Kelley, Shamika M., Assessment of DNA Transfer Events Involving Routine Human Behavior. Master of Science (Forensic Genetics), May, 2010, 43 pp., 4 tables, 29 figures, reference list, 10 titles.

DNA transfer events are affected by routine human actions and can impact the interpretation of forensic evidence results. Some scientists have inferred that secondary transfer events lead to only minimal amount of DNA yield and when two people are involved, the DNA profile of the primary person who had contact with the item is typically prominent.

To assess the effects of secondary DNA transfer events on DNA quantity, methods similar to those of Lowe *et al.* [1] were used. We have recruited 12 volunteers (subjects) to participate in a 4-part study consisting of every day human routine behaviors. These routine behaviors include handshaking, holding a pen in the mouth, and licking the thumb before turning the page.

Sufficient quantities of DNA were obtained via secondary and tertiary transfer. DNA profiles could be observed from an individual to an object even though that individual did not directly touch the object.

KEYWORDS: forensic science, transfer, touch DNA

ASSESSMENT OF DNA TRANSFER EVENTS INVOLVING HUMAN ROUTINE BEHAVIOR

INTERNSHIP PRACTICUM REPORT

Presented to the Graduate Council of the

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For the Degree of

MASTER OF SCIENCE

By

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TABLE OF CONTENTS

Page

LIST OF TABLES

Page

LIST OF FIGURES

Page

CHAPTER I

INTRODUCTION

In 1997, van Oorschot *et al.* [2] introduced the possibility of obtaining an individual's DNA profile from objects that have been touched. This method of obtaining DNA from items that have been handled is often referred to as "touch DNA" analysis. Touch DNA refers to DNA that is transferred to items through casual contact. Using touch DNA analysis, evidentiary items such as bedding [3] cartridge cases [4] and fingerprints [5] have been successfully typed for DNA profiles. Touch DNA analysis is becoming more widely utilized.

Now, that the amount of DNA being considered for analysis is substantially reduced the majority of touch samples fall into low copy number (LCN) range. Budowle *et al.* [6] define LCN typing generally as the analysis of any sample containing less than 200 picograms of template DNA but more aptly as any DNA sample where the results are below the stochastic threshold for reliable interpretation.

The foundation of touch DNA is based on Locard's Exchange Principle [7] which theorizes that when two objects come into contact, there is some form of exchange of material. Transfer of DNA can occur from person to object or from one person to another person and then to an object. Primary transfer occurs when DNA is directly transferred from a person to an object. Secondary transfer involves two DNA transfer events. For example, secondary transfer occurs when the DNA deposited on one object is transferred to a second object or person.

Previous studies [1, 8] have demonstrated that secondary transfer of DNA from one individual to another or an object by casual contact may occur under certain 'ideal' conditions, *e.g.* using a clean object that is touched with washed hands. Based on the results of these studies, scientists assert that secondary transfer events lead to only minimal amounts of DNA yield and when two people are involved, the DNA profile of the primary person who had contact with the item is typically prominent. However, many of these studies have not taken into account more typical ways that people transfer DNA by contact and, hence, transfer their DNA to objects [6], likely transferring relatively large quantities of DNA. For instance, when people hold pens in their mouths and lick their thumbs to turn a page, DNA is present at higher amounts due to these activities as opposed to washed hands performing a handshake. Therefore, this study investigates the potential to detect DNA profiles resulting from secondary transfer under conditions and time intervals that better mimic routine human behaviors.

Specific Aims

The analysis of DNA from touched objects, transferred through primary or secondary transfer events, has become the focus of recent forensic investigations. Primary transfer is the transfer of DNA from an individual to an item. For example, when a person touches a pencil, we know that, depending on a number of variables, it is possible for DNA-bearing cells to slough off the person's hand and adhere to the surface of the pencil. In secondary transfer, two transfer events take place. For example, Person A shakes Person B's hand and transfers his/her DNA to Person B. Person B then touches the pencil transferring the DNA to the pencil. During this secondary transfer event, Person B acted as the vector for the DNA to be deposited from Person A to the item. This would mean that even though Person A never actually touched the pencil, his/her DNA could be present on it.

