ANNUAL REPORT SUMMARY FOR TESTING IN 2004

Prepared by the Relationship Testing Program Unit

PREFACE

This year the 7th edition of AABB's *Standards for Relationship Testing Laboratories (RT Standards)* was published. The guidance document to the 7th edition contains suggestions that laboratories begin to consider alternative methods of incorporating apparent mutations into the paternity index. For the more commonly used polymerase chain reaction methods (short tandem repeats) with discrete alleles, the method of Fimmers et al (1992), is now suggested as a more appropriate calculation method (see *Guidance for Standards for Relationship Testing Laboratories* for more detail).

One of the goals of this year's annual report was to collect data that may be used in calculating the mutation paternity index. This was also the first year that an attempt was made to track "non-legal" testing.

Surveys were received from 42 laboratories.[*] These surveys were mostly from accredited laboratories in the United States, although several of the laboratories were from Canada and Europe. Many of the laboratories report testing a broad range of cases, including relationship tests for routine paternity testing, immigration issues, prenatal evaluations, and postmortem evaluations. Of the laboratories reporting, 97% performed immigration testing and 85% performed reconstruction (family study) cases. Approximately 92% of the laboratories use AABB mutation tables for calculations.

*Two of the reporting laboratories indicated that they sent their cases to other laboratories for testing; thus the data presented here are from the remaining 40 laboratories that actually performed the testing.

In this report, AABB provides some commentary for the lay public on common misconceptions relating to paternity testing. The Relationship Testing Standards Program Unit would also like to remind readers that the *Guidance for Standards for Relationship Testing Laboratories* discusses the *RT Standards* in some detail and provides suggestions on how to comply with the *RT Standards*. It also contains explanations of the standards, various calculations used, and addresses other issues in relationship testing.

TESTING WITHOUT THE MOTHER

Many laboratories were represented at the meeting of the Relationship Testing Special Interest Group during the 2005 AABB Annual Meeting (October 2005, Seattle, Washington). These laboratories voiced a strong concern about the apparent increase in the number of clients submitting disputed paternity cases without samples from the mother. Testing without the mother presents several problems. First, the paternity index is, on average, cut in half. This also greatly reduces the ability to detect a falsely accused man. In some cases, such as incest, this can easily produce false inclusions. When an apparent inconsistency (mutation) is present, it may not be possible to render an opinion of paternity without obtaining a sample from the mother. A maternal sample is also an important quality control step. The mother exclusion may indicate a problem in the testing. The testing of the mother may also allow for the detection of fraud, such as welfare fraud on the part of the mother or cases where the alleged father brings a child he knows is his, but is not the child of the mother. Thus, the testing of the mother, even if maternity is not disputed, is important in evaluating the questioned relationship as it improves the chance of obtaining clear results and is a quality control check for both the scientific and legal community. The laboratories that participated in the survey strongly felt that testing without the mother should be performed only when the mother's location is unknown or she is deceased. Otherwise, every effort should be made to test the mother.

ANNUAL VOLUME OF TESTING

The reported volume of cases tested in 2004 was 390,928. This is an increase of 36,917 cases (10.4%) over the 2003 volume. On the basis of these case numbers, it can be estimated that over one million persons were tested in 2004. A summary of the totals of all years since 1988 is shown in Table 1 and Figure 1.

Table 1. The Number of Relationship Cases Reported for 1988-2004

Year	No. of Cases	Year	No. of Cases
1988	77,000	1997	237,981
1989	85,231	1998	247,317
1990	120,436	1999	280,510
1991	143,459	2000	300,626
1992	161,000	2001	310,490
1993	189,904	2002	340,798
1994	193,000	2003	354,011
1995	149,100	2004	390,928
1996	172,316		

The totals include data from relationship testing laboratories in the United States, Canada, and the United Kingdom.

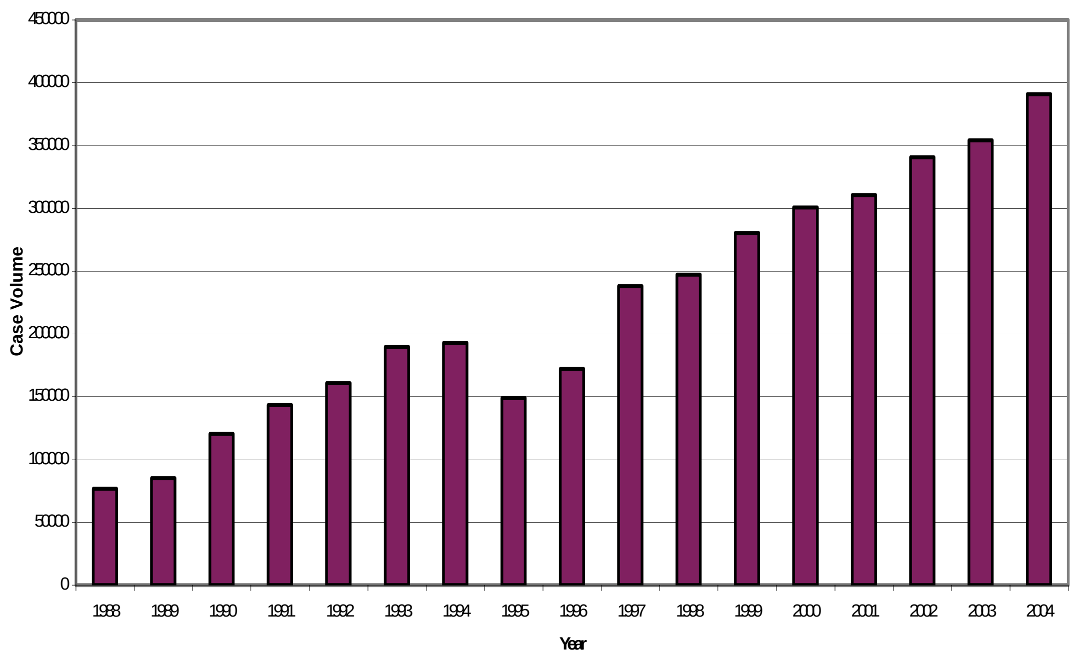

Figure 1. Graph of the case volume for 1988-2004.

Laboratories responding to the survey were asked if they were testing cases where the chain of custody did not meet the requirements of the *Standards for Relationship Testing Laboratories.* Samples for these so called “non-legal” tests are generally collected by the individuals without an impartial or third party witness (see *RT Standards*). AABB has taken the position that it cannot prohibit accredited laboratories from performing these types of tests, but reminds laboratories that they cannot claim or advertise that their “non-legal” testing meets AABB standards. Of the participating laboratories, 48.5% reported that they performed testing of this type. Those laboratories reported 18,025 non-legal cases, which amounts to 4.6% of the total cases reported. Some laboratories did not track the number of non-legal cases they evaluated, but a liberal estimate would be that no more than 10% of all cases reported were of a “non-legal” type.

LABORATORIES BY VOLUME OF REPORTED CASES

Table 2 indicates the size of the various responding laboratories by volume of cases reported. It is important to note that this breakdown is by each laboratory, but a single legal 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	2004
1-500	40	26	25	20	19	19	13	17	14	18	16
501-1,000	6	4	8	7	6	5	6	6	2	3	2
1,001-5,000	7	9	6	10	11	9	11	11	13	11	7
5,001-10,000	6	4	3	5	0	3	3	5	1	3	7
10,001-50,000	1	2	3	5	5	7	8	6	7	7	6
50,001-100,000	2	1	1	1	2	1	1	1	0	0	1
>100,000	0	0	0	0	0	0	0	0	1	1	1
Total laboratories	62	46	46	48	43	44	42	46	38	43	40

EXCLUSION RATE

One laboratory participating in the survey did not track the number of exclusions reported. For the laboratories tracking exclusions, there were 374,171 cases completed and 100,588 (26.88%) were reported as exclusions. The average exclusion rate for the laboratories reporting exclusions was 25.92%, with a standard deviation of 7.27. The median exclusion rate was 27.00% with a range of 11.11% to 39.48%. The explanation for the range of exclusion rates is complex but appears to be related to the laboratory's volume and client base. Anecdotal explanations for the various exclusion rates include differences in the type of case (private vs public contracts), and the geographic source of the case (rural vs metropolitan areas).

MISCONCEPTIONS IN PATERNITY TESTING – EXCLUSION RATE

During the past year, AABB has continued to receive inquiries from the media and the public concerning the exclusion rate. AABB has seen the exclusion rate misused by several organizations trying to claim that 30% of men are misled into believing they are biological fathers of children when the mother knows this not to be true. This claim is incorrect. The exclusion rate includes a number of factors. One is that 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 discover they are not. The testing merely sorts out which of these men is the biological father and excludes the others. Another factor is that typically an unexcluded alleged father, as part of his defense, will allege the mother had multiple sexual partners during the time of conception. These other partners are subsequently tested. Sometimes testing of a man is required because of a legal presumption. When the mother identifies the correct biological father, but the child is the product of a marriage [she is (was) married to someone other than the biological father], there is a legal presumption that the husband is the father. The husband is then tested to rebut the legal presumption, even though no one believes that he is the biological father of the child. In short there simply is no evidence that a large number of the men excluded in the testing were misled into believing they are the biological father of a given child.

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 (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 categories of clients (private vs 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 50% of laboratories using this value (range, 100 to 100,000). This is the first year that a laboratory claimed 100,000 as the minimum CPI needed for an acceptable result. For mother not tested cases, the most common minimum CPI is 100 with 64% of laboratories using this value (range, 100 to 10,000). For the family study or reconstruction cases, 49% indicated that they report "whatever was obtained" and 83% considered a combined paternity index of 101 or less as reportable.

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 in which 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.

Another 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 no relationship, and may still be a strong indicator of a relationship. A CPI of 0 or much less than 1 is considered an indicator of no relationship. 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. Understanding this 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 Minimum Combined Likelihood Ratios for Standard Trios, One Parent [Mother (or Father) Not Tested (MNT)] and Reconstruction Cases*

CPI	**Type of Case**		
	Trio	**One Parent**	**Family Study (Reconstruction)**
Whatever is obtained	0	0	17
10	0	0	2
100	19	25	10
101	0	0	1
150	3	3	1
200	3	3	2
400	1	0	0
500	1	1	1
1,000	7	5	1
1,001	1	1	0
10,000	2	1	0
100,000	1	0	0

*Note: Not all laboratories indicated a CPI for each type of case.

