ANNUAL REPORT SUMMARY FOR TESTING IN 2003
Prepared by the Parentage Testing Standards Program Unit
October 2004

PREFACE

This year marks the 20th anniversary of the AABB parentage laboratory accreditation program. At a joint conference of the AMA/ABA in 1977, the need for accreditation was recognized. AABB assumed the role of accreditation organization of parentage laboratories as the same testing technology used in the blood bank was also used in parentage testing. Over the past twenty years, paternity tests have moved towards different technologies. With AABB's expanded mission into the area of cellular therapies, the testing used to evaluate the success of some cellular therapies is the same as that used in parentage testing, renewing the alliance of technologies. This year's annual report for 2003 continues the past precedent of providing basic summary statistics for testing that took place in the previous year.

AABB sent surveys to 60 organizations that indicated they performed parentage testing and 44 (73%) laboratories returned the surveys. Although these surveys were mostly from accredited laboratories in the United States, several of the laboratories were from Canada and Europe. Many of the laboratories reported testing a broad range of cases, including relationship tests for routine parentage testing, immigration, prenatal evaluations, and post-mortem evaluations.

In this report, AABB provides some commentary regarding misconceptions relating to the significance of the survey results. Some of the commentary from last year is included in this year's report, as the commentary remains relevant to issues raised this year.

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 standards; various calculations used, and addresses other issues in parentage testing.

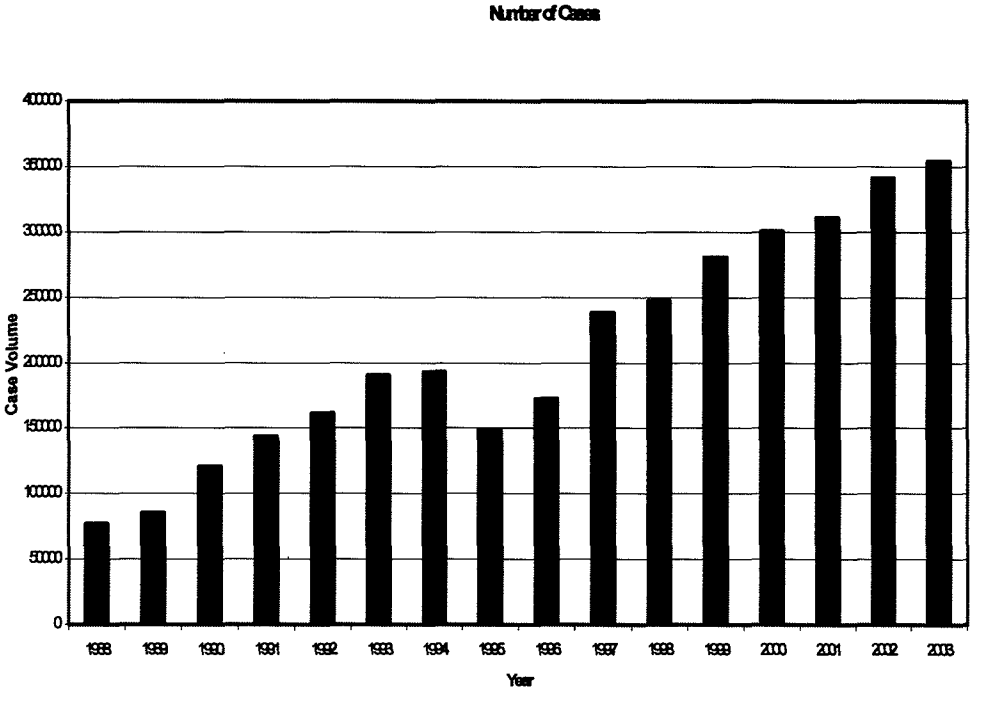
ANNUAL VOLUME OF TESTING

The volume reported for cases tested in 2003 was 354,011, a 3.9% increase over the 2002 reported volume and an approximately 700% increase since 1984. Based on these case numbers, approximately 991,000 persons were tested in 2003. 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 1988-2003.

Year	No. of Cases	Year	No. of Cases
1988	77000	1996	172316
1989	85231	1997	237981
1990	120436	1998	247317
1991	143459	1999	280510
1992	161000	2000	300626
1993	189904	2001	310490
1994	193000	2002	340798
1995	149100	2003	354011

Figure 1. Graph of the Case Volume for 1988-2003.



The totals include data from parentage laboratories worldwide. A total of 44 laboratories responded to the survey, six more than last year.

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 entity may own several laboratories. The size distribution remains about the same as the distribution seen in the last several years.

Table 2. Laboratories by the Volume of Cases Reported.

Case Volumes	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003
1-500	40	26	25	20	19	19	13	17	14	18
501-1,000	6	4	8	7	6	5	6	6	2	3
1,001-5,000	7	9	6	10	11	9	11	11	13	11
5,001-10,000	6	4	3	5	0	3	3	5	1	3
10,001-50,000	1	2	3	5	5	7	8	6	7	7
50,001 – 100,000	2	1	1	1	2	1	1	1	0	0
>100,000	0	0	0	0	0	0	0	0	1	1
Total Laboratories	62	46	46	48	43	44	42	46	38	43*

***one of the 44 participants did not respond to this request**

EXCLUSION RATE

For the laboratories tracking exclusions, there were 353,387 cases completed and 99,174 (28.06%) were reported as exclusions. One of the 44 responding laboratories did not track the number of exclusions. The average exclusion rate for the laboratories reporting exclusions is 27.40% with a standard deviation of 6.01. The median exclusion rate is 27.98% with a range of 11.94% to 41.18% (two laboratories reported completing three cases, with two exclusion cases (66.67%) but because of the small sample size, they were not included in these statistics). 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 verses public contracts) and the geographic source of the case (rural versus metropolitan areas).

MISCONCEPTIONS IN PARENTAGE TESTING

It is important to understand the significance of the exclusion rate, especially since the statistic has been misinterpreted in the past. For example, several organizations have used the exclusion rate to suggest improperly that 30% of men are misled into believing they are biological fathers of children. This suggestion is incorrect. The exclusion rate includes a number of factors. One is that the men are alleged to be fathers. This is important as a woman may allege several men as possible fathers

because she was sexually active with these individuals. These are not men who were misled into believing they were fathers and then later discovered they are not. The testing merely sorts out which man is the biological father so presumably that man can assume his parental role. Another factor is that sometimes men are accused and tested because a man who is not excluded is alleging that the mother had multiple sexual partners as part of his defense. Sometimes a man is required to be tested because of a legal presumption, that is, when the mother properly names the correct father but because she is (was) married to someone else, there is a legal presumption that the husband is the father. The husband is then tested to rebut the legal presumption, not because he was misled into believing he is the biological father of the child.

COMBINED PATERNITY INDEX

The laboratories surveyed were asked to indicate what combined paternity index (CPI) they considered acceptable for cases with a standard trio (mother, child, father), mother (or father) not tested 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 verses public contracts, or for different technologies). 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 26 out of 44 (59%) laboratories using this value, with a range of 100 to 10,000. For mother not tested cases the most common minimum CPI is 100 with 30 of 44 (68%) laboratories using this value, with a range of 100 to 10,000. A couple of laboratories indicated that for these cases they used "whatever was obtained." One laboratory qualified this by saying that the CPI was whatever was obtained after evaluating 18 loci. For the family study or reconstruction cases, the majority of laboratories (66%) 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. This additional testing may result in non-exclusion, exclusion, or inconclusive findings.

Another significant 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 a CPI of less than 100 is not an indicator of non-paternity, unless 0 (or much less than 1), 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. Also remember 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 (Father) 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

CPI	Type of Case		
	Trio	No Mother	Family Study (Reconstruction)
Whatever is obtained	2	2	23
100	26	30	9
101			1
150	2	2	1
200	2	3	1
400	1		
500	2	1	
1000	6	4	
1001	1	1	
10000	2	1	

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 93.26% of reported cases, while RFLP analysis was used in 2.48% of reported cases.

For the first time SNP technology was reported in paternity evaluation. SNP was used in 3.99% of reported cases, exceeding the use of RFLP methods. All other technologies were used in about 0.27% 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 for Class I HLA methods reported using serologic tables for calculating paternity indices.

