Collaborative Testing Services, Inc
FORENSIC TESTING PROGRAM

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DNA Interpretation Test No. 24-5881
Summary Report

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

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

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

Manufacturer's Information

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

SAMPLE PREPARATION: Item 1 was created using blood collected from a female donor. Item 2 was created using blood collected from a male donor. Item 3 was created by combining one part of blood from the Item 1 female donor and one part of blood from the Item 2 male donor. Item 4 was created by combining one part of blood from the Item 1 female donor, one part of blood from the Item 2 male donor, and two parts of blood from an additional female donor whose known standard was not provided.

VERIFICATION: Predistribution results were consistent with each other and the manufacturer’s preparation information with the exception of one participant who was missing an allele at locus D22S1045.

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

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

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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	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
	13,14	30,31	15,17	X,X	11,11	20,25
	*	*	19,27.2	6,7	8,11	14,16
	NM	NM	NM	NM		
2	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
	16,16	27,33.2	11,17	X,Y	9,10	22,22
	*	*	17,20	6,6	8,9	15,18
	10	*	*	2		
3	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12,12	9,11,12,13	12,15,18
	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
	*	*	17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10	*	*	2		
4	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
	*	*	17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10	*	*	2		

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

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

YSTR Results

Results compiled from predistribution laboratories and a consensus of participants.

Item	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
	DYS437	**DYS438**	**DYS439**	**DYS448**	**DYS449**	**DYS456**	**DYS458**	**DYS460**	**DYS481**
	DYS518	**DYS533**	**DYS549**	**DYS570**	**DYS576**	**DYS627**	**DYS635**	**DYS643**	**YGATAH4**
2	35,36	14	11,15	13	29	24	10	13	13
	15	12	12	19	27	15	18	10	25
	36	12	12	17	18	21	23	10	12
3	35,36	14	11,15	13	29	24	10	13	13
	15	12	12	19	27	15	18	10	25
	36	12	12	17	18	21	23	10	12
4	35,36	14	11,15	13	29	24	10	13	13
	15	12	12	19	27	15	18	10	25
	36	12	12	17	18	21	23	10	12

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Summary Comments

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

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

DNA Analysis
All 31 participants that returned results evaluated the provided STR data.

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

For YSTR results, all participants reported consistent results.

For Item 3, a consensus was achieved for the full Item 3 profile (unseparated). Nine 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). No participants attempted the deconvolution of this mixture; therefore, a consensus was not formed for major or minor profiles.

DNA Interpretations
For Item 3, all participants identified that two (or at least two) individuals contributed to the mixture. All participants included the victim (Item 1) and the suspect (Item 2) as possible contributors to the stain.

For Item 4, all participants identified that three (or at least three) individuals contributed to the mixture. All but three participants included the victim (Item 1) as a possible contributor to the stain. The remaining three participants reported "Inconclusive/Uninterpretable;" one of which noted in their Additional Comments that their lab does not interpret mixtures of three or more contributors. All participants included the suspect (Item 2) as a possible contributor to the stain.

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STR Interpretation Guidelines

TABLE 1

WebCode	Analytical Threshold (rfu)	Peak Height Ratio (%)	Stochastic Threshold (rfu)
2LP44T	160	60	630
6YEQCT	130	60	800
8Q4PFM	[Participant did not provide interpretation guidelines]		
A7PUZL	100	65	600
B2ZLFM	130	60	800
CLWRXH	60	50	
EJ2NHF	180	50	370
F9DEBX	150	60	400
FK8VXD	120	60	360
GTNJVG	130		800
H7K3LC	120	60	360
MALE83	75	60	100
N8VV48	75	60	
NPDUBQ	[Participant did not provide interpretation guidelines]		
PRFCK7	160	60	630
PVWJ96	120	60	360
RM36L6	50	65	200
RRHDA6	130		800
TER4Z6	130	60	800
TQBTDK	75	60	100
V6QPRZ	130		800
V7G24Y	75	60	100
V9P2NZ	130	60	800
VER4PY	75	60	100
WU27NY	160	60	630
X9JGRF	75	60	100
XVRRWG	75	60	100
YAEBCX	130	60	800
YEEZ6V	50	60	865
YWYQ4V	80	60	250
ZNJ8KV	50	50	900

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YSTR Interpretation Guidelines

TABLE 2

WebCode	Analytical Threshold (rfu)	Peak Height Ratio (%)	Stochastic Threshold (rfu)
2LP44T	100	60	600
6YEQCT	50	60	724
8Q4PFM	[Participant did not provide interpretation guidelines]		
A7PUZL	[Participant did not provide interpretation guidelines]		
B2ZLFM	50	70	725
CLWRXH	60	50	
EJ2NHF	[Participant did not provide interpretation guidelines]		
F9DEBX	[Participant did not provide interpretation guidelines]		
FK8VXD	75	50	75
GTNJVG	50		800
H7K3LC	75	50	75
MALE83	[Participant did not provide interpretation guidelines]		
N8VV48	75	50	
NPDUBQ	[Participant did not provide interpretation guidelines]		
PRFCK7	100	60	600
PVWJ96	75	50	75
RM36L6	50	65	175
RRHDA6	50		800
TER4Z6	[Participant did not provide interpretation guidelines]		
TQBTDK	75	50	75
V6QPRZ	50		800
V7G24Y	75	50	75
V9P2NZ	50	70	725
VER4PY	75	50	75
WU27NY	100	60	600
X9JGRF	75	50	75
XVRRWG	75	50	75
YAEBCX	50	70	
YEEZ6V	[Participant did not provide interpretation guidelines]		
YWYQ4V	80	50	75
ZNJ8KV	[Participant did not provide interpretation guidelines]		

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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

2LP44T	GlobalFiler™ (HID Format)					
	16,16.3	21,25	11,13	15	11,12	10,11
	10,14	14,15	18,22	12	9,12	12,15
1	13,14	30,31	15,17	X	11	20,25
			19,27.2	6,7	8,11	14,16
6YEQCT	GlobalFiler™ (STRmix version 2.10)					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
			19,27.2	6,7	8,11	14,16
	-			-		
8Q4PFM	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format) (Likelihood Ratio (Lab Retriever))					
	16,16.3	21,25	11,13	15	11,12	10,11
	10,14	14,15	18,22	12	9,12	12,15
1	13,14	30,31	15,17	X	11	20,25
	10,12	12,17	19,27.2	6,7	8,11	14,16
A7PUZL	Investigator® 24plex (PDF Format)					
	16,16.3	21,25	11,13	15	11,12	10,11
	10,14	14,15	18,22	12	9,12	12,15
1	13,14	30,31	15,17	X	11	20,25
			19,27.2	6,7	8,11	14,16
	-					
B2ZLFM	GlobalFiler™ (PDF Format), (HID Format)					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
			19,27.2	6,7	8,11	14,16
	-			-		
CLWRXH	GlobalFiler™ (PDF Format)					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
			19,27.2	6,7	8,11	14,16

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TABLE 3

Item 1 - STR Results

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
	D8S1179	D10S1248	D12S391	D13S317	D16S539	D18S51
Item	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO	FGA
	Penta D	Penta E	SE33	TH01	TPOX	vWA
	DYS391	DYS570	DYS576	Y Indel		
EJ2NHF	Investigator® 24plex					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
	N/A	N/A	19,27.2	6,7	8,11	14,16
	N/A	N/A	N/A	N/A		
F9DEBX	GlobalFiler™ (PDF Format)					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
			19,27.2	6,7	8,11	14,16
	--			--		
FK8VXD	GlobalFiler™ (PDF Format)					
	16,16.3	21,25	11,13	15	11,12	10,11
	10,14	14,15	18,22	12	9,12	12,15
1	13,14	30,31	15,17	X,X	11	20,25
			19,27.2	6,7	8,11	14,16
	NM			NM		
GTNJVG	GlobalFiler™ (PDF Format), (HID Format) (STRMIX)					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
			19,27.2	6,7	8,11	14,16
H7K3LC	GlobalFiler™ (PDF Format)					
	16,16.3	21,25	11,13	15	11,12	10,11
	10,14	14,15	18,22	12	9,12	12,15
1	13,14	30,31	15,17	X,X	11	20,25
			19,27.2	6,7	8,11	14,16
	NM			NM		
MALE83	GlobalFiler™ (PDF Format)					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
			19,27.2	6,7	8,11	14,16

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TABLE 3

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

Item 1 - STR Results

N8VV48	GlobalFiler™ (HID Format) (Lab Retriever)					
	16,16.3	21,25	11,13	15	11,12	10,11
	10,14	14,15	18,22	12	9,12	12,15
1	13,14	30,31	15,17	X	11	20,25
			19,27.2	6,7	8,11	14,16
NPDUBQ	GlobalFiler™					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
			19,27.2	6,7	8,11	14,16
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PRFCK7	GlobalFiler™ (HID Format)					
	16,16.3	21,25	11,13	15	11,12	10,11
	10,14	14,15	18,22	12	9,12	12,15
1	13,14	30,31	15,17	X	11	20,25
			19,27.2	6,7	8,11	14,16
PVWJ96	GlobalFiler™ (PDF Format)					
	16,16.3	21,25	11,13	15	11,12	10,11
	10,14	14,15	18,22	12	9,12	12,15
1	13,14	30,31	15,17	X,X	11	20,25
			19,27.2	6,7	8,11	14,16
	NM			NM		
RM36L6	PowerPlex® Fusion 5C (PDF Format)					
	16,16.3	21,25	11,13	15	11,12	10,11
	10,14	14,15	18,22	12	9,12	12,15
1	13,14	30,31	15,17	X	11	20,25
	10,12	12,17	-	6,7	8,11	14,16
	-	-	-	-		
RRHDA6	GlobalFiler™ (STRMix)					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
			19,27.2	6,7	8,11	14,16