TECHNOLOGY USE

In 2004, the survey showed a continued trend toward the increased use of polymerase chain reaction (PCR) technology (STR analysis) with a decrease in the use of restriction fragment length polymorphism (RFLP) methods. PCR technology was used in 98.34% of reported cases, up from 93.26% in 2003. RFLP analysis decreased from 2.48% in 2003 to 1.48% of reported cases. This is also the first year that no cases were evaluated using red cell antigens. The utilization of Y chromosome analysis increased from 0.018% to 0.056% of cases.

Single nucleotide polymorphism (SNP) technology was reported in paternity evaluation for the first time last year. Apparently, this technology did not catch on and declined from a utilization rate in 2003 of 3.99% of reported cases to a utilization rate of 0.0026% cases in 2004. All other technologies were used in less than 1% of reported cases. Table 4 provides a breakdown of the technology used to resolve the reported paternity cases. The three 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 2004

Technology*	**No. of Cases**	**Utilization (%)**
STR	372,563	98.34
RFLP	5,611	1.48
HLA Class II Molecular	341	0.0901
Y Chromosome	213	0.056
HLA Class I Molecular	123	0.032
SNP	10	0.0026
HLA Serology	1	0.00026
Red Cell Antigens	0	0
Red Cell Enzymes/ Serum Proteins	0	0
Allotyping	0	0
Total of all technologies	378,862	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. In some situations, multiple technologies were used in the same case.

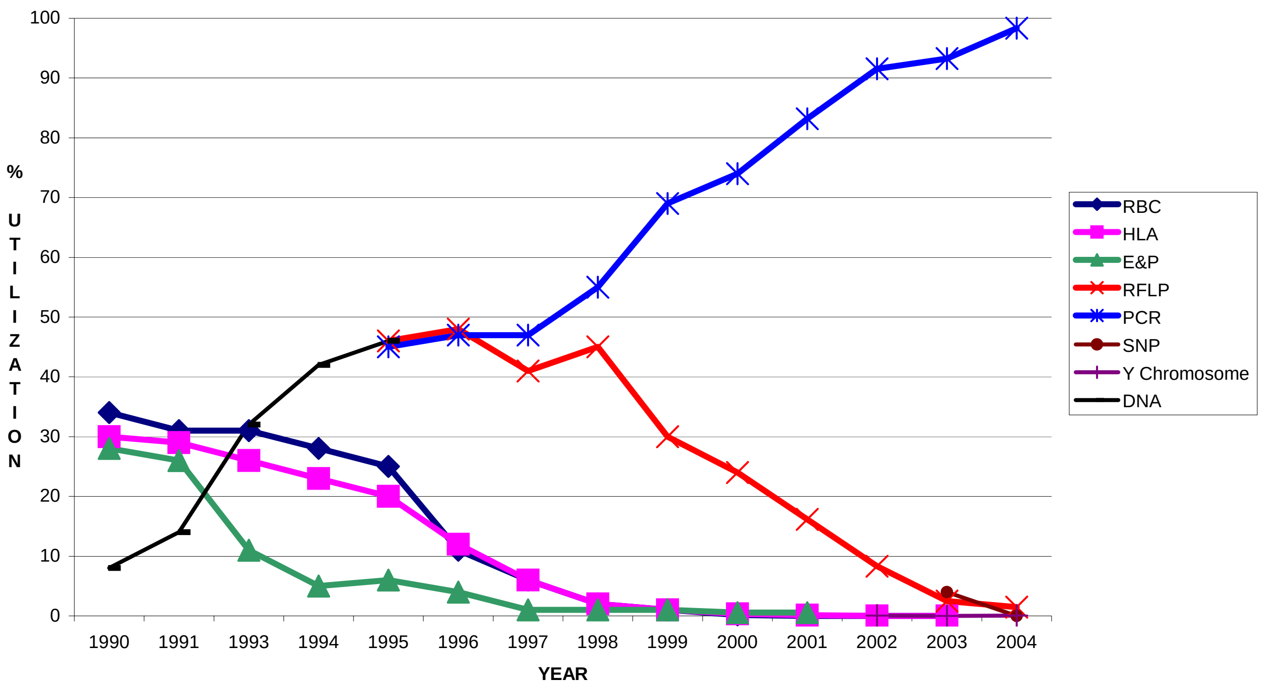

Figure 2. The use of various technologies since 1990.

SAMPLE SOURCE

Laboratories reported approximately 896,155 samples used for the casework in 2004. Not all laboratories reported the samples they used. Of these samples, buccal swabs accounted for 97.27% of the samples. Whole blood samples accounted for 1.74%. The use of blood spot cards decreased from previous years to 0.98% of samples. Teeth were also used, but the numbers were not reported. Various other samples were also reported in extremely small numbers (see Table 5).

Table 5. Sample Source in 2004

Sample	Number	Percent of Total
Buccal Swabs	870,833	97.27
Blood	15,544	1.74
Blood Spot Cards	8,808	0.98
Amniotic Fluid	589	0.066
Misc. Tissues	292	0.033
Paraffin Blocks	23	0.0026
Hair	14	0.0016
Chorionic Villus Sampling	6	0.00067
Personal item	3	0.00033
Bone	3	0.00033
Total	896,115	

MUTATION REPORTS

Another area of concern is the number of inconsistencies necessary to render an opinion of non-paternity. The laboratories were surveyed regarding cases 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 118 cases with double mutations and no cases with triple mutations as inclusions. Most laboratories report these “double mutation” cases with the inconsistencies noted and statistically considered. These results illustrate the importance of accurate assessments of potential mutations and null alleles. This year was the first year the report tried to gather data for more accurate calculations.

MUTATION CALCULATION AND FREQUENCIES

Single inconsistencies are routinely seen in the testing of paternity cases. If a laboratory reaches 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 appear to be using one of several calculation methods. Some laboratories are using the mutation rate as the PI, while others, most commonly, are using the mutation rate divided by the average probability of exclusion. Some laboratories used the mutation rate as a transmission frequency and some of the laboratories used Brenner’s method in looking at the repeat length difference between STR alleles.

A summary of the mutation frequencies for each STR locus is provided in Appendixes 1A and 1B. In Appendixes 2A and 2B, 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 3.

One objective of this year's report is to begin to collect data on STR loci to provide laboratories with frequencies for use in the mutation calculation. The committee is also recommending a move to the method of Fimmers et al (1992). The guidance document for the 7th edition of *RT Standards* contains a discussion of this method. One problem encountered with the data was racial designations. Several laboratories used the term "Asian" for race, which unfortunately does not have biological significance because it could refer to those from as far west as Turkey or India and as far east as China. For next year's survey, specific racial designations will be provided. One limitation of this data set is if the laboratory did not see any mutations, the laboratory did not provide data on the maternal and paternal meiosis. Also, there are differences between the total meioses reported in Appendix 1 and those in Appendixes 3 and 4. This difference reflects the ability to use more data for Appendix 1 because Appendix 1 does not require knowledge of the changes as presented in Appendixes 3 and 4. This was a design flaw in the reporting form, which will be fixed with next year's report. Not all laboratories track this information, or track only part of the information. Only the most complete data were used to compile the information in Appendixes 3 and 4. In these appendices, data are provided for observations where the mutation is indeterminate as to the maternal or paternal origin (Appendix 4) and where the mutation is most likely from one parent (Appendix 3). Even when the data appear to be of paternal origin, there may be some ambiguity as to which allele mutated. Incorporating all these data into a frequency for a single mutation event is open to discussion, as such a specific frequency table has not been created. At the 2005 AABB Annual Meeting, one approach was discussed and will be presented below.

In order to determine the specific mutation frequency at locus *D3S1358* for the apparent paternal mutation event of the alleged father's allele 16 changing to an allele 17 in the child, consider the following steps: Appendix 3 shows that, for the Black population, allele 16 changed to allele 17 in 16 of 79,247 meioses reported, or a frequency of 0.000202. However, there are several other explanations for this change. The same appendix identifies five instances where the alleged father's 16 could have changed to either a 15 or 17 (child is a clone of the mother or mother was not tested). To incorporate these data, one approach is to calculate the relative chance that the change was 16 to 17 rather than 16 to 15. From the appendix note the clear changes and calculate the relative chance of each change. Multiply the relative chance times the number of changes where the allele is 16 to 15 or 17 (five in this data set) to obtain the relative portion attributable to a 16 to 17 change.

Table 6. Relative Chance of Allele 16 Changing to 15 or 17

Change	**Observed**	**Relative Chance**	**Portion of 5**
16 to 17	16	16/31 = 0.516	5 * 0.516 = 2.58
16 to 15	15	15/31 = 0.484	5 * 0.484 = 2.42
Total	31	1	5

From these data, add 2.56 to the 16 observed potential changes from 16 to 17 to get the total of 18.56. Similarly, there were seven observations where the alleged father has alleles 16 and 18, either of which could mutate to a 17.

Table 7. Relative Chance of Allele 16 or 18 Changing to 17

Change	Observed	Relative Chance	Portion of 7
16 to 17	16	16/26 = 0.615	7 * 0.615 = 4.305
18 to 17	10	10/26 = 0.385	7 * 0.385 = 2.695
Total	26	1	5

From these data, add 4.305 to the 18.56 potential changes (paragraph above) from 16 to 17 to get the total of 22.865.

The calculation is not finished, as there was one case in Appendix 3 where the father's alleles 16 and 19 could have changed to a 17 or 18. To incorporate these data a similar approach is used.

Table 8. Relative Chance of Allele 16 or 19 Changing to 17 or 18

Change	Observed	Relative Chance	Portion of 1
16 to 17	16	16/21 = 0.762	1 * 0.762 = 0.762
16 to 18	0	0/21 = 0	1*0 = 0
19 to 17	0	0/21 = 0	1*0 = 0
19 to 18	5	5/21 = 0.238	1* 0.238 = 0.238
Total	31	1	1

From these data, add 0.762 to the 22.865 above yielding 23.627.

