ANNUAL REPORT SUMMARY FOR TESTING IN 2002

Prepared by the Parentage Testing Program Unit
November 2003

PREFACE

This year's annual report continues the past precedent of providing basic summary statistics for testing that took place in the previous year, in this case, 2002. The emphasis of the survey questions this year, however, was on apparent mutations and null alleles. Laboratories were asked how they incorporated mutations into the final report and how they handled situations in which there were two or three inconsistencies. As in the past mutations observed for 2002 are provided in table form.

In this report AABB provides some commentary on commonly asked questions. The Parentage Testing Standards Program Unit would also like to remind readers that shortly after publication of each edition of *Standards for Parentage Testing Laboratories,* the AABB publishes a guidance document that discusses the *Standards* in some detail. The *Guidance for Standards for Parentage Testing Laboratories* provides suggestions on how to comply with the standards and contains explanations of the various calculations used, and addresses other issues in parentage testing.

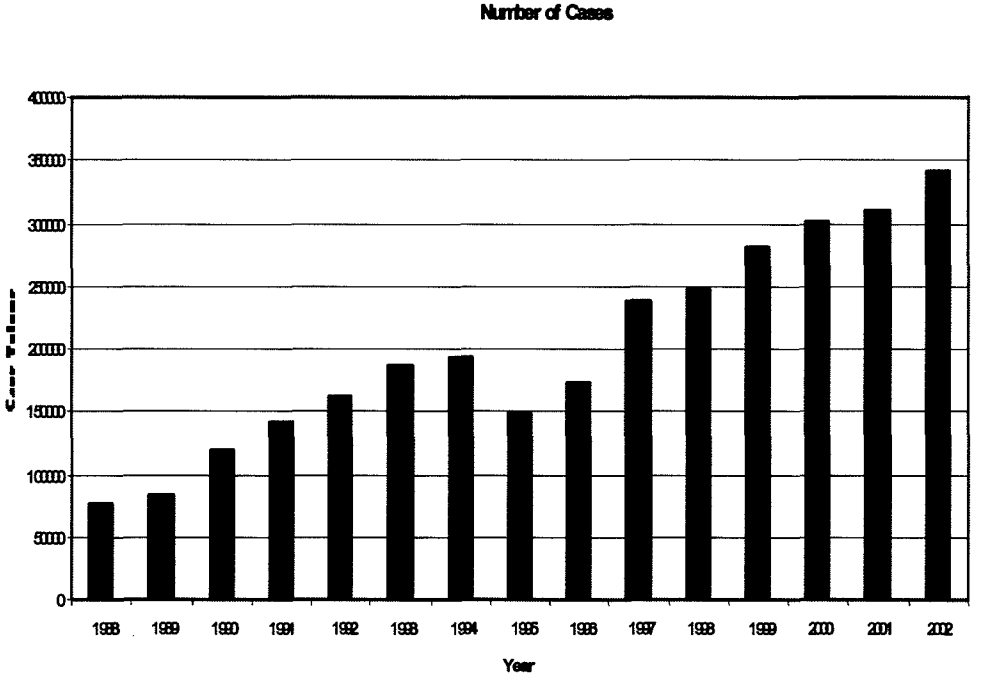
ANNUAL VOLUME OF TESTING

The volume reported for cases tested in 2002 was 340,798, an increase of about 10% over the previous year's volume. A summary of the totals of all years since 1988 is shown in Table 1 and Figure 1.

Table 1. The Number of Parentage Cases Reported for 1988-2002.

Year	No. of Cases	Year	No. of Cases
1988	77000	1996	172316
1989	83000	1997	237981
1990	120000	1998	247317
1991	142000	1999	280510
1992	161000	2000	300626
1993	187000	2001	310490
1994	193000	2002	340798
1995	149100		

Figure 1. Graph of the Case Volume for 1988-2002.



The totals include data from AABB-accredited laboratories in the United States and worldwide as well as data from one non-AABB-accredited laboratory outside the United States. A total of 38 laboratories responded to the survey.

LABORATORIES BY SIZE

Table 2 indicates the size of the various responding laboratories by volume of cases reported. Note that this breakdown is by each laboratory, but a single corporation may own several laboratories.

Table 2. Laboratories by the Volume of Cases Reported.

Case Volumes	1994	1995	1996	1997	1998	1999	2000	2001	2002
1-500	40	26	25	20	19	19	13	17	14
501-1,000	6	4	8	7	6	5	6	6	2
1,001-5,000	7	9	6	10	11	9	11	11	13
5,001-10,000	6	4	3	5	0	3	3	5	1
10,001-50,000	1	2	3	5	5	7	8	6	7
50,001 – 100,000	2	1	1	1	2	1	1	1	0
>100,000	0	0	0	0	0	0	0	0	1
Total Laboratories	62	46	46	48	43	44	42	46	38

EXCLUSION RATE

Of 340,798 cases reported, 97,681 (28.70%) were reported as exclusions. The average exclusion rate for the laboratories is 27.12% with a standard deviation of 7.80. The median exclusion rate is 28.12% with a range of 3.70% to 48.10%. The explanation for the range of exclusion rates is complex but appears to be related to the laboratory's client base. Anecdotal explanations for the various exclusion rates include differences with the type of case (private vs public contracts), and the source of the case (rural versus metropolitan areas). Neither the testing method nor the minimum acceptable combined paternity index level used by the laboratory accounts for the range of exclusion rates.

COMBINED PATERNITY INDEX

The laboratories were asked to indicate what combined paternity index (CPI) they considered acceptable for cases with a standard trio (mother, child, father), mother not tested (MNT) cases, and reconstruction cases (cases where the disputed parent is missing and other relatives are used to evaluate parentage). Some laboratories reported using different CPIs for different classes of clients (private vs public contracts). For these laboratories the higher CPI was used for this report.

The results for the laboratories that responded are shown in Table 3. The most common minimum CPI for a standard trio is 100 with 20 out of 35 (57%) laboratories using this value, with a range of 100 to 10,000. For mother not tested cases the most common minimum CPI for standard trio is 100 with 23 of 34 (68%) laboratories using this value, with a range of 100 to 10,000. A number of laboratories indicated that for these cases they used "whatever was obtained." It is interesting to note that one of the two laboratories using a CPI of 10,000 for trio cases dropped their minimum to 10 for MNT cases. For the family study or reconstruction cases, the majority of laboratories indicated that they report "whatever was obtained."

A common issue is the significance of the paternity index and the reliability of the AABB standard requiring a CPI of 100 to 1. First and foremost, this level was chosen because it provides reasonable evidence of paternity in a standard case where a trio is tested. Generally, when a laboratory tests a case, if the disputed person is not excluded and does not reach the laboratory's minimum value, additional testing is performed to evaluate this person. This additional testing may result in non-exclusion, exclusion, or inconclusive reports.

The second issue arises with regard to performing other relationship analyses such as reconstruction cases, trios with genetic anomalies, and samples from exhumations, coroners, and postmortem testing. It is important to note that in some cases a CPI of less than 100 is not an indicator of non-paternity and may still in fact be a strong indicator of paternity. Practical difficulties exist with the ability to obtain results from degraded samples, as happens in postmortem testing, and in the mathematical analysis of the relationships in reconstruction cases. This concept is particularly important for legislators who establish presumption levels based on paternity calculations, and contract administrators, who need to differentiate between reasonable science and what might be achieved under ideal conditions. The other important concept is that a laboratory's minimum combined paternity index, which may reflect scientific reality, is not necessarily the laboratory's testing goal or median combined paternity index.

Table 3. The Number of Laboratories Using Various Combined Paternity Indices for Standard Trios, Mother not Tested (MNT) and Reconstruction Cases. (Note: not all laboratories indicated a CPI for each type of case.)

Minimum Acceptable CPI in Your Laboratory Under the Following Conditions
(Check one box under each column,
if you have multiple CPIs for any type of case, please explain on the back of this page)

CPI	Type of Case		
	Trio	No Mother	Family Study (Reconstruction)
Whatever is obtained	1	2	19
10		1	1
100	20	23	4
101			1
150	2	2	2
200	2	3	2
300	1		
500	1		
1000	5	1	
1001	1	1	
10000	2	1	
Other (Specify)			

TECHNOLOGY USE

The survey showed a continued trend toward the increased use of polymerase chain reaction (PCR) technology with a decrease in the use of restriction fragment length polymorphism (RFLP) methods. PCR short tandem repeat (STR) technology was used in 91.52% of reported cases, while RFLP analysis was used in 8.31% of reported cases. All other technologies were used in about 0.17% of

reported cases. Table 4 provides a breakdown of the technology used to resolve the reported paternity cases. The laboratories using HLA molecular methods were asked to identify the source of the frequencies. Laboratories using HLA molecular methods reported using serologic tables for calculating Class I molecular results. No laboratories reported using single nucleotide polymorphism (SNP) technology and a few laboratories reported using Y Chromosome analysis in their testing programs.

