16	13	30	23	11	14	14
1	14	11	12	21	27	15	16	10	24
	38	11	N/A	17	19	19	22	N/A	11
CL64AJ	PowerPlex® Y23 (HID Format)								
		13	15,16	13	30	23	11	14	14
1	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
CMJBXL	Yfiler™ Plus (HID Format)								
	36,37	13	15,16	13	30	23	11	14	14
1	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
ETMEXQ	PowerPlex® Y23 (HID Format)								
		13	15,16	13	30	23	11	14	14
1	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
GNJ2TH	Yfiler™ Plus (PDF Format)								
	36,37	13	15,16	13	30	23	11	14	14
1	14	11	12	21	27	15	16	10	24
	38	11	N/A	17	19	19	22	N/A	11
GYDFTE	PowerPlex® Y23 (HID Format)								
		13	15,16	13	30	23	11	14	14
1	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
JP2ZZB	PowerPlex® Y23 (HID Format)								
		13	15,16	13	30	23	11	14	14
1	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
JTMK6F									
		13	15,16	13	30	23	11	14	14
1	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
KLXLRC	PowerPlex® Y23 (PDF Format), (HID Format)								
		13	15,16	13	30	23	11	14	14
1	14	11	12	21		15	16		24
		11	12	17	19		22	10	11

TABLE 4

WebCode	Amplification Kits (File Format)								
	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
Item	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4
Item 1 - YSTR Results									
N2K7XA	PowerPlex® Y23 (PDF Format)								
		13	15,16	13	30	23	11	14	14
1	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
NPQP99	PowerPlex® Y23 (PDF Format)								
		13	15,16	13	30	23	11	14	14
1	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
NQL8BA	PowerPlex® Y23								
		13	15,16	13	30	23	11	14	14
1	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
PGB7PA	(PDF Format)								
		13	15,16	13	30	23	11	14	14
1	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
Q2UUC7	Yfiler™ Plus (PDF Format)								
	36,37	13	15,16	13	30	23	11	14	14
1	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
QJEKB7	Yfiler™ Plus (PDF Format)								
	36,37	13	15,16	13	30	23	11	14	14
1	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
RN3K37	Yfiler™ Plus (PDF Format)								
	36,37	13	15,16	13	30	23	11	14	14
1	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
RWXPW8	Yfiler™ Plus								
	36,37	13	15,16	13	30	23	11	14	14
1	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
T3Y2R6	PowerPlex® Y23								
		13	15,16	13	30	23	11	14	14
1	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
WHKKY3	PowerPlex® Y23								
		13	15,16	13	30	23	11	14	14
1	14	11	12	21		15	16		24
		11	12	17	19		22	10	11

TABLE 4

WebCode	Amplification Kits (File Format)								
	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
Item	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4
	Item 1 - YSTR Results								
XTFDKX	Yfiler™ Plus (HID Format)								
	36,37	13	15,16	13	30	23	11	14	14
1	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
YDE2PY	Yfiler™ Plus (HID Format)								
	36,37	13	15,16	13	30	23	11	14	14
1	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
ZDUK9W	Yfiler™ Plus (PDF Format)								
	36,37	13	15,16	13	30	23	11	14	14
1	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11

TABLE 4

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

Item 3 - YSTR Results

WebCode / Item									
2UCZPX	PowerPlex® Y23 (PDF Format), (HID Format)								
		13	15,16	13	30	23	11	14	14
3	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
3QVXHT	PowerPlex® Y23 (HID Format)								
		13	15,16	13	30	23	11	14	14
3	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
4NM3CV	PowerPlex® Y23 (HID Format)								
		13	15,16	13	30	23	11	14	14
3	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
6PQHXR	Yfiler™ Plus (HID Format)								
	36,37	13	15,16	13	30	23	11	14	14
3	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
6X648V	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	36,37	13	15,16	13	30	23	11	14	14
3	14	11	12	21	27	15	16	10	24
	38	11	12	17	19	19	22	10	11
7463VP	Yfiler™ Plus (PDF Format)								
	36,37	13	15,16	13	30	23	11	14	14
3	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
7DECMP	PowerPlex® Y23 (HID Format)								
		13	15,16	13	30	23	11	14	14
3	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
9RPU8N	Yfiler™ Plus (PDF Format)								
	36,37	13	15,16	13	30	23	11	14	14
3	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
	36,37	13	15,16	13	30	23	11	14	14
3major	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
AECRLQ	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	36,37	13	15,16	13	30	23	11	14	14
3	14	11	12	21	27	15	16	10	24
	38	11	12	17	19	19	22	10	11

TABLE 4

WebCode	Amplification Kits (File Format)								
	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
Item	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4
	Item 3 - YSTR Results								
AQ9XFN	PowerPlex® Y23 (PDF Format)								
	-	13	15,16	13	30	23	11	14	14
3	14	11	12	21	-	15	16	-	24
	-	11	12	17	19	-	22	10	11
AXRZMQ	Yfiler™ Plus (PDF Format)								
	36,37	13	15,16	13	30	23	11	14	14
3	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
BJ79CP	Yfiler™ Plus (HID Format)								
	36,37	13	15,16	13	30	23	11	14	14
3	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
CL64AJ	PowerPlex® Y23 (HID Format)								
		13	15,16	13	30	23	11	14	14
3	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
CMJBXL	Yfiler™ Plus (HID Format)								
	36,37	13	15,16	13	30	23	11	14	14
3	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
ETMEXQ	PowerPlex® Y23 (HID Format)								
		13	15,16	13	30	23	11	14	14
3	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
GNJ2TH	Yfiler™ Plus (PDF Format)								
	36,37	13	15,16	13	30	23	11	14	14
3	14	11	12	21	27	15	16	10	24
	38	11	N/A	17	19	19	22	N/A	11
GYDFTE	PowerPlex® Y23 (HID Format)								
		13	15,16	13	30	23	11	14	14
3	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
JP2ZZB	PowerPlex® Y23 (HID Format)								
		13	15,16	13	30	23	11	14	14
3	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
JTMK6F	PowerPlex® Y23 (HID Format)								
		13	15,16	13	30	23	11	14	14
3	14	11	12	21		15	16		24
		11	12	17	19		22	10	11