Data from those cases where the mutation is either maternal or paternal may be incorporated (Appendix 4). From the data in Appendix 4 there were seven instances where the mutation to a 17 could have been from a paternal 16. The approach to incorporate these data is similar to the above. First look to Appendix 3 to determine the frequency of the changes.

Table 9. Relative Chance of Allele 16 Changing to 17

Change	Observed	Relative Chance	Portion of 7
16 to 17 Maternal	1 / 67521 = 1.481e-5	1.481e-5 / 2.167e-4 = 0.0683	7 * 0.0683 = 0.478
16 to 17 Paternal	16 / 79247 = 2.019e-4	2.019e-4 / 2.167e-4 = 0.9317	7 * 0.9317 = 6.522
Total	2.167e-4	1	7

Finally, add 6.522 to the 23.627 yielding 30.149. Thus, for the Black population, the frequency of paternal mutation from a 16 to a 17 is 30.149 / 79247 = 0.00038 as compared to the 0.000202 without incorporating all possible mutation events. Readers are invited to comment on alternative methods of determining the mutation frequencies.

AMELOGENIN

The amelogenin locus is now used in a number of laboratories to test for the gender of the sample. Several males lacking the Y or X amelogenin allele have been observed. Laboratories were asked to measure the apparent X males observed in their laboratory. Similar to other DNA loci, amelogenin is subject to mutations. Therefore, on occasion, normal males have a female amelogenin phenotype or a Y phenotype. The X male phenotype was most commonly seen in Hispanic populations, in about 1/3,165 men. The Y male phenotype was most commonly seen in the Black population, in about 1/1,733 men.

Table 10. A Summary of Data on Apparent X and Y Males Seen with ABI Primers

	Black	**White**	**Hispanic**
Number X Males Observed	5	15	7
%	0.007	0.024	0.032
Number Y Males Observed	40	5	2
%	0.057	0.008	0.009
Total Number of Males Tested	69,333	62,783	22,152

Appendix 1A. Summary of Apparent Paternal Mutations at Various Loci Analyzed by PCR*

2004 Paternal Mutation Frequencies by Locus and Race

Locus	Black			Caucasian			Hispanic		
	Number Observed	Total Meioses	Number / Total	Number Observed	Total Meioses	Number / Total	Number Observed	Total Meioses	Number / Total
D2S1338	37	30,179	0.00123	65	33,891	0.00192	4	6,933	0.00058
D3S1358	143	89,526	0.00160	105	74,030	0.00142	30	23,139	0.00130
D5S818	118	68,898	0.00171	84	64,830	0.00130	19	23,739	0.00080
D7S820	59	64,974	0.00091	84	63,947	0.00131	27	23,795	0.00113
D8S1179	134	68,081	0.00197	120	68,082	0.00176	52	25,698	0.00202
D13S317	82	51,186	0.00160	100	63,566	0.00157	49	24,376	0.00201
D16S539	81	76,903	0.00105	77	70,091	0.00110	28	21,480	0.00130
D18S51	272	112,946	0.00241	178	99,840	0.00178	64	26,335	0.00243
D19S433	22	31,817	0.00069	16	28,928	0.00055	2	4,382	0.00046
D21S11	153	93,693	0.00163	123	85,407	0.00144	31	25,760	0.00120
FGA	257	88,874	0.00289	239	84,892	0.00282	115	26,856	0.00428
CSF1PO	94	51,070	0.00184	99	53,639	0.00185	34	19,964	0.00170
FESFPS	0	53	<0.18868	0	103	<0.00971	0	25	<0.04000
F13A01	0	48	<0.02083	0	83	<0.01205	0	16	<0.06250
F13B	0	59	<0.01695	0	111	<0.00901	0	24	<0.04167
LPL	0	44	<0.02273	0	93	<0.01075	0	20	<0.05000
THO1	3	69,391	0.00004	1	44,430	0.00002	1	5,657	0.00018
TPOX	10	48,314	0.00021	7	47,807	0.00015	5	16,209	0.00031
Penta D	4	3,124	0.00128	4	5,851	0.00068	2	790	0.00253
Penta B	0	67	<0.01493	0	149	<0.00671	0	42	<0.02381
Penta C	0	73	<0.01370	0	15	<0.06667	0	37	<0.02703
Penta E	2	3,381	0.00059	7	6,503	0.00108	1	630	0.00159
SE33	2	40	0.05000	0	54	<0.01852	0	19	<0.05263
WA	248	91,521	0.00271	226	88,192	0.00256	60	26,015	0.00231

*Number observed refers to the inconsistencies reported

Appendix 1B. Summary of Apparent Maternal Mutations at Various Loci Analyzed by PCR*

2004 Maternal Mutation Frequencies by Locus and Race									
Locus	Black			Caucasian			Hispanic		
	Number Observed	Total Meioses	Number / Total	Number Observed	Total Meioses	Number / Total	Number Observed	Total Meioses	Number / Total
D2S1338	5	20,635	0.00024	8	22,647	0.00035	0	1,281	<0.00078
D3S1358	8	63,011	0.00013	12	63,768	0.00019	1	14,265	0.00007
D5S818	15	45,309	0.00033	15	44,976	0.00033	4	14,293	0.00028
D7S820	6	43,611	0.00014	11	46,619	0.00024	4	14,230	0.00028
D8S1179	15	66,436	0.00023	9	64,998	0.00014	3	14,274	0.00021
D13S317	19	45,651	0.00042	9	46,415	0.00019	7	14,109	0.00050
D16S539	29	64,053	0.00045	14	65,204	0.00021	4	14,156	0.00028
D18S51	39	63,151	0.00062	36	64,903	0.00055	8	15,974	0.00050
D19S433	6	22,080	0.00027	3	23,461	0.00013	1	2,136	0.00047
D21S11	77	69,835	0.00110	74	69,968	0.00106	14	15,412	0.00091
FGA	30	65,751	0.00046	26	66,205	0.00039	10	14,868	0.00067
CSF1PO	28	44,985	0.00062	14	45,332	0.00031	3	13,910	0.00022
FESFPS	0	11	<0.09091	0	32	<0.03125	0	8	<0.12500
F13A01	0	7	<0.14286	0	29	<0.03448	0	6	<0.16667
F13B	0	10	<0.10000	0	39	<0.02564	0	8	<0.12500
LPL	0	5	<0.20000	0	26	<0.03846	0	7	<0.14286
THO1	1	42,501	0.00002	3	63,735	0.00005	1	14,216	0.00007
TPOX	1	42,071	0.00002	3	44,933	0.00007	1	15,193	0.00007
Penta D	0	15	<0.06667	0	42	<0.02381	0	7	<0.14286
Penta B	0	0	0.00000	0	3	<0.33333	0	2	<0.50000
Penta C	0	0	0.00000	0	5	<0.20000	0	2	<0.50000
Penta E	0	16	<0.06250	0	52	<0.01923	0	12	<0.08333
SE33	2	7	0.28571	0	25	<0.04000	0	3	<0.33333
vWA	23	65,352	0.00035	28	68,325	0.00041	6	14,194	0.00042

* Number observed refers to the inconsistencies reported

Appendix 2A. The Distance (Repeat Lengths) from the Obligatory Allele – Paternal Mutations (Expressed as Frequency of Total Number of Mutations)

	Black						Caucasian						Hispanic					
	STR Distance from Obligatory Allele						STR Distance from Obligatory Allele						STR Distance from Obligatory Allele					
Locus	**+1**	**-1**	**+2**	**-2**	**Other**	**Total**	**+1**	**-1**	**+2**	**-2**	**Other**	**Total**	**+1**	**-1**	**+2**	**-2**	**Other**	**Total**
D2S1338	0.303	0.636	0.061	0.000	0.000	33	0.446	0.554	0.000	0.000	0.000	56	0.333	0.667	0.000	0.000	0.000	3
D3S1358	0.523	0.477	0.000	0.000	0.000	107	0.514	0.459	0.014	0.014	0.000	74	0.536	0.429	0.000	0.036	0.000	28
D5S818	0.510	0.480	0.010	0.000	0.000	98	0.507	0.478	0.014	0.000	0.000	69	0.750	0.250	0.000	0.000	0.000	16
D7S820	0.569	0.431	0.000	0.000	0.000	51	0.446	0.554	0.000	0.000	0.000	74	0.421	0.579	0.000	0.000	0.000	19
D8S1179	0.593	0.393	0.000	0.007	0.007	135	0.556	0.426	0.019	0.000	0.000	108	0.429	0.548	0.024	0.000	0.000	42
D13S317	0.415	0.569	0.000	0.015	0.000	65	0.463	0.512	0.000	0.000	0.024	82	0.405	0.568	0.000	0.000	0.027	37
D16S539	0.500	0.471	0.000	0.015	0.015	68	0.557	0.443	0.000	0.000	0.000	61	0.667	0.333	0.000	0.000	0.000	21
D18S51	0.500	0.452	0.005	0.038	0.005	208	0.618	0.361	0.007	0.007	0.007	144	0.474	0.526	0.000	0.000	0.000	57
D19S433	0.850	0.050	0.000	0.000	0.100	20	0.385	0.538	0.000	0.000	0.077	13	0.000	1.000	0.000	0.000	0.000	1
D21S11	0.647	0.316	0.015	0.015	0.008	133	0.737	0.237	0.009	0.000	0.018	114	0.679	0.321	0.000	0.000	0.000	28
CSF1PO	0.526	0.474	0.000	0.000	0.000	76	0.500	0.484	0.016	0.000	0.000	64	0.333	0.625	0.000	0.000	0.042	24
FGA	0.614	0.361	0.000	0.012	0.012	241	0.635	0.330	0.005	0.020	0.010	200	0.500	0.469	0.010	0.010	0.010	98
F13A	0.000	0.000	0.000	0.000	0.000	0	0.000	0.000	0.000	0.000	0.000	0	0.000	0.000	0.000	0.000	0.000	0
F13B	0.000	0.000	0.000	0.000	0.000	0	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	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	0.000	0.000	0.000	0.000	0.000	0
PENTA D	0.250	0.500	0.000	0.250	0.000	4	1.000	0.000	0.000	0.000	0.000	3	0.500	0.500	0.000	0.000	0.000	2
PENTA E	0.000	1.000	0.000	0.000	0.000	1	0.333	0.667	0.000	0.000	0.000	6	0.000	1.000	0.000	0.000	0.000	1