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TABLE 3

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

Item 1 - STR Results

TER4Z6	GlobalFiler™ (HID Format)					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
			19,27.2	6,7	8,11	14,16
TQBTDK	PowerPlex® Fusion 6C (PDF Format)					
	16,16.3	21,25	11,13	15	11,12	10,11
	10,14	14,15	18,22	12	9,12	12,15
1	13,14	30,31	15,(16),17	X	11	20,25
	10,12	12,17	19,27.2	6,7	8,11	14,16
V6QPRZ	GlobalFiler™					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
	-	-	19,27.2	6,7	8,11	14,16
	-	-	-	-		
V7G24Y	GlobalFiler™ (PDF Format)					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
	N/A	N/A	19,27.2	6,7	8,11	14,16
	NSD	N/A	N/A	NSD		
V9P2NZ	GlobalFiler™					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
			19,27.2	6,7	8,11	14,16
	-			-		
VER4PY	GlobalFiler™ (PDF Format)					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
			19,27.2	6,7	8,11	14,16

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TABLE 3

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

Item 1 - STR Results

WU27NY	GlobalFiler™ (HID Format)					
	16,16.3	21,25	11,13	15	11,12	10,11
	10,14	14,15	18,22	12	9,12	12,15
1	13,14	30,31	15,17	X	11	20,25
			19,27.2	6,7	8,11	14,16
X9JGRF	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format) (LR Mix Studio)					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
	10,12	12,17	19,27.2	6,7	8,11	14,16
XVRRWG	GlobalFiler™ (HID Format)					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
			19,27.2	6,7	8,11	14,16
	N/A			N/A		
YAEBCX	GlobalFiler™ (HID Format) (STRmix)					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
			19,27.2	6,7	8,11	14,16
YEEZ6V	GlobalFiler™ (PDF Format) (LRmix Studio ver. 2.1.5 Community Edition)					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
			19,27.2	6,7	8,11	14,16
YWYQ4V	GlobalFiler™ (PDF Format)					
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
1	13,14	30,31	15,17	X,X	11,11	20,25
			19,27.2	6,7	8,11	14,16
	-			-		

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TABLE 3

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

Item 1 - STR Results

ZNJ8KV	GlobalFiler™ (HID Format) (STRmix)					
1	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
	13,14	30,31	15,17	X,X	11,11	20,25
			19,27.2	6,7	8,11	14,16
	NR			NR		

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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 2 - STR Results			
2LP44T	GlobalFiler™ (HID Format)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12	11,13	15,18
2	16	27,33.2	11,17	X,Y	9,10	22
			17,20	6	8,9	15,18
	10			2		
6YEQCT	GlobalFiler™ (STRmix Version 2.10)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18
	10			2		
8Q4PFM	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format) (Likelihood Ratio (Lab Retriever))					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12	11,13	15,18
2	16	27,33.2	11,17	X,Y	9,10	22
	12,13	7	17,20	6	8,9	15,18
	10	17	18	2		
A7PUZL	Investigator® 24plex (PDF Format)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12	11,13	15,18
2	16	27,33.2	11,17	X,Y	9,10	22
			17,20	6	8,9	15,18
	10					
B2ZLFM	GlobalFiler™ (PDF Format), (HID Format)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18
	10			2		
CLWRXH	GlobalFiler™ (PDF Format)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18
	10			2		

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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 2 - STR Results			
EJ2NHF	Investigator® 24plex					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
	N/A	N/A	17,20	6,6	8,9	15,18
	10	N/A	N/A	N/A		
F9DEBX	GlobalFiler™ (PDF Format)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18
	10			2		
FK8VXD	GlobalFiler™ (PDF Format)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12	11,13	15,18
2	16	27,33.2	11,17	X,Y	9,10	22
			17,20	6	8,9	15,18
	10			2		
GTNJVG	GlobalFiler™ (PDF Format), (HID Format) (STRMIX)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18
	10			2		
H7K3LC	GlobalFiler™ (PDF Format)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12	11,13	15,18
2	16	27,33.2	11,17	X,Y	9,10	22
			17,20	6	8,9	15,18
	10			2		
MALE83	GlobalFiler™ (PDF Format)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18
	10			2		

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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 2 - STR Results						
N8VV48	GlobalFiler™ (HID Format) (Lab REtriever)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12	11,13	15,18
2	16	27,33.2	11,17	X,Y	9,10	22
			17,20	6	8,9	15,18
	10			2		
NPDUBQ	GlobalFiler™					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18
	10			2		
PRFCK7	GlobalFiler™ (HID Format)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12	11,13	15,18
2	16	27,33.2	11,17	X,Y	9,10	22
			17,20	6	8,9	15,18
	10			2		
PVWJ96	GlobalFiler™ (PDF Format)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12	11,13	15,18
2	16	27,33.2	11,17	X,Y	9,10	22
			17,20	6	8,9	15,18
	10			2		
RM36L6	PowerPlex® Fusion 5C (PDF Format)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12	11,13	15,18
2	16	27,33.2	11,17	X,Y	9,10	22
	12,13	7	-	6	8,9	15,18
	10	-	-	-		
RRHDA6	GlobalFiler™ (STRMix)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18

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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 2 - STR Results			
TER4Z6	GlobalFiler™ (HID Format)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18
	10			2		
TQBTDK	PowerPlex® Fusion 6C (PDF Format)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
	12,13	7,7	17,20	6,6	8,9	15,18
	10	17	18			
V6QPRZ	GlobalFiler™					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18
	10			2		
V7G24Y	GlobalFiler™ (PDF Format)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
	N/A	N/A	17,20	6,6	8,9	15,18
	10	N/A	N/A	2		
V9P2NZ	GlobalFiler™					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18
	10			2		
VER4PY	GlobalFiler™ (PDF Format)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18
	10			2		

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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 2 - STR Results			
WU27NY	GlobalFiler™ (HID Format)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12	11,13	15,18
2	16	27,33.2	11,17	X,Y	9,10	22
			17,20	6	8,9	15,18
	10			2		
X9JGRF	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format) (LR Mix Studio)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
	12,13	7,7	17,20	6,6	8,9	15,18
	10	17	18	2		
XVRRWG	GlobalFiler™ (HID Format)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18
	10			2		
YAEBCX	GlobalFiler™ (HID Format) (STRmix)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18
	10			2		
YEEZ6V	GlobalFiler™ (PDF Format) (LRmix Studio ver. 2.1.5 Community Edition)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18
	10			2		
YWYQ4V	GlobalFiler™ (PDF Format)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18
	10			2		

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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 2 - STR Results

ZNJ8KV	GlobalFiler™ (HID Format) (STRmix)					
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
2	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18
	10			2		

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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 3 - STR Results			
2LP44T	GlobalFiler™ (HID Format)					
	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
3	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10			2		
6YEQCT	GlobalFiler™ (STRmix version 2.10)					
	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
3	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10			2		
8Q4PFM	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format) (Likelihood Ratio (Lab Retriever))					
	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
3	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
	10,12,13	7,12,17	17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10	17	18	2		
A7PUZL	Investigator® 24plex (PDF Format)					
	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
3	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10					
	_	21,25	11,13	15	11,12	10,11
	10,14	14,15	_	12	9,12	12,15
3major	_	30,31	15,17	X	11	_
			19,27.2	6+	8,11	14,16
	_					
	_	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	_	12	11,13	15,18
3minor	_	27,33.2	11,17	X,Y	9,10	_
			17,20	-	8,9	15,18
	10					

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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 3 - STR Results						
B2ZLFM	GlobalFiler™	(PDF Format)	(STRmix v 2.10)			
	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,23,24	12	9,11,12,13	12,15,18
3	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10			2		
CLWRXH	GlobalFiler™	(PDF Format)				
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
3major		30,31	15,17	X,X	11,11	
			19,27.2		8,11	14,16
	13,15	17,20	12,14	17	13	8
	12,13	12,13	21,24		11,13	18
3minor		27,33.2	11	Y	9,10	
			17,20		9	15,18
	10			2		
EJ2NHF	Investigator® 24plex	(HID Format)				
	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
3	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
	N/A	N/A	17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10	N/A	N/A	N/A		
F9DEBX	GlobalFiler™	(PDF Format)				
	{13},{15},16,16.3	{17},{20},21,25	11,{12},13,{14}	15,17	11,12,{13}	{8},10,11
	10,{12},{13},14	{12},{13},14,15	18,{21},22,{24}	12,12	9,{11},12,{13}	12,15,{18}
3	13,14,{16}	{27},30,31,{33.2}	{11},15,17	X,{Y}	{9},{10},11	20,{22},25
			{17},19,{20},27.2	6,7	8,{9},11	14,{15},16,{18}
	10			2		
FK8VXD	GlobalFiler™	(PDF Format)				
	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
3	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10			2		

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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 3 - STR Results					
GTNJVG	GlobalFiler™ (PDF Format), (HID Format) (STRMIX)					
3	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,23,24	12	9,11,12,13	12,15,18
	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10			2		
H7K3LC	GlobalFiler™ (PDF Format)					
3	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10			2		
MALE83	GlobalFiler™ (PDF Format)					
3	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,23,24	12	9,11,12,13	12,15,18
	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10			2		
3major	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
	13,14	30,31	15,17	X,X	11,11	20,25
			19,27.2	6,7	8,11	14,16
3minor	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18
	10			2		
N8VV48	GlobalFiler™ (HID Format) (Lab Retriever)					
3	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10			2		
NPDUBQ	GlobalFiler™					
3	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12,12	9,11,12,13	12,15,18
	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10			2		

TABLE 3

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

Item 3 - STR Results

PRFCK7	GlobalFiler™ (HID Format)					
	13,15,16,16.3	17,20,21,25	11,12,13,14		11,12,13	8,10,11
	10,12,13,14	12,13,14,15			9,11,12,13	
3	13,14,16					20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
				15		
			18,22	12		12,15
3major		30,31	15,17	X	11	
				17		
			21,24			18
3minor		27,33.2	11	Y	9,10	
	10			2		
PVWJ96	GlobalFiler™ (PDF Format)					
	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
3	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10			2		
RM36L6	PowerPlex® Fusion 5C (PDF Format)					
	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
3	13,15,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
	10,12,13	7,12,17	-	6,7	8,9,11	14,15,16,18
	10	-	-	-		
	16,16.3	21,25	11,13	15	11,12	10,11
	10,14	14,15	18,22	12	9,12	12,15
3major	13,14	30,31	15,17	X	11	20,25
	10,12	12,17	-	6,7	8,11	14,16
	-	-	-	-		
	13,15	17,29	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12	11,13	15,18
3minor	16	27,33.2	11,17	X,Y	9,10	22
	12,13	7	-	6	8,9	15,18
	10	-	-	-		