TABLE 4

WebCode	**Amplification Kits (File Format)**								
	DYF387S	**DYS19**	**DYS385**	**DYS389-I**	**DYS389-II**	**DYS390**	**DYS391**	**DYS392**	**DYS393**
Item	**DYS437**	**DYS438**	**DYS439**	**DYS448**	**DYS449**	**DYS456**	**DYS458**	**DYS460**	**DYS481**
	DYS518	**DYS533**	**DYS549**	**DYS570**	**DYS576**	**DYS627**	**DYS635**	**DYS643**	**YGATAH4**
				Item 3 - YSTR Results					
KLXLRC	PowerPlex® Y23 (PDF Format), (HID Format)								
		13	15,16	13	30	23	11	14	14
3	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
N2K7XA	PowerPlex® Y23 (PDF Format)								
		13	15,16	13	30	23	11	14	14
3	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
NPQP99	PowerPlex® Y23 (PDF Format)								
		13	15,16	13	30	23	11	14	14
3	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
NQL8BA	PowerPlex® Y23								
		13	15,16	13	30	23	11	14	14
3	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
PGB7PA	(HID Format)								
		13	15,16	13	30	23	11	14	14
3	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
Q2UUC7	Yfiler™ Plus (PDF Format)								
	36,37	13	15,16	13	30	23	11	14	14
3	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
QJEKB7	Yfiler™ Plus (PDF Format)								
	36,37	13	15,16	13	30	23	11	14	14
3	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
RN3K37	Yfiler™ Plus (PDF Format)								
	36,37	13	15,16	13	30	23	11	14	14
3	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
RWXPW8	Yfiler™ Plus								
	36,37	13	15,16	13	30	23	11	14	14
3	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
T3Y2R6									
		13	15,16	13	30	23	11	14	14
3	14	11	12	21		15	16		24
		11	12	17	19		22	10	11

TABLE 4

WebCode	Amplification Kits (File Format)								
	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
Item	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4
	Item 3 - YSTR Results								
WHKKY3	PowerPlex® Y23								
		13	15,16	13	30	23	11	14	14
3	14	11	12	21		15	16		24
		11	12	17	19		22	10	11
XTFDKX	Yfiler™ Plus (HID Format)								
	36,37	13	15,16	13	30	23	11	14	14
3	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
YDE2PY	Yfiler™ Plus (HID Format)								
	36,37	13	15,16	13	30	23	11	14	14
3	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		11
ZDUK9W	Yfiler™ Plus (PDF Format)								
	36,37	13	15,16	13	30	23	11	14	14
3	14	11	12	21	27	15	16	10	24
	38	11		17	19	19	22		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

	Item 3 Conclusion			Item 4 Conclusion		
WebCode	**# of Contributors**	**Item 1**	**Item 2**	**# of Contributors**	**Item 1**	**Item 2**
2LMCUV	at least 3, one male	Included	Included	2	Excluded	Included
2UCZPX	4	Included	Included	2	Excluded	Included
3QVXHT	3	Included	Included	2	Excluded	Included
4NM3CV	3 person mixture	Included	Included	2	Excluded	Included
6PQHXR	3	Included	Included	2	Excluded	Included
6X648V	3	Included	Included	2	Excluded	Included
7463VP	3	Included	Included	2	Excluded	Included
7DECMP	at least 3, one male	Included	Inconclusive / Uninterpretable	two females	Excluded	Included
9RPU8N	3	Included	Included	2	Excluded	Included
ABDFQQ	3	Included	Included	2	Excluded	Included
AECRLQ	≥3 contributors (including ≥1 male)	Included	Included	≥2 contributors (male DNA not detected)	Excluded	Included
AQ9XFN	3	Included	Included	2	Excluded	Included
AXRZMQ	3	Included	Included	2	Excluded	Included
BJ79CP	3	Included	Included	2	Excluded	Included
CL64AJ	STR 3, YSTR 1	Included	Included	2	Excluded	Included
CMJBXL	3	Included	Included	2	Excluded	Included
ETMEXQ	3	Included	Included	2	Excluded	Included
EUBPBH	3	Included	Included	2	Excluded	Included
GNJ2TH	3 or more	Included	Included	2	Excluded	Included
GYDFTE	3	Included	Included	2	Excluded	Included

TABLE 5

	Item 3 Conclusion			Item 4 Conclusion		
WebCode	**# of Contributors**	**Item 1**	**Item 2**	**# of Contributors**	**Item 1**	**Item 2**
JP2ZZB	STR-3; YSTR-1	Included	Included	STR-2	Excluded	Included
JTMK6F	3	Included	Included	2	Excluded	Included
K78LZC	3	Included	Included	2	Excluded	Included
KLXLRC	3	Included	Included	2	Excluded	Included
LXR3GD	3	Included	Included	2	Excluded	Included
N2K7XA	3	Included	Included	2	Excluded	Included
NPQP99	at least 3	Included	Included	at least 2	Excluded	Included
NQL8BA	3 contributors	Included	Included	2 contributors	Excluded	Included
PGB7PA	Three	Included	Included	Two	Excluded	Included
Q2UUC7	3	Included	Included	2	Excluded	Included
QJEKB7	3	Included	Included	2	Excluded	Included
RN3K37	3	Included	Included	2	Excluded	Included
RWXPW8	More than 2 (probably 3)	Included	Included	Most probably two	Excluded	Included
T3Y2R6	Three	Included	Included	Two	Excluded	Included
T7XCN4	AT LEAST 3			2	Excluded	Included
WHKKY3	3	Included	Included	2	Excluded	Included
XTFDKX	3	Included	Included	2	Excluded	Included
YBTHJV	3	Included	Included	2	Excluded	Included
YDE2PY	3	Included	Included	2	Excluded	Included
ZDUK9W	3	Included	Included	2	Excluded	Included

Conclusions Response Summary

Participants reporting conclusions: 40

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	**39**	**38**	**0**	**40**
Excluded	**0**	**0**	**40**	**0**
Inconclusive/ Uninterpretable	**0**	**1**	**0**	**0**
No Response	**1**	**1**	**0**	**0**
Total	**40**	**40**	**40**	**40**