THO1	0.333	0.667	0.000	0.000	0.000	3	0.000	1.000	0.000	0.000	0.000	1	1.000	0.000	0.000	0.000	0.000	1
TPOX	0.200	0.700	0.000	0.000	0.100	10	0.857	0.143	0.000	0.000	0.000	7	0.500	0.500	0.000	0.000	0.000	4
VWA	0.441	0.559	0.000	0.000	0.000	204	0.460	0.540	0.000	0.000	0.000	176	0.500	0.477	0.023	0.000	0.000	44
TOTALS	**0.532**	**0.445**	**0.004**	**0.012**	**0.007**	**1,457**	**0.553**	**0.430**	**0.006**	**0.005**	**0.006**	**1,252**	**0.498**	**0.484**	**0.007**	**0.005**	**0.007**	**426**

Appendix 2B. The Distance (Repeat Lengths) from the Obligatory Allele – Maternal Mutations.
(Expressed as Frequency of Total Number of Mutations)

	Black						Caucasian						Hispanic					
	STR Distance from Obligatory Allele						STR Distance from Obligatory Allele						STR Distance from Obligatory Allele					
Locus	**+1**	**-1**	**+2**	**-2**	**Other**	**Total**	**+1**	**-1**	**+2**	**-2**	**Other**	**Total**	**+1**	**-1**	**+2**	**-2**	**Other**	**Total**
D2S1338	0.200	0.800	0.000	0.000	0.000	5	0.571	0.429	0.000	0.000	0.000	7	0.000	0.000	0.000	0.000	0.000	0
D3S1358	0.429	0.429	0.000	0.000	0.143	7	0.400	0.500	0.000	0.000	0.100	10	0.000	1.000	0.000	0.000	0.000	1
D5S818	0.714	0.214	0.000	0.071	0.000	14	0.545	0.455	0.000	0.000	0.000	11	1.000	0.000	0.000	0.000	0.000	3
D7S820	0.800	0.200	0.000	0.000	0.000	5	0.100	0.900	0.000	0.000	0.000	10	0.750	0.250	0.000	0.000	0.000	4
D8S1179	0.467	0.533	0.000	0.000	0.000	15	0.429	0.571	0.000	0.000	0.000	7	0.500	0.500	0.000	0.000	0.000	2
D13S317	0.667	0.250	0.083	0.000	0.000	12	0.875	0.125	0.000	0.000	0.000	8	0.667	0.333	0.000	0.000	0.000	6
D16S539	0.300	0.700	0.000	0.000	0.000	20	0.091	0.909	0.000	0.000	0.000	11	0.000	1.000	0.000	0.000	0.000	3
D18S51	0.706	0.265	0.000	0.000	0.029	34	0.758	0.242	0.000	0.000	0.000	33	0.625	0.250	0.000	0.000	0.125	8
D19S433	0.000	0.750	0.000	0.250	0.000	4	1.000	0.000	0.000	0.000	0.000	1	1.000	0.000	0.000	0.000	0.000	1
D21S11	0.300	0.683	0.000	0.017	0.000	60	0.266	0.578	0.000	0.141	0.016	64	0.417	0.583	0.000	0.000	0.000	12
CSF1PO	0.333	0.600	0.000	0.067	0.000	15	0.750	0.250	0.000	0.000	0.000	12	1.000	0.000	0.000	0.000	0.000	2
FGA	0.720	0.280	0.000	0.000	0.000	25	0.571	0.381	0.000	0.000	0.048	21	0.333	0.667	0.000	0.000	0.000	6
F13A	0.000	0.000	0.000	0.000	0.000	0	0.000	0.000	0.000	0.000	0.000	0	0.000	0.000	0.000	0.000	0.000	0
F13B	0.000	0.000	0.000	0.000	0.000	0	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	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	0.000	0.000	0.000	0.000	0.000	0
PENTA D	0.000	0.000	0.000	0.000	0.000	0	0.000	0.000	0.000	0.000	0.000	0	0.000	0.000	0.000	0.000	0.000	0
PENTA E	0.000	0.000	0.000	0.000	0.000	0	0.000	0.000	0.000	0.000	0.000	0	0.000	0.000	0.000	0.000	0.000	0

THO1	0.000	0.000	0.000	0.000	0.000	0	0.500	0.500	0.000	0.000	0.000	2	0.000	1.000	0.000	0.000	0.000	2
TPOX	1.000	0.000	0.000	0.000	0.000	1	0.333	0.667	0.000	0.000	0.000	3	0.000	1.000	0.000	0.000	0.000	1
VWA	0.750	0.250	0.000	0.000	0.000	16	0.810	0.143	0.048	0.000	0.000	21	0.400	0.600	0.000	0.000	0.000	5
TOTALS	**0.502**	**0.468**	**0.004**	**0.017**	**0.009**	**233**	**0.493**	**0.448**	**0.005**	**0.041**	**0.014**	**221**	**0.500**	**0.482**	**0.000**	**0.000**	**0.018**	**56**

Appendix 3. Phenotype patterns where the submitting laboratory assigned either a paternal or maternal origin for the inconsistency (mutation) observed. (BLK = Black; CAU = Caucasian; HIS = Hispanic.) See Appendix 4 for other mutations.

Specific Mutations at Locus D19S453

Apparent Mutation		Number of Paternal			Number of Maternal		
From	**To**	**BLK**	**CAU**	**HIS**	**BLK**	**CAU**	**HIS**
Total Meioses		**27186**	**20833**	**5313**	**20122**	**22631**	**896**
12.2	13.2	1					
12	10				1		
13.2	11.2	1					
13	14	1				1	
13 or 15	14				1		
14	13				1		
14.2	13.2				1		
14	13 or 15				1		
14	15	5	2				
14 or 16	15					1	
15	14			2			
15	16	3	1				
15.2	16.2	2					
16	15		2				
16	17	1					
16.2	15.2	1	1				
16.2	17.2	1					
17	16			1			
17	18						1

Specific Mutation at Locus D5S818

Apparent Mutation		Number of Paternal			Number of Maternal		
From	**To**	**BLK**	**CAU**	**HIS**	**BLK**	**CAU**	**HIS**
Total Meioses		**58503**	**45337**	**19300**	**59766**	**59438**	**20102**
9	10	1	1				
9 or 11	10		1				
10 or 12	11					1	
10	11	1		2			
11	10	4	3				
11	12	6	2	1		1	1
11 or 13	12	6	3	1		2	1
11	13	1					
12	10				1		
12	11	4	7		1	1	
12	11 or 13		1				
12	13	14	12	2	5	3	1
12 or 14	13	2	1		1	1	
12	10 or 11	1					
13	12	11	6	1	1	1	
13	14	14	10	3	5	2	
13	12 or 14	1					
14	13	14	12	2	1	2	
14	15	1					1
15	14	4	2				
17	18	1					
10 or 14	9 or 13	1					
11 or 12	13 or 14			1			
12 or 14	11 or 13	2	1				

Specific Mutation Events D8S1179

Apparent Change		Number of Paternal			Number of Maternal		
From	To	BLK	CAU	HIS	BLK	CAU	HIS
Total Meioses		89643	79676	26309	70700	74338	20528
9	10		1				
10	11	1	4	2	1		1
10 or 12	11		1				
11	7	1					
11	10	2	3	1		1	
11	12	3					
11 or 13	12	1	1				1
12	11	1	4	1			
12	13	5	5	3			
12	11 or 13	1					
12 or 14	13	1	4	1			
13	12	5	4	2	2		
13	14	3	12	5	2	1	
13	12 or 14			1			
13 or 14	15		1				
13 or 15	14	3	5				
13	15			1			
14	13	8	10	6	3	2	1
14	15	29	11	4	1	2	1
14	13 or 15	2					
14 or 16	15	4	3				
15	14	11	9	4	2		
15	16	16	5	1	2		
15 or 17	16	1					
16	15	9	7	5	1		
16	17	12	2	1	1		
16	15 or 17					1	
16	18		1				
17	16	7		1			
17	18	1					
18	17	3	1			1	
10 or 13	11 or 14			1			
12 or 13	11 or 14		1				
12 or 14	11 or 13		1				
12 or 15	13 or 14					1	
11 or 13	10 or 12	1					
13 or 14	12 or 15	1					
13 or 16	14 or 15		1				
12 or 15	13 or 14	1					
13 or 15	12 or 14	1					

13 or 15	14 or 16	1					
13 or 16	12 or 17	1					
13 or 16	14 or 15	1					
14 or 16	13 or 15			2			
15 or 18	14 or 17	1					

Specific Mutations in D16S539

Apparent Mutation		**Number of Paternal**			**Number of Maternal**		
From	**To**	**BLK**	**CAU**	**HIS**	**BLK**	**CAU**	**HIS**
Total Meioses		**66483**	**52187**	**17061**	**64198**	**65919**	**16929**
8	9	1					
9	10	1	2				
10	11	3	2	1			
10	9 or 11	3					
10 or 12	11			2			1
11	10	1			1		
11	12	5	3	4	3		
11 or 13	12		3	1	5	1	
12	11	11	7	2	1	2	1
12	13	6	8	5	2	1	
12	11 or 13					1	
12 or 14	13	4	2	1			
13	9	1					
13	11	1					
13	12	10	4	2		2	1
13	14	9	14	1	6		
13 or 15	14		1		1		
14	13	6	5	1	6	6	
14	15	2					
15	14						1
15	16		1				
9 or 12	10 or 11				1		
9 or 13	10 or 12			1			
10 or 12	9 or 13	1	1				
10 or 12	11 or 13		2				
11 or 14	10 or 13				1		
11 or 15	12 or 14		1				
12 or 15	13 or 14				1		