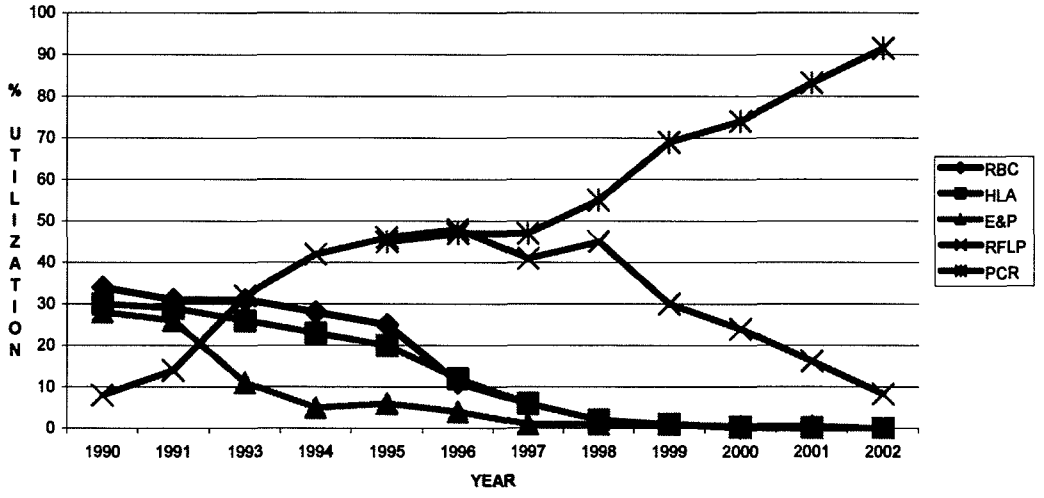
Table 4. The Technology Used and Number of Relationship Cases Reported in 2002

Technology	Number of Cases	Utilization (%)
Red Cell Antigens	**10**	**0.00364**
HLA Serology	**1**	**0.00035**
HLA Class 1 Molecular	**42**	**0.01455**
HLA Class II Molecular	**356**	**0.12332**
Red Cell Enzymes/Serum Proteins	**0**	**0**
Allotyping	**0**	**0**
RFLP	**23982**	**8.30776**
STR	**264198**	**91.52250**
SNP	**0**	**0**
Y Chromosome	**81**	**0.02806**
Total of All Technologies	**288670**	**100**

***Note that some cases used more than one technology. Not all laboratories responded to this question.**

Figure 2 shows the use of various technologies since 1990. As indicated above, the most commonly used technologies in 1990 (red cell antigens, HLA, and red cell enzymes and serum proteins) now account for less than 1% of all casework. The change in DNA technologies from RFLP to PCR technology is also obvious. Prior to 1995 the use of PCR was not tracked in the Annual Reports, although the technology was in use. Note that in some cases multiple technologies were used in the same case.

Figure 2. The Use of Various Technologies Since 1990.
[From AABB Annual Report Summary for 2002 (Nov. 2003)]



SAMPLE SOURCE

There were approximately 918,623 samples used for the casework in 2002. Of these, buccal swabs account for 839,387 (91.37%). The other samples used included 74,822 (8.15%) whole blood samples, 3,461 (0.38%) blood spot cards, 88 (0.01%) amniotic fluid samples and 865 (0.09%) other samples that included various tissues, bone, hair and undefined samples.

PROBABILITY OF EXCLUSION

None of the loci/probe/enzyme combinations evaluated with RFLP testing were used (reported) by more than five laboratories. These data were reported for all loci even if a locus was used by one laboratory. Therefore, because of the small sample size, these data should be viewed with caution. Appendix 1 contains a table showing the probability of exclusions calculated for the various loci submitted. Table 5 shows the data for the most commonly used loci.

Table 5. The Average Probability of Exclusion for the Most Commonly Used Loci Evaluated with RFLP Technology (from Appendix 1).

LOCUS	PROBE	ENZYME	PE	# Labs
D1S1339	SLI1335	HAEIII	0.8949	5
D6S132	SLI1090	HAEIII	0.8274	5
D2S44	YNH24	HAEIII	0.9161	4
D4S163	SLI604	HAEIII	0.8608	4

Appendix 2 shows the average probability of exclusion for the various PCR loci reported. Note that several loci seen in 2001 appeared not to be in use during 2002. For the CODIS loci a sufficient sample size was available to make statistical analysis, although without regard to the database source as this was not always clear from the information provided. Table 6 shows the statistical analysis of the probabilities of exclusion provided for the CODIS loci. The range of probabilities of exclusion may have been caused by using different frequency tables (population sampling differences) or by varying methods of determining the probability of exclusion. This same observation was made in 2001.

Table 6. The Mean, Standard Deviation, Mode, Median, Range and Number of Laboratories Reporting Results for the CODIS Loci.

Locus	**Mean**	**StDev**	**Mode**	**Median**	**Range**	**# Labs**
TPOX	0.4068	0.0697	0.3500	0.3901	0.278 - 0.572	25
D5S818	0.4731	0.0313	0.4554	0.4571	0.428 - 0.559	25
CSF1P0	0.5124	0.0510	0.4854	0.5020	0.369 - 0.633	26
D13S317	0.5295	0.0698	0.5948	0.5333	0.408 - 0.715	26
TH	0.5389	0.0321	0.5418	0.5405	0.436 - 0.618	28
D16S539	0.5497	0.0414	0.5252	0.5660	0.470 - 0.623	26
D3S1358	0.5610	0.0331	0.5797	0.5560	0.514 - 0.588	25
D7S820	0.5961	0.0259	0.6307	0.5904	0.539 - 0.637	26
D8S1179	0.6120	0.0370	0.6128	0.6128	0.527 - 0.690	26
VWA	0.6270	0.0300	0.6170	0.6245	0.588 - 0.761	28
D21S11	0.6862	0.0430	0.6835	0.6835	0.529 - 0.783	26
FGA	0.7289	0.0303	0.7173	0.7220	0.644 - 0.836	26
D18S51	0.7344	0.0210	0.7414	0.7410	0.647 - 0.749	26

A common question is: What is the most powerful test, RFLP or PCR? The answer is not straightforward. The powers of exclusion in Appendix 1 for the

RFLP technology appear to be more powerful per locus tested than the probabilities of exclusion in Appendix 2 for PCR technology. This has been the basis of misleading statements that RFLP technology produces a more powerful paternity test. The power of a paternity test is determined by the average probability of exclusion, not the technology used or the number of loci evaluated.

When RFLP was commonly used, laboratories evaluated three or four loci in their test battery. For example, the four most commonly used loci for RFLP testing in the 2002 data are shown in Table 5. If the average probability of exclusion is calculated for these four loci, an average probability of exclusion of 99.979% is obtained. The average probability of exclusion for the thirteen CODIS loci in Table 6 is 99.999%. In this example, the PCR paternity test would be more powerful than the RFLP testing. Therefore, the answer to the question about the most powerful test is not straightforward. Neither the type of technology used nor the number of loci tested determines the power of a test. The power of a test is ascertained by calculating the average probability of exclusion for the test battery chosen by the laboratory.

The hypothetical comparison given in the above paragraph is intended for illustrative purposes only and does not reflect an accreditation requirement or a required standard of practice. Accredited laboratories are free to create any test battery they wish as long as that battery conforms to AABB standards. A laboratory following AABB accreditation requirements should be able to tell their client what the average probability of exclusion is for their test battery.

MUTATION REPORTS

One area of concern is the number of inconsistencies necessary to render an opinion of non-paternity. The laboratories were asked if they had seen any case where, in the opinion of the expert, the inconsistencies were double or triple "mutations" and not sufficient to render an opinion of non-paternity. The laboratories reported 69 cases with double mutations (0.020% of all reported cases) and six cases with triple mutations (0.002% of all reported cases) as inclusions. These findings were similar to those observed in 2001. Most laboratories report these cases with the inconsistencies noted and statistically considered. This illustrates the importance of accurate assessments of potential mutations and null alleles. With PCR-STR technology, this assessment is made easier as the repeat differences between the obligatory allele and the closest allele in the disputed parent can be evaluated as part of this process.

MUTATION CALCULATION AND FREQUENCIES

Single inconsistencies are routinely seen in the testing of paternity cases. If a laboratory comes to the conclusion that the inconsistency is a mutation, then the mutation result must be incorporated into the reported results. Laboratories were asked how they calculated the paternity index (PI) for these loci. The most significant change from 2001 is that no laboratory reported using arbitrary numbers for the mutation PI. Those laboratories all appear to be using one of several calculation methods. Some laboratories are using the mutation rate as the PI (8% of laboratories), while others (66%) used the mutation rate divided by the average probability of exclusion. Some laboratories (16%) used the mutation rate as a transmission frequency and 8% of the laboratories used Brenner's method in looking at the repeat length difference between STR alleles.

The mutation frequency for the PCR loci can be found in Appendix 3. As indicated in the table, the data are from 2002 and previous years. Unlike previous years, the null allele frequencies have been removed from this table and placed in a different section of this report. RFLP mutations data are presented in Appendix 4.

In order to obtain data to possibly better evaluate mutation calculations, laboratories were asked to provide information on specific mutations that they observed. These data are summarized in Appendix 5. When mutations were first observed, calculation methods were developed with various strengths and weaknesses, as the type of data in Appendix 5 was not available. A summary of the repeat difference for PCR-STR cases is provided in Appendix 6. For most of these cases a single repeat difference is seen between the child's obligatory allele and an allele in the disputed person.

NULL ALLELES

This year laboratories were asked to provide details about cases where the parent had an apparent single allele and the child had a different single allele (homozygous for different alleles). These inconsistencies are different than mutations and the paternity index for the locus with an apparent null allele is calculated in a different manner than mutations. Null alleles appear to be caused by a mutation in the primer site. The presence of a possible null allele can be determined by evaluating a number of factors. These factors include:

* The possible null alleles are about equal in maternal vs paternal cases.

* The presence of the null allele will vary in frequency in different ethnic groups.

* The STR difference in the apparent homozygous alleles may be large.

* Alternate primers for the same locus do not yield a "null phenotype," but the presence of an allele is not observed with the other primers.

* There is an excess of observed homozygotes when calculating Hardy-Weinberg.