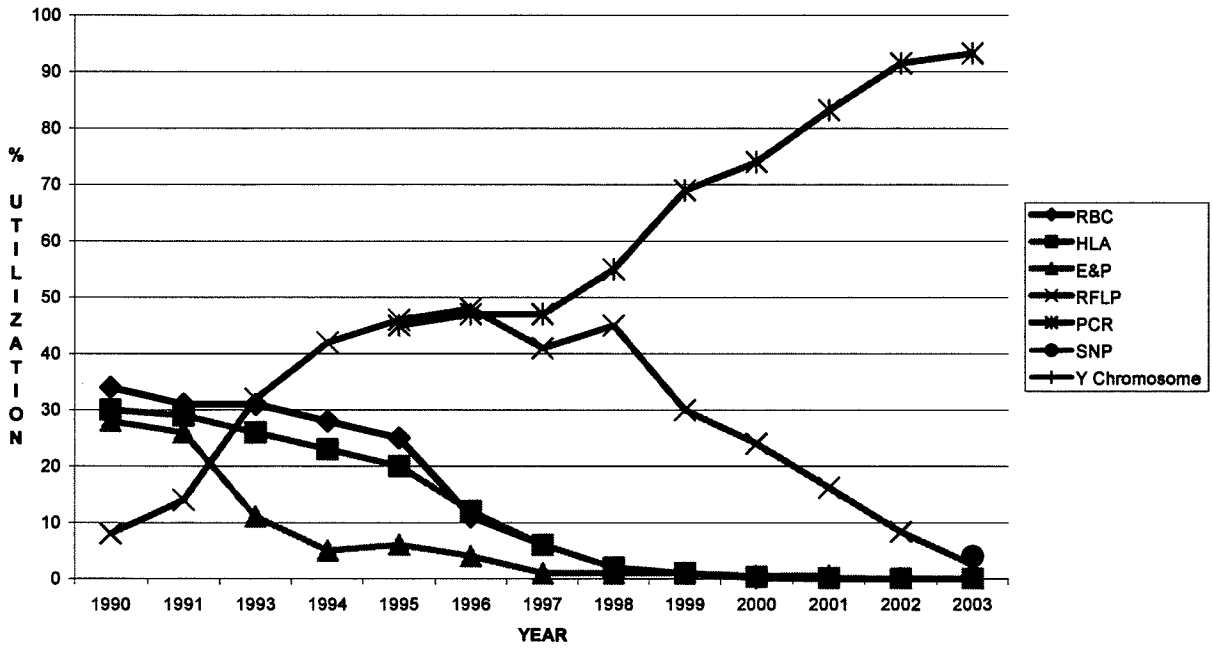
Table 4. The Technology Used in Cases Reported in 2003

Technology	Number of Cases	Utilization (%)
Red Cell Antigens	**3**	**0.00085**
HLA Serology	**3**	**0.00085**
HLA Class 1 Molecular	**95**	**0.02689**
HLA Class II Molecular	**777**	**0.21995**
Red Cell Enzymes/Serum Proteins	**0**	**0**
Allotyping	**0**	**0**
RFLP	**8744**	**2.475**
STR	**329467**	**93.263**
SNP	**14111**	**3.994**
Y Chromosome	**65**	**0.018**
Total of All Technologies	**353265**	**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. Note the appearance of SNP technology for the first time. 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.



SAMPLE SOURCE

Laboratories reported approximately 889,926 samples used for the casework in 2003. Of these, buccal swabs account for 814,942 (91.57%). Whole blood samples accounted for 29,182 (3.28) samples, a reduction of about 61% over the use of whole blood in 2002. The use of blood spot cards increased from 3,461 samples to 44,543 (5.01%) samples, an increase over 2002 numbers. In 2002 blood spot cards only accounted for 0.38% of samples. The reason for this change appears to be that one laboratory changed from whole blood to blood spots as their sample of choice. Lastly, various tissues accounted for 1,259 (0.14%) of the samples submitted. About half of these tissues were amniotic fluid samples (42.65%) and Chorionic Villus Samples (CVS) (6.83%). Hair, paraffin blocks, bones, and other undefined tissues were also evaluated.

PROBABILITY OF EXCLUSION

So few laboratories use RFLP technology that probability of exclusion data and mutation/null allele data were not tracked. With the small number of laboratories using RFLP, statistically significant numbers could not be achieved. For those seeking information on RFLP, please review previous annual reports (available at www.AABB.org) or the appendices of *Guidance for Standards for Parentage Testing Laboratories* published by AABB.

Appendix 1 shows the average probability of exclusion for the various PCR loci reported. For the CODIS loci a sufficient sample size is available to make statistical analysis of the laboratory's probabilities of exclusion. This was done without regard to the database used. Table 5 shows the statistical analysis of the probabilities of exclusion provided for the CODIS loci. The range of probabilities of exclusion seen is partly 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 previous years.

Table 5. The Mean Probability of Exclusion, Standard Deviation, Mode, Median, Range and Number of Laboratories Reporting Results for the CODIS Loci in 2003.

Locus	Mean	StDev	Mode	Median	Range	Δ Range	# Labs
VWA	61.96	2.36	62.5	62.5	52.3 - 64.7	12.4	35
D7S820	59.50	2.83	58.2	59.0	51.3 - 63.7	12.4	35
TH	54.57	2.63	56.6	54.2	46.4 - 59.2	12.8	34
D18S51	73.13	2.96	73.1	74.1	64.7 - 78.0	13.3	33
D16S539	53.96	4.55	56.6	55.8	44.8 - 63.0	18.2	34
CSF1P0	50.43	3.64	49.6	49.6	38.1 - 57.0	18.9	34
D3S1358	58.5	4.22	63.0	58.0	48.3 - 67.5	19.2	33
D21S11	68.25	4.32	70.8	68.7	52.9 - 72.3	19.4	33
D5S818	46.18	3.81	44.0	45.5	34.0 - 56.1	22.1	34
FGA	72.81	3.98	76.6	72.4	60.7 - 83.6	22.9	33
TPOX	37.16	5.69	32.9	35.9	27.8 - 51.2	23.4	34
D8S1179	63.05	5.46	68.0	61.5	52.7 - 78.9	26.2	33
D13S317	52.86	6.62	48.7	52.3	44.2 - 71.5	27.3	35

In order to evaluate the effects of different frequency tables the probability of exclusion was calculated for the two loci at the extremes, D13S317 and VWA. The formula used was that of Garber and Morris (*R. A. Garber & J. W. Morris. General Equations for the Average Power of Exclusion for Genetic Systems of n Codominant Alleles in One-Parent and No-Parent Cases of Disputed Parentage. In R. H. Walker, ed., Inclusion Probabilities in Parentage Testing. AABB, pg. 277-280 (1983).*

$$\hat{A} = \sum_{i=1}^{n} P_i(1-P_i)^2 + \sum_{\substack{i,j \\ i<j}}^{n} (P_iP_j)^2(3P_i+3P_j-4)$$

Where Ā is the average probability of exclusion, in an n allele codominant system that has alleles a, b,..., i, j,....n and allele frequencies of P_a, P_b, ..., P_i, P_j,... P_n.

Table 6. The average probability of exclusion obtained using the formula above and published Caucasian data. FBI, ABI, and Promega were indicated as sources for frequencies used by the laboratories in Table 5. NIST is provided as another published frequency table, but was apparently not used by any laboratories.

	LOCUS							
	D13S317				VWA			
Frequency Table	FBI[1]	ABI[2]	PROMEGA[2]	NIST[3]	FBI[1]	ABI[2]	PROMEGA[2]	NIST[3]
# Alleles	392	400	420	604	392	400	426	604
Ā (%)	56.8	59.5	57.6	59.2	62.5	61.7	62.8	62.2
X ± SD	58.28±1.29				62.3±0.469			

[1] Budowle, et al, J Forensic Sci 1999;44(6).
[2] Provided by company as part of their kit
[3] Butler, et al, J Forensic Sci 2003;48(4).

The probabilities of exclusions obtained by the reporting laboratories for each frequency source is shown in Table 7. In looking at D13S539 the reason for the large range that appears in Table 5 may be the frequency table used by laboratories using frequency provided by Promega. In Table 6 available data was analyzed and the Promega frequencies for the available data were comparable to the other frequency tables. Promega may have more than one frequency table available, which may explain the difference between Table 6 and 7 Promega data. NIST used PowerPlex 16 to obtain the frequencies shown in Table 6, and NIST's average probability of exclusion is comparable to the probability of exclusion obtained with other data sources. Laboratories using Promega frequency tables should review the power of exclusion they are using.

Table 7. The average probabilities of exclusion separated by the source of the frequencies used by the participating laboratories.

Allele Frequency Source	Locus	# Labs	Mean (%)	SD	Range	**Δ Range**
FBI	D13S317	10	54.2	5.3	47.0 - 60.0	13
ABI	D13S317	12	52.9	4.3	48.7 - 59.5	10.8
PROMEGA	D13S317	4	44.6	0.4	44.3 - 45.2	0.9
IN HOUSE	D13S317	6	55.1	7.5	44.2 - 64.0	19.8
FBI	VWA	10	62.4	1.1	61.7-64.5	2.8
ABI	VWA	12	61.7	1.9	56.1-62.8	6.7
PROMEGA	VWA	4	64.3	0.3	64.0-64.7	0.7
IN HOUSE	VWA	6	61.5	1.8	58.7-64.0	5.3

MISCONCEPTIONS IN TESTING

Last year's AABB report dealt with the issue of how to determine the power of a test. As indicated in that report it is the probability of exclusion not the number of systems or type of technology used that determines the power of a test. Ultimately the answer is - was a satisfactory combined paternity index (or probability of paternity) achieved? With the changing technologies laymen become confused as to the meaning of their test results. If one had a combined paternity index (CPI) of 1,000 (99.9%) with red cell antigens and HLA does it mean something different than a CPI of 1,000 (99.9%) with RFLP DNA methods or a CPI of 1,000 (99.9%) with PCR DNA methods? The answer is that a CPI of 1,000 (99.9%) means the same thing regardless of technology. The misconception that they mean something different has even spilled over into state contracts for paternity testing. In one state, the contract specified that cases tested with RFLP methods needed a CPI of 1,000 (99.9%) while those tested with PCR methods needed a CPI of 10,000 (99.99%). Contract managers should be cautious of claims that the CPI means something different with differing technologies.

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. Seventeen laboratories stated they had reported cases with double or triple mutations. Eighteen laboratories did not observe any mutations. The laboratories reported 67 cases with double mutations (0.019% of all reported cases) and four cases with triple mutations (0.001% of all reported cases) as inclusions. These findings were

similar to those observed in 2001 and 2002. 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 than RFLP technology as the repeat differences between the obligatory allele and the closest allele in the disputed parent can be evaluated as part of the evaluation 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 laboratories all appear to be using one of several calculation methods. Interestingly, several laboratories use different methods for different cases. The rational for using different methods in different cases is not known to the committee. Some laboratories are using the mutation rate as the PI (8% of laboratories), while others (61%) used the mutation rate divided by the average probability of exclusion. Some laboratories (5.9%) used the mutation rate as a transmission frequency and 17.6% of the laboratories used Brenner's method in looking at the repeat length difference between STR alleles.