Specific Mutations at Locus VWA

Apparent Mutation		Number of Paternal			Number of Maternal		
From	To	BLK	CAU	HIS	BLK	CAU	HIS
Total Meioses		81516	69414	21712	67780	68999	19201
10 or 12	11			1			
14	13	1					
14	15	1	1				
14 or 16	15		1	1			
14 or 18	16				1		
15	14	3	4	1			
15	16	10	6	1	6	2	
15 or 17	16	3	3		2	3	
15 or 18	16					1	
16	15	11	3	2			
14 or 16	15	1					
16	17	15	6	5	3	5	2
16	18			1			
16 or 18	17	9	6	3	2	1	
17	16	16	16	4	1		2
17	18	16	15	1		4	
17	16 or 18	1	1	1			
17 or 19	18	6	8	1	1	1	
18	17	23	17	6	1	1	
18	19	18	21	2	3	3	
18	17 or 19	1	1			1	
18	20					1	
18 or 20	19	2		2			
19	18	21	18	3			
19	20	14	16	3			
19 or 21	20	1					
20	19	16	18	4	1		
20	21	7	5	1			
21	20	3	2				1
21	22	1					
22	21	1					
14 or 16	15 or 17	2					
14 or 18	15 or 17		1				
15 or 17	14 or 18		1				
15 or 17	16 or 18	2			1		
15 or 18	16 or 17	2	1	1			
15 or 18	16 or 19		1				
15 or 19	14 or 20	1					
16 or 17	15 or 18	1					
16 or 18	15 or 17			1	1		

16 or 18	17 or 19		1			1	
16 or 19	15 or 18	1					
16 or 19	17 or 18	2					
17 or 20	16 or 19	1	1				
17 or 20	18 or 19		1				
18 or 20	17 or 19			1			

Specific Mutations at Locus CSF1PO

Apparent Mutation		Number of Paternal			Number of Maternal		
From	**To**	**BLK**	**CAU**	**HIS**	**BLK**	**CAU**	**HIS**
Total Meioses		**43165**	**36097**	**16641**	**45108**	**47643**	**17749**
7	8				1		
8	9	1					
9	10				1		
10	8				1		
10	9		1			1	
9 or 11	10		1	1			
10	11	1	2		1		
10 or 12	11	1	4	2			
11	10	9	1	1	1	1	
11	12	4	8	1	1	2	
11	10 or 12	1	3	1	1	1	1
11 or 13	12	2	10	5			
11	15			1			
12	11	6	3	4	4		
12	13	20	4	5	1	4	
12	11 or 13		2				
12 or 14	13		4				
13	12	15	9	4	4	1	
13	14	3	5			2	
14	13	3	7	2			
14	15	1					
10 or 11	9 or 12				1		
10 or 12	9 or 11	1				1	
11 or 12	10 or 13	1			11		
11 or 13	10 or 12	1	1				

Specific Mutations at Locus D2S1338

Apparent Mutation		Number of Paternal			Number of Maternal		
From	To	BLK	CAUC	HISP	BLK	CAUC	HISP
Total Meioses		**23803**	**22449**	**4535**	**18693**	**21667**	**3648**
18	17 or 19		1				
19	18	1		1			
19	20	2	3				
20	19	2	1			1	
20	21	1	4				
21	20		1				
21	22	2	2				
21 or 23	22	1					
22	21	1	1				
22	23		1				
23	22	1	1	1			
23	24		2				
23	25	1					
23 or 25	24		1				
24	23	1	4			1	
24	25		1			1	
25	24	1	5		1		
25	26	1	2		1	1	
26	25	4	2		2		
27	26	1					
20 or 24	19 or 23		1				

Specific Mutations at Locus D3S1358

Apparent Mutation		Number of Paternal			Number of Maternal		
From	To	BLK	CAU	HIS	BLK	CAU	HIS
Total Meioses		79247	56022	21707	67521	66237	20030
14	15	7					
14 or 16	15	1	1				
15	12	0			1		
15	14	3	1	4			
15	14 or 16		1				
15	16	9	6	2	1	1	
15 or 17	16	8	5	1	1		
16	15 or 17	5					
16	15	15	3	1		1	1
16	17	16	3	5	1	1	
16 or 18	17	7	7	1			
17	15		1				
17	16	11	7	2	2	1	
17	16 or 18		1				
17 or 18	16	1	1				
17 or 19	18	3	1				
17	18	8	10	1		2	
17	19		1				
18	16 or 17		1				
18	17	10	12	3		3	
18	19	4	8	4			
19	18	5	4	1			
19	20		3				
20	19	1					
20	21			1			
14 or 17	15 or 16	2					
15 or 17	14 or 16	2					
15 or 17	16 or 18		1				
15 or 19	16 or 18		1				
16 or 17	15 or 18					1	
16 or 19	17 or 18	1					

Specific Mutations at Locus D13S317

Apparent Mutation		Number of Paternal			Number of Maternal		
From	**To**	**BLK**	**CAU**	**HIS**	**BLK**	**CAU**	**HIS**
Total Meioses		**56211**	**47459**	**20555**	**59214**	**61338**	**19671**
8	9		1				
9	10	1	1				
10	9		1	1	1		
10	11			2			1
10 or 12	11	1		1			
10	15			1			
11	9				1		
11	10	5	3				
11	12	4	7	2	3	2	
11 or 13	12	4	5	1		1	1
11	15		2				
12	9		1				
12	11	11	9	2	1		
12	13	11	12	6	2	2	2
12	11 or 13	2	1	1	1		
12 or 14	13	2	3	5			
13	12	17	8	6			1
13	14	7	5	2	2	1	
13	12 or 14	1					
14	13	9	9	6			1
14	15	5	5	1	1	2	
15	14		2	3		1	
8 or 12	9 or 13				1		
8 or 12	11 or 9		1				
10 or 13	11 or 12		2				
11 or 12	10 or 13	1					
11 or 13	12 or 14	1			1		
11 or 14	12 or 13				1		
12 or 13	11 or 14		1				
12 or 14	11 or 13	1			1		

Specific Mutations at Locus D18S51

Apparent Mutation		Number of Paternal			Number of Maternal		
From	**To**	**BLK**	**CAU**	**HIS**	**BLK**	**CAU**	**HIS**
Total Meioses		**77949**	**62761**	**22269**	**74675**	**78736**	**21544**
11	12				1		
11 or 13	12	1					
12	10	1	1				
12	11	1	2				
12	13	2	9				
12 or 14	13					1	
13	12	1	1			3	
13	14	1	2	2		1	
13 or 15	14				1		
14	11		1		1		
14	12	1					
14	13	4	3				
14	15	4	8	3	1	3	1
14 or 16	15	3				1	
15	12	1					
15	14	2	1			1	
15	16	4	8		2	3	
15 or 17	16	2	1	1			
16	14	1					
16	15	7	5	3	1		
16	17	13	6	2	7	5	
16	15 or 17				1		
16	18	1					
16 or 18	17	3		2			
17	14						1
17	15	1					
17	16	8	5	5		1	1
17	18	14	11	3		3	
17 or 19	18	6	1				
17	23	1					
18	16	1					
18	17	6	10	2	3		
18	19	10	8	2	2		1
18 or 20	19	3	1				
19	18	15	2	3	2	2	1
19	20	20	4	2	6	1	
19	18 or 20	1					
19 or 20	20	2					
20	18	2					

20	19	18	5	4	2	1	
20	21	11	9	2	3	2	1
20	22		1				
20 or 22	21		1				
20.2	19.2	1					
21	20	11	7	3	1		
21	22	6	2	2	1	2	
22	21	4	2	3			
22	23	1	2	1	1		1
23	22	6		1			
23	24	1	1				
24	23		1	1			
24	25	1					
25	24		1	2			
25	26			1			
13 or 15	12 or 16	1					
13 or 17	12 or 16		1				
13 or 16	12 or 17					1	
13 or 17	14 or 16		1				
13 or 18	12 or 17	1					
13.2 or 19	16	1					
14 or 15	13 or 16		1				
14 or 17	15 or 18		1				
15 or 16	14 or 17	1	1				
15 or 17	16 or 18	1			1		
15 or 18	16 or 19				1		
16 or 18	15 or 19		1				
17 or 19	16 or 18		1				

Specific Mutations at Locus D21S11

Apparent Mutation		Number of Paternal			Number of Maternal		
From	To	BLK	CAU	HIS	BLK	CAU	HIS
Total Meioses		80952	67031	21332	81248	71434	20859
23	29		1				
26	27	1					
27	28	1	1		1		
27 or 29	28				1		
28	26	1					
28	27		1				
28	27.2		1				
28	29	11	6		3		
28	27 or 29	2					
28 or 30	29	3	1		4		
29	28	4	3	2	5	1	1
29	30	6	7	2	1	1	
29	28 or 30				1		
29 or 31	30	3	1		4	4	1
30	28					6	
30	29	9	2	3	7	5	2
30	29 or 31		1				
30	31	15	18	5	6	3	1
30	32	1					
30 or 32	31		1			2	
30 or 31.2	31		1				
31	30	9	6	1	13	14	2
30 or 32	31				1		
31	31.2	1					
31	32	7	11	2	4	3	1
30.2	31.2		5				
31.2	31			1			
31.2	30.2	1			2		
31.2	32.2	11	1	3	4		
31.2 or 33.2	32.2	2				1	
32.2	31.2 or 33.2			1			
32	31	1	2		3	4	
32	33	2		1		1	
32.2	31.2	2	1		4	1	
32.2	33.2	11	13	4	3	2	2
33	32	2				1	
33.2	32.2	5	3	1	6	6	2

33.2	34.2	7	5	1	1	3	
33.2	32.2 or 34.2	1					
34	33	2	1		4		
34	35	3					
34.2	32.2				1		
34.2	33.2	1	1		5	3	
34.2	35.2	1					
35.2	34.2					1	
35	34	1			1		
35	36	2					
36	35	1		1			
36	37	1					
36.2	35.2	1					
37	36	1			2		
16 or 19	14 or 20	1					
27 or 29	28 or 30	2					
28 or 29	29 or 30	1					
28 or 30	27 or 31	1					
28 or 31	29 or 30	1				1	
29 or 30	28 or 31	1					
29 or 31	28 or 30	1			1		
29 or 32	30 or 31					1	
28 or 32.2	29 or 31.2				1		
30 or 32.2	31 or 33.2			1			