For the locus D8S1179 the Federal Bureau of Investigation observed an excess of homozygotes and showed that this was caused by a primer mutation. The data submitted in this report also indicate the presence of a null allele at this locus. The manufacturer of the primers used by the FBI has recently released a new kit with a new primer for D8S1179 that eliminated the apparent null allele. Therefore, the number of null alleles observed at this locus will change with time. The presence of potential null alleles is summarized in Table 7. Appendix 7 shows a compilation of the raw data for the null alleles and Appendix 8 provides frequencies for some of the loci with significant findings. Null alleles were seen for primers from both Applied Biosystems (ABI) and Promega Corporation. Two loci, D16S539 and CSF1PO, using primers from ABI had no evidence of a null allele. For many loci insufficient information was submitted.

The other important aspect of these data is that the frequency of the null allele cannot be ascertained. In order to obtain the null allele frequency, counts of cases where no allele was observed are needed (that is, counts of individual homozygous for the null allele). This may prove difficult to obtain, but the presence of null alleles may also provide, in part, an explanation as to why in certain cases, results are not obtained at a particular locus. This is important for the careful evaluation of inconsistencies with apparent null alleles. Guidance on this matter will be provided at a later time. If the null allele frequency were known, the proper calculation of the paternity index would be:

Calculation of the PI with a Null Allele
(Assume the child's phenotype is Q and the alleged father is P)

$$PI = \frac{n}{(q+n)(p+2n)}$$

n = null allele frequency
p = frequency of the allele seen in the father
q = frequency of the allele seen in the child

Table 7. The Presence of Possible "Null Alleles" at Various Loci Using ABI or Promega Primers. A "?" indicates there are Insufficient Data to Hypothesize as to the Presence of a Null Allele. (Note: YES means observations consistent with the presence of a null allele.)

LOCUS	PRIMER SOURCE	
	ABI	PROMEGA
D3S1358	YES	?
D5S818	YES	?
D7S820	YES	?
D13S317	YES	YES
D16S539	NO	YES
D18S51	YES	?
D21S11	YES	YES
PENTA D	N/A	YES
PENTA E	N/A	YES
THO1	YES	YES
TPOX	YES	?
VWA	YES	YES
FGA	YES	YES
D2S1338	YES	N/A
D19S433	?	N/A
D8S1179	YES	?
CSF1PO	NO	?

AMELOGENIN

The amelogenin locus is now used in a number of laboratories to test for the gender of the sample. A number of males lacking the Y amelogenin allele have been observed. Laboratories were asked to measure the apparent X males observed in their laboratory. Like other DNA loci, amelogenin is subject to mutations. Therefore, occasionally normal males have a female amelogenin phenotype. The frequencies may vary by primer source and the following tables show a summary of X males observed using primers developed by either ABI or Promega Corporation. Several laboratories also indicated that they observed Y males, that is males with no apparent X amelogenin allele. These apparent Y males will be tracked in next year's report. The following two tables summarize the data submitted for primers from ABI and Promega.

Table 8. A Summary of Data on Apparent X Males Seen with ABI Primers

	Race/Ethnicity					
	Black	**White**	**Hispanic**	**American Indian**	**Oriental**	**Other**
Number X Males Observed	**25**	**20**	**22**	**2**	**5**	**1**
Total Number of Males Tested	**65,061**	**46,842**	**11,135**	**544**	**210**	**1,037**
%	**0.0384**	**0.0427**	**0.1976**	**0.3676**	**2.3810**	**0.0964**

Table 9. A Summary of Data on Apparent X Males Seen with Promega Primers.

	Race/Ethnicity					
	Black	**White**	**Hispanic**	**American Indian**	**Oriental**	**Other**
Number X Males Observed	**6**	**4**	**0**	**0**	**0**	**0**
Total Number of Males Tested	**13831**	**8578**	**1192**	**50**	**86**	**769**
%	**0.0434**	**0.0466**				

Appendix 1. The Probability of Exclusion (PE) Reported for Various Loci Evaluated Using RFLP Methods. (Note: no loci had more than five laboratories using a particular locus / probe / enzyme combination.)

LOCUS	PROBE	ENZYME	PE	# Labs
D10S28	TBQ7	HAEIII	0.8967	3
D10S28	SLI917	HAEIII	0.8787	3
D12S11	SLI737	PST1	0.8800	1
D12S11	MS43A	PST1	0.9150	2
D14S13	CMM101	HAEIII	0.8100	1
D16S85	SLI779	HAEIII	0.8500	1
D17S26	EFD52	HAEIII	0.8992	3
D17S26	SLI936	HAEIII	0.9000	1
D17S79	SLI986	PST1	0.7000	1
D17S79	V1	HAEIII	0.7200	2
D17S79	SLI441	HAEIII	0.7330	3
D17S79	SLI441	PST1	0.7200	2
D5S110	PLH1	HAEIII	0.9190	3
D5S110	LH1	HAEIII	0.9827	1
D18S27	SLI604	PST1	0.6800	1
D18S27	SLI605	PST1	0.7550	2
D1S1339	SLI1335	HAEIII	0.8949	5
D1S339	PAC425	HAEIII	0.9100	1
D2S44	YNH24	HAEIII	0.9161	4
D2S44	SLI106	PST1	0.7933	3
D2S44	SLI106	HAEIII	0.8683	3
D2S44	YNH24	HINF1	0.9587	1
D2S92	SLI874	HAEIII	0.9275	2
D4S139	PH30	HAEIII	0.9291	2
D4S163	SLI604	PST1	0.8350	2
D4S163	SLI604	HAEIII	0.8608	4
D6S132	SLI1090	PST1	0.8850	2
D6S132	SLI1090	HAEIII	0.8274	5
D7S467	SLI989	PST1	0.8450	2
D7S467	PAC415	HAEIII	0.8050	2
D7S467	SLI989	HAEIII	0.9100	3

Labs = number of laboratories using the particular locus, probe, enzyme combination.

Appendix 2. The Probability of Exclusion for Various Loci Evaluated Using PCR. (Note: for some loci only a single laboratory reported results.)

LOCUS	PE	LOCUS	PE	LOCUS	PE
D3S1358	0.561	D2S1338	0.7471	D18S849	0.457
VWA	0.627	D19S433	0.5992	D1S533	0.527
FGA	0.7289	F13A01	0.516	D9S304	0.527
D5S818	0.4731	FESFPS	0.443	D9S302	0.81
D13S317	0.5295	F13B	0.4557	D22S683	0.783
D7S820	0.5961	LPL	0.4521	D18S535	0.58
D8S1179	0.612	PENTA E	0.7618	D7S1804	0.579
D21S11	0.6862	PENTA D	0.6908	D3S2387	0.707
D18S51	0.7344	D1S80	0.6261	D4S2366	0.569
TH	0.5389	D17S5	0.605	D5S1719	0.698
TPOX	0.4068	HPRTB	0.428		
CSF1P0	0.5124	D12S1090	0.861		
D16S539	0.5497	D3S1744	0.695		

Appendix 3. Summary of Apparent Mutations at Various Loci Analyzed by PCR. The Number Observed Refers to the Inconsistencies Reported.

Locus	PATERNAL			MATERNAL			Number of Either Mat. Or Pat.
	Number Observed	Total Meioses	Number / Total	Number Observed	Total Meioses	Number / Total	
D1S80*	75	199543	0.00038	4	14052	0.00028	NR
D122131*	3	1240	0.00242	0	1212	<0.00083	NR
D1S533*	6	3830	0.00157	?	?	?	NR
D2S1338	61	81960	0.00074	2	25271	0.00008	31
D2S548*	0	1240	<0.00081	1	1212	0.00083	NR
D3S1358	429	336208	0.00128	37	244484	0.00015	266
D3S1744*	84	20290	0.00414	16	10141	0.00158	NR
D3S2386*	1	1240	0.00081	0	1212	<0.00083	NR
D5S818	537	468366	0.00115	84	316102	0.00027	303
D7S820	550	461457	0.00119	43	334886	0.00013	218
D8S306*	3	1240	0.00242	1	1212	0.00083	NR
D8S1179	396	264350	0.00150	54	237235	0.00023	225
D9S302*	49	11179	0.00438	19	8332	0.00228	NR
D10S1214*	114	2938	0.03880	28	2903	0.00965	NR
D12S1090	113	12886	0.00877	9	4894	0.00184	NR
D13S317	608	435530	0.00140	142	348395	0.00041	402
D14S297*	0	1240	0.00000	0	1212	<0.00083	NR
D16S539	350	317146	0.00110	77	300742	0.00026	256
D17S5*	7	6568	0.00107	0	228	<0.00439	NR
D17S1185*	0	1240	<0.00081	0	1212	<0.00439	NR
D18S51	623	278098	0.00224	83	130206	0.00064	330
D18S535*	2	2624	0.00076	1	2676	0.00037	NR
D18S849*	18	10440	0.00172	0	4291	<0.00023	NR
D19S253*	17	3247	0.00524	8	2997	0.00267	NR
D19S433	16	38983	0.00041	22	28027	0.00078	37
D21S11	454	306198	0.00148	284	258795	0.00110	423
D21S1437*	1	1240	0.00081	0	1212	<0.00083	NR
D22S445*	1	1240	0.00081	2	1212	0.00165	NR
D22S683*	9	2625	0.00343	2	2670	0.00075	NR
ACTBP2*	330	51610	0.00639	0	330	<0.00303	NR
CYP19*	205	177210	0.00116	6	343	0.01749	NR
CYAR04*	?	?	?	2	3539	0.00057	NR
FGA	1481	473924	0.00312	134	238378	0.00056	495
CSF1PO	727	504342	0.00144	70	179353	0.00039	303
FESFPS	79	149028	0.00053	3	18918	0.00016	NR
F13A01	37	65347	0.00057	1	10474	0.00010	3
F13B	8	27183	0.00029	2	13157	0.00015	1
LPL	9	16943	0.00053	0	8821	<0.00011	4
THO1	29	346518	0.00008	23	189478	0.00012	23
TPOX	43	328067	0.00013	16	299186	0.00005	24
Penta D	10	15088	0.00066	12	18701	0.00064	21
Penta E	58	44152	0.00131	22	39121	0.00056	55
vWA	907	646851	0.00140	133	400560	0.00033	628

*Data from last years report. No new data submitted
RED refers to cumulative data (last year's data plus new data)
NR = None Reported

Appendix 4. Mutation Rates Summarized for Loci Analyzed by Using RFLP methods. (Note: The data presented are a cumulative compilation of current and previous AABB data. The data under these column headings refers to the number of inconsistencies/number of total meioses expressed as a percentage.)