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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 3 - STR Results

RRHDA6	GlobalFiler™ (STRMix)					
3	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
TER4Z6	GlobalFiler™ (HID Format) (STRMix)					
3	13,15,16,16.3	17,20,21,25FB	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
	13,14,16	27,20,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10			2		
TQBTDK	PowerPlex® Fusion 6C (PDF Format)					
3	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12,12	9,11,12,13	12,15,18
	13,14,16	27,30,31,33.2	11,15,16,17	X,Y	9,10,11	20,22,25
	10,12,13	7,12,17	17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10	17	18			
V6QPRZ	GlobalFiler™ (STRmix)					
3	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12,12	9,11,12,13	12,15,18
	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10			2		
3major	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
	13,14	30,31	15,17	-	11,11	20,25
			19,27.2	6,7	8,11	14,16
	-			-		
3minor	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
	16,16	27,33.2	11,17	-	9,10	22,22
			17,20	6,6	8,9	15,18
	-			-		
V7G24Y	GlobalFiler™ (PDF Format)					
3	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
	N/A	N/A	17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10	N/A	N/A	2		

TABLE 3

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

Item 3 - STR Results

V9P2NZ	GlobalFiler™	(STRMix v 2.10)				
	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
3	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10			2		
VER4PY	GlobalFiler™	(PDF Format)				
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
3major		30,31	15,17	X,X	11,11	
			19,27.2		8,11	14,16
	13,15	17,20	12,14	17	13	8
	12,13	12,13	21,24		11,13	18
3minor		27,33.2	11	X,Y	9,10	
			17,20		9	15,18
	10			2		
WU27NY	GlobalFiler™	(HID Format)				
	13,15,16,16.3	17,20,21,25	11,12,13,14		11,12,13	8,10,11
	10,12,13,14	12,13,14,15			9,11,12,13	
3	13,14,16					20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
				15		
			18,22	12		12,15
3major		30,31	15,17	X	11	
				17		
			21,24			18
3minor		27,33.2	11	X,Y	9,10	
	10			2		
X9JGRF	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format) (LR Mix Studio)					
	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
3	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
	10,12,13	7,12,17	17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10	17	18	2		

TABLE 3

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

Item 3 - STR Results

XVRRWG	GlobalFiler™ (HID Format)					
	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
3	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10			2		
YAEBCX	GlobalFiler™ (HID Format) (STRmix)					
	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
3	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10			2		
YEEZ6V	GlobalFiler™ (PDF Format) (LRmix Studio ver. 2.1.5 Community Edition)					
	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
3	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10			2		
YWYQ4V	GlobalFiler™ (PDF Format) (LRmixStudio-2.1.5-CommunityEdition)					
	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12	9,11,12,13	12,15,18
3	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10			2		
	16,16.3	21,25	11,13	15,15	11,12	10,11
	10,14	14,15	18,22	12,12	9,12	12,15
3major	13,14	30,31	15,17	X,X	11,11	20,25
			19,27.2	6,7	8,11	14,16
	-			-		
	13,15	17,20	12,14	15,17	11,13	8,10
	12,13	12,13	21,24	12,12	11,13	15,18
3minor	16,16	27,33.2	11,17	X,Y	9,10	22,22
			17,20	6,6	8,9	15,18
	10			2		
ZNJ8KV	GlobalFiler™ (HID Format) (STRmix)					
	13,15,16,16.3	17,20,21,25	11,12,13,14	15,17	11,12,13	8,10,11
	10,12,13,14	12,13,14,15	18,21,22,24	12,12	9,11,12,13	12,15,18
3	13,14,16	27,30,31,33.2	11,15,17	X,Y	9,10,11	20,22,25
			17,19,20,27.2	6,7	8,9,11	14,15,16,18
	10			2		

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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			
2LP44T	GlobalFiler™ (HID Format)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		
6YEQCT	GlobalFiler™ (STRmix version 2.10)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		
8Q4PFM	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format) (Likelihood Ratio (Lab Retriever))					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
	10,12,13	5,7,12,17	17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10	17	18	2		
A7PUZL	Investigator® 24plex (PDF Format)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	-
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	_	9,10,11,12	19,20,22,23,25
			_	6,7,9.3	8,9,11,12	14,15,16,17,18
	10					
B2ZLFM	GlobalFiler™ (PDF Format), (HID Format) (STRmix v 2.10)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		
CLWRXH	GlobalFiler™ (PDF Format)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		

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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

EJ2NHF	Investigator® 24plex (HID Format)					
4	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
		N/A	17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10	N/A	N/A	N/A		
F9DEBX	GlobalFiler™ (PDF Format)					
4	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		
FK8VXD	GlobalFiler™ (PDF Format)					
4	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		
GTNJVG	GlobalFiler™ (PDF Format), (HID Format) (STRMIX)					
4	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		
H7K3LC	GlobalFiler™ (PDF Format)					
4	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		
MALE83	GlobalFiler™ (PDF Format)					
4	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		

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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					
N8VV48	GlobalFiler™ (HID Format) (Lab Retriever)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		
NPDUBQ	GlobalFiler™					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		
PRFCK7	GlobalFiler™ (HID Format)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		
PVWJ96	GlobalFiler™ (PDF Format)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		
RM36L6	PowerPlex® Fusion 5C (PDF Format)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,16,17	X,Y	9,10,11,12	19,20,22,23,25
	10,12,13	5,7,12,17	-	6,7,9.3	8,9,11,12	14,15,16,17,18
	10	-	-	-		
RRHDA6	GlobalFiler™					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18

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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

WebCode	Amplification Kits (File Format) (Probabilistic Genotyping)					
TER4Z6	GlobalFiler™ (HID Format) (STRMix)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		
TQBTDK	PowerPlex® Fusion 6C (PDF Format)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,16,17	X,Y	9,10,11,12	19,20,22,23,25
	10,12,13	5,7,12,17	17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10	17	18			
V6QPRZ	GlobalFiler™ (STRmix)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		
V7G24Y	GlobalFiler™ (PDF Format)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
	N/A	N/A	17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10	N/A	N/A	2		
V9P2NZ	GlobalFiler™ (STRMix v 2.10)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		
VER4PY	GlobalFiler™ (PDF Format)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		

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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

WU27NY	GlobalFiler™ (HID Format)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		
X9JGRF	GlobalFiler™, Investigator® 24plex, PowerPlex® Fusion 5C, PowerPlex® Fusion 6C (PDF Format), (HID Format) (LR Mix Studio)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,16,17	X,Y	9,10,11,12	19,20,22,23,25
	10,12,13	5,7,12,17	17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10	17	18	2		
XVRRWG	GlobalFiler™ (HID Format)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		
YAEBCX	GlobalFiler™ (HID Format) (STRmix)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,177	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		
YEEZ6V	GlobalFiler™ (PDF Format) (LRmix Studio ver. 2.1.5 Community Edition)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		
YWYQ4V	GlobalFiler™ (PDF Format) (LRmixStudio-2.1.5-CommunityEdition)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		

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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

ZNJ8KV	GlobalFiler™ (HID Format) (STRmix)					
	13,15,16,16.3,17.3	17,20,21,25	10,11,12,13,14	15,16,17	11,12,13	8,10,11,12
	10,12,13,14	12,13,14,15	18,20,21,22,24	11,12	9,11,12,13	12,15,18
4	13,14,14.2,16	27,30,31,31.2,32.2,33.2	11,15,17	X,Y	9,10,11,12	19,20,22,23,25
			17,19,20,27.2	6,7,9.3	8,9,11,12	14,15,16,17,18
	10			2		

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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 2 - YSTR Results

2LP44T	PowerPlex® Y23 (HID Format)								
		14	11,15	13	29	24	10	13	13
2	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
6YEQCT	PowerPlex® Y23								
		14	11,15	13	29	24	10	13	13
2	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
8Q4PFM	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	35,36	14	11,15	13	29	24	10	13	13
2	15	12	12	19	27	15	18	10	25
	36	12	12	17	18	21	23	10	12
B2ZLFM	PowerPlex® Y23 (PDF Format), (HID Format)								
		14	11,15	13	29	24	10	13	13
2	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
CLWRXH	PowerPlex® Y23 (PDF Format)								
		14	11,15	13	29	24	10	13	13
2	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
FK8VXD	Yfiler™ Plus (PDF Format)								
	35,36	14	11,15	13	29	24	10	13	13
2	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12
GTNJVG	PowerPlex® Y23 (PDF Format)								
		14	11,15	13	29	24	10	13	13
2	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
H7K3LC	Yfiler™ Plus (PDF Format)								
	35,36	14	11,15	13	29	24	10	13	13
2	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12
N8VV48	Yfiler™ Plus (HID Format)								
	35,36	14	11,15	13	29	24	10	13	13
2	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12
NPDUBQ	Yfiler™ Plus								
	35,36	14	11,15	13	29	24	10	13	13
2	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12