Statistical Analysis for Item 3

TABLE 6

WebCode	Item 3 Methods & Results
2LMCUV	**Method(s):** Combined Probability of Exclusion/Inclusion **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 13 million (10^6) **Database(s):** NIST 1036 (Revision 2017)
2UCZPX	**Method(s):** Likelihood Ratio **Stats Analysis:** The DNA result obtained from the swab (Item 3) allegedly taken from sidewalk outside victim's home is consistent with a mixture from at least four (4) contributors, including at least one (1) male:- a) This mixture is approximately 1.08 x 10^16 times more likely to occur (strong support for inclusion) if the deceased male and three (3) unknown, unrelated individuals are contributors, rather than if four (4) unknown, unrelated individuals are contributors. b) This mixture is approximately 8.92 x 10^14 times more likely to occur (strong support for inclusion) if the suspected female and three (3) unknown, unrelated individuals are contributors, rather than if four (4) unknown, unrelated individuals are contributors. **Database(s):** FBI_EXTENDED_SE_HISP; FBI_EXTENDED_SE_HISP_0820_21; FBI_EXTENDED_SW_HISP
3QVXHT	**Method(s):** Likelihood Ratio **Stats Analysis:** (STR): The DNA profile from this item is at least 310 sextillion times more likely if it originated from Victim and two unknown individuals than if it originated from three unknown, unrelated individuals. The DNA profile from this item is at least 19 sextillion times more likely if it originated from Suspect and two unknown individuals than if it originated from three unknown, unrelated individuals. (YSTR): The DNA profile is at least 1,030 times more likely if the profile originated from Victim (or a patrilineal relative) than if it originated from a randomly selected individual. **Database(s):** Most conservative population group 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
4NM3CV	**Method(s):** Likelihood Ratio **Stats Analysis:** The DNA result obtained from Item 3 is consistent with a mixture of three (3) contributors including at least one (1) male individual. The mixture is approximately 4.38 x10^20 more likely to occur if the male complainant (Item 1) and two (2) unknown, unrelated individuals are contributors, rather than if three (3) unknown, unrelated individuals are contributors. The mixture is approximately 1.73 x10^18 more likely to occur if the female suspect (Item 2) and two (2) unknown, unrelated individuals are contributors, rather than if three (3) unknown, unrelated individuals are contributors. **Database(s):** FBI extended_SE_Hisp_082021
6PQHXR	**Method(s):** Likelihood Ratio **Stats Analysis:** This DNA result is approximately 4.87 quadrillion times more likely if Item 1 and 2 unknown individuals were the sources of the mixture DNA profile than if 3 unknown individuals were the sources. This favors support that Item 1 is included as a contributor to the DNA profile from Item 3. This DNA result is approximately 1.09 quadrillion times more likely if Item 2 and 2 unknown individuals were the sources of the mixture DNA profile than if 3 unknown individuals were the sources. This favors support that Item 2 is included as a contributor to the DNA profile from Item 3. **Database(s):** National Institute of Standards and Technology (NIST 2017 Revision)
6X648V	**Method(s):** Likelihood Ratio **Stats Analysis:** The DNA profile from item 3 is 1 billion times more likely if it is a result of contribution from victim and two unknown persons than if it is a result of contribution from 3 unknown persons. The DNA profile from item 3 is 1 billion times more likely if it is a result of contribution from suspect and two unknown persons than if it is a result of contribution from 3 unknown persons. **Database(s):** 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.

TABLE 6

WebCode	Item 3 Methods & Results
7463VP	**Method(s):** Likelihood Ratio **Stats Analysis:** A mixed DNA profile of three individuals was developed from "Item 3". The DNA profile obtained from "Item 1" and "Item 2" are being the contributors to the mixed DNA profile. The mixed DNA profile is 1.3 septillion, 560 septillion and 53 septillion TIMES more likely if it originated from "Item 1", "Item 2" and one unknown RATHER THAN; IF it originated from three unknown, unrelated individuals as calculated based on the [Location Identifying Population]. **Database(s):** [Location Identifying Database]
7DECMP	**Method(s):** YSTR haplotype frequency **Stats Analysis:** INCLUDED as a possible contributor: Item 1 (Victim). 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):** 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.
9RPU8N	**Method(s):** Likelihood Ratio **Stats Analysis:** The DNA profile obtained from Questioned sample (Item 3: Blood on the sidewalk) provides a strong support for the inclusion on the male victim (LR= 1725671.1207) as a contributor. Additionally, it provides an extreme support for female suspect inclusion (LR= 4.0164E12) as a possible second contributor. LRmixStudio 2.1.3 used to calculate Likelihood Ratio (LR). **Database(s):** [Location Identifying Database]
ABDFQQ	**Method(s):** Random Match Probability **Stats Analysis:** Item 1: [Location] (allele frequencies) RMP=3.38036E+28 , US HISPANIC SE (allele frequencies) RMP=6.62495E+26. Item 2: [Location] (allele frequencies) RMP=3.2762E+34, US HISPANIC SE (allele frequencies) RMP =6.0877E+33. **Database(s):** [Location Identifying Database]
AECRLQ	**Method(s):** Likelihood Ratio **Stats Analysis:** Statistical Results (Autosomal): Under the assumption that the VICTIM (Item 1) and 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 SIDEWALK OUTSIDE VICTIM'S HOME (Item 3) is ≥1,000,000 times greater (actual LR available upon request) than if it is assumed that three 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 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 SIDEWALK OUTSIDE VICTIM'S HOME (Item 3) is ≥1,000,000 times greater (actual LR available upon request) than if it is assumed that three unknown unrelated persons selected at random from the general population are contributors to this mixed-source profile. Statistical Results (YSTR): The VICTIM (Item 1), 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 THE SIDEWALK OUTSIDE VICTIM'S HOME (Item 3). Given a theta-value of 2.0x10-05 and a 95% UCI of the combined Haplotype frequency of 1 in 3,131 (no matches in 9,379 Haplotypes at U.S. subpopulations without Native American), the corrected Match Probability is 1 in 2,947. **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

TABLE 6

WebCode	**Item 3 Methods & Results**
AQ9XFN	**Method(s):** Likelihood Ratio **Stats Analysis:** The DNA result obtained from stain (Item 3) on sidewalk outside victim's house is consistent with a mixture from at least three (3) contributors, including at least one (1) male: a. The mixture is approximately 1.24 x 10^18 times more likely to occur (very strong support for inclusion) if the suspect and two (2) unknown, unrelated individuals are contributors, rather than if three (3) unknown, unrelated individuals are contributors. b. The mixture is approximately 3.88 x 10^20 times more likely to occur (very strong support for inclusion) if the victim and two (2) unknown, unrelated individuals are contributors, rather than if three (3) unknown, unrelated individuals are contributors. **Database(s):** [Participant did not report database(s).]
CL64AJ	**Method(s):** Likelihood Ratio **Stats Analysis:** STR: The DNA profile from this item is at least 450 sextillion times more likely if it originated from Item 1 (victim) and two unknown individuals than if it originated from three unknown, unrelated individuals. The DNA profile from this item is at least 49 sextillion times more likely if it originated from Item 2 (suspect) and two unknown individuals than if it originated from three unknown, unrelated individuals. YSTR: The DNA profile is at least 1,030 times more likely if the profile originated from Item 1 (victim) (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.
CMJBXL	**Method(s):** Likelihood Ratio **Stats Analysis:** The DNA result from Item 3 is consistent with mixture from at least 3 contributors. The mixture is approximately 6,6x10^15 times more likely to occur if the victim and two unknown individuals are contributors, rather than if the DNA is from three unknown individuals. The DNA result from Item 3 is consistent with mixture from at least 3 contributors. The mixture is approximately 7,53x10^14 times more likely to occur if the suspect and two unknown individuals are contributors, rather than if the DNA is from three unknown individuals. **Database(s):** Imported from STRideR population American.
ETMEXQ	**Method(s):** Likelihood Ratio **Stats Analysis:** [Participant did not report statistical analysis.] **Database(s):** Local database
EUBPBH	**Method(s):** Likelihood Ratio **Stats Analysis:** [Participant did not report statistical analysis.] **Database(s):** NIST1036_Hisp
GNJ2TH	**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).]