System	Maternal (%)	Paternal (%)	Null (%)**	Multi-banded (%)
D1S7*	9/580=1.55	11/721=1.52	1/560=0.17	2/461=<0.43
S1S339	219/91289=0.24	411/108325=0.38	103/97212=0.11	204/75647=0.27
D2S44	361/223008=0.16	274/270176=0.10	658/284877=0.23	459/296422=0.15
D4S139	43/80119=0.05	987/103687=0.95	27/82364=0.03	918/87419=1.05
D4S163	8/34282=0.02	93/86257=0.11	110/103300=0.11	24/86966=0.03
D5S110	144/25505=0.56	462/25780=1.79	13/28948=0.04	521/33441=1.56
D5SS43*	0/525=<0.19	0/536=<0.19	UNK.	UNK.
D6S132	15/71362=0.02	98/129839=0.08	4/158424=0.003	42/182453=0.02
D7S21*	20/1073=1.86	41/1398=2.93	UNK.	1/1235=0.08
D7S22*	15/2843=0.52	91/3292=2.76	UNK.	UNK.
D7S467	18/108543=0.02	206/187911=0.11	22/218900=0.01	48/210821=0.02
D10S28	357/201367=0.18	215/230241=0.09	116/212285=0.05	225/215222=0.10
D12S11	7/20366=0.03	19/24803=0.08	3/30094=0.01	10/27271=0.04
D14S13*	19/30596=0.06	108/33085=0.33	3/21391=0.01	119/26343=0.45
D16S309*	0/286=<0.35	2/2234=0.09	UNK.	UNK.
D16S85*	0/565=<0.18	3/614=0.50	4/795=0.50	0/795=<0.13
D17S26	61/63797=0.10	179/69527=0.26	6/23765=0.03	45/58597=0.08
D17S79	7/19292=0.04	29/25499=0.11	15/17880=0.08	29/25287=0.11

* Data from 2001 AABB Annual Report (no data submitted for these systems)
** Null alleles are assumed when cases of paternal or maternal inconsistencies occur due to the child having an apparent single allele and the disputed parent having a different single allele (different homozygous banding patterns).

Appendix 5. The Observed Apparent Changes for Mutation Cases Submitted for Analysis by the Laboratories. (Note: Each locus is shown is broken down by paternal or maternal observations. Observed is the number reported and % Total is the percent of the total number of mutations observed at a specific locus.)

Maternal and Paternal FGA Mutations Observed in 2002

Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	% Total
50.2	49.2	1	0.20%		
31.2	30.2	2	0.40%		
29	28	3	0.60%		
28	29	5	0.90%	1	1.50%
28	27	18	3.40%	1	1.50%
27	29	1	0.20%		
27	28	3	0.60%		
27	26	19	3.60%	2	2.90%
26	27	32	6.00%	6	8.80%
26	25	36	6.80%	8	11.80%
25.2	24.2	1	0.20%		
25	27	1	0.20%		
25	26	47	8.90%	9	13.20%
25	24	30	5.70%	7	10.30%
25	23	1	0.20%		
25	19	1	0.20%		
24.2	23	1	0.20%		
24	27	1	0.20%		
24	25	62	11.70%	7	10.30%
24	23	30	5.70%	3	4.40%
24	22	1	0.20%		
23.2	24.2	1	0.20%		
23	24	47	8.90%	3	4.40%
23	22.2	1	0.20%	1	1.50%
23	22	20	3.80%	2	2.90%
23	19	1	0.20%		
23	27			1	1.50%
22.2	24.2	1	0.20%		
22.2	23.2	2	0.40%		
22.2	23	1	0.20%		
22	23	38	7.20%	1	1.50%
22	22.2	1	0.20%		
22	21	27	5.10%	3	4.40%
22	20	1	0.20%		
22	24			1	1.50%
22	25			1	1.50%
22	17			1	1.50%
21.1	22.2	4	0.80%		
21	23	2	0.40%		
21	22	34	6.40%	2	2.90%

21	20	10	1.90%	3	4.40%
21	19			1	1.50%
20.2	21.2	2	0.40%		
20.2	19.2	1	0.20%		
20	22	2	0.40%		
20	21	12	2.30%		
20	19	4	0.80%		
20	18	2	0.40%		
19.2	18.2	2	0.40%		
19	20	8	1.50%	3	4.40%
19	18	3	0.60%		
19	17	1	0.20%		
18.2	19.2	3	0.60%		
18	19			1	1.50%
17.2	18.2	1	0.20%		
17	18	1	0.20%		
17	16	1	0.20%		
		530	100.00%	136	100.00%

Maternal and Paternal VWA Mutations Observed in 2002

Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
21	22	1	0.2%		
21	20	10	2.1%	1	2.0%
20	21	16	3.4%	2	4.1%
20	19	41	8.7%	1	2.0%
19	20	37	7.8%	8	16.3%
19	18	58	12.3%	2	4.1%
18	19	56	11.8%	8	16.3%
18	17	59	12.5%	2	4.1%
17	19	1	0.2%		
17	18	53	11.2%	14	28.6%
17	16	35	7.4%	1	2.0%
17	15	1	0.2%		
17	14	1	0.2%		
16	18	2	0.4%		
16	17	37	7.8%	3	6.1%
16	15	22	4.7%	1	2.0%
15	16	11	2.3%	3	6.1%
15	14	27	5.7%		
14	15	3	0.6%	3	6.1%
14	13	2	0.4%		
		473	100.0%	49	100.0%

Maternal and Paternal D7S820 Mutations Observed in 2002

Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
15	14	1	0.7%		
14	15	2	1.4%		
14	13	13	9.1%	1	9.1%
13	14	5	3.5%	1	9.1%
13	12	15	10.5%	3	27.3%
12	13	19	13.3%	2	18.2%
12	11	17	11.9%		
11	12	17	11.9%	1	9.1%
11	10	7	4.9%	2	18.2%
10	11	24	16.8%		
10	9	11	7.7%		
9	10	4	2.8%		
9	8	1	0.7%		
8	9	7	4.9%	1	9.1%
		143	100.0%	11	100.0%

Maternal and Paternal D13S317 Mutations Observed in 2002

Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
16	17	1	0.5%		
15	16	1	0.5%		
15	14	9	4.8%	3	6.7%
14	15	10	5.3%	7	15.6%
14	13	31	16.5%	1	2.2%
13	15	1	0.5%		
13	14	21	11.2%	8	17.8%
13	12	25	13.3%	2	4.4%
13	8	1	0.5%		
12	13	42	22.3%	10	22.2%
12	11	17	9.0%	4	8.9%
11	12	15	8.0%		
11	10	1	0.5%	2	4.4%
10	11	5	2.7%	4	8.9%
10	9	1	0.5%		
9	10	5	2.7%		
9	8	1	0.5%		
8	9	1	0.5%		
		188	100.0%	45	100.0%

Maternal and Paternal D18S51 Mutations Observed in 2002

Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
24	25	2	0.6%	1	1.3%
24	21	1	0.3%		
23	24	2	0.6%	1	1.3%
23	22	6	1.8%		
22	23	5	1.5%		
22	21	12	3.6%	3	3.8%
21	22	8	2.4%		
21	20	18	5.3%		
20.2	18	1	0.3%		
20	21	10	3.0%	3	3.8%
20	19	27	8.0%	3	3.8%
20	18	1	0.3%		
19	21			1	1.3%
19	20	23	6.8%	8	10.3%
19	19	1	0.3%		
19	18	24	7.1%	2	2.6%
18.1	18	1	0.3%		
18	19	25	7.4%	3	3.8%
18	17	19	5.6%	1	1.3%
18	16	4	1.2%		
17	19			1	1.3%
17	18	12	3.6%	11	14.1%
17	16	13	3.8%	1	1.3%
17	15			1	1.3%
17	14			1	1.3%
16	17	24	7.1%	7	9.0%
16	15	9	2.7%	2	2.6%
16	14	1	0.3%		
16	13	1	0.3%		
15	16	24	7.1%	7	9.0%
15	14	13	3.8%	2	2.6%
15	13			2	2.6%
14.2	13	1	0.3%		
14	15	18	5.3%	4	5.1%
14	13	5	1.5%	1	1.3%
14	12	1	0.3%	1	1.3%
13	17	1	0.3%		
13	15	1	0.3%		
13	14	8	2.4%	4	5.1%
13	12	3	0.9%	1	1.3%
13	10	1	0.3%		
12	13	5	1.5%	5	6.4%
12	11	2	0.6%	1	1.3%
12	10	1	0.3%		
11	12	3	0.9%		
8	12	1	0.3%		
		338	100.0%	78	100.0%

Maternal and Paternal D5S818 Mutations Observed in 2002

Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
15	16	1	0.6%		
15	14	4	2.4%	1	3.4%
14	15	6	3.6%		
14	13	24	14.5%	4	13.8%
13	14	39	23.6%	7	24.1%
13	12	25	15.2%	3	10.3%
12	13	25	15.2%	9	31.0%
12	11	13	7.9%	3	10.3%
12	8	1	0.6%		
11	12	11	6.7%	1	3.4%
11	10	11	6.7%	1	3.4%
11	7	1	0.6%		
10	11	1	0.6%		
10	9	1	0.6%		
9	10	2	1.2%		
		165	100.0%	29	100.0%