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TABLE 4

WebCode	Amplification Kits (File Format)								
	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
Item	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4
	Item 2 - YSTR Results								
PRFCK7	PowerPlex® Y23 (HID Format)								
		14	11,15	13	29	24	10	13	13
2	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
PVWJ96	Yfiler™ Plus (PDF Format)								
	35,36	14	11,15	13	29	24	10	13	13
2	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12
RM36L6	PowerPlex® Y23 (PDF Format)								
	-	14	11,15	13	29	24	10	13	13
2	15	12	12	19	-	15	18	-	25
	-	12	12	17	18	-	23	10	12
RRHDA6	PowerPlex® Y23								
		14	11,15	13	29	24	10	13	13
2	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
TQBTDK	PowerPlex® Y23 (PDF Format)								
		14	11,15	13	29	24	10	13	13
2	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
V6QPRZ	PowerPlex® Y23 (PDF Format)								
		14	11,15	13	29	24	10	13	13
2	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
V7G24Y	Yfiler™ Plus (PDF Format)								
	35,36	14	11,15	13	29	24	10	13	13
2	15	12	12	19	27	15	18	10	25
	36	12	N/A	17	18	21	23	N/A	12
V9P2NZ	PowerPlex® Y23								
		14	11,15	13	29	24	10	13	13
2	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
VER4PY	PowerPlex® Y23 (PDF Format)								
		14	11,15	13	29	24	10	13	13
2	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
WU27NY	PowerPlex® Y23 (HID Format)								
		14	11,15	13	29	24	10	13	13
2	15	12	12	19		15	18		25
		12	12	17	18		23	10	12

TABLE 4

WebCode	**Amplification Kits (File Format)**								
	DYF387S	**DYS19**	**DYS385**	**DYS389-I**	**DYS389-II**	**DYS390**	**DYS391**	**DYS392**	**DYS393**
Item	**DYS437**	**DYS438**	**DYS439**	**DYS448**	**DYS449**	**DYS456**	**DYS458**	**DYS460**	**DYS481**
	DYS518	**DYS533**	**DYS549**	**DYS570**	**DYS576**	**DYS627**	**DYS635**	**DYS643**	**YGATAH4**
	Item 2 - YSTR Results								
X9JGRF	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	35,36	14	11,15	13	29	24	10	13	13
2	15	12	12	19	27	15	18	10	25
	36	12	12	17	18	21	23	10	12
XVRRWG	Yfiler™ Plus (HID Format)								
	35,36	14	11,15	13	29	24	10	13	13
2	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12
YAEBCX	PowerPlex® Y23 (HID Format)								
		14	11,15	13	29	24	10	13	13
2	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
YEEZ6V	Yfiler™ Plus (PDF Format)								
	35,36	14	11,15	13	29	24	10	13	13
2	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12
YWYQ4V	Yfiler™ Plus (PDF Format)								
	35,36	14	11,15	13	29	24	10	13	13
2	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12

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TABLE 4

Item 3 - YSTR Results

WebCode Item	Amplification Kits (File Format)								
	DYF387S	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4
2LP44T	PowerPlex® Y23 (HID Format)								
		14	11,15	13	29	24	10	13	13
3	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
6YEQCT	PowerPlex® Y23								
		14	11,15	13	29	24	10	13	13
3	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
8Q4PFM	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	35,36	14	11,15	13	29	24	10	13	13
3	15	12	12	19	27	15	18	10	25
	36	12	12	17	18	21	23	10	12
B2ZLFM	PowerPlex® Y23								
		14	11,15	13	29	24	10	13	13
3	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
CLWRXH	PowerPlex® Y23 (PDF Format)								
		14	11,15	13	29	24	10	13	13
3	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
FK8VXD	Yfiler™ Plus (PDF Format)								
	35,36	14	11,15	13	29	24	10	13	13
3	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12
GTNJVG	PowerPlex® Y23 (PDF Format)								
		14	11,15	13	29	24	10	13	13
3	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
H7K3LC	Yfiler™ Plus (PDF Format)								
	35,36	14	11,15	13	29	24	10	13	13
3	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12
N8VV48	Yfiler™ Plus								
	35,36	14	11,15	13	29	24	10	13	13
3	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12
NPDUBQ	Yfiler™ Plus								
	35,36	14	11,15	13	29	24	10	13	13
3	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12

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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								
PRFCK7	PowerPlex® Y23 (HID Format)								
		14	11,15	13	29	24	10	13	13
3	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
PVWJ96	Yfiler™ Plus (PDF Format)								
	35,36	14	11,15	13	29	24	10	13	13
3	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12
RM36L6									
	-	14	11,15	13	29	24	10	13	13
3	15	12	12	19	-	15	18	-	25
	-	12	12	17	18	-	23	10	12
RRHDA6	PowerPlex® Y23								
		14	11,15	13	29	24	10	13	13
3	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
TQBTDK	PowerPlex® Y23 (PDF Format)								
		14	11,15	13	29	24	10	13	13
3	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
V6QPRZ	PowerPlex® Y23 (PDF Format)								
		14	11,15	13	29	24	10	13	13
3	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
V7G24Y	Yfiler™ Plus (PDF Format)								
	35,36	14	11,15	13	29	24	10	13	13
3	15	12	12	19	27	15	18	10	25
	36	12	N/A	17	18	21	23	N/A	12
V9P2NZ	PowerPlex® Y23								
		14	11,15	13	29	24	10	13	13
3	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
VER4PY	PowerPlex® Y23 (PDF Format)								
		14	11,15	13	29	24	10	13	13
3	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
WU27NY	PowerPlex® Y23 (HID Format)								
		14	11,15	13	29	24	10	13	13
3	15	12	12	19		15	18		25
		12	12	17	18		23	10	12

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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								
X9JGRF	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	35,36	14	11,15	13	29	24	10	13	13
3	15	12	12	19	27	15	18	10	25
	36	12	12	17	18	21	23	10	12
XVRRWG	Yfiler™ Plus (HID Format)								
	35,36	14	11,15	13	29	24	10	13	13
3	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12
YAEBCX	PowerPlex® Y23 (HID Format)								
		14	11,15	13	29	24	10	13	13
3	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
YEEZ6V	Yfiler™ Plus (PDF Format)								
	35,36	14	11,15	13	29	24	10	13	13
3	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12
YWYQ4V	Yfiler™ Plus (PDF Format)								
	35,36	14	11,15	13	29	24	10	13	13
3	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12

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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 4 - YSTR Results									
2LP44T	PowerPlex® Y23 (HID Format)								
		14	11,15	13	29	24	10	13	13
4	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
6YEQCT	PowerPlex® Y23								
		14	11,15	13	29	24	10	13	13
4	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
8Q4PFM	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	35,36	14	11,15	13	29	24	10	13	13
4	15	12	12	19	27	15	18	10	25
	36	12	12	17	18	21	23	10	12
B2ZLFM	PowerPlex® Y23 (PDF Format)								
		14	11,15	13	29	24	10	13	13
4	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
CLWRXH	PowerPlex® Y23 (PDF Format)								
		14	11,15	13	29	24	10	13	13
4	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
FK8VXD	Yfiler™ Plus (PDF Format)								
	35,36	14	11,15	13	29	24	10	13	13
4	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12
GTNJVG	PowerPlex® Y23 (PDF Format)								
		14	11,15	13	29	24	10	13	13
4	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
H7K3LC	Yfiler™ Plus (PDF Format)								
	35,36	14	11,15	13	29	24	10	13	13
4	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12
N8VV48	Yfiler™ Plus (HID Format)								
	35,36	14	11,15	13	29	24	10	13	13
4	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12
NPDUBQ	Yfiler™ Plus								
	35,36	14	11,15	13	29	24	10	13	13
4	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12

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 4 - YSTR Results

PRFCK7	PowerPlex® Y23 (HID Format)								
		14	11,15	13	29	24	10	13	13
4	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
PVWJ96	Yfiler™ Plus (PDF Format)								
	35,36	14	11,15	13	29	24	10	13	13
4	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12
RM36L6									
		14	11,15	13	29	24	10	13	13
4	15	12	12	19	-	15	18	-	25
	-	12	12	17	18	-	23	10	12
RRHDA6	PowerPlex® Y23								
		14	11,15	13	29	24	10	13	13
4	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
TQBTDK	PowerPlex® Y23 (PDF Format)								
		14	11,15	13	29	24	10	13	13
4	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
V6QPRZ	PowerPlex® Y23 (PDF Format)								
	-	14	11,15	13	29	24	10	13	13
4	15	12	12	19	-	15	18	-	25
	-	12	12	17	18	-	23	10	12
V7G24Y	Yfiler™ Plus (PDF Format)								
	35,36	14	11,15	13	29	24	10	13	13
4	15	12	12	19	27	15	18	10	25
	36	12	N/A	17	18	21	23	N/A	12
V9P2NZ	PowerPlex® Y23								
		14	11,15	13	29	24	10	13	13
4	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
VER4PY	PowerPlex® Y23 (PDF Format)								
		14	11,15	13	29	24	10	13	13
4	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
WU27NY	PowerPlex® Y23 (HID Format)								
		14	11,15	13	29	24	10	13	13
4	15	12	12	19		15	18		25
		12	12	17	18		23	10	12

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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 4 - YSTR Results								
X9JGRF	Yfiler™ Plus, PowerPlex® Y23 (PDF Format), (HID Format)								
	35,36	14	11,15	13	29	24	10	13	13
4	15	12	12	19	27	15	18	10	25
	36	12	12	17	18	21	23	10	12
XVRRWG	Yfiler™ Plus (HID Format)								
	35,36	14	11,15	13	29	24	10	13	13
4	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12
YAEBCX	PowerPlex® Y23 (HID Format)								
		14	11,15	13	29	24	10	13	13
4	15	12	12	19		15	18		25
		12	12	17	18		23	10	12
YEEZ6V	Yfiler™ Plus (PDF Format)								
	35,36	14	11,15	13	29	24	10	13	13
4	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12
YWYQ4V	Yfiler™ Plus (PDF Format)								
	35,36	14	11,15	13	29	24	10	13	13
4	15	12	12	19	27	15	18	10	25
	36	12		17	18	21	23		12