During the 2004 annual meeting a presentation summarizing research among both European and American statisticians indicating general consensus that the future of mutation calculations is the method described by Fimmers, et.al. (*Fimmers, R., L. Henke, J. Henke & M.P. Baur. 1992. How to deal with mutations in DNA-testing, pp. 285-287 in Advances in Forensic Haemogenetics 4, edited by C. Rittner & P.M. Schneider. Springer-Verlag, Berlin).* The presentation at the 2004 Annual Meeting is, in part, based the data collected on specific mutation changes reported in last years AABB Annual Report Summary for 2002. The data collected for 2003 is reported in this year's report. Based on the observation of the statistician evaluating this issue and those laboratories present at the annual meeting, the committee will be asking contributing laboratories to present the specific mutation changes by ethnic group for the 2004 cases.

A summary of the mutation frequencies for each STR locus is provided in Appendix 2. In Appendix 3 a summary of the distance (repeat lengths) from the obligatory allele is provided. The frequencies for changes from one allele to another are presented in Appendix 6.

NULL ALLELES

Null allele data was similar to last year's report. As with last year's report the frequency of the null phenotype is separated from the mutation rate, as these frequencies do not represent the frequency of the null allele. Laboratories should be careful in evaluating case with potential null alleles. The use of alternative primers may resolve these cases. In next years report the laboratories will not be asked to provide null allele data in order to concentrate on the mutation calculation issue. Very little data was presented from laboratories using Promega primers, therefore the summary table contains last years data. ABI data is summarized in Appendix 4 and Appendix 5. For a further discussion see the Annual Report Summary for Testing in 2002. The raw data is presented in Appendix 7.

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 or X amelogenin allele have been observed. Laboratories were asked to measure the apparent X males observed in their laboratory. No laboratory using Promega primers reported X or Y male phenotypes, although in last year's report several laboratories reported seeing amelogenin mutations. Like other DNA loci, amelogenin is subject to mutations. Therefore, occasionally normal males have a female amelogenin phenotype or a Y phenotype. The X male phenotype was most commonly seen in the "oriental" populations, in about 1/628 men. The Y male phenotype was most commonly seen in the Black population in about 1/2221 Black males.

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

	Race/Ethnicity				
	Black	**White**	**Hispanic**	**American Indian**	**Oriental**
Number X Males Observed	**34**	**33**	**13**	**1**	**4**
%	**0.033**	**0.039**	**0.102**	**0.079**	**0.159**
Number Y Males Observed	**46**	**5**	**1**	**0**	**1**
%	**0.045**	**0.006**	**0.008**		**0.040**
Total Number of Males Tested	**102,176**	**84,925**	**12,752**	**1,270**	**2,512**

Appendix 1. The Probability of Exclusion for Various Loci Evaluated Using PCR in 2003 (Note: for some loci only a single laboratory reported results).

LOCUS	PE	LOCUS	PE
D3S1358	0.5850	D2S1338	0.7148
VWA	0.6196	D19S433	0.5560
FGA	0.7281	F13A01	0.5393
D5S818	0.4618	FESFPS	0.4321
D13S317	0.5286	F13B	0.4521
D7S820	0.5950	LPL	0.4821
D8S1179	0.6305	PENTA E	0.7406
D21S11	0.6825	PENTA D	0.6801
D18S51	0.7313	D1S80	0.6400
TH	0.5457	D17S5	0.7000
TPOX	0.3716	HPRTB	0.4972
CSF1P0	0.5043	D12S1090	0.8610
D16S539	0.5396	D3S1744	0.6950
D18S849	0.4570		

Appendix 2. Summary of Apparent Mutations at various Loci analyzed by PCR. The Number Observed Refers to the Inconsistencies Reported.

	PATERNAL			MATERNAL			Number of Either Mat. Or Pat.
Locus	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	157	152310	0.00103	15	72830	0.00021	90
D2S548*	0	1240	<0.00081	1	1212	0.00083	NR
D3S1358	713	558836	0.00128	60	405452	0.00015	379
D3S1744*	84	20290	0.00414	16	10141	0.00158	NR
D3S2386*	1	1240	0.00081	0	1212	<0.00083	NR
D5S818	763	655603	0.00116	111	451736	0.00025	385
D7S820	745	644743	0.00116	59	440562	0.00013	285
D8S306*	3	1240	0.00242	1	1212	0.00083	NR
D8S1179	779	489968	0.00159	96	409869	0.00023	364
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	881	621146	0.00142	192	482136	0.00040	485
D14S297*	0	1240	<0.00081	0	1212	<0.00083	NR
D16S539	540	494465	0.00109	129	467774	0.00028	372
D17S5*	7	6568	0.00107	0	228	<0.00439	NR
D17S1185*	0	1240	<0.00081	0	1212	<0.00083	NR
D18S51	1094	494098	0.00221	186	296244	0.00063	466
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	78	103489	0.00075	38	70001	0.00054	71
D21S11	772	526708	0.00147	464	435388	0.00107	580
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	2210	692776	0.00319	205	408230	0.00050	710
CSF1PO	982	643118	0.00153	95	304307	0.00031	410
FESFPS*	79	149028	0.00053	3	18918	0.00016	NR
F13A01	39	69178	0.00056	1	10474	0.00010	5
F13B*	8	27183	0.00029	2	13157	0.00015	1
LPL*	9	16943	0.00053	0	8821	<0.00011	4
THO1	41	452382	0.00009	31	327172	0.00009	28
TPOX	54	457420	0.00012	18	400061	0.00004	28
Penta D	21	22501	0.00093	12	18701	0.00064	24
Penta E	75	55719	0.00135	29	44311	0.00065	59
vWA	1482	873547	0.00170	184	564398	0.00033	814

*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 3. The distance (repeat lengths) from the obligatory allele.

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	0.583	0.333	0.000	0.083	0.000	12	0.432	0.543	0.012	0.012	0.000	81
D3S1744	0.000	0.000	0.000	0.000	0.000	0	0.000	0.000	0.000	0.000	0.000	0
D3S1358	0.474	0.526	0.000	0.000	0.000	19	0.521	0.465	0.009	0.005	0.000	213
D5S818	0.632	0.368	0.000	0.000	0.000	19	0.575	0.409	0.000	0.016	0.000	186
D7S820	0.200	0.800	0.000	0.000	0.000	10	0.512	0.482	0.006	0.000	0.000	166
D8S1179	0.297	0.676	0.000	0.000	0.027	37	0.516	0.465	0.013	0.000	0.006	314
D12S1090	0.000	0.000	0.000	0.000	0.000	0	0.000	0.000	0.000	0.000	0.000	0
D13S317	0.646	0.292	0.021	0.042	0.000	48	0.457	0.530	0.000	0.009	0.000	233
D16S539	0.233	0.744	0.000	0.000	0.023	43	0.493	0.493	0.007	0.007	0.000	150
D18S51	0.702	0.223	0.011	0.032	0.032	94	0.571	0.408	0.002	0.009	0.009	422
D18S849	0.000	0.000	0.000	0.000	0.000	0	0.000	0.000	0.000	0.000	0.000	0
D19S433	0.313	0.687	0.000	0.000	0.000	16	0.451	0.549	0.000	0.000	0.000	51
D21S11	0.167	0.782	0.006	0.013	0.032	156	0.696	0.266	0.010	0.003	0.024	286
CSF1PO	0.417	0.417	0.000	0.125	0.042	24	0.495	0.495	0.005	0.005	0.000	190
FGA	0.397	0.586	0.000	0.017	0.000	58	0.554	0.410	0.002	0.018	0.017	663
F13A	0.000	0.000	0.000	0.000	0.000	0	0.333	0.667	0.000	0.000	0.000	3
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	0.000	0.000	0.000	0.000	0.000	0
LPL	0.000	0.000	0.000	0.000	0.000	0	0.000	0.000	0.000	0.000	0.000	0
PENTA D	0.000	0.000	0.000	0.000	0.000	0	0.400	0.200	0.400	0.000	0.000	5
PENTA E	0.375	0.625	0.000	0.000	0.000	8	0.400	0.400	0.000	0.100	0.100	10
THO1	0.167	0.667	0.000	0.000	0.167	6	0.545	0.364	0.000	0.000	0.091	11
TPOX	0.000	1.000	0.000	0.000	0.000	2	0.364	0.545	0.000	0.091	0.000	11
VWA	0.787	0.191	0.000	0.000	0.021	47	0.414	0.571	0.002	0.011	0.002	471
TOTALS	**0.422**	**0.531**	**0.005**	**0.020**	**0.022**	**599**	**0.524**	**0.453**	**0.005**	**0.010**	**0.008**	**3466**