Maternal and Paternal TPOX Mutations Observed in 2002

Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
16	15			1	12.5%
12	11	1	7.1%	2	25.0%
11	12	5	35.7%	1	12.5%
11	10	2	14.3%	1	12.5%
10	11	1	7.1%		
10	9	1	7.1%		
10	7			1	12.5%
9	11	1	7.1%		
9	8			1	12.5%
8	10	1	7.1%		
8	9	1	7.1%	1	12.5%
8	7	1	7.1%		
		14	100.0%	8	100.0%

Maternal and Paternal CSF1PO Mutations Observed in 2002

Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
15	14	6	4.5%		
14	15	7	5.2%		
14	13	12	9.0%	2	8.7%
13	14	8	6.0%	1	4.3%
13	12	29	21.6%	1	4.3%
12	13	29	21.6%	4	17.4%
12	11	9	6.7%	1	4.3%
12	10	2	1.5%	1	4.3%
11	12	11	8.2%	5	21.7%
11	10	10	7.5%	3	13.0%
10	12	1	0.7%		
10	11	6	4.5%	2	8.7%
10	8	1	0.7%	1	4.3%
9	12	1	0.7%		
9	10			2	8.7%
8	9	1	0.7%		
7	8	1	0.7%		
		134	100.0%	23	100.0%

Maternal and Paternal D16S539 Mutations Observed in 2002

Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
15	16	1	0.8%		
15	14	3	2.5%	3	8.6%
14	15	5	4.1%	1	2.9%
14	13	8	6.6%	9	25.7%
13	14	28	23.0%		
13	12	11	9.0%	8	22.9%
13	11			1	2.9%
12	13	22	18.0%	1	2.9%
12	11	12	9.8%	5	14.3%
12	9	1	0.8%		
11	13	1	0.8%		
11	12	10	8.2%	3	8.6%
11	10	4	3.3%		
11	9	1	0.8%		
10	11	9	7.4%		
10	9			1	2.9%
9	12	1	0.8%		
9	10	5	4.1%	3	8.6%
		122	100.0%	35	100.0%

Maternal and Paternal D21S11 Mutations Observed in 2002

Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
37	36			1	0.6%
36	37	1	0.4%		
35.2	34	1	0.4%	1	0.6%
35	36	1	0.4%		
35	34			2	1.3%
34.2	35	3	1.2%	2	1.3%
34.2	33			11	6.9%
34	35			1	0.6%
33.2	34	13	5.3%		
33.2	32	3	1.2%	23	14.4%
33	34	1	0.4%		
33	32	5	2.0%	2	1.3%
32.2	33	23	9.3%	11	6.9%
32.2	32			1	0.6%
32.2	31	4	1.6%	4	2.5%
32	33	4	1.6%	2	1.3%
32	31	5	2.0%	13	8.1%
31.2	32	13	5.3%	6	3.8%
31.2	30	5	2.0%		
31	32	26	10.5%	7	4.4%
31	30	14	5.7%	32	20.0%
30.2	31	4	1.6%	2	1.3%
30	31	38	15.4%	5	3.1%
30.2	31	2	1.3%	2	1.3%
30	31	38	15.4%	5	3.1%
30	29.2	2	0.8%		
30	29	24	9.7%	14	8.8%
29	32.2	1	0.4%		
29	30.2	1	0.4%		
29	30	20	8.1%	7	4.4%
29	28	10	4.0%	7	4.4%
28.2	30	1	0.4%		
28	29	17	6.9%	4	2.5%
28	27	2	0.8%	1	0.6%
27	28	4	1.6%		
25	28	1	0.4%		
		247	100.0%	160	100.0%

Maternal and Paternal D8S1179 Mutations Observed in 2002

Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
18	17	4	1.6%		
17	18	0	0.0%		
17	16	15	6.1%	2	5.9%
16	17	15	6.1%	2	5.9%
16	15	21	8.5%	2	5.9%
15	16	26	10.5%	6	17.6%
15	14	32	13.0%		
14	16	2	0.8%		
14	15	40	16.2%	6	17.6%
14	14			1	2.9%
14	13	22	8.9%	5	14.7%
14	12	1	0.4%		
13	16	1	0.4%		
13	14	15	6.1%	2	5.9%
13	12	23	9.3%	4	11.8%
12	13	9	3.6%		
12	11	6	2.4%	1	2.9%
11	12	6	2.4%	3	8.8%
11	10	2	0.8%		
10	13	1	0.4%		
10	11	3	1.2%		
9	10	0	0.0%		
8	9	3	1.2%		
		247	100.0%	34	100.0%

Maternal and Paternal D19S433 Mutations Observed in 2002

Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
17.2	16.2			1	6.7%
16.2	17.2	1	8.3%		
16.2	15.2	2	16.7%	4	26.7%
16	17			1	6.7%
16	15	2	16.7%	2	13.3%
15.2	16.2	1	8.3%		
15	14	1	8.3%	2	13.3%
14.2	13.2			1	6.7%
14	15	1	8.3%	1	6.7%
14	13	2	16.7%		
13	14	0	0.0%	1	6.7%
13	12	0	0.0%	1	6.7%
12	13	1	8.3%	1	6.7%
11	12	1	8.3%		
		12	100.0%	15	100.0%

Maternal and Paternal THO1 Mutations Observed in 2002

Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
9.3	10			1	20.0%
9	10	1	16.7%		
9	8	2	33.3%	2	40.0%
8	9.3			1	20.0%
8	7	1	16.7%	1	20.0%
6	7	1	16.7%		
5	7	1	16.7%		
		6	100.0%	5	100.0%

Maternal and Paternal D2S1338 Mutations Observed in 2002

Apparent Change		Paternal		Maternal	
From	To	Observed	From	To	Observed
27	26	2	4.1%		
26	25	6	12.2%		
25	26	4	8.2%	1	50.0%
25	24	5	10.2%		
24	25	3	6.1%		
24	23	2	4.1%		
23	24	1	2.0%		
23	22	6	12.2%	1	50.0%
22	23	2	4.1%		
22	21	1	2.0%		
21	22	1	2.0%		
21	20	3	6.1%		
20	21	3	6.1%		
20	19	2	4.1%		
19	20	1	2.0%		
19	18	1	2.0%		
18	19	2	4.1%		
18	17	1	2.0%		
17	18	1	2.0%		
16	17	1	2.0%		
16	15	1	2.0%		
		49	100.0%	2	100.0%

Maternal and Paternal Penta D Mutations Observed in 2002

Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
13	14	1	12.5%	1	14.3%
13	11			1	14.3%
12	13			2	28.6%
12	11	1	12.5%	2	28.6%
11	10	3	37.5%		
10	13	1	12.5%		
10	11	1	12.5%		
9	11	1	12.5%		
9	10			1	14.3%
		8	100.0%	7	100.0%

Maternal and Paternal Penta E Mutations Observed in 2002

Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
23	22	1	5.3%		
20	21	1	5.3%		
19	20	1	5.3%		
19	18	1	5.3%	1	9.1%
18	19	1	5.3%	1	9.1%
17	18			1	9.1%
17	16	1	5.3%		
17	13			1	9.1%
16	17			1	9.1%
16	15	2	10.5%		
16	12	2	10.5%		
15	16	1	5.3%		
15	14	1	5.3%		
13	14	1	5.3%		
13	12			1	9.1%
12	14			1	9.1%
12	13	2	10.5%		
12	11			1	9.1%
11	10	1	5.3%		
10	12	1	5.3%		
10	9			1	9.1%
9	12			1	9.1%
9	16	1	5.3%		
9	10			1	9.1%
7	10	1	5.3%		
		19	100.0%	11	100.0%

Appendix 6. The Distance (Repeat Lengths) from the Obligatory Allele for PCR-STR Cases.

PCR MUTATIONS: DISTANCE FROM OBLIGATORY ALLELE (Expressed as Percent of Total Number of Mutations)												
	Maternal						Paternal					
	STR Distance From Obligatory Allele						STR Distance From Obligatory Allele					
GENETIC SYSTEM	+1	-1	+2	- 2	OTHER	TOTAL #	+1	-1	+2	- 2	OTHER	TOTAL #
D2S1338	0.000	0.000	0.000	0.000	0.000	0	1.000	0.000	0.000	0.000	0.000	1
D3S1744	0.000	0.000	0.000	0.000	0.000	0	0.000	1.000	0.000	0.000	0.000	1
D3S1358	0.440	0.550	0.000	0.000	0.000	10	0.540	0.420	0.025	0.000	0.008	118
D5S818	0.410	0.500	0.090	0.000	0.000	24	0.580	0.380	0.030	0.000	0.013	172
D7S820	0.810	0.180	0.000	0.000	0.000	11	0.620	0.340	0.010	0.020	0.010	106
D8S1179	0.600	0.400	0.000	0.000	0.000	18	0.460	0.520	0.020	0.000	0.000	112
D12S1090	0.000	0.000	0.000	0.000	0.000	0	0.660	0.340	0.000	0.000	0.000	3
D13S317	0.520	0.480	0.000	0.000	0.000	122	0.650	0.330	0.023	0.000	0.000	188
D16S539	0.830	0.110	0.050	0.000	0.000	20	0.680	0.310	0.000	0.000	0.000	86
D18S51	0.400	0.570	0.030	0.000	0.000	32	0.500	0.470	0.009	0.017	0.000	129
D18S849	0.000	0.000	0.000	0.000	0.000	0	1.000	0.000	0.000	0.000	0.000	3
D19S433	0.670	0.330	0.000	0.000	0.000	3	1.000	0.000	0.000	0.000	0.000	1
D21S11	0.630	0.360	0.013	0.000	0.013	84	0.350	0.610	0.020	0.009	0.009	113
CSF1PO	0.550	0.450	0.000	0.000	0.000	26	0.750	0.220	0.030	0.008	0.000	148
FGA	0.380	0.590	0.000	0.023	0.000	49	0.490	0.500	0.005	0.005	0.000	220
F13A	0.000	1.000	0.000	0.000	0.000	1	0.500	0.000	0.000	0.500	0.000	2
F13B	0.000	0.000	0.000	0.000	0.000	0	0.000	0.000	0.000	0.000	0.000	0
FESFPS	0.000	0.000	0.000	0.000	0.000	0	1.000	0.000	0.000	0.000	0.000	1
LPL	0.000	0.000	0.000	0.000	0.000	0	0.330	0.330	0.330	0.000	0.000	4
PENTA D	0.800	0.000	0.000	0.000	0.200	5	0.500	0.000	0.000	0.000	0.500	2
PENTA E	0.550	0.220	0.110	0.000	0.110	9	0.750	0.200	0.000	0.000	0.050	22
THO1	0.860	0.140	0.000	0.000	0.000	7	0.250	0.250	0.000	0.500	0.000	7
TPOX	0.400	0.400	0.200	0.000	0.000	5	0.500	0.330	0.000	0.160	0.000	6
VWA	0.430	0.560	0.000	0.000	0.000	35	0.640	0.340	0.010	0.003	0.003	295