TABLE 6

WebCode	Item 3 Methods & Results
GYDFTE	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile from this item is at least 530 sextillion times more likely if it originated from Victim and two unknown individuals than if it originated from three unknown, unrelated individuals. The DNA profile from this item is at least 10 sextillion times more likely if it originated from Suspect and two unknown individuals than if it originated from three unknown, unrelated individuals. The DNA profile is at least 1,030 times more likely if the profile originated from Victim (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
JP2ZZB	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile from this item is at least 490 sextillion times more likely if it originated from Victim and two unknown individuals than if it originated from three unknown, unrelated individuals. The DNA profile from this item is at least 15 sextillion times more likely if it originated from Suspect and two unknown individuals than if it originated from three unknown, unrelated individuals. The YSTR DNA profile is at least 1,030 times more likely if the profile originated from Victim (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.
JTMK6F	**Method(s)**: Likelihood Ratio **Stats Analysis:** The mixture is approximately 4.19E19 times more likely to occur (very strong support for inclusion) if the victim and an unknown, unrelated individual are contributors, rather than if two unknown, unrelated individuals are contributors. The mixture is approximately 5.83E17 times more likely to occur (very strong support for inclusion) if the suspect and an unknown, unrelated individual are contributors, rather than if two unknown, unrelated individuals are contributors. **Database(s):** FBI_EXTENDED_SE_HISP, FBI_EXTENDED_SW_HISP, NIST1036_HISP and FBI_EXTENDED_SE_HISP_0820. The stratified LR was reported.
K78LZC	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 3 (bloodstain on sidewalk outside victim's home) presents a genetic profile of more than two persons. Assuming that the profile of the item comes from at least three contributors and two of the contributors are Male Victim [Item#1], Female Suspect [Item#2] and an unknown contributor, we conclude that: The genetic profile of the Item 3 (bloodstain on sidewalk outside victim's home) is approximately: 66 Quatrillions using the Hispanic population database 67 Quatrillions using the Caucasian population database 194 Quatrillions using the Afro-American population database times more likely to have come from Male Victim [Item#1], Female Suspect [Item#2] and an unrelated person, than Male Victim [Item#1] and any other two unrelated persons chosen randomly. Male Victim [Item#1], Female Suspect [Item#2] and an unrelated person cannot be excluded of being the contributors of the genetic profile on the Item. This probability is very strong supported by the statistical data. **Database(s):** The Database used in the statistical analysis for Item 3 was the NIST's U.S. STR Population Database for Caucasian (Cau), African American (Blk), Hispanic (Hsp), Asian (Asn) and Combined Population Groups (August 2017).

TABLE 6

WebCode	Item 3 Methods & Results
KLXLRC	**Method(s)**: Random Match Probability **Stats Analysis:** RMP for item#3 female Major (suspect): The probability of selecting a random individual having a DNA profile identical to item 3 major at the observed loci is 1 in 3.63 E+34 for Hispanic Americans. RMP for item #3 minor: The probability of selecting random unrelated individual having a DNA profile identical to item #3 minor at th loci observed is 1 in 5.43E+29 for African Americans, 1 in 1.28E+30 for Caucasian Americans, 1 in 6.54 E+28 for Hispanic Americans, 1 in 2.08 E +33 for Asian Americans. **Database(s):** Promega & NIST databases
LXR3GD	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA result obtained from ITEM 3 is consistent with a mixture from at least three (3) contributors, including at least one (1) male: (a) The mixture is approximately 5.54 x 10^20 times more likely to occur (very strong support for inclusion) if ITEM 1 (victim) and two (2) unknown, unrelated individuals are contributors, rather than if three (3) unknown, unrelated individuals are contributors. (b) The mixture is approximately 2.11 x 10^18 times more likely to occur (very strong support for inclusion) if ITEM 2 (suspect) and two (2) unknown, unrelated individuals are contributors, rather than if three (3) unknown, unrelated individuals are contributors. **Database(s):** STRmix, FBI_extended_SE_Hisp_082021
N2K7XA	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA result obtained from the stain on sidewalk outside victim's home (Item 3) is consistent with a mixture from at least three (3) contributors, including at least one (1) male: a) The mixture is approximately 4.83 x 10^20 times more likely to occur (very strong support for inclusion) if the male victim and two (2) unknown, unrelated individuals are contributors rather than if three (3) unknown, unrelated individuals are contributors. b) The mixture is approximately 1.76 x 10^18 times more likely to occur (very strong support for inclusion) if the female suspect and two (2) unknown, unrelated individuals are contributors rather than if three (3) unknown, unrelated individuals are contributors. **Database(s):** FBI Extended SE Hisp 082021
NQL8BA	**Method(s)**: Likelihood Ratio **Stats Analysis:** Victim is included (cannot be excluded) as a possible contributor to the DNA obtained from Item 3, LR = 6.98 x 10 20. Suspect is included (cannot be excluded) as a possible contributor to the DNA obtained from Item 3, LR = 2.44 x 10 18. CONCLUSION: The DNA result obtained from the stain [Internal Test Number] allegedly taken from sidewalk outside victim's house is consistent with a mixture from at least three (3) contributors, including at least one (1) male: A) The mixture is approximately 2.44 x 10 18 (very strong support for inclusion) times more likely to occur if the suspect and two (2) unknown, unrelated individuals are contributors, rather than if three (3) unknown, unrelated individuals are contributors. B) The mixture is approximately 6.98 x 10 20 (very strong support for inclusion) times more likely to occur if the victim and two (2) unknown, unrelated individuals are contributors, rather than if three (3) unknown, unrelated individuals are contributors. END OF REPORT **Database(s):** [Participant did not report database(s).]
PGB7PA	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA result obtained from the stain(Item 3) on sidewalk outside victim's home is consistent with a mixture from at least three (3) contributors, including at least one (1) male: a) The mixture is approximately 1.29 x 10^20 times more likely to occur (very strong support for inclusion) if the male victim and two (2) unknown, unrelated individuals are contributors, rather than if three (3) unknown, unrelated individuals are contributors. b) The mixture is approximately 1.16 x 10^18 times more likely to occur (very strong support for inclusion) if the female suspect and two (2) unknown, unrelated individuals are contributors, rather than if three (3) unknown, unrelated individuals are contributors. **Database(s):** FBI_EXTENDED_SW_HISP and FBI_EXTENDED_SE_HISP_082021