Appendix 4. The Number and Frequency of Maternal and Paternal Cases that Have an Apparent "Null Allele" Phenotype Pattern using ABI primers. Note that these frequencies are Not the Same as the Frequency of the Null Allele, which Cannot be Directly Ascertain 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	1	0.000025	7	0.000153	3	0.000053	8	0.000137			Hisp 2	0.00012
D5S818	4	0.00009	14	0.00025	3	0.000066	2	0.000047	Hisp. 3	0.000066	Hisp. 2	0.000047
D7S820	1	0.000026	3	0.000091	4	0.00010	10	0.000329				
D8S1179	10	0.00019	20	0.00038	4	0.000061	13	0.00015	Hisp. 3 Asian 4 Pac I 8	Hispanic 0.00015 Asian 0.012 Pac I 0.0394	Hisp. 4 Asian 2 Pac I 18	Hispanic 0.00025 Asian 0.0013 Pac I 0.0634
D13S317	7	0.00018	14	0.00032	5	0.00011	6	0.00020	Hisp 2	Hispanic 0.00013	Hisp 3	Hispanic 0.00015
D18S51	6	0.00012	9	0.00015	2	0.00027	7	0.000165	Hisp 6	Hispanic 0.00047	Hisp 11	Hispanic 0.00056
D21S11	12	0.000235	11	0.00016	7	0.000151	13	0.000171				
THO1	11	0.00025	7	0.00015	2	0.000052	1	0.000038	Hisp 1	Hispanic 0.000075	Hisp 5	Hispanic 0.00042
VWA	4	0.00007	10	0.00018	5	0.00008	12	0.00018	Hisp 3	Hispanic 0.00015	Hisp 6	Hispanic 0.00031
FGA	28	0.000564	31	0.00048	6	0.00016	12	0.00016	Hisp. 1	0.00021	Hisp. 2	0.00015
D2S1338			3	0.00015	1	0.000086	2	0.000076				

Pac I = Pacific Island

Locus	BLACK				CAUCASIAN				OTHER RACE			
	# Mat	Freq. Mat.	# Pat.	Freq. Pat	# Mat	Freq. Mat.	# Pat.	Freq. Pat	# Mat	Freq. Mat.	# Pat.	Freq. Pat
TPOX			2	0.000057			1	0.00024			Hisp 2	0.00013
D5S818	4	0.00009	14	0.00025	3	0.000066	2	0.000047	Hisp. 3	0.000066	Hisp. 2	0.000047
CSF1PO	2	0.000053	5	0.00012	2	0.000053	12	0.00028			Hisp 2	0.00018
D16S539	1	0.000026	6	0.00010	6	0.00013	4	0.000073	Hisp 2	0.00039	Hisp 2	0.00017
D19S433	3	0.00021	4	0.00021	1	0.000087	2	0.000085			Hisp 3	0.00082

Appendix 5. This appendix provides a summary of the potential null alleles based on the data supplied. The sample for the 2003 Promega mutation data was insufficient to draw a conclusion so the 2002 data is presented. Note that the use of the term YES means the data is consistent with the presence of a null allele. See the Annual Report Summary for Testing in 2002 for a complete discussion of the method used to make a determination.

LOCUS	PRIMER SOURCE	
	ABI (2003)	PROMEGA (2002)
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	?

Appendix 6. Apparent mutation changes from on allele to another.

Maternal and Paternal D3S1358 Mutations Observed in 2003					
Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
20	19	2	0.94%		
19	20	5	2.35%		
19	18	13	6.10%	4	21.05%
18	19	29	13.62%	3	15.79%
18	17	26	12.21%	3	15.79%
17	18	33	15.49%		0.00%
17	16	21	9.86%	2	10.53%
17	15	1	0.47%		
16	18	1	0.47%		
16	17	27	12.68%	4	21.05%
16	15	24	11.27%	1	5.26%
15	16	13	6.10%		

15	14	13	6.10%		
14	15	3	1.41%	2	10.53%
13	15	1	0.47%		
13	14	1	0.47%		
		213	100.00%	19	100.00%

Maternal and Paternal D5S818 Mutations Observed in 2003					
Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
16	15	2	1.08%		
15	16	1	0.54%		
15	14	3	1.61%		
14	15	6	3.23%	1	5.26%
14	13	26	13.98%	3	15.79%
13	14	40	21.51%	5	26.32%
13	12	28	15.05%	3	15.79%
12	13	40	21.51%	2	10.53%
12	11	11	5.91%	1	5.26%
12	10	1	0.54%		
11	12	14	7.53%	2	10.53%
11	10	5	2.69%		
11	9	1	0.54%		
10	11	3	1.61%	2	10.53%
10	9	1	0.54%		
9	10	3	1.61%		
9	7	1	0.54%		
		186	100.00%	19	100.00%

Maternal and Paternal D7S820 Mutations Observed in 2003					
Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
15	14	2	1.20%		
14	15				
14	13	16	9.64%	2	22.22%
13.1	12.1			1	11.11%
13	14	8	4.82%		
13	12	24	14.46%	2	22.22%
12	13	26	15.66%		
12	11	21	12.65%	2	22.22%
11	12	19	11.45%		
11	10	5	3.01%	1	11.11%
10	11	22	13.25%		
10	9	9	5.42%		
9	10	5	3.01%		
9	8	3	1.81%		
8	10	1	0.60%		
8	9	5	3.01%	1	11.11%
		166	100.00%	9	100.00%

Maternal and Paternal D8S1179 Mutations Observed in 2003					
Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
18	17	1	0.32%	3	8.11%
17	18	1	0.32%		
17	16	15	4.78%	4	10.81%
16	17	12	3.82%		
16	15	38	12.10%	2	5.41%
15	16	40	12.74%	2	5.41%
15	14	32	10.19%	5	13.51%
14	15	47	14.97%	4	10.81%
14	14.2			1	2.70%
14	13	32	10.19%	4	10.81%
14	10	1	0.32%		
13	15	3	0.96%		
13	14	27	8.60%	1	2.70%
13	12	19	6.05%	5	13.51%
12	13	11	3.50%	2	5.41%
12	11	8	2.55%	2	5.41%
11	13	1	0.32%		
11	12	13	4.14%	1	2.70%
11	10	1	0.32%		
10	11	7	2.23%	1	2.70%
9	13	1	0.32%		
9	10	3	0.96%		
8	9	1	0.32%		
		314	100.00%	37	100.00%

Maternal and Paternal D13S317 Mutations Observed in 2003					
Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
16	15	1	0.43%		
15	16	1	0.43%	1	2.04%
15	14	14	6.01%	4	8.16%
15	13	1	0.43%		
14	15	14	6.01%	8	16.33%
14	13	40	17.17%		
13	14	21	9.01%	6	12.24%
13	12	34	14.59%	5	10.20%
13	11	1	0.43%	2	4.08%
12	13	48	20.60%	11	22.45%
12	11	26	11.16%	1	2.04%
11	13			1	2.04%
11	12	15	6.44%	3	6.12%
11	10	8	3.43%	3	6.12%
10	11	2	0.86%		
10	9	1	0.43%		
9	10	6	2.58%		
9	8			1	2.04%
8	9			3	6.12%
		233	100.00%	49	100.00%

Maternal and Paternal D16S539 Mutations Observed in 2003					
Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
16	15			1	2.33%
15	16				
15	14	3	2.00%	1	2.33%
14	15	2	1.33%	1	2.33%
14	13	23	15.33%	6	13.95%
13	14	31	20.67%	4	9.30%
13	12	31	20.67%	13	30.23%
12	13	19	12.67%	2	4.65%
12	11	13	8.67%	9	20.93%
12	9			1	2.33%
11	13	1	0.67%		
11	12	13	8.67%	2	4.65%
11	10	2	1.33%	1	2.33%
11	9	1	0.67%		
10	11	7	4.67%	1	2.33%
10	9	2	1.33%	1	2.33%
9	10	2	1.33%		
		150	100.00%	43	100.00%

Maternal and Paternal TPOX Mutations Observed in 2003					
Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
12	13	1	9.09%		
12	11	4	36.36%	2	100.00%
11	12	1	9.09%		
11	10	2	18.18%		
10	11				
10	9				
10	8	1	9.09%		
9	10	1	9.09%		
9	8				
8	9	1	9.09%		
8	7				
		11	100.00%	2	100.00%

Maternal and Paternal TH01 Mutations Observed in 2003					
Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
12	13	1	9.09%		
10	9	1	9.09%	1	16.67%
9.3	10			1	16.67%
9	10	2	18.18%		
9	8	1	9.09%	1	16.67%
8	9	3	27.27%		
8	7	1	9.09%	2	33.33%
7	8			1	16.67%
7	6	1	9.09%		
6	9	1	9.09%		
6	7				
		11	100.00%	6	100.00%

Maternal and Paternal F13A01 Mutations Observed in 2003					
Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
7	6	1	33.33%		
6	5	1	33.33%		
5	6	1	33.33%		
		3	100.00%		

Maternal and Paternal CSF1P0 Mutations Observed in 2003					
Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
15	14	10	5.26%		
14	15	3	1.58%	1	4.17%
14	13	17	8.95%		
13	15	1	0.53%		
13	14	16	8.42%	2	8.33%
13	12	33	17.37%	4	16.67%
12	13	43	22.63%	4	16.67%
12	11	19	10.00%	1	4.17%
12	10	1	0.53%	2	8.33%
11	12	23	12.11%	2	8.33%
11	10	12	6.32%	4	16.67%
11	9			1	4.17%
10	11	7	3.68%		
10	9	3	1.58%	1	4.17%
10	7			1	4.17%
9	10	1	0.53%	1	4.17%
8	9	1	0.53%		
		190	100.00%	24	100.00%