Appendix 7. The Apparent Null Alleles Reported by the Various Laboratories. (Note: Each locus is broken down by the primer source. Some laboratories did not provide complete information. Therefore, a race and the total number in the system may not be provided.)

Null alleles in CSF1PO

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
CSF1PO	**10**	**11**	**10** **11**	1	BLACK	28862
CSF1PO	**11**	**12**	**11** **12**	1	BLACK	28862
CSF1PO	**10** **11**	**10**	**11**	1	CAUCA	25072
CSF1PO	**11**	**11**	**10**	1	CAUCA	5867
CSF1PO	**11**	**12**	**11** **12**	2	CAUCA	25072
CSF1PO	**9** **13**	**13**	**12**	1	HISPANIC	9908

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
CSF1PO	**13**	**11**		1	?	?
CSF1PO	**12**	**11**		1	?	?
CSF1PO		**12**	**11**	1	?	?
CSF1PO	**10**	**11**		1	?	?

Null alleles in D2S1338

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D2S1338		**19**	**20**	1	BLACK	2849
D2S1338	**19 20**	**20**	**21**	1	BLACK	2849
D2S1338	**17 22**	**17**	**22**	1	CAUCA	2300
D2S1338	**23**	**18**	**18 21**	1	CAUCA	2300
D2S1338	**19 20**	**19**	**21**	1	CAUCA	5917
D2S1338	**17 22**	**22**	**23**	1	HISPA	1424
D2S1338	**25**	**23**		1	?	?
D2S1338	**25**	**19**		1	?	?

Null alleles in PENTA D

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
PENTA D	**11**	**8**		1	?	?
PENTA D	**12**	**`9**		1	?	?
PENTA D	**9 12**	**9**	**12**	1	CAUCA	3297
PENTA D		**14**	**9**	1	CAUCA	?
PENTA D		**9**	**10**	1	BLACK	?

Null alleles in D3S1358

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D3S1358		**14**	**15**	1	BLACK	2666
D3S1358		**15**	**16**	1	BLACK	28862
D3S1358	**17**	**15**	**15 17**	1	BLACK	28862
D3S1358	**16**	**15**		1	BLACK	2341
D3S1358	**15 16**	**16**	**17**	2	BLACK	28862
D3S1358	**14**	**17**	**14 17**	1	BLACK	28862
D3S1358		**17**	**15**	1	BLACK	2666
D3S1358	**15**	**15**	**16**	1	CAUCA	25072
D3S1358	**16**	**16**	**17**	1	CAUCA	3951
D3S1358	**15 17**	**17**	**15**	1	CAUCA	5537
D3S1358	**16 17**	**17**	**18**	1	CAUCA	25072
D3S1358		**16**	**15**	1	BLACK	?
D3S1358		**16**	**15**	1	CAUCA	?

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D3S1358	**15 16**	**16**	**18**	1	BLACK	1460
D3S1358	**15**	**16**		2	?	?
D3S1358		**16**	**17**	1	?	?
D3S1358		**17**	**16**	1	?	?
D3S1358		**17**	**18**	1	CAUCA	?

Null alleles in D5S818

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D5S818		**10**	**13**	1	BLACK	19607
D5S818	**12 13**	**13**	**12**	1	BLACK	28862
D5S818	**11**	**11**	**12**	1	BLACK	28862
D5S818	**13 14**	**13**	**11**	1	BLACK	19607
D5S818	**12 13**	**13**	**11**	1	BLACK	1391
D5S818	**12**	**12**	**11**	1	CAUCA	25072
D5S818	**12**	**12**	**11**	1	CAUCA	6476
D5S818		**12**	**11**	1	CAUCA	6476
D5S818		**12**	**13**	1	CAUCA	6476
D5S818	**11 13**	**13**	**9**	1	CAUCA	25072
D5S818	**12**	**13**	**13**	1	CAUCA	25072
D5S818	**13**	**13**	**10**	1	ASIAN	335
D5S818	**11 12**	**11**	**12**	1	HISPANIC	123
D5S818		**13**	**12**	1	HISPA	1559

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D5S818	**13**	**12**		1	?	?
D5S818		**11**	**13**	1	CAUCA	?
D5S818		**12**	**13**	1	CAUCA	?
D5S818		**12**	**13**	1	BLACK	?

Null alleles in D7S820

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D7S820	**13**	**11**	**10** **11**	1	AMERICAN INDIAN	786
D7S820	**8** **10**	**8**	**11**	1	BLACK	2270
D7S820	**8** **9**	**9**	**8**	1	BLACK	28862
D7S820	**9** **11**	**11**	**10**	2	BLACK	28862
D7S820	**10**	**7**	**7** **9**	1	CAUCA	25072
D7S820	**11**	**10**	**9** **10**	1	CAUCA	25072
D7S820	**11** **13**	**11**	**12**	1	CAUCA	3854
D7S820	**10**	**13**	**9** **13**	1	CAUCA	3890

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D7S820	**11**	**10**		1	?	?
D7S820		**8**	**10**	1	?	?

Null alleles in D8S1179

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D8S1179	**14**	**10**	**12 15**	1	BLACK	28862
D8S1179	**13**	**13**	**14**	1	BLACK	28862
D8S1179	**14**	**13**	**13 15**	1	BLACK	28862
D8S1179	**8**	**13**	**13**	1	BLACK	28862
D8S1179	**13 15**	**13**	**11**	1	BLACK	28862
D8S1179	**13 14**	**13**	**14**	1	BLACK	28862
D8S1179	**13 14**	**14**	**13**	1	BLACK	1937
D8S1179	**13 14**	**14**	**15**	1	BLACK	28862
D8S1179	**13 14**	**14**	**16**	1	BLACK	28862
D8S1179	**14 15**	**14**	**15**	1	BLACK	2331
D8S1179	**14**	**14**	**12**	1	BLACK	28862
D8S1179	**12**	**15**	**11 15**	1	BLACK	28862
D8S1179	**15**	**16**	**15 16**	1	BLACK	28862
D8S1179		**16**	**15**	1	BLACK	?
D8S1179		**10**	**13**	1	CAUCA	?
D8S1179	**12 13**	**13**	**16**	1	CAUCA	25072
D8S1179		**13**	**14**	1	CAUCA	?
D8S1179	**14 15**	**14**	**15**	2	CAUCA	25072
D8S1179	**13**	**14**	**13 14**	1	CAUCA	25072
D8S1179	**11 13**	**11**	**15**	1	HISPANIC	9908
D8S1179	**14**	**11**		1	HISPANIC	4099
D8S1179	**15**	**11**		1	HISPANIC	9908
D8S1179		**11**	**13**	1	HISPANIC	3775

D8S1179	14	13		1	HISPANIC	4099
D8S1179	15	14		1	HISPANIC	4099
D8S1179	13	14		1	HISPANIC	9908
D8S1179	11 14	14	13	1	HISPANIC	3775
D8S1179	13	15		1	HISPANIC	9908
D8S1179	13 16	16	14	1	HISPANIC	3775
D8S1179	11 15	11	15	1	ASIAN	146
D8S1179	13	12		1	ASIAN	381
D8S1179	13	12	12 13	1	ASIAN	600
D8S1179	10	13		1	ASIAN	381
D8S1179	11	13	13 14	1	ASIAN	356
D8S1179	12	13		1	ASIAN	381
D8S1179	13 15	13	14	1	ASIAN	146
D8S1179	14	13		1	ASIAN	381
D8S1179	10 14	14	13	1	ASIAN	333
D8S1179	10 14	14	15	1	ASIAN	333
D8S1179	10 14	14	16	1	ASIAN	333
D8S1179	13	15		1	ASIAN	381
D8S1179	10 15	15	11	1	ASIAN	333
D8S1179	11 13	11	10	1	PACIFIC ISLANDER	339
D8S1179	13	11	12 15	1	PACIFIC ISLANDER	339
D8S1179	13	11	11 14	1	PACIFIC ISLANDER	339
D8S1179	13	11	11 13	1	PACIFIC ISLANDER	339
D8S1179	10	12	12 14	1	PACIFIC ISLANDER	339
D8S1179	13	12	12 13	1	PACIFIC ISLANDER	339
D8S1179	10	13	11 14	1	PACIFIC ISLANDER	339
D8S1179	15	13	11 13	1	PACIFIC ISLANDER	339
D8S1179	13	13	14	1	PACIFIC ISLANDER	339

D8S1179	13	14	10 14	1	PACIFIC ISLANDER	339
D8S1179		14	15	1	PACIFIC ISLANDER	339
D8S1179	12 14	14	12	1	PACIFIC ISLANDER	339
D8S1179	13	14	14	1	PACIFIC ISLANDER	339
D8S1179	12	15	13 14	1	PACIFIC ISLANDER	339
D8S1179	11	15	12 13	1	PACIFIC ISLANDER	339
D8S1179	14	15	13 15	1	PACIFIC ISLANDER	339
D8S1179	14	15	14 15	1	PACIFIC ISLANDER	339
D8S1179	13 16	16	14	1	PACIFIC ISLANDER	339
D8S1179	13	16		1	BLACK	?
D8S1179	15	14		1	?	?