TABLE 6

WebCode	Item 3 Methods & Results
Q2UUC7	**Method(s):** Likelihood Ratio **Stats Analysis:** H1 : the mixture is made up of the victim's genetic profile (item 1) and the genetic profile of two unknown unrelated person. H2 : the mixture is made up of the genetic profils of three unknown unrelated people. LR= 1,16E6 (Personnal Data base, drop-out=0.1, drop-in=0.05, Theta=0.01). H1 : the mixture is made up of the suspect's genetic profile (item 2) and the genetic profile of two unknown unrelated person. H2 : the mixture is made up of the genetic profils of three unknown unrelated people. LR= 1,91E11 (Personnal Data base, drop-out=0.1, drop-in=0.05, Theta=0.01). **Database(s):** https://strider.online/frequencies
QJEKB7	**Method(s):** Likelihood Ratio **Stats Analysis:** A mixed DNA profile of three individuals was developed from "Item 3". The DNA profiles obtained from reference samples "Item 1" and "Item 2" are consistent being the contributors to this mixed DNA profile. The mixed DNA profile is 1.3 septillion (1.3 x 10e24) , 560 septillion (560 x 10e24) and 53 septillion (53 x 10e24) times more likely if they originated from "Item 1" , "Item 2" and one unknown individual rather than, if they originated from three unknown unrelated individuals as calculated based on the [Location Identifying Population]. **Database(s):** [Location Identifying Database]
RN3K37	**Method(s):** Likelihood Ratio **Stats Analysis:** LR = VICTIM + SUSPECT + UNKNOWN / 3 UNKNOWNS. LR = 1,62092 x E22. drop out for VICTIM = 0. drop out for SUSPECT = 0. drop out for UNKNOWN = 0,01. **Database(s):** Global Filer PCR Amplification Kit user guide.Caucasion popolation base.
RWXPW8	**Method(s):** Combined Probability of Exclusion/Inclusion **Stats Analysis:** [Participant did not report statistical analysis.] **Database(s):** [Participant did not report database(s).]
T7XCN4	**Method(s):** [Participant did not report a method.] **Stats Analysis:** The DNA information obtained from this item is not suitable for manual comparison due to the complexity of the mixture profile and stochastic effects throughout the profile. However, the DNA information obtained may be suitable for probabilistic genotyping. **Database(s):** [Participant did not report database(s).]
WHKKY3	**Method(s):** Likelihood Ratio **Stats Analysis:** The DNA result obtained from stain (Item 3) on sidewalk outside victim's home is consistent with a mixture from at least three (3) contributors: a) The mixture is approximately 5.06 x 10^19 times more likely to occur (very strong support for inclusion) if the victim and two unknown, unrelated individuals are contributors, rather than if three (3) unknown, unrelated individuals are contributors. b) The mixture is approximately 9.48 x 10^17 times more likely to occur (very strong support for inclusion) if the suspect and two unknown, unrelated individual are contributors, rather than if three (3) unknown, unrelated individuals are contributors. **Database(s):** NIST1036_Hisp population
XTFDKX	**Method(s):** Likelihood Ratio, YSTR Profile Probability **Stats Analysis:** STR Results: This DNA result is approximately 4.95 quadrillion times more likely if Item 1, Male Victim and 2 unknown individuals were the sources of the mixture DNA profile than if 3 unknown individuals were the sources. This DNA result is approximately 1.23 quadrillion times more likely if Item 2, Female Suspect and 2 unknown individuals were the sources of the mixture DNA profile than if 3 unknown individuals were the sources. YSTR Results: The Yfiler Plus DNA profile obtained from sample Item 3 is a single source profile and matches the DNA profile from Item 1, Male Victim. Therefore, Item 1, Male Victim and any of his biological paternal relatives cannot be excluded as possible contributors to this DNA profile. The profile from Item 3 has a frequency of approximately 1 in 13,630 male individuals. **Database(s):** NIST 1036 (2017) for STR Results. US National Database in YHRD, R63 for YSTR results.

TABLE 6

WebCode	Item 3 Methods & Results
YBTHJV	**Method(s):** Likelihood Ratio **Stats Analysis:** The evidence is 1.3 sextillion times more likely if the Male Victim (item 1) is a contributor to the DNA mixture than if he is not a contributor. The evidence is 39 quintillion times more likely if the Female Suspect (item 2) is a contributor to the DNA mixture than if she is not a contributor. Further comparisons may be done for the remaining component of the mixture. **Database(s):** FBI expanded
YDE2PY	**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 48.1 million 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. The genetic profile obtained from Item 3 is interpreted as a mixture of DNA from three contributors. Item 2 (suspect) cannot be excluded as a possible contributor to this mixture. Given this genetic profile, assuming three contributors, and assuming the presence of the victim's profile, it is 3.07 quadrillion times more likely to observe this genetic profile if Item 2 (suspect) and Item 1 (victim) are contributors than if Item 1 (victim) and two unknown individuals are the contributors. **Database(s):** NIST
ZDUK9W	**Method(s):** Likelihood Ratio **Stats Analysis:** A mixed DNA profile of three (3) contributors was developed from “Item 3”. The DNA profile obtained from “Item 1” and “Item 2” is consistent with being the contributors to this mixed DNA profile. The mixed DNA profile are 1.3 septillion (1.3 x 10e24), 560 septillion (560 x 10e24) and 53 septillion (53 x 10e24) TIMES more likely IF they originated from “Item 1” (victim), “Item 2” (suspect) and one unknown individual RATHER THAN; IF they originated from three unknown unrelated individuals as calculated based on the [Location Identifying Population]. **Database(s):** [Location Identifying Database]

Statistical Analysis for Item 4

TABLE 7

WebCode	Item 4 Methods & Results
2LMCUV	**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 750 trillion (10^12) **Database(s):** NIST 1036 (Revision 2017)
2UCZPX	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result obtained from the swab (Item 4) allegedly taken from the shirt of the deceased is consistent with a mixture from at least two (2) contributors. This mixture is approximately 1.96 x 10^17 times more likely to occur (strong support for inclusion) is the suspected female and one (1) unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. The deceased male has been excluded as being a contributors to this mixture. **Database(s):** FBI_EXTENDED_SE_HISP; FBI_EXTENDED_SE_HISP_0820_21; FBI_EXTENDED_SW_HISP
3QVXHT	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA profile from this item is at least 130 quadrillion times more likely if it originated from Suspect and an unknown individual than if it originated from two unknown, unrelated individuals. Victim is excluded from this DNA profile. **Database(s):** Most conservative population group 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.
4NM3CV	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result obtained from Item 4 is consistent with a mixture of two (2) contributors. The male complainant (Item 1) has been excluded as being a contributor to this mixture. The mixture is approximately 1.21 x10^19 more likely to occur if the female suspect (Item 2) and one (1) unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. **Database(s):** FBI extended_SE_Hisp_082021
6PQHXR	**Method(s)**: Likelihood Ratio **Stats Analysis**: Item 1 is excluded as a contributor to the DNA profile from Item 4. This DNA result is approximately 19.5 trillion 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):** National Institute of Standards and Technology (NIST 2017 Revision)
6X648V	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA profile from item 4 is 1 billion times more likely if it is a result of contribution from suspect and one unknown persons than if it is a result of contribution from 2 unknown persons. **Database(s):** 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.
7463VP	**Method(s)**: Likelihood Ratio **Stats Analysis**: A mixed DNA profile of two female individuals was developed from "Item 4". The DNA profile obtained from "Item 2" is being one of the contributors to the mixed DNA profile. The mixed DNA profile is 40 quintillion, 760 quintillion and 140 quintillion TIMES more likely if it originated from "Item 2" and one unknown RATHER THAN; IF it originated from two unknown, unrelated individuals as calculated based on the Malaysian Malay, Chinese and Indian DNA population databases respectively. **Database(s):** Malaysian Malay, Chinese and Indian DNA population Databases.