Maternal and Paternal D18S51 Mutations Observed in 2003					
Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
26	25	1	0.24%		
25	24	5	1.18%		
25	23	2	0.47%		
24	25				
24	23	3	0.71%		
23	24	4	0.95%	2	2.13%
23	22	9	2.13%	1	1.06%
22	23	5	1.18%	1	1.06%
22	21	10	2.37%	3	3.19%
22	20	1	0.24%		
21	22	18	4.27%	4	4.26%
21	20	20	4.74%	2	2.13%
21	19			1	1.06%
20	23			1	1.06%
20	21	21	4.98%	8	8.51%
20	19	28	6.64%		
19	20	31	7.35%	13	13.83%
19	18	17	4.03%	3	3.19%
19	17			1	1.06%
18	19	40	9.48%	5	5.32%
18	17	16	3.79%	5	5.32%
18	15	1	0.24%		
17	18	36	8.53%	5	5.32%
17	16	21	4.98%		
16	17	31	7.35%	9	9.57%
16	15	17	4.03%	3	3.19%
16	14	1	0.24%		
16	13	1	0.24%		
15	16	27	6.40%	5	5.32%
15	14	9	2.13%	3	3.19%
14	16			2	2.13%
14	15	14	3.32%	5	5.32%
14	13	5	1.18%		
13.2	14.2	2	0.47%		
13.2	13	1	0.24%		
13	18			1	1.06%
13	15	1	0.24%		
13	14	5	1.18%	2	2.13%
13	12	6	1.42%	1	1.06%
12	13	6	1.42%	6	6.38%
12	11	4	0.95%		
12	19			1	1.06%
11	12	1	0.24%		
11	10	1	0.24%		
10	13	1	0.24%		
10	11			1	1.06%
		422	100.00%	94	100.00%

Maternal and Paternal D21S11 Mutations Observed in 2003					
Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
38	37	1	0.35%		
37	38	2	0.70%		
37	36	1	0.35%		
36	37	2	0.70%		
36	35			1	0.64%
35	36	3	1.05%		
35	34				
34.2	33.2			11	7.01%
34	35	5	1.75%		
34	33	1	0.35%		
33.2	34.2	12	4.20%		
33.2	32.2	6	2.10%	21	13.38%
33.2	29.2			1	0.64%
33	34	1	0.35%		
33	32	3	1.05%	3	1.91%
32.2	34.2	1	0.35%		
32.2	33.2	18	6.29%	4	2.55%
32.2	33	3	1.05%		
32.2	31.2	6	2.10%	6	3.82%
32.2	31	1	0.35%		
32	33	12	4.20%	3	1.91%
32	31	5	1.75%	14	8.92%
31.2	32.2	9	3.15%		
31.2	32	1	0.35%		
31.2	30.2	3	1.05%	4	2.55%
31.2	30			1	0.64%
31	32	24	8.39%	2	1.27%
31	30	15	5.24%	33	21.02%
31	29			1	0.64%
30.2	31.2	1	0.35%	2	1.27%
30.2	29	1	0.35%		
30	33.2			1	0.64%
30	31.2			1	0.64%
30	31	44	15.38%	3	1.91%
30	30.2			1	0.64%
30	29	18	6.29%	16	10.19%
30	27	1	0.35%		
29	31	1	0.35%		
29	30	36	12.59%	7	4.46%
29	28	13	4.55%	13	8.28%
29	27	1	0.35%	1	0.64%
28	30	1	0.35%	1	0.64%
28	29	24	8.39%	5	3.18%
28	27	4	1.40%	1	0.64%
27	28	6	2.10%		
		286	100.00%	157	100.00%

Maternal and Paternal FGA Mutations Observed in 2003					
Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
51	52	1	0.15%		
50	51	1	0.15%		
46.2	45.2	1	0.15%		
46	46.2	1	0.15%		
45.2	46.2	1	0.15%		
43.2	44.2	1	0.15%		
33.2	32.2	1	0.15%		
30.2	31.2	1	0.15%		
29	30	1	0.15%		
28	29	9	1.36%	2	3.45%
28	27	7	1.06%		
27	28	11	1.66%	1	1.72%
27	26	24	3.62%	1	1.72%
27	25	3	0.45%		
26	27	23	3.47%	1	1.72%
26	25	50	7.54%	4	6.90%
26	24	1	0.15%		
25.2	24	1	0.15%		
25	26	52	7.84%	1	1.72%
25	24	67	10.11%	8	13.79%
25	19	1	0.15%		
24	25	88	13.27%	2	3.45%
24	23	41	6.18%	4	6.90%
24	22	1	0.15%		
24	21	2	0.30%		
23	24	64	9.65%	4	6.90%
23	22	31	4.68%	5	8.62%
23	21	1	0.15%		
23	20	1	0.15%		
23	19	1	0.15%		
22.2	23.2	4	0.60%		
22.2	23	1	0.15%		
22	23	40	6.03%	4	6.90%
22	21	27	4.07%	7	12.07%
22	20	1	0.15%		
22	19	1	0.15%		
21.1	22.2	2	0.30%		
21	24	1	0.15%		
21	22	39	5.88%	4	6.90%
21	20	10	1.51%	4	6.90%
21	19	5	0.75%		
20.2	19.2	1	0.15%		
20	23	1	0.15%		
20	22	1	0.15%		
20	21	17	2.56%	3	5.17%
20	19	5	0.75%		
20	18			1	1.72%

19	20	9	1.36%	1	1.72%
19	18	6	0.90%	1	1.72%
18.2	17.2	1	0.15%		
18	19	3	0.45%		
		663	100.00%	58	100.00%

Maternal and Paternal vWA Mutations Observed in 2003					
Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
23	22	1	0.21%		
22	21	7	1.49%		
21	22	2	0.42%	1	2.13%
21	20	17	3.61%	1	2.13%
20	21	12	2.55%	4	8.51%
20	19	33	7.01%		
19	20	19	4.03%	4	8.51%
19	18	67	14.23%	1	2.13%
19	17	1	0.21%		
18	19	56	11.89%	8	17.02%
18	17	69	14.65%	4	8.51%
18	16	2	0.42%		
17	18	48	10.19%	8	17.02%
17	16	53	11.25%	1	2.13%
17	15	1	0.21%		
16	19	1	0.21%		
16	18	1	0.21%		
16	17	29	6.16%	7	14.89%
16	15	18	3.82%	2	4.26%
16	14	1	0.21%		
15	16	24	5.10%	3	6.38%
15	14	3	0.64%		
14	17			1	2.13%
14	15	4	0.85%	1	2.13%
14	13	1	0.21%		
13	14	1	0.21%		
12	13			1	2.13%
		471	100.00%	47	100.00%

Maternal and Paternal D19S433 Mutations Observed in 2003					
Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
17.2	16.2	2	3.92%		
17	18	1	1.96%		
17	16	2	3.92%	1	6.25%
16.2	17.2	1	1.96%		
16.2	15.2	2	3.92%		
16	17	2	3.92%		
16	15	1	1.96%	1	6.25%
15.2	16.2	2	3.92%	1	6.25%
15.2	14.2	2	3.92%		
15	16	7	13.73%		
15	14	1	1.96%	3	18.75%
14.2	13.2	3	5.88%	2	12.50%
14	15	4	7.84%	2	12.50%
14	13	11	21.57%	4	25.00%
13.2	14.2	2	3.92%		
13.2	12.2	1	1.96%		
13	14	4	7.84%		
13	12	2	3.92%		
12	13			1	6.25%
11	12	1	1.96%		
9	10			1	6.25%
		51	100.00%	16	100.00%

Maternal and Paternal Penta D Mutations Observed in 2003					
Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
13	14				
12	13				
12	11	1	20.00%		
11	13	1	20.00%		
11	10				
10	11				
9	11	1	20.00%		
9	10	2	40.00%		
		5	100.00%		

Maternal and Paternal D2S1338 Mutations Observed in 2003					
Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
27	26	6	7.41%		
26	27	1	1.23%		
26	25	11	13.58%	2	16.67%
25	26	5	6.17%	3	25.00%
25	24	8	9.88%		
25	23	1	1.23%	1	8.33%
24	25	2	2.47%	1	8.33%
24	23	2	2.47%		
23	24	7	8.64%	1	8.33%
23	22	3	3.70%		
22	23	3	3.70%		
22	21	5	6.17%		
21	22	1	1.23%		
21	20	1	1.23%	2	16.67%
20	21	5	6.17%	1	8.33%
20	19	3	3.70%		
19	20	2	2.47%		
19	18	1	1.23%		
18	20	1	1.23%		
18	19	5	6.17%		
18	17	3	3.70%		
17	18	3	3.70%		
17	16	1	1.23%		
16	17			1	8.33%
16	15				
15	16	1	1.23%		
		81	100.00%	12	100.00%

Maternal and Paternal Penta E Mutations Observed in 2003					
Apparent Change		Paternal		Maternal	
From	To	Observed	% Total	Observed	%Total
23	22	1	10.00%		
20	21	1	10.00%		
19	20	1	10.00%		
19	18				
18	19	1	10.00%	1	12.50%
18	17			1	12.50%
17	18				
17	16	1	10.00%		
17	15	1	10.00%		
16	17			1	12.50%
16	15	2	20.00%	2	25.00%
15	16				
15	14				
14	13			1	12.50%
13	14				
13	12				
12	13	1	10.00%		
12	11				
11	12			1	12.50%
11	10				
10	9				
9	10				
7	6			1	12.50%
5	8	1	10.00%		
		10	100.00%	8	100.00%

Appendix 7. Apparent Null Alleles for the Loci Submitted for the 2003 Annual Report.