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D8S1179	14	12	14 12	1	BLACK	?
D8S1179	15	13	14 13	1	CAUCA	?
D8S1179	14	15	14 15	1	CAUCA	500
D8S1179	13	15	15 13	1	CAUCA	?
D8S1179		13	14	2	?	?
D8S1179		14	15	1	?	?
D8S1179		14	13	1	?	?
D8S1179		14	13	1	CAUCA	?

Null alleles in D13S317

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D13S317	**11 12**	**11**	**12**	1	ASIAN	356
D13S317	**12 13**	**12**	**8**	1	ASIAN	356
D13S317	**12 13**	**12**	**13**	1	BLACK	28862
D13S317	**12**	**12**	**13**	1	BLACK	28862
D13S317	**11 12**	**12**	**13**	1	BLACK	28862
D13S317	**11 13**	**13**	**12**	1	BLACK	28862
D13S317	**11**	**11**	**13**	1	CAUCA	25072
D13S317	**12**	**11**		1	CAUCA	5585
D13S317	**13**	**11**		1	CAUCA	25072
D13S317	**12**	**12**	**13**	2	CAUCA	25072
D13S317	**12**	**12**	**11**	1	CAUCA	25072
D13S317	**8**	**13**		1	CAUCA	25072
D13S317	**9**	**8**		1	HISPANIC	9908
D13S317		**10**	**11**	1	HISPA	1567
D13S317	**12**	**11**		1	HISPANIC	4134
D13S317	**9**	**12**		1	HISPANIC	9908
	13	**11**	**8 11**	1	ORIENTAL	146

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D13S317	**10 12**	**11**	**12**	1	BLACK	251
D13S317	**11 12**	**11**	**12**	1	BLACK	1611
D13S317	**13**	**11**	**11 12**	1	BLACK	?
D13S317	**12**	**12**	**11**	1	BLACK	100
D13S317	**8**	**12**	**12**	1	BLACK	100
D13S317	**12**	**12**	**13**	1	BLACK	251
D13S317	**11**	**12**	**12**	1	BLACK	251
D13S317	**10**	**12**		1	?	?
D13S317	**10**	**14**		1	?	?
D13S317	**13**	**11**		1	?	?
D13S317	**11**	**13**		1	?	?
D13S317	**14**	**11**		1	BLACK	?
D13S317	**13**	**12**		1	BLACK	?
D13S317	**12**	**14**		1	BLACK	?
D13S317	**12**	**13**		1	BLACK	?
D13S317	**11**	**12**		1	BLACK	?
D13S317	**11**	**9**		1	BLACK	?
D13S317	**9**	**12**		1	CAUCA	?
D13S317		**13**	**12**	2	BLACK	?
D13S317		**12**	**13**	1	BLACK	?
D13S317		**12**	**11**	1	BLACK	?
D13S317		**11**	**12**	1	BLACK	?
D13S317		**12**	**9**	1	CAUCA	?

Null alleles in D16S539

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D16S539		**12**	**11**	1	CAUCA	?

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D16S539	**13**	**9**		1	?	?
D16S539	**9**	**10**		1	?	?
D16S539	**12**	**11**		2	?	?
D16S539		**12**	**11**	1	?	?
D16S539	**12**	**12**	**9**	1	CAUCA	3366
D16S539		**13**	**10**	1	BLACK	?

Null alleles in D18S51

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D18S51	**16**	**14**	**14 15**	1	BLACK	28862
D18S51	**12**	**15**	**15 18**	1	BLACK	28862
D18S51		**15**	**13**	1	BLACK	28862
D18S51	**17**	**16**	**16**	1	BLACK	28862
D18S51	**15**	**17**		1	BLACK	28862
D18S51	**13 17**	**17**	**15**	1	BLACK	28862
D18S51	**18**	**11**		1	CAUCA	25072
D18S51	**12**	**12**	**13**	1	CAUCA	1626
D18S51	**15 17**	**15**	**12**	1	CAUCA	22512
D18S51	**15 17**	**15**	**16**	1	CAUCA	25072
D18S51		**15**	**14**	1	CAUCA	25072
D18S51	**14 16**	**16**	**15**	1	CAUCA	3849
D18S51	**12 17**	**17**	**19**	1	CAUCA	3890
D18S51	**15 17**	**15**	**14**	1	HISPANIC	9908
D18S51	**13**	**16**		1	HISPANIC	5419
D18S51	**15**	**16**		1	HISPANIC	9908
D18S51	**16 18**	**16**	**15**	1	HISPANIC	3700
D18S51	**18**	**18**	**15**	1	HISPANIC	9908
D18S51	**17 18**	**18**	**12**	1	HISPANIC	9908
D18S51	**14**	**19**	**18 19**	1	HISPANIC	9908
D18S51	**12 20**	**20**	**14**	1	HISPANIC	9908

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D18S51		**14**	**13**	1	CAUCA	3391
D18S51	**17**	**18**		1	?	?
D18S51	**16**	**14**		1	?	?
D18S51		**16**	**17**	1	?	?
D18S51		**15**	**14**	1	?	?
D18S51		**15**	**16**	1	?	?
D18S51		**10**	**11**	1	CAUCA	?

Null alleles in TPOX

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
TPOX	**12**	**8**		1	BLACK	28862
TPOX	**11**	**9**	**9**	1	BLACK	28862
TPOX	**8**	**8**	**10**	1	CAUCA	25072
TPOX	**8**	**11**	**11**	1	CAUCA	25072
TPOX	**8** **11**	**8**	**9**	1	CAUCA	25072

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
TPOX	**8**	**9**		1	?	?
TPOX	**8**	**11**		1	CAUCA	?

Null alleles in THO1

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
THO1	7	6	6 9	1	BLACK	28862
THO1	6	6	7	1	BLACK	28862
THO1	6 8	6	8	1	BLACK	28862
THO1	6 9.3	6	9	2	BLACK	28862
THO1	6 9	6	10	1	BLACK	28862
THO1	7 9.3	7	9.3	1	BLACK	28862
THO1	7 8	7	6	3	BLACK	28862
THO1	7	8	7 8	2	BLACK	28862
THO1	8	8	7	1	BLACK	28862
THO1	8 9.3	8	7	1	BLACK	28862
THO1	7	9	7 9	3	BLACK	29462
THO1	8	9	8 9	1	BLACK	28862
THO1	9 9.3	9	7	1	BLACK	28862
THO1	7	9.3		1	BLACK	?
THO1	9.3	6	6	1	CAUCA	25072
THO1	6	7		1	CAUCA	25072
THO1	7 9.3	9.3	6	1	CAUCA	25072
THO1	18	12	12 13	1	YEMENI	516
THO1	7	6	6 7	1	HISPANIC	9908
THO1	7	8	8	1	HISPANIC	9908
THO1	7	9	6 9	1	HISPANIC	9908
THO1	7 9.3	9.3	7	1	HISPANIC	9908
THO1	6	9.3	9.3	1	HISPANIC	9908
THO1	6 10	10	9.3	1	HISPANIC	9908

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
THO1	**7**	**6**		2	?	?
THO1	**9.3**	**10**		1	?	?
THO1	**10**	**9.3**		2	?	?
THO1	**6**	**9.3**		1	?	?
THO1	**6**	**7**		1	?	?
THO1		**7**	**6**	1	?	?
THO1		**9.3**	**8**	1	?	?

Null alleles in D19S433

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D19S433	**13 14**	**14**	**13**	1	BLACK	2286
	13	**12**		1	?	?
		13	**14**	1	?	?
		14	**13**	1	BLACK	?

Null alleles in VWA

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
VWA	**16, 18**	**16**	**17**	1	ASIAN	335
VWA	**17 19**	**19**	**15**	1	AMERICAN INDIAN	786
VWA	**16**	**15**		1	BLACK	?
VWA		**15**	**17**	1	BLACK	28862
VWA		**15**	**16**	1	BLACK	?
VWA	**15 17**	**15**	**16**	1	BLACK	1937
VWA	**15 17**	**15**	**17**	1	BLACK	19607
VWA	**15 19**	**15**	**20**	1	BLACK	28862
VWA	**16**	**16**	**17**	1	BLACK	2342
VWA	**16 19**	**16**	**20**	1	BLACK	28862
VWA	**15 17**	**17**	**16**	1	BLACK	2342
VWA	**17 18**	**17**	**16**	1	BLACK	28862
VWA	**13**	**17**	**15 17**	1	BLACK	28862
VWA	**19**	**17**	**17 18**	1	BLACK	28862
VWA	**16**	**17**	**17 18**	1	BLACK	28862
VWA	**15 17**	**17**	**18**	1	BLACK	2342
VWA		**17**	**18**	1	BLACK	2851
VWA	**17**	**18**		1	BLACK	?
VWA	**17 18**	**18**	**14**	1	BLACK	19607
VWA	**17 18**	**18**	**15**	1	BLACK	19607
VWA	**16 18**	**18**	**16**	1	BLACK	19607
VWA	**18**	**18**	**17**	1	BLACK	28862
VWA	**16 19**	**19**	**16**	1	BLACK	28862
VWA	**15 19**	**19**	**18**	1	BLACK	1937