TABLE 7

WebCode	Item 4 Methods & Results
7DECMP	**Method(s)**: Combined Probability of Exclusion/Inclusion **Stats Analysis**: INCLUDED as a possible contributor: Item 2 (Suspect). EXCLUDED as a possible contributor: Item 1 (Victim). The estimated frequency of a random, unrelated individual being included as a possible contributor to the profile is rarer than 1 in 330 billion. **Database(s):** STR population frequency statistics calculated in Popstats using Expanded FBI STR 2015 Caucasian and African American populations as well as [Location Identifying Population]. Only the most common frequency among the five populations or 1 in 330 billion is reported, whichever is more common.
9RPU8N	**Method(s)**: Likelihood Ratio **Stats Analysis**: The Female Mixture profile obtained from Questioned sample (Item 4: Blood on shirt) is not applicable for Male victim DNA reference inclusion. On the other hand, it provides a strong support (LR= 5.8032E17) for female suspect inclusion as a major contributor. LRmixStudio 2.1.3 used to calculate Likelihood Ratio (LR). **Database(s):** [Location Identifying Database]
ABDFQQ	**Method(s)**: Random Match Probability **Stats Analysis**: Item 2: [Location] (allele frequencies) RMP=3.2762E+34, US HISPANIC SE (allele frequencies) RMP =6.0877E+33 **Database(s):** [Location Identifying Database]
AECRLQ	**Method(s)**: Likelihood Ratio **Stats Analysis**: 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 VICTIM'S SHIRT (Item 4) is ≥1,000,000 times greater (actual LR available upon request) than if it is assumed that the VICTIM (Item 1) and one unknown unrelated person selected at random from the general population are contribuotors to this mixed-source profile. Under the assumption that the SUSPECT (Item 2) and one unknown unrelated person selected at random from the general population are contributors, the likelihood of observing the mixed source profile developed from the STAIN ON VICTIM'S SHIRT (Item 4) is ≥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. **Database(s):** Statistical Calculations employed the following databases: Revised-NIST-1036-Allele Frequencies; ABI ID Allele Frequencies; and Promega PowePlex Fusion Allele Frequencies.
AQ9XFN	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result obtained from stain (Item 4) on victim's shirt is consistent with a mixture from at least two (2) contributors: a. The victim (Item 1) has been excluded as being a contributor to this mixture. b. The mixture is approximately 2.65 x 10^17 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):** [Participant did not report database(s).]
AXRZMQ	**Method(s)**: Likelihood Ratio **Stats Analysis**: The genetic results obtained from item 4 consisted of a DNA mixture, which I interpreted as originating from at least 2 individuals. It is more than 23 quadrillion times more likely to observe this DNA mixture if it originated from Item 2 (suspect) and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals. **Database(s):** NIST 1036 population dataset

TABLE 7

WebCode	Item 4 Methods & Results
CL64AJ	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA profile from this item is at least 730 quadrillion times more likely if it originated from Item 2 (suspect) and an unknown individual than if it originated from two unknown, unrelated individuals. **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.
CMJBXL	**Method(s)**: Random Match Probability **Stats Analysis**: Item 4 RMP 2,9x10^32 for female suspect **Database(s):** Imported from STRideR population American.
ETMEXQ	**Method(s)**: Likelihood Ratio **Stats Analysis**: [Participant did not report statistical analysis.] **Database(s):** Local database
EUBPBH	**Method(s)**: Likelihood Ratio **Stats Analysis**: [Participant did not report statistical analysis.] **Database(s):** NIST1036_Hisp
GNJ2TH	**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).]
GYDFTE	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA profile from this item is at least 800 quadrillion times more likely if it originated from Suspect and an unknown individual than if it originated from two unknown, unrelated individuals. **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.
JP2ZZB	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA profile from this item is at least 420 quadrillion times more likely if it originated from Suspect 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.
JTMK6F	**Method(s)**: Likelihood Ratio **Stats Analysis**: The mixture is approximately 3.01E17 times more likely to occur (very strong support for inclusion) if the suspect and an unknown, unrelated individual are contributors, rather than if two unknown, unrelated individuals are contributors. The mixture is approximately 0 times more likely to occur (very strong support for exclusion) if the victim and an unknown, unrelated individual are contributors, rather than if two unknown, unrelated individuals are contributors. **Database(s):** FBI_EXTENDED_SE_HISP, FBI_EXTENDED_SW_HISP, NIST1036_HISP and FBI_EXTENDED_SE_HISP_0820. The stratified LR was reported.