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D3S1358		17	18	1	American Indian	864
D3S1358	15, 16	15	14	1	Black	33405
D3S1358	16	15	15, 16	1	Black	39496
D3S1358	15, 16	15	16	1	Black	33405
D3S1358		**16**	**15**	2	Black	?
D3S1358		**16**	**15**	1	Black	12,323

D3S1358		16	15	1	Black	33405
D3S1358	15, 16	16	15	1	Black	33405
D3S1358	15, 16	16	17	1	Black	33405
D3S1358	15, 17	17	16	1	Black	33405
D3S1358		**15**	**14**	1	Caucasian	12,292
D3S1358	**15**	**16**		1	Caucasian	12,193
D3S1358	16, 18	16	15	1	Caucasian	26555
D3S1358	15	16	16, 17	1	Caucasian	39074
D3S1358		**16**	**17**	1	Caucasian	12,292
D3S1358	**15, 17**	**17**	**16**	1	Caucasian	4,278
D3S1358	17	17	16	1	Caucasian	26555
D3S1358	**16**	**17**	**15, 17**	1	Caucasian	5,824
D3S1358	16, 18	18	17	1	Caucasian	26555
D3S1358	**17, 18**	**18**	**17**	1	Caucasian	15,314
D3S1358		**19**	**14**	1	Caucasian	15,314
D3S1358	**14, 15**	**14**	**15**	1	Hispanic	4,539
D3S1358	16, 18	16	15	1	Hispanic	12200

PCR LOCUS	Phenotypes of The Observed Alleles			**PROMEGA**	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D3S1358						

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**	**10**	**12**	1	Asian	2,106
D5S818	**11, 12**	**12**	**11**	1	Asian Indian	265
D5S818		**12**	**11**	1	Black	**868**

D5S818	10, 13	10	12	1	Black	33235
D5S818	**10, 12**	**10**	**13**	1	Black	18,607
D5S818	**10, 12**	**12**	**18**	1	Black	1379
D5S818	**11**	**11**	**12**	1	Black	2,611
D5S818	11	11	13	1	Black	33235
D5S818	**11**	**12**	**10, 12**	1	Black	2,545
D5S818	11	13	12, 13	1	Black	39262
D5S818	11, 12	11	12	1	Black	33235
D5S818	11, 12	12	13	1	Black	33235
D5S818	11, 13	13	11	1	Black	33235
D5S818	**11, 12**	**12**	**13**	1	Black	1379
D5S818	12	12	13	2	Black	33235
D5S818	12	12	11	1	Black	33235
D5S818	12, 13	12	13	1	Black	33235
D5S818	**13**	**10**	**10**	1	Black	2,733
D5S818	13	12	10, 12	1	Black	39262
D5S818	9, 13	13	12	1	Black	33235
D5S818		**12**	**11**	2	Caucasian	16,415
D5S818	11	13	11, 13	1	Caucasian	38827
D5S818	11, 12	11	13	1	Caucasian	26402
D5S818	**12**	**`10**	**10, 12**	1	Caucasian	651
D5S818	**13**	**11**	**11, 13**	1	Caucasian	5,826
D5S818	11	11	12	1	Hispanic	11838
D5S818	**11**	**12**	**11, 12**	1	Hispanic	4,607
D5S818	11	13	13	1	Hispanic	13307
D5S818	**9, 11**	**11**	**13**	1	Other	1,007

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	Black	?
D5S818		**11**	**12**	1	Caucasian	1,208
D5S818						

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D7S820	11	11	12	1	American Indian	866
D7S820	10	10	9	1	Black	32830
D7S820	11	11	10	1	Black	32830
D7S820	10,11	11	10	1	Black	32830
D7S820	12	11		1	Black	38756
D7S820	**8**	**8**	9	1	Caucasian	4,263
D7S820	9, 10	9	7	1	Caucasian	4,263
D7S820		11	12	1	Caucasian	4,263
D7S820		7	11	1	Caucasian	26124
D7S820	13	9	9, 12	1	Caucasian	38415
D7S820	9	9	10	1	Caucasian	26124
D7S820	9, 11	9	10	1	Caucasian	26124
D7S820	11	11	12	1	Caucasian	26124
D7S820	11	11	10	1	Caucasian	26124
D7S820	10, 11	11	10	1	Caucasian	26124
D7S820	12	12	9	1	Caucasian	26124
D7S820	**8**	10	10, 12	1	Caucasian	38415
D7S820	7	10	8, 10	1	Caucasian	38415
D7S820	**8**	11	11	1	Caucasian	38415
D7S820	11, 12	12	11	1	Hispanic	12535

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

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D8S1179	14	14	13	1	American Indian	848
D8S1179	13, 14	13	12	1	American Indian	404
D8S1179	13, 16	13	14	1	American Indian	404
D8S1179	13	8		1	Asian	331
D8S1179	13	10	10	1	Asian	331
D8S1179	15	10	10, 14	1	Asian	331
D8S1179	14	13	13, 15	1	Asian	331
D8S1179	11, 13	13	14	1	Asian	?
D8S1179	13, 14	13	17	1	Asian	462
D8S1179		16	13	1	Asian	1,024
D8S1179		9	14	1	Black	12,978
D8S1179	11	10	10, 11	1	Black	39321
D8S1179	11	10	10, 11	1	Black	39321
D8S1179		10	14	1	Black	12,978
D8S1179	12, 14	12	13	1	Black	1,347
D8S1179		12	14	1	Black	33247
D8S1179	13, 14	13	12	1	Black	2,474
D8S1179		13	14	1	Black	33247
D8S1179	13, 14	13	14	1	Black	33247

D8S1179	13, 15	13	14	1	Black	33247
D8S1179	13	14		1	Black	39321
D8S1179	15	14	12, 14	1	Black	39321
D8S1179	15	14	12, 14	1	Black	39321
D8S1179	14	14	13	1	Black	2,606
D8S1179	15	14	14	1	Black	39321
D8S1179	14, 15	14	15	1	Black	2,606
D8S1179	13, 14	14	15	1	Black	33247
D8S1179	13	15		1	Black	12,976
D8S1179	10	15	11, 15	1	Black	39321
D8S1179	14, 15	15	13	1	Black	33247
D8S1179		15	14	1	Black	?
D8S1179	12	15	14, 15	1	Black	39321
D8S1179	12, 15	15	14	1	Black	33247
D8S1179	13, 15	15	14	1	Black	33247
D8S1179	14, 15	15	14	1	Black	33247
D8S1179	15, 16	15	14	1	Black	33247
D8S1179	12, 15	15	16	1	Black	33247
D8S1179		16	14	1	Black	12,978
D8S1179		16	15	1	Black	12,978
D8S1179	13	17	13, 17	1	Black	39321
D8S1179	10, 15	10	12	1	Caucasian	38820
D8S1179	10, 13	10	14	1	Caucasian	26389
D8S1179	13	12	10, 12	1	Caucasian	38820
D8S1179	13	12	10, 12	1	Caucasian	38820
D8S1179		12	11	1	Caucasian	12,944
D8S1179	11	13	11, 13	1	Caucasian	38820
D8S1179	13, 14	13	12	1	Caucasian	26389

D8S1179	13, 14	13	12	1	Caucasian	26389
D8S1179	14	13	13, 14	1	Caucasian	26389
D8S1179	13	13	14	1	Caucasian	26389
D8S1179	10, 14	14	13	1	Caucasian	3,764
D8S1179	13, 14	14	13	1	Caucasian	26389
D8S1179	13, 14	14	13	1	Caucasian	26389
D8S1179	13, 14	14	13	1	Caucasian	26389
D8S1179	13, 14	14	15	1	Caucasian	26389
D8S1179	13, 15	15	14	1	Caucasian	4,268
D8S1179	14, 15	15	14	1	Caucasian	26389
D8S1179	13	10	10, 12	1	Hispanic	1,629
D8S1179	13	10	10, 16	1	Hispanic	4,605
D8S1179	10	13	13	1	Hispanic	13522
D8S1179	11, 13	13	14	1	Hispanic	12022
D8S1179	13, 14	14	12	1	Hispanic	12022
D8S1179	12, 14	14	13	1	Hispanic	4,148
D8S1179	10, 14	14	13	1	Hispanic	12022
D8S1179	15	15	14	1	Hispanic	4,148
D8S1179	14	10		1	PI	203
D8S1179	10, 11	10	13	1	PI	284
D8S1179	10, 16	10	14	1	PI	284
D8S1179	14	12		2	PI	203
D8S1179	12	12	13	1	PI	284
D8S1179	10	13	8, 13	1	PI	203
D8S1179	14	13	10, 13	1	PI	203
D8S1179	14	13	13	1	PI	203
D8S1179	16	13	13, 14	1	PI	203
D8S1179	12, 13	13	14	1	PI	284

D8S1179	12, 13	13	14	1	PI	284
D8S1179	13	13	14	1	PI	284
D8S1179	10, 13	13	14	1	PI	284
D8S1179	13	13	15	1	PI	284
D8S1179	12, 14	14	10	1	PI	284
D8S1179	13	14	11, 14	1	PI	203
D8S1179	13, 14	14	12	1	PI	284
D8S1179	14, 15	14	12	1	PI	284
D8S1179		14	13	1	PI	284
D8S1179	10, 14	14	13	1	PI	284
D8S1179	14	14	13	1	PI	284
D8S1179	14, 15	14	13	1	PI	284
D8S1179	13, 14	14	13	1	PI	284
D8S1179	13, 14	14	13	1	PI	284
D8S1179	16	14	14, 16	1	PI	203
D8S1179	15	15	10	1	PI	284

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D8S1179	8	13	14, 16	1	Caucasian	?
D8S1179	12	14	10, 14	1	Caucasian	?
D8S1179	13	14	13, 14	1	Caucasian	?
D8S1179	13	15	14, 15	1	Black	?
D8S1179						