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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
2LP44T	2 contributors, 1 male	Included	Included	at least 3, one male	Inconclusive / Uninterpretable	Included
6YEQCT	2	Included	Included	3	Included	Included
8Q4PFM	≥2 contributors (including ≥1 male)	Included	Included	≥3 contributors (including ≥1 male)	Included	Included
A7PUZL	2	Included	Included	3	Included	Included
B2ZLFM	2	Included	Included	3	Included	Included
CLWRXH	2	Included	Included	3	Included	Included
EJ2NHF	2	Included	Included	3	Included	Included
F9DEBX	2	Included	Included	3	Included	Included
FK8VXD	2	Included	Included	3	Included	Included
GTNJVG	Two	Included	Included	3	Included	Included
H7K3LC	2	Included	Included	3	Included	Included
MALE83	at least 2	Included	Included	at least 3	Included	Included
N8VV48	2	Included	Included	3	Included	Included
NPDUBQ	Two contributors	Included	Included	More than 2 contributors (most probably 3 contributors)	Included	Included
PRFCK7	2	Included	Included	at least 3	Inconclusive / Uninterpretable	Included
PVWJ96	2	Included	Included	3	Included	Included
RM36L6	2	Included	Included	minimum 3	Included	Included
RRHDA6	2	Included	Included	3	Included	Included
TER4Z6	2	Included	Included	3	Included	Included
TQBTDK	2	Included	Included	3	Included	Included

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TABLE 5

WebCode	Item 3 Conclusion # of Contributors	 Item 1	 Item 2	Item 4 Conclusion # of Contributors	 Item 1	 Item 2
V6QPRZ	2	Included	Included	3	Included	Included
V7G24Y	2	Included	Included	3 or more	Included	Included
V9P2NZ	2	Included	Included	3	Included	Included
VER4PY	2	Included	Included	3	Included	Included
WU27NY	STR: 2 YSTR:1	Included	Included	STR: at least 3; YSTR: 1	Inconclusive / Uninterpretable	Included
X9JGRF	2	Included	Included	3	Included	Included
XVRRWG	2	Included	Included	3	Included	Included
YAEBCX	2	Included	Included	3	Included	Included
YEEZ6V	2	Included	Included	3	Included	Included
YWYQ4V	2	Included	Included	3	Included	Included
ZNJ8KV	2	Included	Included	3	Included	Included

Conclusions Response Summary

Participants reporting conclusions: 31

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

Responses	Item 3 Item 1	 Item 2	Item 4 Item 1	 Item 2
Included	**31**	**31**	**28**	**31**
Excluded	**0**	**0**	**0**	**0**
Inconclusive	**0**	**0**	**3**	**0**
No Response	**0**	**0**	**0**	**0**
Total	**31**	**31**	**31**	**31**

Statistical Analysis for Item 3

TABLE 6

WebCode	Item 3 Methods & Results
2LP44T	**Method(s)**: Combined Probability of Exclusion/Inclusion, YHRD - counting method **Stats Analysis:** The estimated probability (18 loci) of selecting an unrelated individual at random that can be included as one of the possible contributors to the DNA profile obtained from this sample is rarer than 1 in at least 7 billion. Due to possible drop out and/or stutter masking, the following loci are not suitable for calculation of population frequency statistics: CSF1PO, TPOX, and D22S1045. This Y-STR profile is not expected to occur more frequently than 1 in 140 male individuals. **Database(s):** STR population frequency statistics calculated in Popstats using Expanded FBI STR 2015 Caucasian and African American populations as well as [State] expanded core 2017 (includes [Location Identifying Populations]). Only the most common frequency among the five populations or 1 in 330 billion is reported, whichever is more common. Y-STR population frequency statistics calculated in YHRD.org using the Y17 dataset with the National Database (with Subpopulations, 2014 SWGDAM compliant) - [Location Identifying Populations]. Only the most common frequency is reported, using the 95% confidence interval.
6YEQCT	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA result obtained from the stain on the kitchen floor (23-19625.01G - Item 3) is consistent with a mixture from at least two (2) contributors, including at least one (1) male: a) The mixture is approximately 2.39E25 times more likely to occur (very strong support for inclusion) if the victim and an unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. b) The mixture is approximately 2.50E29 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):** The African American 2015 Expanded FBI STR Loci Allele Frequencies. [Location Identifying Database]
8Q4PFM	**Method(s)**: Likelihood Ratio **Stats Analysis:** Under the assumption that the VICTIM (Item 1) and one unrelated person selected at random from the general population are contributors to this mixture, the likelihood of observing the mixed source profile on Item 3 is ≥1,000,000 times greater (actual LR available upon request) than if it is assumed that two unrelated persons selected at random from the general population are contributors to this mixed-source sample. Under the assumption that the SUSPECT (Item 2) and one unrelated person selected at random from the general population are contributors to this mixture, the likelihood of observing the mixed source profile on Item 3 is ≥1,000,000 times greater (actual LR available upon request) than if it is assumed that two unrelated persons selected at random from the general population are contributors to this mixed-source sample. YSTR Conclusion: The SUSPECT (Item 2), his paternally-related male relatives, and an unknown number of males in the general population cannot be excluded as the potential source of the YSTR haplotype developed from Item 3. Given a theta-value of 6.0 x 10-05 and a 95%% UCI of the combined Haplotype frequency of 1 in 8,568 (no matches in 25,666 Haplotypes at [Location Identifying Population]), the corrected Match Probability is 1 in 5,659. **Database(s):** Revised-NIST-1036-Allele Frequencies, ABI ID Database + Promega PP Fusion YHRD database (Release 69)

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TABLE 6

WebCode	Item 3 Methods & Results
A7PUZL	**Method(s):** Likelihood Ratio, Random Match Probability **Stats Analysis:** The deduced major DNA profile obtained from this item is consistent with female origin and matches the Victim (001-AA Item 1). The frequency of occurrence of an unrelated individual in a random population having the same genetic profile as the deduced major DNA profile obtained from this item is approximately 1 in 108 quintillion (1.08 x 10^20) African Americans, 1 in 187 quintillion (1.87 x 10^20) Caucasians, and 1 in 768 quintillion (7.68 x 10^20) Southwestern Hispanics. The mixed DNA profile obtained from this item is consistent with the combined DNA profiles from the Victim (001-AA Item 1) and the Suspect (001-AB Item 2). This mixed DNA profile is approximately 142 septillion (1.42 x 10^26) times more likely to be observed if the Victim (001-AA Item 1) and the Suspect (001-AB Item 2) are the contributors than if the Victim (001-AA Item 1) and a random, unrelated African American are the contributors; approximately 3.30 octillion (3.30 x 10^27) times more likely than if the Victim (001-AA Item 1) and a random, unrelated Caucasian are the contributors; and approximately 34.5 nonillion (3.45 x 10^31) times more likely than if the Victim (001-AA Item 1) and a random, unrelated Southwestern Hispanic are the contributors. **Database(s):** PopStats
B2ZLFM	**Method(s):** Likelihood Ratio **Stats Analysis:** The DNA result from Item 3 is consistent with a mixture from at least two (2) contributors, including at least one (1) male. The mixture is approximately 5.60E29 times more likely if the victim and the suspect are contributors, rather than if the victim and one (1) unknown, unrelated individual are contributors. This result gives very strong support for the inclusion of the suspect. **Database(s):** FBI Caucasian STR Allele Frequency Database (2015).
CLWRXH	**Method(s):** Likelihood Ratio **Stats Analysis:** I would consider two sets of alternatives for statistical evaluation: First set of alternatives: Victim + one unknown/two unknowns. Second set of alternatives (assuming a contribution of DNA from the victim): Victim + Suspect/Victim + one unknown. Unable to carry out the statistical evaluations detailed above as currently we do not have allele frequency datasets for Globalfiler. **Database(s):** [Participant did not report database(s).]
EJ2NHF	**Method(s):** Likelihood Ratio **Stats Analysis:** Item 3 (Stain from kitchen floor) presents a genetic profile of more than one person. Assuming that the genetic profile detected on Item 3 (Stain from kitchen floor) came from at least two contributors, Female Victim (Item 1) and Male Suspect (Item 2) we concluded that: The genetic profile detected on Item 3 (Stain from kitchen floor) is approximately: 6 Octillions more likely using the Caucasian database; 182 Septillions more likely using the African American database; 157 Octillions more likely using the Hispanic database to have come from Female Victim (Item 1) and Male Suspect (Item 2), than from any other unknown person chosen randomly. Female Victim (Item 1) and Male Suspect (Item 2) can not be excluded from being the donors of the genetic profile on the Item. This probability is strongly supported by the statistical data. **Database(s):** The data base used in the statistical analysis for item 3 (Stain from kitchen floor) 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).
F9DEBX	**Method(s):** Random Match Probability **Stats Analysis:** RMP Item 1= 1.40805E+27. RMP Item 2=1.96053E+32. **Database(s):** [Location Identifying Database]
FK8VXD	**Method(s):** Likelihood Ratio **Stats Analysis:** The mixed DNA profile are 12 tredecillion , 1.3 quattuordecillion and 130 tredecillion TIMES more likely; IF they originated from Item 1 (victim) and Item 2 (suspect) RATHER THAN; IF they originated from two unknown unrelated individuals as calculated based on the [Location Identifying Population] databases respectively. **Database(s):** [Location Identifying Database]

TABLE 6

WebCode	Item 3 Methods & Results
GTNJVG	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA result obtained from Item 3 is consistent with a mixture from at least two (2) contributors, including at least one (1) male: a) The mixture is approximately 2.65 x 10^25 times more likely to occur (very strong support for inclusion) if the victim and an unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. b) The mixture is approximately 2.94 x 10^29 times more likely to occur (very strong support for inclusion) if the suspect and an unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. **Database(s):** FBI_extended_Cauc
H7K3LC	**Method(s)**: Likelihood Ratio **Stats Analysis:** A mixed DNA profile of two individuals was developed from the bloodstain on kitchen floor "Item 3". The donors of reference sample "Item 1" and "Item 2" are consistent being the contributors to this mixed DNA profile. The mixed DNA profile is 12 tredecillion (12 x 10e42), 1.3 quattuordecillion (1.3 x 10e45) and 130 tredecillion (130 x 10e42) times more likely if they originated from "Item 1" and "Item 2" rather than, if they originated from two unknown unrelated individuals as calculated based on the [Location Identifying Population] database respectively. **Database(s):** [Location Identifying Database]
MALE83	**Method(s)**: Likelihood Ratio **Stats Analysis:** H1: The victim and the suspect are contributors to the mixture in item 3. H2: The victim and an unknown, unrelated individual are contributors to the mixture in item 3. LR: 11.052 x 10^28 or 110,520,000,000,000,000,000,000,000,000. The DNA results are extremely more likely under H1 than under H2. **Database(s):** DNAStatistX version 1.3.5
N8VV48	**Method(s)**: Likelihood Ratio **Stats Analysis:** The genetic profile obtained from Item 3 is interpreted as a mixture of DNA from two contributors. Item 1 (victim) cannot be excluded as a possible contributor to this mixture. Given this genetic profile, assuming two contributors, it is 1.93 trillion times more likely to observe this genetic profile if Item 1 (victim) and one unknown individual are contributors than if 2 unknown individuals are the contributors. The genetic profile obtained from Item 3 is interpreted as a mixture of DNA from two contributors. Item 2 (suspect) cannot be excluded as a possible contributor to this mixture. Given this genetic profile, assuming two contributors, and assuming the presence of the victim's profile, it is 3.5 septillion times more likely to observe this genetic profile if Item 2 (suspect) and Item 1 (victim) are contributors than if Item 1 (victim) and one unknown individual are the contributors. **Database(s):** NIST
NPDUBQ	**Method(s)**: Combined Probability of Exclusion/Inclusion **Stats Analysis:** [Participant did not report statistical analysis.] **Database(s):** [Participant did not report database(s).]