TABLE 7

WebCode	Item 4 Methods & Results
K78LZC	**Method(s)**: Likelihood Ratio **Stats Analysis**: Item 4 (bloodstain on victim's shirt) presents a genetic profile of more than one person. Assuming that the genetic profile detected on Item 4 (bloodstain on victim's shirt) came from at least two contributors, and one of the contributors is Female Suspect (Item 2) we concluded that: The genetic profile detected on Item 4 (bloodstain on victim's shirt) is approximately: 2 Quintillons using the Caucasian population database, 106 Quintillons using the African American population database, 5 Quintillions using the Hispanic population database, times more likely to have come from Female Suspect (Item 2) and one unrelated unknown person, than any other two unrelated unknown persons chosen randomly. Female Suspect (Item 2) cannot be excluded from being one of the contributors from the genetic profile on the Item. This probability is very strongly supported by the statistical data. Male Victim (Item 1) is excluded to be one of the contributors of the genetic profile in the Item. **Database(s):** The Database used in the statistical analysis for Item 4 was the NIST's U.S. STR Population Database for Caucasian (Cau), African American (Blk), Hispanic (Hsp), Asian (Asn) and Combined Population Groups (August 2017).
KLXLRC	**Method(s)**: Random Match Probability **Stats Analysis**: RMP for major female component: The probability for selecting a random unrelated individual having a DNA profile identical to item 4 major at the loci observed is 1 in 6.52 E+34 for Hispanic Americans. RMP for minor female component: The probability of selecting a random unrelated individual having a DNA profile identical to item 4 minor is 1 in 7.98 E+34 for African Americans, 1 in 1.81E+34 for Caucasian Americans, 1 in 8.92 E+34 for Hispanic Americans, 1 in 2.18E+34 for Asian Americans **Database(s):** Promega & NIST databases
LXR3GD	**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) Item 1 (victim) has been excluded as being a contributor to this mixture. (b) The mixture is approximately 2.16 x 10^17 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):** STRmix, FBI_extended_SE_Hisp_082021
N2K7XA	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result obtained from the stain on victim's shirt (Item 4) is consistent with a mixture from at least two (2) contributors: a) The mixture is approximately 2.74 x 10^17 times more likely to occur (very strong support for inclusion) if the female suspect and one (1) unknown, unrelated individual are contributors rather than if two (2) unknown, unrelated individuals are contributors. b) The male victim has been excluded as being a contributor to this mixture. **Database(s):** FBI Extended SE Hisp 082021
NQL8BA	**Method(s)**: Likelihood Ratio **Stats Analysis**: CONCLUSION: The DNA result obtained from the stain [Internal Test Number] allegedly taken from victim's shirt is consistent with a mixture from at least two (2) contributors: A) The mixture is approximately 2.86 x 10 17 times more likely to occur (very strong support for inclusion) if the suspect and one (1) unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. B) The victim has been excluded as being a contributor to this mixture. END OF REPORT **Database(s):** [Participant did not report database(s).]
PGB7PA	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result obtained from the stain(Item 4) on victim's shirt is consistent with a mixture from at least two (2) contributors, including at least one (1) male. The mixture is approximately 2.24 x 10^17 times more likely to occur (very strong support for inclusion) if the female suspect and an unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. The male victim has been excluded as being a contributor to this mixture. **Database(s):** FBI_EXTENDED_SW_HISP and FBI_EXTENDED_SE_HISP_082021

TABLE 7

WebCode	Item 4 Methods & Results
Q2UUC7	**Method(s)**: Likelihood Ratio **Stats Analysis**: H1 : the mixture is made up of the suspect’s genetic profile (item 2) and the genetic profile of one unknown unrelated person. H2 : the mixture is made up of the genetic profils of two unknown unrelated people. LR= 1,90E16 (Personnal Data base, drop-out=0.1, drop-in=0.05, Theta=0.01) **Database(s)**: https://strider.online/frequencies
QJEKB7	**Method(s)**: Likelihood Ratio **Stats Analysis**: A mixed DNA profile of two individuals was developed from the bloodstain from the victim's shirt "Item 4". The DNA profile obtained from reference sample "Item 2" is consistent being one of the contributor to this mixed DNA profile. The mixed DNA profile is 40 quintillion (40 x 10e18), 760 quintillion (760 x 10e18) and 140 quintillion (140 x 10e18) times more likely if they originated from "Item 2" and one unknown individual rather than if they originated from two unknown unrelated individual as calculated based on the [Location Identifying Population]. **Database(s)**: [Location Identifying Database]
RN3K37	**Method(s)**: Likelihood Ratio **Stats Analysis**: LR = SUSPECT + UNKNOWN / 2 UNKNOWNS. LR = 7,17125 x E16. drop out for SUSPECT = 0. drop out for UNKNOWN = 0,01. **Database(s)**: Global Filer PCR Amplification Kit user guide. Caucasion popolation base.
RWXPW8	**Method(s)**: Combined Probability of Exclusion/Inclusion **Stats Analysis**: [Participant did not report statistical analysis.] **Database(s)**: [Participant did not report database(s).]
T7XCN4	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA information obtained from this item is more than 8 billion times more likely to be observed if the DNA originated from the suspect and one unrelated,unknown contributor than if it originated from two unrelated, unknown contributors. **Database(s)**: Combined Population from the NIST 1036 Revised U.S. Population Dataset (July 2017).
WHKKY3	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result obtained from stain (Item 4) on victim's shirt is consistent with a mixture from at least two (2) contributors: a) The male victim has been excluded as being a contributor to this mixture. b) The mixture is approximately 3.61 x 10^17 times more likely to occur (very strong support for inclusion) if the female suspect and an unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. **Database(s)**: NIST1036_Hisp population
XTFDKX	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA profile from Item 1, Male Victim was compared to Item 4. Item 1, Male Victim is excluded as a contributor to the DNA profile from Item 4. This DNA result is approximately 18.3 trillion times more likely if Item 2, Female Suspect and 1 unknown individual were the sources of the mixture DNA profile than if 2 unknown individuals were the sources. **Database(s)**: NIST 1036 (2017)
YBTHJV	**Method(s)**: Likelihood Ratio **Stats Analysis**: The evidence is 180 trillion times more likely if the Female Suspect (item 2) is a contributor to the DNA mixture than if she is not a contributor. Further comparisons may be done for the remaining component of the mixture. **Database(s)**: FBI Expanded
YDE2PY	**Method(s)**: [Participant did not report a method.] **Stats Analysis**: No statistics necessary on this sample. Results are not probative as victim is excluded from mixture. Suspect's DNA on her own clothing is not a probative result. **Database(s)**: [Participant did not report database(s).]

TABLE 7

WebCode	Item 4 Methods & Results
ZDUK9W	**Method(s)**: Likelihood Ratio **Stats Analysis**: A mixed DNA profile of two (2) contributors was developed from “Item 4”. The DNA profile obtained from “Item 2” is consistent with being one of the contributors to this mixed DNA profile. The DNA profile obtained from “Item 1” is excluded from being the other contributor to this mixed DNA profile. The mixed DNA profile are 40 quintillion (40 x 10e18), 760 quintillion (760 x 10e18) and 140 quintillion (140 x 10e18) TIMES more likely IF they originated from “Item 2” (suspect) and one unknown individual RATHER THAN; IF they originated from two unknown unrelated individuals as calculated based on the [Location Identifying Population]. **Database(s):** [Location Identifying Database]