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
FGA	22, 23	22	21	1	Asian	2,069
FGA	18.2 19.2	18.2	26	1	Black	17865
FGA	22	19		1	Black	12,171
FGA	26	19	19, 22	1	Black	37459
FGA		19	21	1	Black	31801
FGA	19, 22	19	21	1	Black	31801
FGA	23	20	20, 22	1	Black	37459
FGA	27	20	20, 21.2	1	Black	37459
FGA	20, 22	20	22	2	Black	31801
FGA		20	23	1	Black	31801
FGA	20, 21	20	24	1	Black	31801
FGA	20, 21	20	26	1	Black	31801
FGA	23	21		1	Black	37459
FGA	22	21	21, 25	1	Black	37459
FGA	22	21	21, 23	1	Black	37459
FGA	21, 22	21	23	1	Black	31801
FGA	23	22	21, 22	1	Black	37459
FGA	23	22	22, 24	1	Black	37459
FGA	22, 23	22	23	1	Black	2,474
FGA	21	22	23, 25	1	Black	37459
FGA	22, 24	22	23	1	Black	31801
FGA	22, 25	22	24	1	Black	31801
FGA	22, 26	22	24	1	Black	31801
FGA	22	23	20, 23	1	Black	37459
FGA	23	23	21	1	Black	31801
FGA	22	23	22, 23	1	Black	37459

FGA	22, 23	23	22	1	Black	31801
FGA	22	23	23, 25	1	Black	37459
FGA	22, 23	23	24	1	Black	31801
FGA	23, 24	23	24	1	Black	31801
FGA	23, 25	23	24	1	Black	31801
FGA		23	27	1	Black	?
FGA	20	24		1	Black	12,171
FGA	22	24		1	Black	12,171
FGA	23	24		1	Black	12,171
FGA	24, 26	24	18.2	1	Black	31801
FGA	22, 24	24	19	1	Black	31801
FGA		24	20	1	Black	11,998
FGA	24	24	21	1	Black	31801
FGA	21	24	23, 24	1	Black	37459
FGA	23	24	23, 24	1	Black	37459
FGA	22, 24	24	23	1	Black	31801
FGA	24, 25	24	23	1	Black	31801
FGA	22	24	24, 27	1	Black	37459
FGA	23	24	24, 27	1	Black	37459
FGA	24, 26	24	25	1	Black	31801
FGA	23	25		1	Black	37459
FGA	24	25		1	Black	37459
FGA		25	18.2	1	Black	11,998
FGA	23, 25	25	20	1	Black	31801
FGA	22.2	25	22, 25	1	Black	37459
FGA	23, 25	25	22	1	Black	31801
FGA	25	25	23	1	Black	31801
FGA	27	25	23, 25	1	Black	37459

FGA	18.2	25	24, 25	1	Black	37459
FGA	18.2	25.2	23, 25.2	1	Black	37459
FGA	22	26	22, 26	1	Black	37459
FGA	24, 26	26	23	1	Black	2,474
FGA	20, 26	26	23	1	Black	17865
FGA	22	28	22, 28	1	Black	37459
FGA		29	23	1	Black	31801
FGA	18, 22	18	24	1	Caucasian	13379
FGA	20, 22	20	24	1	Caucasian	25614
FGA		21	20	1	Caucasian	11,968
FGA	20	21	21	1	Caucasian	37542
FGA	22	21	21, 24	1	Caucasian	37542
FGA		22	23	1	Caucasian	16,131
FGA	22, 23	23	21	1	Caucasian	3,764
FGA		23	22	1	Caucasian	16,131
FGA		23	22	1	Caucasian	11,968
FGA		24	22	1	Caucasian	25614
FGA		24	23	1	Caucasian	4,266
FGA	24	24	23	1	Caucasian	25614
FGA	20	25		1	Caucasian	37542
FGA	20	25		1	Caucasian	37542
FGA	20	25	23, 25	1	Caucasian	37542
FGA	22, 25	25	24	1	Caucasian	4,266
FGA	20	26		1	Caucasian	37542
FGA	21, 26	26	21	1	Caucasian	4,266
FGA	21	21	23	1	Hispanic	4,141
FGA	20	21	20, 21	1	Hispanic	4,862
FGA		22	26	1	Hispanic	11440

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
FGA						

PCR LOCUS	Phenotypes of The Observed Alleles			**PROMEGA**	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
PENTA E	14	13	13, 15	1	Hispanic	?
PENTA E	11, 22	22	14	1	Hispanic	?
PENTA E						

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
THO1	9	8	7, 8	1	American Indian	490
THO1		7	9.3	1	Black	33312
THO1		8	7	1	Black	12,865
THO1		9.3	7	1	Black	12,865
THO1	6, 7	6	8	1	Black	33312
THO1	6, 9	6	7	1	Black	33312
THO1	6	7		1	Black	?
THO1	6, 9.3	9.3	7	1	Black	33312
THO1	7	6	6	1	Black	2,418
THO1	7	6	6, 9	1	Black	39369
THO1	7	8		1	Black	?
THO1	7	9	7, 9	1	Black	39369
THO1	7	9		2	Black	39369
THO1	7	9.3	8, 9.3	1	Black	39369
THO1	8	8	6	1	Black	33312
THO1	8	9	7, 8	1	Black	1379
THO1	8	9	8, 9	1	Black	39369
THO1	8	9	9	1	Black	39369
THO1	8	9.3	8, 9.3	2	Black	1379

THO1	9	8		1	Black	?
THO1	9	9.3	9, 9.3	1	Black	39369
THO1	9.3	9	9, 9.3	1	Black	2,418
THO1	6	7		1	Caucasian	38825
THO1	6	7	6, 7	1	Caucasian	38825
THO1	7, 9	7	9	1	Caucasian	26375
THO1	6	6	9.3	1	Hispanic	11793
THO1	6, 7	7	9.3	1	Hispanic	11793
THO1	7	7	9.3	1	Hispanic	11793
THO1	8, 9	8	6	1	Hispanic	11793
THO1	9	9.3	6, 9.3	1	Hispanic	13269
THO1	9.3	9.3	7	1	Hispanic	11793
THO1	7	7	6	1	PI	175

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
THO1						

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
TPOX	10, 11	10	11	1	Black	32853
TPOX	8, 11	8	11	1	Black	2,470
TPOX	8, 11	11	12	1	Caucasian	4,102
TPOX	8, 9	9	11	1	Hispanic	11756
TPOX	8, 11	11	8	1	Hispanic	3,965

PCR LOCUS	Phenotypes of The Observed Alleles	**PROMEGA**	RACE OR ETHNICITY	Total Tests in the same System by Race

	M	C	F			
TPOX	8	8	10	1	Caucasian	212
TPOX		13	11	1	Hispanic	456
TPOX	8, 22	8	5	1	Hispanic	456

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
CSF1PO	11, 12	12	13	1	American Indian	822
CSF1PO		12	11	1	Black	7,574
CSF1PO	10	11	11	1	Black	37725
CSF1PO	10	11	11, 12	1	Black	37725
CSF1PO	11	11	10	1	Black	2,291
CSF1PO	11, 12	12	11	1	Black	31976
CSF1PO	12	12	13	1	Black	31976
CSF1PO	12	12	13	1	Black	31976
CSF1PO		12	13	1	Caucasian	13,342
CSF1PO	10, 11	11	12	1	Caucasian	25502
CSF1PO	10, 12	12	11	1	Caucasian	25502
CSF1PO	11	11	12	1	Caucasian	3,744
CSF1PO	11	11	12	1	Caucasian	25502
CSF1PO	11	11	13	1	Caucasian	25502
CSF1PO	11	12	12	1	Caucasian	37539
CSF1PO	11, 12	12	11	2	Caucasian	25502
CSF1PO	11, 12	11	10	1	Caucasian	3,744
CSF1PO	11, 12	11	12	1	Caucasian	3,744
CSF1PO	12	13	12, 13	1	Caucasian	37539
CSF1PO	12, 13	13	12	1	Caucasian	13,342
CSF1PO	9, 13	9	11	1	Caucasian	25502

CSF1PO	9, 10	10	11	1	Caucasian	25502
CSF1PO	10	10	11	1	Hispanic	11397
CSF1PO	12	12	13	1	Hispanic	11397

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
CSF1PO						
CSF1PO						

PCR LOCUS	Phenotypes of The Observed Alleles			**ABI**	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D13S317	10	10	9	1	American Indian	842
D13S317	14	8	8, 12	1	Asian	2,175
D13S317	8, 11	8	12	1	Asian	2,035
D13S317		11	12	1	Asian	2,035
D13S317	13	11	8, 11	1	Asian	2,175
D13S317	9	8	9, 13	1	Asian Indian	869
D13S317	8	9	9, 11	1	Asian Indian	869
D13S317	9, 11	11	9	1	Asian Indian	869
D13S317	12	9	9, 11	1	Black	38683
D13S317	10, 11	11	12	1	Black	32792
D13S317	11, 13	11	12	1	Black	32792
D13S317	11, 12	11	12	1	Black	2,583
D13S317	9, 11	11	13	1	Black	32792
D13S317		12	11	1	Black	9,006
D13S317	11	12	11, 12	1	Black	38683
D13S317	11	12	12	1	Black	38683
D13S317	11	12	12	1	Black	38683