TABLE 6

WebCode	Item 3 Methods & Results
PRFCK7	**Method(s)**: Combined Probability of Exclusion/Inclusion, Random Match Probability, Estimated Frequency via Counting Method **Stats Analysis:** The estimated frequency (7 loci) of the STR profile from the major component of the above sample is 1 in at least 597 million. Because the major and minor components could not be separated at all loci, only the following loci are suitable for calculation of population frequency statistics for the major component: D3S1358, CSF1PO, D21S11, D18S51, D22S1045, D13S317 and D12S391. The estimated probability (18 loci) of selecting an unrelated individual at random that can be included as one of the possible contributors to the STR mixture profile obtained from this sample is 1 in at least 7 billion. Owing to possible data below detection, the following STR loci are not suitable for inclusion in the probability calculation: D3S1358, TPOX, and D22S1045. This Y-STR profile is not expected to occur more frequently than 1 in 140 male individuals. **Database(s):** STR population frequency statistics calculated in Popstats using Expanded FBI STR 2015 Caucasian and African American populations as well as [State] expanded core 2017 (includes [Location Identifying Populations]). Only the most common frequency among the five populations or 1 in 330 billion is reported, whichever is more common. Y-STR population frequency statistics calculated in YHRD.org using the Y17 dataset with the National Database (with Subpopulations, 2014 SWGDAM compliant) - [Location Identifying Populations]. Only the most common frequency is reported, using the 95% confidence interval.
PVWJ96	**Method(s)**: Likelihood Ratio **Stats Analysis:** A mixed DNA profile of two individuals was developed from the bloodstain on kitchen floor "Item 3". The donors of reference sample "Item 1" and "Item 2" are consistent being the contributors to this mixed DNA profile. The mixed DNA profile is 12 tredecillion (12 x 10e42), 1.3 quattuordecillion (1.3 x 10e45) and 130 tredecillion (130 x 10e42) times more likely if they originated from "Item 1" and "Item 2" rather than, if they originated from two unknown unrelated individuals as calculated based on the [Location Identifying Population] databases respectively. **Database(s):** [Location Identifying Database]
RM36L6	**Method(s)**: Random Match Probability **Stats Analysis:** The DNA profile of CTS-24-5881-3 (major) is consistent with the DNA profile of CTS-24-5881-1.The probability of selecting a random unrelated individual having a profile identical to CTS-24-5881-1 at the observed loci is 1 in 6.04 E+28 for African Americans, 1 in 1.11 E+28 for caucasian Americans, 1 in 4.79E+27 for Hispanic Americans ; and 1 in 1.02E+29 for Asian Americans. The DNA profile of CTS-24-5881-3 (minor) is consistent with the DNA profile of CTS-24-5881-2 (suspect). Probability of selecting a random unrelated individual having a DNA profile identical is 1 in 4.84E+33 for African American, 3.83 E+32 for Caucasians, 1 in 8.84E34 for Hispanic and 1 in 4.45 E+36 in Asian Americans. **Database(s):** In house RMB database
RRHDA6	**Method(s)**: Likelihood Ratio **Stats Analysis:** The LR for Item 1 is 2.39 E25 and the LR for Item 2 is 2.36 E29. **Database(s):** STRmix
TER4Z6	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA result obtained from the stain on the kitchen floor is consistent with a mixture from at least two (2) contributors, including at least one (1) male: a) The mixture is approximately 2.53 x 10^25 times more likely to occur (very strong support for inclusion) if the female victim and an unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. b) The mixture is approximately 2.52 x 10^29 times more likely to occur (very strong support for inclusion) if the male suspect and an unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. **Database(s):** FBI Extended Caucasian

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TABLE 6

WebCode	Item 3 Methods & Results
V6QPRZ	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA result obtained from stain on kitchen floor (Item 3) is consistent with a mixture from at least two (2) contributors, including at least one (1) male: a. The mixture is approximately 2.79 x 10^25 times more likely to occur (very strong support for inclusion) if the victim (Item 1) and an unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. b. The mixture is approximately 3.08 x 10^29 times more likely to occur (very strong support for inclusion) if the suspect (Item 2) and an unknown, unrelated individual are contributors, rather than if two (2) unknown, unrelated individuals are contributors. **Database(s):** [Participant did not report database(s).]
V7G24Y	**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).]
V9P2NZ	**Method(s)**: Likelihood Ratio **Stats Analysis:** Victim + Unknown vs 2 Unknowns = 2.6506EXP25. Suspect + Unknown vs 2 Unknowns = 2.8674EXP29. **Database(s):** FBI_extended_cauc population
VER4PY	**Method(s)**: [Participant did not report a method.] **Stats Analysis:** No statistical evaluation attempted as we have no validated tool for the STR kits used in the PT. **Database(s):** [Participant did not report database(s).]
WU27NY	**Method(s)**: Combined Probability of Exclusion/Inclusion, Random Match Probability, YHRD **Stats Analysis:** STR results: DNA from two individuals was observed in this sample. A single source DNA profile from the major component of this sample (7 loci) MATCHED the DNA profile from Item 1 (victim). Therefore, Item 1 cannot be excluded as the source of DNA detected in the major component from this sample. Because the major and minor components could not be separated, the following loci are not suitable for calculation of population frequency statistics: vWA, D16,TPOX, D8, D2S441, D19, TH01, FGA, D5, D7, SE33, D10, D1, and D2S1338. The estimated frequency (7 loci) of the genetic profile from the major component from this sample is 1 in at least 597 million. Item 2 (suspect) was INCLUDED as possible contributor to the DNA mixture from this sample (19 loci). Data below the reporting threshold may be present at the following core loci: TPOX and D22. Therefore, population frequency statistics are not reported for these loci. The estimated probability (19 loci) of selecting an unrelated individual at random that can be included as one of the possible contributors to the DNA profile obtained from this sample is 1 in at least 27 billion. Y-STR analysis was performed on this sample. The single source Y-STR DNA profile from this sample MATCHED the Y-STR profile from Item 2 (suspect). Therefore, Item 2 (suspect) cannot be excluded as the source of DNA detected in this sample. Assuming no mutations in the Y chromosome, all paternal male relatives of Item 2 (suspect) also cannot be excluded. This Y-STR profile is not expected to occur more frequently than 1 in 140 male individuals. **Database(s):** STR population frequency statistics calculated in Popstats using Expanded FBI STR 2015 Caucasian and African American populations as well as [State] expanded core 2017 (includes [Location Identifying Populations]). Only the most common frequency among the five populations or 1 in 330 billion is reported, whichever is more common. Y-STR population frequency statistics calculated in YHRD.org using the Y17 dataset with the National Database (with Subpopulations, 2014 SWGDAM compliant) - [Location Identifying Populations]. Only the most common frequency is reported, using the 95% confidence interval.

TABLE 6

WebCode	Item 3 Methods & Results
X9JGRF	**Method(s):** Likelihood Ratio **Stats Analysis:** The mixed DNA profile obtained from item 3 is 1 billion times more likely if victim and suspect are contributing to the profile than if victim and an unrelated person are contributing to the profile. **Database(s):** NIST
YAEBCX	**Method(s):** Likelihood Ratio **Stats Analysis:** This mixture is approximately 24,700,000,000,000,000,000,000,000 times more likely to occur if the victim and an unknown, unrelated individual are contributors, rather than if two unknown, unrelated individuals are contributors. This mixture is approximately 60,200,000,000,000,000,000,000,000,000 times more likely to occur if the suspect and an unknown, unrelated individual are contributors, rather than if two unknown, unrelated individuals are contributors. **Database(s):** Caucasian
YEEZ6V	**Method(s):** Likelihood Ratio **Stats Analysis:** LR = VICTIM + SUSPECT / 2 UNKNOWN. LR = 5,55598 x E38. drop out for VICTIM = 0,00. drop out for SUSPECT = 0,00. drop out for unknown = 0,01. **Database(s):** Global Filer PCR Amplification Kit user guide. Caucatian population base.
YWYQ4V	**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 an unknown unrelated person. H2:the mixture is made up of the genetic profiles of two unknown unrelated people. LR=6.38E11 (caucasian population, drop-out = 0.1, drop-in = 0.05, Theta = 0.01). H1:the mixture is made up of the suspect's genetic profile (item 2) and the genetic profile of an unknown unrelated person. H2:the mixture is made up of the genetic profiles of two unknown unrelated people. LR=3.45E14 (caucasian population, drop-out = 0.1, drop-in = 0.05, Theta = 0.01). H1:the mixture is made up of the victim's genetic profile (item 1) and the suspect's genetic profile (item 2). H2:the mixture is made up of the genetic profiles of two unknown unrelated people. LR= 8.96E36 (caucasian population, drop-out = 0.1, drop-in = 0.05, Theta = 0.01). **Database(s):** Personal Databases
ZNJ8KV	**Method(s):** Likelihood Ratio **Stats Analysis:** The evidence is 1.5 septillion times more likely if the Female victim is a contributor to the DNA mixture than if she is not a contributor. The evidence is 440 septillion times more likely if the Male suspect is a contributor to the DNA mixture than if he is not a contributor. **Database(s):** FBI Extended