Specific Mutations at Locus FGA

Apparent Mutation		Number of Paternal			Number of Maternal		
From	**To**	**BLK**	**CAU**	**HIS**	**BLK**	**CAU**	**HIS**
Total Meioses		**78883**	**65749**	**22169**	**62801**	**81372**	**17460**
17.2	18.2	2					
18.2	19.2	2					
19	20	4	1				
19 or 21	20			1			
20	19 or 21					1	
19.2	20.2	2					
20	19		3		2	1	
20	21	4	4	1	2		
20 or 22	21	1	1			2	
21	18	1					
21	19	1	1	1			
21	20	4	2	1			1
21	22	6	11	4			
21 or 23	22		1	1			
21.2	22.2		1				
21.2	21					1	
22	20	1					
22	21	7	5	1			
22	21 or 23	1	1	1		1	
22	23	19	17	8		1	1
22 or 24	23		5	2		1	2
22.2	22		1				
22.2	21.2		1				
22.2	23.2	1	1				
23	21		1				
23	22	6	7	4	1	3	2
23	24	19	21	1	2	1	
23 or 25	24	4	3	1	1		
23.2	24.2		1				
24	22		1				
24	23	18	10	8		3	
24	23 or 25			1			
24	25	42	23	9	4	3	1
24 or 26	25	1	1	3	2		
24	27	1					
24.3	25.3					1	
25	24	18		8	1	1	
25	24 or 26				1		
25	26	14	27	9	3	2	

25	27		1				
25 or 27	26		9	1			
26	25	6	7	7	1		
26	27	9	8	3	1	1	
26 or 28	27			1			
27	26	8	6	7			
27	28	1	2	3	3		
28	27	2	1	4	1		
28	29	2			1		
29	28	1			1		
30.2	31.2				1		
33.2	34.2						1
45.2	46.2	1					
19 or 24	21 or 25			1			
20 or 24	19 or 25		1				
22 or 24	21 or 25	1					
22 or 24	23 or 25		1				1
22 or 26	21 or 25		1				
22 or 26	23 or 25				1		
23 or 25	22 or 26	1					
24 or 26	23 or 25			1			

Specific Mutations at Locus THO1

Apparent Mutation		Number of Paternal			Number of Maternal		
From	**To**	**BLK**	**CAU**	**HIS**	**BLK**	**CAU**	**HIS**
Total Meioses		**59206**	**31394**	**1285**	**40391**	**58389**	**12874**
6	7					1	
7	6	1	1				
7	8	1		1			
8	7	1					
8	9.3		1				
8 or 10	9				1		
9	8					1	
10	8						1
6 or 8	7 or 9					1	

Specific Mutations at Locus TPOX

Apparent Mutation		Number of Paternal			Number of Maternal		
From	**To**	**BLK**	**CAU**	**HIS**	**BLK**	**CAU**	**HIS**
Total Meioses		**41203**	**29641**	**16220**	**39970**	**39434**	**13828**
8	9		1				
9	10	1			1		
10	9	1					
11	10	1		1		2	
11	12	2	2	1		1	
11	16	1					
12	11	3	1	2			1
12	13		1				
13	12	2					

Appendix 4. Data for cases where the inconsistency (mutation) could not be assigned a paternal or maternal origin by the submitting laboratory. (BLK = Black; CAU = Caucasian; HIS = Hispanic.)

Indeterminate Mutations at Locus D19S5433

Phenotypes Observed			**Number Observed by Race**		
MOTHER'S ALLELES	**CHILD'S ALLELES**	**FATHER'S ALLELES**	**BLK**	**CAU**	**HIS**
Total Maternal Meioses			**20122**	**22631**	**896**
Total Paternal Meioses			**27186**	**20833**	**5313**
13	13, 14	13, 13.2	1		
14, 15	13, 14	14		1	
13, 16	13, 15	13, 14	1		
13, 14	14, 15	13, 14		1	
13, 14	14, 15	14		1	1
13, 15	14, 15	12, 15		1	
14, 16	16, 17	13, 16	1		

Indeterminate Mutations at Locus CSF1PO

Phenotypes Observed			Number Observed by Race		
MOTHER'S ALLELES	**CHILD'S ALLELES**	**FATHER'S ALLELES**	**BLK**	**CAU**	**HIS**
Total Maternal Meioses			**45108**	**47643**	**17749**
Total Paternal Meioses			**43165**	**36097**	**16641**
10, 12	10, 11	10, 12	3	1	1
10, 12	10, 11	10	2		
11	10, 11	11			1
11, 12	10, 11	11, 12			1
11, 12	10, 11	11, 13	1		
10, 11	10, 12	10, 11	1		
10, 11	10, 12	10, 13		1	
10, 13	10, 12	10, 11		1	1
11, 12	10, 12	11		1	
10, 12	10, 13	10, 12			1
10, 12	10, 13	10, 12	1		
10, 11	11, 12	11	1		
10, 11	11, 12	11, 13	2	2	1
10, 12	11, 12	10, 12		1	
11	11, 12	10, 11	1		
11	11, 12	7, 11	1		
11	11, 12	11, 13		1	
11, 13	11, 12	11, 13	1		
12	11, 12	10, 12	1		1
8, 11	11, 12	11			1
8, 11	11, 12	9, 11	1		
9, 11	11, 12	11, 13	2		
9, 12	11, 12	12, 13		1	
11, 12	11, 13	11, 12	1	1	
10, 12	12, 13	12	2	2	
10, 12	12, 13	12			2
10, 13	12, 13	10, 13		1	1
11, 12	12, 13	12			
11, 12	12, 13	10, 13		1	
11, 12	12, 13	11, 12		1	
12	12, 13	8, 12			1
12	12, 13	10, 12		1	1
12	12, 13	11, 12	1	1	1
13	12, 13	10, 13		1	
8, 12	12, 13	8, 12	1		
8, 12	12, 13	12		1	
10, 12	8, 10	10, 12			1
10	9, 10	10, 12	2		2
10, 12	9, 12	11, 12		1	

Indeterminate Mutations at Locus D2S1338

Phenotypes Observed			Number Observed by Race		
MOTHER'S ALLELES	**CHILD'S ALLELES**	**FATHER'S ALLELES**	**BLK**	**CAU**	**HIS**
Total Maternal Meioses			**18693**	**21667**	**3648**
Total Paternal Meioses			**23803**	**22449**	**4535**
17, 19	17, 18	17		1	
17, 25	17, 19	17, 18		1	
17	17, 25	17, 18		1	
17, 26	17, 27	17, 26			1
16, 21	20, 21	19, 21	1		
23, 24	23	20, 24		1	
19, 23	22, 23	20, 23	1		
20, 23	22, 23	21, 23	1		
22	22, 23	21, 22	1		
16, 23	23, 24	21, 23	1		
19, 23	23, 24	23, 25			1
17, 25	24, 25	22, 25		1	
24	24, 26	24, 25		1	
18, 26	25, 26	17, 26	1		

Indeterminate Mutations at Locus D3S1358

Phenotypes Observed			Number Observed by Race		
MOTHER'S ALLELES	**CHILD'S ALLELES**	**FATHER'S ALLELES**	**BLK**	**CAU**	**HIS**
Total Maternal Meioses			**67521**	**66237**	**20030**
Total Paternal Meioses			**79247**	**56022**	**21707**
15, 17	13, 15	15, 16	1		
14, 16	14, 15	14, 16	2		
14, 16	14, 15	14, 18	1		
15, 17	14, 15	15	1		1
15, 18	14, 15	15, 17		1	
16	14, 16	15, 16			1
14, 15	15, 16	15			1
15	15, 16	15, 17	2	1	1
15	15, 16	15, 18	1		1
15, 17	15, 16	15, 17	1	1	
15, 17	15, 16	15			1
15, 18	15, 16	15	1		
16	15, 16	16, 17	2	1	
16	15, 16	14, 16	2		
16	15, 16	13, 16	1		
16, 17	15, 16	16	1		
16, 18	15, 16	16	2		
15, 16	15, 17	15, 16	2		
15, 16	15, 17	15, 18	1	1	
15, 18	15, 17	15, 16	1		
15, 18	15, 17	15, 18		1	
16, 17	15, 17	16, 17	1		
14, 18	15, 18	14, 18		1	
15, 16	15, 18	15			1
18	15, 18	17, 18		1	
15, 16	15, 19	15			1
14, 16	16, 17	15, 16	1		
14, 16	16, 17	16, 18		1	
15, 16	16, 17	15, 16	1		
15, 16	16, 17	16, 18		1	
15, 17	16, 17	15, 17	2	1	1
15, 17	16, 17	17		1	
15, 17	16, 17	17, 18			1
16	16, 17	16, 18	1		
16, 18	16, 17	16	1		
16, 19	16, 17	16	1		
17	16, 17	17, 18	1		
17	16, 17	15, 17	1	1	

16, 17	16, 18	16			1
15, 18	16, 18	17, 18		1	
17, 18	16, 18	17, 18		1	
14, 18	17, 18	15, 18	1		
15, 17	17, 18	15, 17	1		
15, 17	17, 18	16, 17		1	
16, 17	17, 18	16, 17		1	
16, 17	17, 18	17, 19	1		
16, 18	17, 18	16, 18	0	1	
17	17, 18	16, 17	1		
17	17, 18	17	2		
15, 17	17, 19	16, 17	1		
18	18, 19	18, 20			1

Indeterminate Mutations at Locus D5S818

Phenotypes Observed			Number Observed by Race		
MOTHER'S ALLELES	**CHILD'S ALLELES**	**FATHER'S ALLELES**	**BLK**	**CAU**	**HIS**
Total Maternal Meioses			**59766**	**59438**	**20102**
Total Paternal Meioses			**58503**	**45337**	**19300**
11, 12	10, 11	11		1	1
11, 12	10, 11	11, 12	1		1
10, 12	10, 13	10, 12		1	
10, 12	11, 12	12	1	1	
11	11, 12	11, 13		1	
11, 13	11, 12	11, 13		2	
12	11, 12	8, 12	1		
12	11, 12	12	1		
12, 13	11, 12	12	1		
9, 11	11, 12	11		1	
10, 13	11, 13	12, 13	1		
11	11, 13	11, 12		1	
11, 12	11, 13	11, 12	2	1	
12, 13	11, 13	12, 13	1		
11, 12	12, 13	12	1	1	
11, 12	12, 13	12, 14	2	2	
11, 12	12, 13	7, 12	1		1
11, 12	12, 13	9, 12	1		
11, 12	12, 13	12	2		1
11, 12	12, 13	10, 12		1	
11, 13	12, 13	9, 13	1		
12	12, 13	9, 12			1
12	12, 13	11, 12			1
12	12, 13	12, 14	1		
13	12, 13	13	1		
7, 13	12, 13	13	1		
8, 12	12, 13	10, 13	1		
8, 12	12, 13	12, 14	1		
8, 13	12, 13	13	1		
11, 12	12, 14	12, 13		1	
11, 13	13, 14	12, 13	1		
11, 13	13, 14	13	1		
12, 13	13, 14	13		1	
12, 13	13, 14	12, 13			1
12, 13	13, 14	11, 13	4		
7, 11	7, 12	7, 11			1
9, 12	9, 13	9, 12	1		