D13S317	11, 12	12	13	1	Black	32792
D13S317	11, 12	12	11	1	Black	32792
D13S317	11, 12	12	13	1	Black	32792
D13S317	12	12	13	1	Black	32792
D13S317	12	12	13	1	Black	32792
D13S317	12, 14	12	13	1	Black	32792
D13S317	12, 13	12	13	1	Black	32792
D13S317	13	12		1	Black	38683
D13S317	13	12		1	Black	38683
D13S317	11, 13	13	11	1	Black	32792
D13S317	12	13		1	Black	38683
D13S317	12, 13	13	12	1	Black	32792
D13S317	12	9	9, 10	1	Caucasian	38305
D13S317	10, 11	10	11	1	Caucasian	26053
D13S317	13	11	11, 13	1	Caucasian	651
D13S317	9, 11	11	12	1	Caucasian	4,232
D13S317	12	11	11, 12	1	Caucasian	38305
D13S317	8, 11	11	12	1	Caucasian	26053
D13S317	10	12	11, 12	1	Caucasian	5,756
D13S317	12	12	11	1	Caucasian	26053
D13S317	12, 14	12	11	1	Caucasian	26053
D13S317	12, 14	12	11	1	Caucasian	26053
D13S317	12	13	11, 13	1	Caucasian	38305
D13S317		12	15	1	Hispanic	3900
D13S317	11, 12	12	13	1	Hispanic	4,114
D13S317	12	12	11	1	Hispanic	11677
D13S317	9	12		1	Hispanic	15060
D13S317	14	13		1	Hispanic	15060

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D13S317		11	12	2	Black	1,280
D13S317		12	13	1	Black	?
D13S317		10	12	1	Caucasian	1,277
D13S317	14, 12	12	13	1	Caucasian	?

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	Black	9,258
D16S539		12	11	1	Black	425
D16S539		12	13	1	Black	12,670
D16S539	11	12		1	Black	?
D16S539	11	13	9, 13	1	Black	38683
D16S539	12	12	11	1	Black	32806
D16S539	12, 13	12	11	1	Black	32806
D16S539	13	13	12	1	Black	2,481
D16S539		11	12	1	Caucasian	16,308
D16S539		12	11	2	Caucasian	12,637
D16S539		13	12	1	Caucasian	12,637
D16S539	9, 13	9	11	1	Caucasian	26075
D16S539	11	9	9, 12	1	Caucasian	38373
D16S539	12	11	11	1	Caucasian	7,583
D16S539	12	11	9, 11	1	Caucasian	38373

D16S539	12	11	9, 11	1	Caucasian	38373
D16S539	13	12		1	Caucasian	38373
D16S539	13	12	11, 12	1	Caucasian	38373
D16S539	9, 11	9	10	1	Hispanic	11642
D16S539	11, 12	11	12	1	Hispanic	11642
D16S539	13	12	12	1	Hispanic	4,380
D16S539	13	12		1	Hispanic	790
D16S539	13	12	12, 13	1	Yemeni	190

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D16S539						
D16S539						

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D18S51	12, 15	12	17	1	Black	31668
D18S51	12, 19	12	17	1	Black	31668
D18S51	17	14	14, 20	1	Black	37116
D18S51	15	15	17	1	Black	31668
D18S51	15, 16	15	17	1	Black	31668
D18S51	18	16	16	1	Black	37116
D18S51		17	18	1	Black	8,754
D18S51	16	17		1	Black	11,484
D18S51	17	18	17, 18	1	Black	1,062
D18S51	14	18	16, 18	1	Black	37116
D18S51	15	19		1	Black	11,484
D18S51	17, 19	19	16	1	Black	31668

D18S51	21	21	15	1	Black	31668
D18S51	15, 16	15	11	1	Black	17,923
D18S51	17, 21	21	17	1	Black	17,923
D18S51	13	11	11, 16	1	Caucasian	5,768
D18S51	16	12	12, 14	1	Caucasian	1642
D18S51		12	13	1	Caucasian	1619
D18S51		14	18	1	Caucasian	15,420
D18S51		14	15	1	Caucasian	25385
D18S51	14, 20	14	15	1	Caucasian	25385
D18S51	16	15		1	Caucasian	?
D18S51		15	17	1	Caucasian	11,315
D18S51	12, 16	16	17	1	Caucasian	25385
D18S51	14, 15	14	12	1	Caucasian	15,420
D18S51	12, 14	12	17	1	Hispanic	11371
D18S51	12, 15	12	15	1	Hispanic	11371
D18S51	10	12		1	Hispanic	12784
D18S51	17	12	12, 15	1	Hispanic	12784
D18S51	12, 14	14	13	1	Hispanic	11371
D18S51	16	14	14, 15	1	Hispanic	12784
D18S51	14, 15	14	20	1	Hispanic	11371
D18S51	17	14		1	Hispanic	12784
D18S51	15, 21	15	18	1	Hispanic	11371
D18S51	13	15	14, 15	1	Hispanic	12784
D18S51	13, 15	15	16	1	Hispanic	11371
D18S51	16, 17	17	13	1	Hispanic	11371
D18S51	13, 18	18	17	1	Hispanic	11371
D18S51	13	23	15, 23	1	Hispanic	12784
D18S51	13, 21	21	18	1	Hispanic	4,098

D18S51	15, 17	17	12	1	Hispanic	4,098
D18S51	16, 17	16	13	1	Hispanic	3,775
D18S51	15, 16	16	13	1	Other	970
D18S51	17	18	18	1	Yemeni	190

PCR LOCUS	Phenotypes of The Observed Alleles			PROMEGA	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D18S51						

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D19S433	12	13		1	Asian	1,685
D19S433	14	14	13	1	Asian	1,577
D19S433	12	12	14	2	Black	1,062
D19S433	14	13		1	Black	11,518
D19S433	13	14	14	1	Black	1,379
D19S433	13	14	14	2	Black	1,062
D19S433	14	14	13	1	Black	6,979
D19S433		14	12	1	Black	6,979
D19S433	15	14		1	Black	?
D19S433		15	15.2	1	Black	11,412
D19S433		15.2	14	1	Black	?
D19S433		17.2	14	1	Black	6,979
D19S433	14	13		1	Caucasian	11,489
D19S433	14.2 15	15	13	1	Caucasian	12,294
D19S433		15	14	1	Caucasian	11,382
D19S433	13, 15	13	14	1	Hispanic	3,644

D19S433	14, 14.2	14	15.2	1	Hispanic	3,644
D19S433		14	15.2	1	Hispanic	3,644

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D21S11		31.2	32.2	1	Asian	2,095
D21S11	31.2 32.2	31.2	30	1	Asian	2,095
D21S11		28	30	1	Black	11,760
D21S11		30	28	1	Black	1379
D21S11	27, 33.2	27	31.2	1	Black	33120
D21S11	27	29	29, 33.2	1	Black	39101
D21S11	27	29		1	Black	39101
D21S11	27	29	28, 32.2	1	Black	39101
D21S11	28, 32.2	28	27	1	Black	33120
D21S11	28, 29	28	29	1	Black	33120
D21S11	28, 29	28	29	1	Black	33120
D21S11	28, 31	28	33.2	1	Black	33120
D21S11	28	30		1	Black	39101
D21S11	29	29	30	1	Black	2,474
D21S11	30	29		1	Black	11,954
D21S11	30, 31.2	30	33.2	1	Black	33120
D21S11	30	32.2		1	Black	39101
D21S11	31	28	28	1	Black	39101
D21S11	32	29	29, 30	1	Black	39101
D21S11	32.2	29	26, 29	1	Black	39101
D21S11	33.2	29	29, 30	1	Black	39101
D21S11	33.2	32.2	32.2 34	1	Black	39101
D21S11	32,2	30	30	1	Black	39101

D21S11	30, 30.2	30	28	1	Black	18,255
D21S11	32, 35	32	27	1	Black	18,255
D21S11		28	29	1	Caucasian	16,326
D21S11		29	30	1	Caucasian	11,729
D21S11		30	32.2	1	Caucasian	16,326
D21S11	24.2 28	28	30.2	1	Caucasian	13,671
D21S11	28, 29	29	31	1	Caucasian	26378
D21S11	29	29	28	1	Caucasian	26378
D21S11	29, 31	29	30	1	Caucasian	26378
D21S11	29, 30	30	31	1	Caucasian	26378
D21S11	29	32.2	30, 32.2	1	Caucasian	38781
D21S11	30	29	29	1	Caucasian	38781
D21S11	30	30	29	1	Caucasian	26378
D21S11	30	32.2		1	Caucasian	38781
D21S11	30	32.2	28, 32.2	1	Caucasian	38781
D21S11	32.2	28	28, 30	1	Caucasian	7,591
D21S11	32.2	33.2	32.2 33.2	1	Caucasian	38781
D21S11	32.2	33.2	32.2 33.2	1	Caucasian	38781
D21S11	28, 31	31	30	1	Caucasian	16,326
D21S11	29, 32.2	32.2	30	1	Caucasian	3,764
D21S11	30, 32.2	32.2	28	1	Caucasian	4,274
D21S11	31, 32	31	30	1	Caucasian	16,326
D21S11	28	29		1	Hispanic	?

PCR LOCUS	Phenotypes of The Observed Alleles			**PROMEGA**	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D21S11						
D21S11						

PCR LOCUS	Phenotypes of The Observed Alleles			ABI	RACE OR ETHNICITY	Total Tests in the same System by Race
	M	C	F			
D2S1338		16	17	1	Black	11,551
D2S1338		20	21	1	Black	8,452
D2S1338		23	22	1	Black	11,551
D2S1338		17	18	1	Caucasian	11,521
D2S1338	22	20		1	Caucasian	11,670
D2S1338	19, 23	23	17	1	Caucasian	14,887
D2S1338	25	23		1	Caucasian	?
D2S1338						