Statistical Analysis for Item 4

TABLE 7

WebCode	Item 4 Methods & Results
2LP44T	**Method(s)**: YHRD: counting method **Stats Analysis**: The Y-STR profile is not expected to occur more frequently than 1 in 140 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 Populations]. Only the most common frequency is reported, using the 95% confidence interval.
6YEQCT	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result obtained from the suspects pants (23-19626.01W - Item 4) is consistent with a mixture from at least three (3) contributors, including at least one (1) male. The mixture is approximately 7.12E13 times more likely to occur (very strong support for inclusion) if the victim, the suspect and one (1) unknown, unrelated individual are contributors, rather than if the suspect and two (2) unknown, unrelated individuals are contributors. **Database(s):** The African American 2015 Expanded FBI STR Loci Allele Frequencies. [Location Identifying Database]
8Q4PFM	**Method(s)**: Likelihood Ratio **Stats Analysis**: Under the assumption that the VICTIM (Item 1) and two unrelated persons selected at random from the general population are contributors to this mixture, the likelihood of observing the mixed source profile on Item 4 is ≥1,000,000 times greater (actual LR available upon request) than if it is assumed that three unrelated persons selected at random from the general population are contributors to this mixed-source sample. Under the assumption that the SUSPECT (Item 2) and two unrelated persons selected at random from the general population are contributors to this mixture, the likelihood of observing the mixed source profile on Item 4 is ≥1,000,000 times greater (actual LR available upon request) than if it is assumed that three unrelated persons selected at random from the general population are contributors to this mixed-source sample. YSTR Conclusion: The SUSPECT (Item 2), his paternally-related male relatives, and an unknown number of males in the general population cannot be excluded as the potential source of the YSTR haplotype developed from Item 4. Given a theta-value of 6.0 x 10-05 and a 95%% UCI of the combined Haplotype frequency of 1 in 8,568 (no matches in 25,666 Haplotypes at [Location Identifying Population]), the corrected Match Probability is 1 in 5,659. **Database(s):** Revised-NIST-1036-Allele Frequencies, ABI ID Database + Promega PP Fusion YHRD database (Release 69)
A7PUZL	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA profile from this item is a mixture of three individuals consistent with male and female origin. The DNA profile obtained from this item is a mixture consistent with the combined DNA profiles from the Victim (001-AA Item 1), the Suspect (001-AB Item 2), and an unidentified individual. This mixed DNA profile is approximately 1.02 trillion (1.02 x 10^12) times more likely to be observed if the Victim (001-AA Item 1) , the Suspect (001-AB Item 2), and an unidentified individual are the contributors than if the Suspect (001-AB Item 2) and two random, unrelated African Americans are the contributors; approximately 320 billion (3.20 x 10^11) times more likely than if the Suspect (001-AB Item 2) and two random, unrelated Caucasians are the contributors; and approximately 10.8 trillion (1.08 x 10^13)) times more likely than if the Suspect (001-AB Item 2), and two random, unrelated Southwestern Hispanics are the contributors. **Database(s):** PopStats
B2ZLFM	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result from Item 4 is consistent with a mixture from at least three (3) contributors, including at least one (1) male. The mixture is approximately 5.56E13 times more likely to occur if the victim, suspect and one (1) unknown, unrelated individual are contributors, rather than if the suspect and two (2) unknown, unrelated individuals are contributors. This result gives very strong support for the inclusion of the suspect and victim. **Database(s):** FBI Caucasian STR Allele Frequency Database (2015).

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TABLE 7

WebCode	Item 4 Methods & Results
CLWRXH	**Method(s)**: Likelihood Ratio **Stats Analysis**: I would consider two sets of alternatives for statistical evaluation: First set of alternatives: Suspect + two unknowns/three unknowns. Second set of alternatives (assuming a contribution of DNA from the Suspect): Suspect + Victim + one unknown/Suspect + two unknowns. Unable to carry out the statistical evaluations detailed above as currently we do not have allele frequency datasets for Globalfiler. **Database(s)**: [Participant did not report database(s).]
EJ2NHF	**Method(s)**: Likelihood Ratio **Stats Analysis**: Item 4 (Suspect's pants) presents a genetic partial profile of more than two persons. Assuming that the genetic partial profile detected on Item 4 (Suspect's pants) came from at least three contributors Female Victim (Item 1), Male Suspect (Item 2) and an unknown contributor we concluded that: The genetic partial profile detected on Item 4 (Suspect's pants) is approximately: 14 Quadrillions using the Caucasian database; 1 Quadrillion using the database African American; 350 Quadrillions using the Hispanic database times more likely to have come from Female Victim(Item 1), Male Suspect (Item 2) and an unknown contributor than from any other three unknown persons chosen randomly. Female Victim (Item 1), Male Suspect (Item 2) and an unknown contributor can not be excluded from being the donors of the genetic partial profile detected on the Item. This probability is strongly supported by the statistical data. **Database(s)**: The data base used in the statistical analysis for item 3 (Stain from kitchen floor) 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).
F9DEBX	**Method(s)**: Random Match Probability **Stats Analysis**: RMP Item 1= 1.40805E+27. RMP Item 2=1.96053E+32. **Database(s)**: [Location Identifying Database]
FK8VXD	**Method(s)**: Likelihood Ratio **Stats Analysis**: The mixed DNA profile are 36 trillion , 280 trillion and 54 trillion TIMES more likely; IF they originated from Item 1 (victim), Item 2 (suspect) and an unknown unrelated individual RATHER THAN; IF they originated from Item 2 (suspect) and two unknown unrelated individuals as calculated based on the [Location Identifying Population] databases respectively. **Database(s)**: [Location Identifying Database]
GTNJVG	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result obtained from Item 4 is consistent with a mixture from at least three (3) contributors, including at least one (1) male. The mixture is approximately 6.14 x 10^13 times more likely to occur (very strong support for inclusion) if the victim, the suspect and one (1) unknown, unrelated individual are contributors, rather than if the suspect and two (2) unknown, unrelated individuals are contributors. **Database(s)**: FBI_extended_Cauc
H7K3LC	**Method(s)**: Likelihood Ratio **Stats Analysis**: A mixed DNA profile of three individuals was developed from the bloodstain from the suspect's pants "Item 4". The donors of reference sample "Item 1" and "Item 2" and an unknown individual are consistent being the contributors to this mixed DNA profile. The mixed DNA profile is 36 trillion (36 x 10e12), 280 trillion (280 x 10e12) and 54 trillion (54 x 10e12) times more likely if they originated from "Item 1", "Item 2" and an unknown individual rather than, if they originated from "Item 2" and two unknown unrelated individuals as calculated based on the [Location Identifying Population] database respectively. **Database(s)**: [Location Identifying Database]
MALE83	**Method(s)**: Likelihood Ratio **Stats Analysis**: H1: The victim and the suspect are contributors to the mixture in item 4. H2: The suspect and an unknown, unrelated individual are contributors to the mixture in item 4. LR: 19.782 x 10^12 or 19,782,000,000,000. The DNA results are extremely more likely under H1 than under H2. **Database(s)**: DNAStatistX version 1.3.5

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TABLE 7

WebCode	Item 4 Methods & Results
N8VV48	**Method(s)**: [Participant did not report a method.] **Stats Analysis**: The genetic profile obtained from Item 4 is interpreted as a mixture of DNA from three contributors. Item 2 (suspect) is an assumed contributor to this mixture. Item 1 (victim) cannot be excluded as a possible contributor to this mixture. Given this genetic profile, assuming three contributors and assuming Item 2 (suspect) is a contributor, it is 1.3 trillion times more likely to observe this genetic profile if Item 1 (victim), Item 2 (suspect) and one unknown individual are contributors than if Item 2 (suspect) and two unknown individuals are the contributors. **Database(s)**: NIST
NPDUBQ	**Method(s)**: Combined Probability of Exclusion/Inclusion **Stats Analysis**: [Participant did not report statistical analysis.] **Database(s)**: [Participant did not report database(s).]
PRFCK7	**Method(s)**: Estimated Frequency via Counting Method **Stats Analysis**: 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 Populations]. Only the most common frequency is reported, using the 95% confidence interval.
PVWJ96	**Method(s)**: Likelihood Ratio **Stats Analysis**: A mixed DNA profile of three individuals was developed from the bloodstain from the suspect's pants "Item 4". The donors of reference sample "Item 1" and "Item 2" and an unknown individual are consistent being the contributors to this mixed DNA profile. The mixed DNA profile is 36 trillion (36 x 10e12), 280 trillion (280 x 10e12) and 54 trillion (54 x 10e12) times more likely if they originated from "Item 1", "Item 2" and an unknown individual rather than, if they originated from "Item 2" and two unknown unrelated individuals as calculated based on the [Location Identifying Population] databases respectively. **Database(s)**: [Location Identifying Database]
RM36L6	**Method(s)**: Likelihood Ratio **Stats Analysis**: Lab retriever version 2.2.1 detected the following unattribute suspected ratios: African American 1.671e+004, Caucasian American 3.1943e+004 and Hispanic Americans 1.6709e+006. Hypothesis 1:1 S 1UNK. Hypothesis 2:00 S 2UNK. **Database(s)**: Lab Retriever
RRHDA6	**Method(s)**: Likelihood Ratio **Stats Analysis**: The LR for Item 1 is 2.64 E13 and the LR for Item 2 is 8.57 E27. **Database(s)**: STRmix
TER4Z6	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result obtained from the suspect's pants is consistent with a mixture from at least three (3) contributors, including at least one (1) male. The mixture is approximately 5.69 x 10^13 times more likely to occur (very strong support for inclusion) if the male suspect, the female victim and an unknown, unrelated individual are contributors, rather than if the male suspect and two (2) unknown, unrelated individuals are contributors. **Database(s)**: FBI Extended Caucasian
V6QPRZ	**Method(s)**: Likelihood Ratio **Stats Analysis**: The DNA result obtained from suspect's pants (Item 4) is consistent with a mixture from at least three (3) contributors, including at least one (1) male: a. The mixture is approximately 2.09 x 10^13 times more likely to occur (very strong support for inclusion) if the victim (Item 1) and an unknown, unrelated individual are contributors, rather than if three (3) unknown, unrelated individuals are contributors. b. The mixture is approximately 8.30 x 10^27 times more likely to occur (very strong support for inclusion) if the suspect (Item 2) and an unknown, unrelated individual are contributors, rather than if three (3) unknown, unrelated individuals are contributors. **Database(s)**: [Participant did not report database(s).]