Indeterminate Mutations at Locus D7S820

Phenotypes Observed			Number Observed by Race		
MOTHER'S ALLELES	**CHILD'S ALLELES**	**FATHER'S ALLELES**	**BLK**	**CAU**	**HIS**
Total Maternal Meioses			**53021**	**53029**	**16943**
Total Paternal Meioses			**54644**	**45776**	**19307**
10	10, 11	10	2		
10	10, 11	8, 10		1	
10	10, 11	10, 12		1	
10, 12	10, 11	9, 10	1		
10, 12	10, 11	10	1		
11	10, 11	11	1		1
11, 12	10, 11	11, 12			1
8, 11	10, 11	11		1	
10, 11	10, 12	10, 13		1	
10, 11	10, 12	10, 11		1	
10, 11	10, 13	10, 12		1	
10, 11	11, 12	10, 11		1	
10, 11	11, 12	11			1
10, 12	11, 12	10, 12			1
10, 12	11, 12	8, 12	1		
10, 12	11, 12	9, 12	1		
10, 12	11, 12	12, 13			1
11, 13	11, 12	11, 13		1	
12, 14	11, 12	10, 12	2		
8, 11	11, 12	11	1		
8, 12	11, 12	8, 12		1	
9, 11	11, 12	9, 11		1	
10, 12	12, 13	10, 12		1	
11, 12	12, 13	9, 12			1
8, 12	12, 13	8, 12			1
8, 11	8, 12	8, 11		1	
8, 13	8, 12	8, 13	1		
8, 12	8, 13	8, 12	1		
8, 11	8, 9	8, 11	1		
10	9, 10	10, 12	1		
8, 10	9, 10	8, 10	1		
8, 9	9, 10	9, 11	1		

Indeterminate Mutations at Locus D8S1179

Phenotypes Observed			Number Observed by Race		
MOTHER'S ALLELES	**CHILD'S ALLELES**	**FATHER'S ALLELES**	**BLK**	**CAU**	**HIS**
Total Maternal Meioses			**70700**	**74338**	**20528**
Total Paternal Meioses			**89643**	**79676**	**26309**
10, 15	10, 11	10, 13		1	
10, 15	10, 16	10, 15		1	
11	11, 12	11, 14		1	
11, 14	11, 12	11, 15			1
10, 13	11, 13	10, 13		1	
10, 12	12, 13	12, 14	1		
11, 13	12, 13	13, 15		1	
12, 14	12, 13	12		1	
13	12, 13	11, 13		1	
13	12, 13	13		1	
13	12, 13	13, 14		1	
13	12, 13	13, 15	1	2	
9, 13	12, 13	13, 14			1
10, 13	12, 15	13, 15	1		
12, 14	12, 15	12, 14	1		
10, 13	13, 14	13		1	
10, 14	13, 14	11, 14			1
11, 13	13, 14	13	1		
11, 13	13, 14	13, 15		2	
11, 14	13, 14	12, 14		1	
11, 14	13, 14	14, 15		1	
12, 14	13, 14	12, 14		1	
13	13, 14	13		1	
13	13, 14	13, 15	1	1	
13, 15	13, 14	12, 13		1	
13, 15	13, 14	13, 15		1	
14	13, 14	12, 14		1	
14	13, 14	14	1		
14	13, 14	14, 15			1
14, 16	13, 14	11, 14		1	
14, 16	13, 14	12, 14	1		
9, 14	13, 14	14		1	
11, 15	13, 15	14, 15	1		
13, 14	13, 15	13, 14		1	
10, 14	14, 15	12, 14	1	1	
10, 14	14, 15	13, 14		2	1
11, 14	14, 15	12, 14	1		
11, 14	14, 15	13, 14	1		

11, 14	14, 15	14	1		
12, 14	14, 15	11, 14	1		
12, 14	14, 15	14, 16	1		
13, 14	14, 15	13, 14			1
13, 14	14, 15	14, 16	1		
13, 15	14, 15	13, 15			1
13, 15	14, 15	15, 16	1		
14	14, 15	11, 14	1		
14	14, 15	12, 14	2		
14	14, 15	14, 16	1		
14, 16	14, 15	12, 14	1	1	
14, 16	14, 15	13, 14			1
14, 17	14, 15	14, 16	1		
15, 16	14, 15	12, 15	1		
15, 16	14, 15	15	1		
15, 16	14, 15	15, 16	1		
9, 15	14, 15	8, 15		1	
14, 15	14, 16	14, 15	1		
11, 15	15, 16	15	1		
12, 15	15, 16	14, 15		1	
13, 15	15, 16	12, 15	1		
13, 15	15, 16	14, 15	1		
14, 15	15, 16	13, 15	2		
14, 15	15, 16	15	1		
14, 16	15, 16	12, 16			1
15	15, 16	13, 15	1		
10, 16	16, 17	13, 16	1		

Indeterminate Mutations at Locus D13S317

Phenotypes Observed			Number Observed by Race		
MOTHER'S ALLELES	**CHILD'S ALLELES**	**FATHER'S ALLELES**	**BLK**	**CAU**	**HIS**
Total Maternal Meioses			**59214**	**61338**	**19671**
Total Paternal Meioses			**56211**	**47459**	**20555**
11	10, 11	9, 11		1	
11, 12	10, 11	11	1		
11, 13	10, 11	11, 12		1	
11, 12	10, 12	11, 12	1		
11	11, 12	10, 11		1	
11, 13	11, 12	11		1	
11, 14	11, 12	11, 13	1		
12	11, 12	12	3		
11	11, 12	11			1
8, 11	11, 12	11		1	
9, 12	11, 12	10, 12			1
9, 12	11, 12	12	1		
11	11, 13	11, 14		1	
11, 12	11, 13	11, 12	2		
11, 12	11, 13	11, 14	1		
11, 12	11, 13	9, 11	1		
11, 14	11, 13	11, 12	1		
12, 13	11, 13	12, 13	1		
10, 12	12, 13	11, 12		1	
10, 13	12, 13	13	1		
10, 13	12, 13	13, 14	1		
10, 13	12, 13	8, 13		1	
11, 12	12, 13	12, 14	1	1	
11, 13	12, 13	11, 13			
11, 13	12, 13	13	1		
12	12, 13	10, 12	1		
12	12, 13	12	2	1	
12	12, 13	12, 14	1		
12	12, 13	9, 12		1	
12, 14	12, 13	11, 12	1		
12, 14	12, 13	12, 14		1	
13	12, 13	13, 14	1		
7, 12	12, 13	11, 12			
8, 12	12, 13	12		1	
8, 13	12, 13	11, 13		1	
8, 13	12, 13	8, 13		1	
9, 13	12, 13	11, 13		1	

12, 13	12, 14	12, 15		1	
12	12, 14	12, 13			1
9, 13	13, 14	12, 13	1		
13, 14	14, 15	11, 14	1		
8, 10	8, 11	8, 12		1	
8, 10	8, 9	8, 11		1	
9, 11	9, 10	9, 12	1		
9, 11	9, 12	9, 10			1

Indeterminate Mutations at Locus D16S539

Phenotypes Observed			Number Observed by Race		
MOTHER'S ALLELES	**CHILD'S ALLELES**	**FATHER'S ALLELES**	**BLK**	**CAU**	**HIS**
Total Maternal Meioses			**64198**	**65919**	**16929**
Total Paternal Meioses			**66483**	**52187**	**17061**
9, 13	9, 10	8, 9	1		
9, 10	9, 11	9, 10		2	
9, 12	9, 11	9, 12	1		
10, 12	10, 11	10, 12			1
9, 12	9, 13	9, 14		1	
10	10, 13	10, 12			1
10, 11	10, 13	10, 12			1
11	11, 12	11		1	
11	11, 12	11, 13		2	
11	11, 12	9, 11	1		
11, 13	11, 12	11		1	
12	11, 12	10, 12		1	
12	11, 12	12, 13		1	
12	11, 12	9, 12		1	1
12, 13	11, 12	12	1		
9, 11	11, 12	11, 13	2		
9, 12	11, 12	12, 13	1		
10, 13	10, 14	10, 15			1
11	11, 13	11, 12		1	
11, 12	11, 13	11, 12	2		
11, 12	11, 13	11, 14	2		
12, 13	11, 13	10, 13	2		
10, 13	12, 13	10, 13		1	
11	11, 14	11, 13	1		
11, 12	12, 13	10, 12		1	
11, 12	12, 13	12		1	
11, 12	12, 13	12, 14	1		
11, 13	12, 13	13		1	
12	12, 13	11, 12	2		
12	12, 13	12		1	
13, 14	12, 13	9, 13	1		
8, 12	12, 13	12		1	
9, 12	12, 13	12	1		
9, 13	12, 13	11, 13			1
11, 13	13, 14	11, 13		1	
11, 13	13, 14	12, 13	1		
12, 13	13, 14	10, 13	1		
12, 13	13, 14	12, 13			1