Additional Comments

TABLE 8

WebCode	Additional Comments
3QVXHT	NR = No Results. Y-STR AT: Blue=45, Green=70, Yellow=65, Red=75, No PHR threshold for Y-STR data utilized.
6PQHXR	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.
7463VP	1. Statistical calculations were carried out using DNAView software version 37.56. 2. NM represents non-male profile.
7DECMP	There was some confusion from the naming conventions used on the electropherograms, e.g., Sample File 25-5881 GLOBALFILER Known Item 1 - Victims Blood Sample (Male) had Sample Name 24-5290 3A. I completed this test assuming that the Sample File information was correct. When this test was digitally received by the Evidence section, they gave it item #INT2. Page 1 of this form indicates that the test is item #INT1. Evidence technician was not able to determine how that number was assigned.
AECRLQ	I noted that there in some of the profiles there was insufficient spectral separation in the red channels (possibly due to an inadequate matrix file). This resulted in a failure to adequately remove the spectral overlap with the black channel The resulting pull up produced erroneous allele calls (e.g., allele 38 at SE33), off ladder allele calls (e.g., peak at 347.35 bp) in the red channel. Since these were limited mostly to the PowerPlex Fusion 6C profiles for known samples (especially item 2) in this case, they were relatively easy to identify and remove. This could have compromised the accurate interpretation of questioned profiles in a questioned sample (such as item 4 - Stain from Victim's Shirt where allele 38 at SE33 and allele 17.3 at vWA were detected in the Fusion 6C profile. Both appear to be false based on the lack of reproducibility with the other chemistries in this proficiencty tesxt. Since most labs do not run the same sample through multiple profiling chemistries, however, it would be harder to know if these were artifacts or a trace contrributor. This underscores the importance of always checking the performance of the matrix file. Unrealted to the DNA interpretation, I was a bit surprised to see the case scenario refer to blood as having been "confirmed". Given that it is generally regcognized that the serological tests for blood (both chemical and antibody based) are presumptive tests, it would be better for the scenario description to say that blood was "indicated" rather than "confirmed".
CL64AJ	NR= No results. Y-STR Analytical Threshold (RFU): Blue=45, Green=70, Yellow=65, Red=75. No PHR threshold for Y-STR data utilized.
ETMEXQ	Based on PCR validation process conducted in our lab, we have established the threshold values for each of the five dyes, depending on DNA quantity and number of cycles, as follows: Blue: 41 RFU. Green: 62 RFU. Yellow: 99 RFU. Red: 80 RFU. Purple: 76 RFU.
GYDFTE	NR=No result; YSTRs AT= 45 (blue), 70 (green), 65 (yellow), 75 (red); No PHR threshold for Y-STR data utilized.
JP2ZZB	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.
K78LZC	CODIS Popstat used for LR calculations.
NPQP99	Components not accounted for by either victim or suspect in results for items 3 and 4 show commonality. Third contributor to item 3 result most likely to be female. Using both results, possible to consider elucidating at least a partial profile for intelligence purposes (ie to search any relevant database if available).
QJEKB7	NM indicates Non-Male. The statistical calculations were carried out using DNA View Software.
RN3K37	DNA Analysis for ITEM 3: LR = VICTIM + SUSPECT + UNKNOWN / 3 UNKNOWNS. LR = 1,62092 x E22. drop out for VICTIM = 0. drop out for SUSPECT = 0. drop out for UNKNOWN = 0,01. The probability of the evidence is 1,62092 x E22 times more likely if the reddish-brown stain on the sidewalk near the victim's home came from Victim (ITEM 1), Suspect (ITEM 2) and 1 unknown unrelated individual, than if it came from three unknowns unrelated individuals. DNA Analysis for ITEM 4: LR =

TABLE 8

WebCode	Additional Comments
	SUSPECT + UNKNOWN / 2 UNKNOWNS LR = 7,17125 x E16 drop out for SUSPECT = 0 drop out for UNKNOWN = 0,01 The probability of the evidence is 7,17125 x E16 times more likely if the reddish-brown stain was identified on the victim's shirt came from Suspect (ITEM 2) and 1 unknown unrelated individual, than if it came from two unknowns unrelated individuals.
RWXPW8	Item 3; is a mixture profile of the male victim, the female suspect and unknown female. Item 4; is a mixture profile of the female suspect and the same unknown female present in item 3.
T7XCN4	Conclusion and statement for Item 3: The DNA information form this item appears to come from a mixture of at least 3 contributors with major and minor components. Due to the complex nature of this mixture profile, it is not suitable for manual comparison due to the stochastic effects throughout the profile. However, the DNA information obtained may be suitable for probabilistic genotyping.
XTFDKX	For STR Stochastic Threshold (ST), the laboratory uses ST based on injection time, 300 RFU for 7 and 10 second injections, and 400 RFU for 15 second injection. The Likelihood Ratio result considering Item 1 (Male Victim) a contributor of Item 4 is zero.
YBTHJV	For item 3, at vWA: Analysis was done using FaSTR interpretation software. The 15 allele was designated as stutter based on the Artificial Neural Network (ANN) information and the RFU ratio with the allele next to it. The 15 allele (stutter) is included with the interpretation of the mixture in STRmix for the 3rd contributor (19% contribution to 3 person mixture), which is associated to the reference sample for the victim (item 1).
ZDUK9W	1. Statistical calculation were carried out using DNA View Software. 2. NM represents non-male profile.

-End of Report-
(Appendix may follow)

Collaborative Testing Services ~ Forensic Testing Program

Test No. 25-5881: DNA Interpretation

DATA MUST BE SUBMITTED BY **June 09, 2025, 11:59 p.m. EDT** TO BE INCLUDED IN THE REPORT

Participant Code: U1234A WebCode: 8ANP6L

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 stabbing case involving a male victim and female suspect. The victim reported to police that the suspect stabbed him several times on the sidewalk just outside his home. The suspect, who has been apprehended, denies any involvement in the stabbing. While a weapon has not been recovered, investigators have identified a reddish-brown stain on the sidewalk near the victim's home, which the Serology Unit confirmed as blood (Item 3). Additionally, a reddish-brown stain was identified on the victim's shirt and was also confirmed as blood (Item 4).

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

Items Submitted (Sample Pack INT1):
Item 1: DNA profile from reference sample (Male Victim - Hispanic)
Item 2: DNA profile from reference sample (Female Suspect - Hispanic)
Item 3: DNA profile from stain on sidewalk outside victim's home
Item 4: DNA profile from stain on victim's shirt

To verify a complete and accurate download, the hash value for the downloaded .ZIP file is as follows:
25-5881 Data for Participants.zip MD5 hash value: 74322a190c87d99fe99f2a26911076e9
25-5881 Data for Participants.zip SHA1 hash value: 8268ad5bc43668662ea8d47c5e4fa281d2a349da

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

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

☐ HID format
☐ PDF format

Report the Probabilistic Genotyping Software Used (if applicable): ☐

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

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

YSTR Results for Known Item 1

YSTR Amplification Kit Used For Item 1:

☐ 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
1									
ITEM	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
1									
ITEM	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	Y GATA H4
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 ☐ PowerPlex® Fusion 5C ☐ PowerPlex® Fusion 6C

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

☐ HID format ☐ PDF format

Report the Probabilistic Genotyping Software Used (if applicable):

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

ITEM	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
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						

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

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

☐ HID format
☐ PDF format

Report the Probabilistic Genotyping Software Used (if applicable):

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

ITEM	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
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
☐ PowerPlex® Fusion 5C
☐ PowerPlex® Fusion 6C

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

☐ HID format
☐ PDF format

Report the Probabilistic Genotyping Software Used (if applicable): ☐

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

ITEM	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
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)

______