VWA		14	17	1	CAUCA	25072
VWA	17	14		1	CAUCA	25072
VWA	17	15	15 18	1	CAUCA	25072
VWA	14 15	15	18	1	CAUCA	22512
VWA	16	16	17	1	CAUCA	25072
VWA	16	16	18	1	CAUCA	25072
VWA	16 19	16	18	1	CAUCA	22512
VWA		16	15	1	CAUCA	?
VWA	16 17	17	14	1	CAUCA	22512
VWA	16	17		1	CAUCA	5602
VWA		17	18	1	CAUCA	?
VWA	16 17	17	18		CAUCA	3420
VWA	17 19	17	18	1	CAUCA	3985
VWA		17	19	1	CAUCA	?
VWA		18	17	1	CAUCA	?
VWA	15 18	18	19	1	CAUCA	5921
VWA	17 18	18	19	1	CAUCA	25072
VWA	17 18	18	16	1	CAUCA	25072
VWA	17	18	17 18	1	CAUCA	25072
VWA	18	19		1	CAUCA	25072
VWA	18 20	20	18	1	CAUCA	25072
VWA	14 18	14	16	1	HISPANIC	9908
VWA	17	16	16	1	HISPANIC	9908
VWA		17	16	1	HISPANIC	3809
VWA	16 17	17	18	1	HISPANIC	99
VWA	16	18		1	HISPANIC	4136
VWA	17 18	18	16	1	HISPANIC	9908
VWA	18 19	19	15	1	HISPANIC	3809

VWA		**19**	**18**	1	HISPANIC	1425
VWA	**16**	**19**	**18** **19**	1	HISPANIC	9908

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
VWA	**16** **17**	**17**	**18**	1	CAUCA	3420
VWA	**17**	**18**		1	?	?
VWA	**16**	**17**		1	?	?
VWA	**21**	**17**		1	?	?
VWA		**17**	**18**	1	?	?
VWA		**18**	**17**	1	?	?
VWA		**16**	**15**	1	?	?
VWA		**16**	**18**	1	?	?
VWA		**19**	**20**	1	?	?
VWA	**17**	**15**		1	BLACK	?
VWA		**15**	**16**	1	BLACK	?
VWA		**15**	**17**	1	BLACK	?
VWA		**17**	**18**	1	CAUCA	?

Null alleles in FGA

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
FGA	**17 23**	**17**	**24**	1	BLACK	28862
FGA	**18.2 25**	**18.2**	**23**	1	BLACK	28862
FGA		**19**	**18.2**	1	BLACK	?
FGA	**26**	**19**	**19 22**	1	BLACK	28862
FGA	**24**	**19**	**19 24**	1	BLACK	28862
FGA	**26**	**19**	**19 22**	1	BLACK	28862
FGA	**24**	**19**	**19 24**	1	BLACK	28862
FGA	**22**	**20**	**20 24**	1	BLACK	28862
FGA	**27**	**20**	**20 23**	1	BLACK	28862
FGA	**19**	**20**	**20 24**	1	BLACK	28862
FGA	**22**	**20**	**20**	1	BLACK	28862
FGA	**19 20**	**20**	**22**	1	BLACK	28862
FGA	**22**	**20**	**20 24**	1	BLACK	28862
FGA	**27**	**20**	**20 23**	1	BLACK	28862
FGA	**19**	**20**	**20 24**	1	BLACK	28862
FGA	**22**	**20**	**20**	1	BLACK	28862
FGA	**21 25**	**21**	**23**	1	BLACK	28862
FGA	**21 25**	**21**	**23**	1	BLACK	28862
FGA	**21 29**	**21**	**25**	1	BLACK	19607
FGA	**21 22**	**22**	**21**	1	BLACK	28862
FGA	**22 24**	**22**	**23**	1	BLACK	28862
FGA	**22 24**	**22**	**21**	1	BLACK	28862
FGA	**22 23**	**22**	**23**	1	BLACK	28862

FGA	20	22	21 22	1	BLACK	28862
FGA	24	22	24	1	BLACK	28862
FGA	21	22	23	1	BLACK	28862
FGA	22 25	22	20	1	BLACK	28862
FGA	22 23	22	23	1	BLACK	28862
FGA	22	22	19	1	BLACK	28862
FGA	21 22	22	21	1	BLACK	28862
FGA	22 24	22	23	1	BLACK	28862
FGA	22 24	22	21	1	BLACK	28862
FGA	22 23	22	23	1	BLACK	28862
FGA	20	22	21 22	1	BLACK	28862
FGA	24	22	24	1	BLACK	28862
FGA	21	22	23	1	BLACK	28862
FGA		23	18.2	1	BLACK	28862
FGA	23 25	23	22	1	BLACK	28862
FGA	24	23	20 23	1	BLACK	28862
FGA	27	23	23 28	1	BLACK	28862
FGA	19	23	19 22	1	BLACK	28862
FGA		23	18.2	1	BLACK	28862
FGA	23 25	23	22	1	BLACK	28862
FGA	24	23	20 23	1	BLACK	28862
FGA	27	23	23 28	1	BLACK	28862
FGA	19	23	19 22	1	BLACK	28862
FGA	22	23		1	BLACK	?
FGA	24	23.2	24 26	1	BLACK	28862
FGA	24	23.2	24 26	1	BLACK	28862
FGA	22	24		1	BLACK	?
FGA	24	24	23	1	BLACK	28862

FGA	24 25	24	21	1	BLACK	28862
FGA	24 25	24	21	1	BLACK	28862
FGA	22	24	21 24	1	BLACK	28862
FGA	19	24	24 25	1	BLACK	28862
FGA	22 24	24	23	1	BLACK	28862
FGA		24	19.2	1	BLACK	28862
FGA	24	24	23	1	BLACK	28862
FGA	24 25	24	21	1	BLACK	28862
FGA	24 25	24	21	1	BLACK	28862
FGA	22	24	21 24	1	BLACK	28862
FGA	19	24	24 25	1	BLACK	28862
FGA	25	25	21	1	BLACK	28862
FGA	22	25	23 25	1	BLACK	28862
FGA		25	24	1	BLACK	28862
FGA	25	25	21	1	BLACK	28862
FGA	22	25	23 25	1	BLACK	28862
FGA	21	26	24 26	1	BLACK	28862
FGA	24	26	23 26	1	BLACK	28862
FGA	21	26	24 26	1	BLACK	28862
FGA	24	26	23 26	1	BLACK	28862
FGA	22	27	23 25	1	BLACK	28862
FGA	22	27	23 25	1	BLACK	28862
FGA	23 28	28	23	1	BLACK	28862
FGA	28 22	28	19	1	BLACK	19607
FGA	26	44.2		1	BLACK	2340
FGA	25	21	21 25	1	CAUCA	25072
FGA		21	22	2	CAUCA	?
FGA		22	20	1	CAUCA	?

FGA		**23**	**21**	1	CAUCA	?
FGA		**23**	**22**	1	CAUCA	6241
FGA	**19** **24**	**24**	**25**	1	CAUCA	3890
FGA		**24**	**25**	1	CAUCA	6241
FGA		**25**	**24**	1	CAUCA	6241
FGA	**22** **25**	**25**	**24**	1	CAUCA	3890
FGA	**25**	**19**		1	HISPANIC	9908
FGA	**23** **24**	**24**	**23**	1	HISPANIC	9908

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
FGA	**17**	**22**	**21** **22**	1	ASIAN	22
FGA	**21**	**20**		1	?	?
FGA	**25**	**23**		1	?	?
FGA	**26**	**24**		1	?	?
FGA		**24**	**19**	1	?	?
FGA		**18**	**23**	1	?	?
FGA		**19**	**23**	1	?	?
FGA		**23**	**21**	1	CAUCA	?

Appendix 8. The Number and Frequency of Maternal and Paternal Cases that Have an Apparent "Null Allele" Phenotype Pattern. (Note: These frequencies are not the same as the frequency of the null allele, which cannot be directly ascertained from the data collected for this report.

	BLACK				CAUCASIAN				OTHER RACE			
Locus	# Mat	Freq. Mat.	# Pat.	Freq. Pat	# Mat	Freq. Mat.	# Pat.	Freq. Pat	# Mat	Freq. Mat.	# Pat.	Freq. Pat
D3S1358	3	0.00009	4	0.00012	0		4	0.00012				
D5S818	0		5	0.00010	1	0.00003	5	0.00016				
D7S820	0		3	0.00010	3	0.00010	1	0.00003				
D8S1179	5	0.00015	8	0.00024	1	0.00004	2	0.00007	Hisp. 6 Asian 6 Pac I 13	Hispanic 0.00034 Asian 0.00814 Pac I 0.03835	Hisp. 4 Asian 6 Pac I 5	Hispanic 0.00022 Asian 0.01253 Pac I 0.01475
D13S317	0		4	0.00014	3	0.00010	3	0.00010	Hisp 3	Hispanic 0.00019	Hisp 1	Hispanic 0.00006
D18S51	4	0.00014	2	0.00007	1	0.00003	6	0.00017	Hisp 3	Hispanic 0.00016	Hisp 5	Hispanic 0.00026
D21S11	6	0.00011	10	0.00019	2	0.00004	2	0.00004				
THO1	8	0.00014	12	0.00021	2	0.00008	1	0.00004	Hisp 4	Hispanic 0.00040	Hisp 2	Hispanic 0.00020
VWA	4	0.00007	10	0.00018	5	0.00008	12	0.00018	Hisp 3	Hispanic 0.00015	Hisp 6	Hispanic 0.00031
FGA	41	0.00081	33	0.00065	1	0.00003	5	0.00014				
D2S1338	0		2	0.00007	1	0.00012	2	0.00024				

Pac I = Pacific Islander