13	13, 14	12, 13		2	
13	13, 14	9, 13	1		

Indeterminate Mutations at Locus D18S51

Phenotypes Observed			Number Observed by Race		
MOTHER'S ALLELES	**CHILD'S ALLELES**	**FATHER'S ALLELES**	**BLK**	**CAU**	**HIS**
Total Maternal Meioses			**74675**	**78736**	**21544**
Total Paternal Meioses			**77949**	**62761**	**22269**
13, 14	11, 13	13, 16		1	
12, 17	12, 18	12, 17		1	
13, 18	13, 14	13, 17		1	
14, 15	13, 15	14, 15		1	
13	13, 17	13, 16		1	
12, 15	14, 15	15, 17			1
13, 14	14, 15	12, 14		1	
14	14, 15	13, 14		1	
14, 16	14, 15	14		1	
14, 21	14, 15	14		1	
15, 18	14, 15	15	1		
13, 16	14, 16	13, 16			1
15, 19	14, 19	19	1		
12, 15	15, 16	12, 15		1	
13, 15	15, 16	14, 15		1	
13, 15	15, 16	15, 19	1		
13, 16	15, 16	16, 20	1		
15	15, 16	13, 15			1
15, 16	15, 17	15, 16	2		
15, 18	15, 19	15, 18		1	
15, 18	15, 26	15, 21	1		
12, 16	16, 17	16, 20	1		
14, 16	16, 17	16, 20	1		
14, 17	16, 17	15, 17	1		
15, 16	16, 17	13, 16		1	
15, 16	16, 17	14, 16			1
15, 17	16, 17	15, 17		3	
15, 17	16, 17	17		1	
16, 18	16, 17	16	1		
16, 17	16, 18	16			1
16, 17	16, 18	16, 17	1		
16, 20	16, 19	16, 20	1		
12, 17	17, 18	15, 17	1		
14, 17	17, 18	16, 17	1		
16, 17	17, 18	15, 17	2		
16, 17	17, 18	16, 17			
16, 18	17, 18	12, 18			1
16, 18	17, 18	16, 18	1		

17	17, 18	10.2, 17	1		
17	17, 18	17	1		
14.2, 17	17, 19	17, 20	1		
14, 18	18, 19	14, 18			2
16, 18	18, 19	18, 20	1		
18, 21	18, 19	12, 18	1		
19	18, 19	16, 19	1		
12, 19	19, 20	15, 19			1
12, 19	19, 20	19	1		
15, 19	19, 20	13, 19			1
16, 19	19, 20	17, 19	1		

Indeterminate Mutations at Locus D21S11

Phenotypes Observed			**Number Observed by Race**		
MOTHER'S ALLELES	**CHILD'S ALLELES**	**FATHER'S ALLELES**	**BLK**	**CAU**	**HIS**
Total Maternal Meioses			**81248**	**71434**	**20859**
Total Paternal Meioses			**80952**	**67031**	**21332**
28	28, 29	28, 30	1		
28, 30	28, 29	28, 31			1
28, 30	28, 29	28, 31.2		1	
28, 31	28, 29	28, 30	1		
29	28, 29	29, 30.2	1		
29, 30	28, 29	29		1	
29, 31.2	28, 29	29, 30		1	
28, 31	28, 30	28, 29		1	
28, 31	28, 30	28, 31.2	1		
28, 29	29, 30	29, 30.2			1
28, 30	29, 30	27, 30	1		
29	29, 30	29	1		
29	29, 30	29, 31.2			1
29	29, 30	29, 32.2		1	
29, 31	29, 30	29		1	
30	29, 30	24.2, 30		2	
30	29, 30	30			1
30, 31	29, 30	30		1	
30, 32.2	29, 30	27, 30			1
30, 32.2	29, 30	30			1
30, 34.2	29, 30	28, 30		1	
30, 31	29, 31	29, 31		1	
28, 31	30, 31	31, 32.2	2		
29 ,30	30, 31	29, 30		1	
29, 30	30, 31	28, 30	1		
30	30, 31	30	1		
30	30, 31	30, 32.2		1	
30, 31.2	30, 31	30, 30.2			1
30, 32.2	30, 31	30, 32.2	1		
31, 31.2	30, 31	31, 31.2		1	
31, 32.2	30, 32.2	28, 32.2		1	
30, 32.2	30, 33.2	30, 33		1	
29, 31.2	31.2, 32.2	30, 31.2			1
31.2	31.2, 32.2	28, 31.2		1	

Indeterminate Mutations at Locus FGA

Phenotypes Observed			Number Observed by Race		
MOTHER'S ALLELES	**CHILD'S ALLELES**	**FATHER'S ALLELES**	**BLK**	**CAU**	**HIS**
Total Maternal Meioses			**62801**	**81372**	**17460**
Total Paternal Meioses			**78883**	**65749**	**22169**
19, 24	19, 20	19, 22		1	
20, 23	20, 22	20, 23		1	
21, 22	20, 22	22, 23		1	
22, 25	20, 22	22, 23		1	
20, 22	20, 23	20, 24		1	
24, 25	20, 24	23, 24	1		
20, 25	20, 26	20, 27			1
20, 25	20, 26	25, 27	1		
19, 21	21, 22	21, 23		1	
20, 21	21, 22	21, 25		1	
21, 24	21, 22	21			1
22, 25	21, 22	22, 24			1
21, 22	21, 23	21, 24		1	
21, 24	21, 25	21, 23			1
21, 24	21, 25	21, 24			1
21, 26	21, 25	20, 21		1	
21, 26	21, 25	21, 26			1
21, 23	21, 26	21, 25			1
18.2, 23	22, 23	21, 23	1		
21, 22	22, 23	22	1		
21, 22	22, 23	22, 24	1		
21, 22	22, 23	22, 25	1		
21, 23	22, 23	21, 23		2	
22	22, 23	22	1		
22	22, 23	22, 24		1	
22	22, 23	22, 25	1		
22, 24	22, 23	22, 25	1		
23, 24	22, 23	23		1	
23, 24	22, 23	23, 46	1		
23, 24	22, 24	21, 24	1		
23, 26	22, 26	23, 26	1		
19, 23	23, 24	18, 23		1	
19, 23	23, 24	22, 24	1		
20, 24	23, 24	22, 24		1	
21, 23	23, 24	20, 23	1		
22, 23	23, 24	23, 25		1	
22, 24	23, 24	20, 24		1	
22, 24	23, 24	24			1
23	23, 24	21, 23	1		

23	23, 24	23		1	
23	23, 24	23, 23.3	1		
23, 25	23, 24	23, 25			1
23, 26	23, 24	23, 25	1		
24	23, 24	20, 24		1	
24, 25	23, 24	22, 24	1		
24, 26	23, 24	21, 24			1
24, 27	23, 24	21, 24		1	
22, 25	23, 25	24, 25	1		
18, 25	24, 25	21, 25			1
18.2, 24	24, 25	23, 24			1
20, 24	24, 25	21, 24		1	
20, 24	24, 25	22, 24		1	
20, 24	24, 25	23, 24			1
21, 24	24, 25	23, 24		1	
21, 24	24, 25	24		1	
22, 24	24, 25	21, 24	1		
22, 24	24, 25	21, 24	1		
22, 25	24, 25	22, 25		1	
23, 24	24, 25	24, 26			1
24	24, 25	20, 24		1	
24	24, 25	21, 24		1	
25, 26	24, 25	23, 25			1
23, 26	25, 26	22.3, 26	1		
23, 26	25, 26	23, 26		1	
25	25, 26	23, 25	1		
26, 27	25, 26	21, 26			1
21, 27	27, 28	24, 27	1		

Indeterminate Mutations at Locus VWA

Phenotypes Observed			Number Observed by Race		
MOTHER'S ALLELES	**CHILD'S ALLELES**	**FATHER'S ALLELES**	**BLK**	**CAU**	**HIS**
Total Maternal Meioses			**67780**	**68999**	**19201**
Total Paternal Meioses			**81516**	**69414**	**21712**
15, 16	12, 16	16, 19	1		
14, 18	14, 15	14	1		
15	14, 15	15, 20	1		
14, 17	14, 18	14, 17		1	
15	15, 16	15, 19		1	
15, 19	15, 16	15, 18	1	1	
16	15, 16	16, 18	1		
16, 17	15, 16	16, 18	1		
15, 18	15, 17	15, 18	1		
15, 17	15, 18	15, 17	1		
17	16, 17	17, 19		1	
14, 16	16, 17	14, 16		1	
14, 16	16, 17	16		1	
15, 16	16, 17	16	1	1	
15, 17	16, 17	17, 18		1	
16	16, 17	15, 16	1		
16	16, 17	16, 18	1		
16, 18	16, 17	15, 16		1	
16, 18	16, 17	16, 18		1	
16, 18	16, 17	16, 19	1	1	
17, 18	16, 17	14, 17	1		
17, 18	16, 17	17		1	1
17, 19	16, 17	17			1
17, 19	16, 17	17, 19	1		
15, 16	16, 18	16, 17			1
16	16, 18	16, 17			1
16, 17	16, 18	16, 17	1		
16, 17	16, 18	16, 19	1	1	1
16, 19	16, 18	16, 17	1		
16, 19	16, 18	16, 19		1	
17, 18	16, 18	17, 18	1		
16	16, 19	16, 18		1	
16, 18	16, 19	16, 20		1	
15, 17	17, 18	17, 19	2		
16, 18	17, 18	18	1		
13, 18	17, 18	15, 18	1		
16, 17	17, 18	16, 17			1
16, 17	17, 18	17, 19		1	

17	17, 18	13, 17	1		
17	17, 18	14, 17	1		
17	17, 18	15, 17	1		
17	17, 18	16, 17		1	
17	17, 18	17			1
17	17, 18	17, 19		1	1
17, 19	17, 18	17			1
18	17, 18	18		1	
18, 19	17, 18	14, 18	1		
18, 20	17, 18	18			1
16, 17	17, 19	17, 20			1
14, 17	17, 20	17, 19		1	
14, 19	18, 19	17, 19	1		
15, 18	18, 19	17, 18	1		
15, 19	18, 19	16, 19	1		
16, 18	18, 19	14, 18			1
16, 18	18, 19	17, 18	1		
17, 18	18, 19	16, 18			1
17, 18	18, 19	18	1		
17, 18	18, 19	18, 20		1	
17, 19	18, 19	19		1	
18	18, 19	16, 18		1	
18, 21	18, 19	17, 18		1	
19, 10	18, 19	17, 19		1	
17, 19	19, 20	16, 19	1		
19, 20	20, 21	18, 20	1		