TABLE 7

WebCode	Item 4 Methods & Results
V7G24Y	**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).]
V9P2NZ	**Method(s)**: Likelihood Ratio **Stats Analysis**: Victim + Unknown vs 2 Unknowns = 1.4782EXP13. Suspect + Unknown vs 2 Unknowns = 7.2104EXP27. **Database(s)**: FBI_extended_cauc population
VER4PY	**Method(s)**: [Participant did not report a method.] **Stats Analysis**: No statistical evaluation attempted as we have no validated tool for the STR kits used in the PT. **Database(s)**: [Participant did not report database(s).]
WU27NY	**Method(s)**: YSTR **Stats Analysis**: STR: DNA from at least three individuals was observed in this sample. Due to the complexity of the genetic profile obtained from this sample, no meaningful comparisons can be made to known reference samples. Y-STR analysis was also performed on this sample. The single source Y-STR DNA profile from this sample MATCHED the Y-STR profile from Item 2 (suspect). Therefore, Item 2 (suspect) cannot be excluded as the source of DNA detected in this sample. Assuming no mutations in the Y chromosome, all paternal male relatives of Item 2 (suspect) also cannot be excluded. 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 Populations]. Only the most common frequency is reported, using the 95% confidence interval.
X9JGRF	**Method(s)**: Likelihood Ratio **Stats Analysis**: The mixed DNA profile from item 4 is 1 billion times more likely if victim, suspect and one unknown person are contributing to the DNA profile than if victim and two unknown persons are contributing to the DNA profile. **Database(s)**: NIST
YAEBCX	**Method(s)**: Likelihood Ratio **Stats Analysis**: This mixture is approximately 81,300,000,000,000 times more likely to occur if the suspect and three unknown, unrelated individuals are contributors, rather than if the suspect and two unknown, unrelated individuals are contributors. **Database(s)**: Caucasian
YEEZ6V	**Method(s)**: Likelihood Ratio **Stats Analysis**: LR = VICTIM + SUSPECT + 1 UNKNOWN / SUSPECT + 2 UNKNOWN. LR = 1,96352 x E12. drop out for VICTIM = 0,00. drop out for SUSPECT = 0,00. drop out for unknown = 0,01. **Database(s)**: Global Filer PCR Amplification Kit user guide. Caucatian population base.
YWYQ4V	**Method(s)**: Likelihood Ratio **Stats Analysis**: H1:the mixture is made up of the suspect's genetic profile (item 2), the victim's genetic profile (item 1) and the genetic profile of an unknown unrelated person. H2:the mixture is made up of the suspect's genetic profile (item 2) and the genetic profile of two unknown unrelated person. LR=4.32E11 (caucasian population, drop-out = 0.1, drop-in = 0.05, Theta = 0.01). **Database(s)**: Personal Databases

TABLE 7

WebCode	Item 4 Methods & Results
ZNJ8KV	**Method(s)**: Likelihood Ratio **Stats Analysis**: Assuming the Male suspect as a contributor to the DNA mixture, the evidence is 38 trillion times more likely if the Female victim is also 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 Extended

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Additional Comments

TABLE 8

WebCode	Additional Comments
2LP44T	Based on laboratory interpretation guidelines, 3 loci in Item 3 were not suitable for calculation of population frequency statistics: CSF1PO, TPOX, and D22S1045. Insufficient information was provided to determine whether the victim could be an assumed contributor in item 3; more communication with the submitting agency would be appropriate in this scenario. If the victim *could* be assumed, this profile would have been a good candidate for deduction, potentially resulting in a more compelling comparison and statistic. Since both contributors could be probative, separation not attempted and mixture stat run.
A7PUZL	+ at TH01 locus for major profile of item 3 indicates obligate allele. For Item 4, Amelogenin, SE33, and D7S820 have likely DNA peaks less than stochastic threshold and these loci were not used in statistical calculations for this item.
FK8VXD	NM indicates non-male profile. Statistical calculations were done using DNAVIEW Software.
H7K3LC	NM indicates Non-Male. The statistical calculations were carried out using DNA View Software.
MALE83	For item 3: An additional allele (23) was obtained at D12S391 which may indicate a third contributor to this mixture.
NPDUBQ	* Item 3: In comparison with the reference samples, item 3 is mixture of the profile of the victim and the suspect. * Item 4:In comparison with the reference samples, item 4 is mixture of the profile of the victim, the suspect and another profile belonging to either female or male from same paternal lineage as the suspect.
PRFCK7	The [Laboratory] does not currently interpret/make comparisons to indistinguishable mixtures of three or more contributors.
PVWJ96	NM indicates Non-Male. The statistical calculations were carried out using DNA View Software.
TER4Z6	The analysis of Item 4 was conditioned on the assumption that the male suspect was a contributor to the DNA mixture obtained as the pants were taken from him.
TQBTDK	Item #1, D22S1045-16, would inc. locus for statistical calculations due to uncertainty regarding whether it is a true allele or a higher than reported stutter artifact (exceeds the sum of the maximum range for forward and back stutter at that location); if sample had not been consumed, it could be re-amped to determine if this was reproducible.
X9JGRF	This section would best serve the community if it contained answers about currently used technologies and concepts to see how the analysts respond in their own words. Labs would be able to identify analysts who need additional training in testimony and it should be part of regular proficiency because as the tech changes, the words and descriptions used by the analyst to explain their results will change.
YEEZ6V	DNA Analysis for Item 3: LR = VICTIM + SUSPECT / 2 UNKNOWN. LR = 5,55598 x E38. drop out for VICTIM = 0,00. drop out for SUSPECT = 0,00. drop out for unknown = 0,01. The probability of the evidence is 5,55598 x E38 times more likely if the reddish-brown stain on the floor came from Female Victim (Item 1) and Male Suspect (Item 2), than if it came from two unknown unrelated individuals. DNA Analysis for Item 4: LR = VICTIM + SUSPECT + 1 UNKNOWN / SUSPECT + 2 UNKNOWN. LR = 1,96352 x E12. drop out for VICTIM = 0,00. drop out for SUSPECT = 0,00. drop out for unknown = 0,01. The probability of the evidence is 1,96352 x E12 times more likely if the reddish-brown stain on the pants came from Female Victim (Item 1), Male Suspect (Item 2) and 1 unknown, unrelated individual, than if it came from Male Suspect (Item 2) and two unknown unrelated individuals.

-End of Report-
(Appendix may follow)

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Test No. 24-5881: DNA Interpretation

DATA MUST BE SUBMITTED BY **June 03, 2024, 11:59 p.m. EDT** TO BE INCLUDED IN THE REPORT

Participant Code: U1234A WebCode: ZDZTGT

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

Scenario:

Police are investigating a homicide involving a female victim and male suspect. The victim’s body was found in her kitchen. The suspect, who is the victim’s estranged husband, was apprehended the same day the victim’s body was located. A reddish-brown stain was identified on the floor near the victim’s body in the kitchen, and was confirmed as blood by the Serology Unit (Item 3). A reddish-brown stain from the pants the suspect was wearing at the time of arrest was also confirmed as blood (Item 4). Both Items have been submitted for DNA analysis.

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

Items Submitted (Sample Pack INT1):

Item 1: DNA profile from reference sample (Female Victim - Caucasian)
Item 2: DNA profile from reference sample (Male Suspect - Caucasian)
Item 3: DNA profile from stain on kitchen floor
Item 4: DNA profile from the suspect's pants

To verify a complete and accurate download, the hash value for the downloaded .ZIP file is as follows:
24-5881 Data For Participants.zip MD5 hash value: 88f283263475436e1435143a927273d1
24-5881 Data For Participants.zip SHA1 hash value: 1e1f2e2f732b8714f612bd24ed77a8d6c1ec1f7e

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						

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						

YSTR Results for Known Item 2

YSTR Amplification Kit Used For Item 2:

☐ YFiler® Plus
☐ PowerPlex® Y23

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

☐ HID format
☐ PDF format

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

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

Part I: DNA ANALYSIS (continued)

STR & Amelogenin Results for Questioned Item 3

- Report alleles in numerical order, separated by a comma.
- Follow your laboratory procedures for reporting homozygotes (i.e. X,X or X) and null responses.
- For each locus, if a major and minor contributor can be distinguished and your laboratory normally reports this distinction, record the results in the appropriately labeled response boxes.

STR Amplification Kit Used For Item 3:

☐ GlobalFiler™
☐ Investigator® 24plex

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

☐ PowerPlex® Fusion 5C
☐ PowerPlex® Fusion 6C
☐ HID format
☐ PDF format

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

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

ITEM	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D7S820
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: ☐

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

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

Part I: DNA ANALYSIS (continued)

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: ☐

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

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

Part II: ADDITIONAL COMMENTS

Comments regarding any part of this Test.

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

Part III: AMPLIFICATION KIT SURVEY (optional)

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

RELEASE OF DATA TO ACCREDITATION BODIES

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

CTS submits external proficiency test data directly to 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)

____