As previously stated, some scientists have inferred that secondary transfer events lead to only minimal amount of DNA yield, and when two people are involved, the DNA profile of the primary person who had contact with the item is typically prominent. Since studies to date have not assessed more common ways people may transfer DNA, we investigated the potential transfer of DNA by a body fluid not tested in current studies, saliva, because it contains many epithelial cells and is routinely found on hands and objects that people handle. We hypothesized that saliva epithelial cells are more likely involved in DNA transfer versus skin cells and that the primary profile is not obtained from the last individual who had direct contact with the item. We addressed this hypothesis with the following specific aims:

1) Assess the quantity of DNA recovered after transfer events
2) Assess the predominant contributor the DNA transfer profiles

To assess the effects of secondary DNA transfer events on DNA quantity, methods similar to those of Lowe *et al.* [1] were used. The Lowe *et al.* study carried out structured secondary transfer experiments but did not consider saliva. We observed DNA recovery after a series of human routine actions at different time intervals. These routine actions include handshaking (without and with moisture to mimic perspiration), holding a pen with the mouth, and the licking of thumbs before turning four pages. This information is essential for assessing the impact of the amount of DNA recovered from an object and whether that amount or the dominant profile can be correlated with a primary or secondary transfer event.

CHAPTER II

MATERIALS AND METHODS

DNA isolation and typing took place in the University of North Texas Center for Human Identification Laboratories located in the Center for BioHealth (CBH), Room 250, at the University of North Texas Health Science Center at Ft. Worth.

Sample collection

A total of 12 individuals, male and female, over 18 years old were recruited to provide biological samples. Participants were recruited from the population of students, faculty and staff at the University of North Texas Health Science Center at Fort Worth. We collected buccal swab samples from these individuals as references. The research subjects were arbitrarily partnered with a second research volunteer. All individuals were anonymized and the study has UNTHSC IRB approval.

At the start of all experiments, the subjects were asked to wash and dry their hands. Tubes were swabbed before (negative control) and after gripping (Figure 1). All handled tubes were swabbed using a double swab technique [9] with a sterile swab moistened with sterile distilled water, followed by a second sterile dry swab. The entire exterior surface of the tubes was swabbed except for the top and bottom. The samples collected during the experiments were labeled using a unique sample naming system (Table 1).

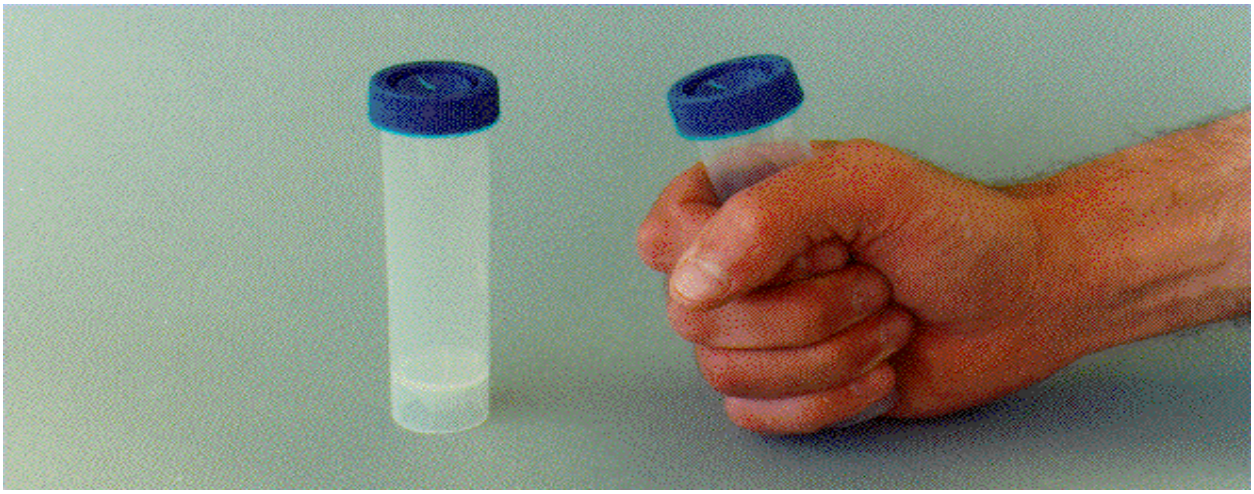

Figure 1. Subjects held 50 mL conical tube for 10 secs. Tubes were swabbed using the double swab technique.

Table 1. Chart listing the naming scheme for the samples collected during the experiments.

Sample Naming System	
Pairs	**P1-P6**
Sample Types	
Lick Thumb	T
Turn Pages	P
Pen Bite	B
Atomizer (Sweat)	S
Time Intervals	
5 min-5 min	A
5 min-30 min	B
30 min-5 min	C
30 min-30 min	D

Experiment 1: Handshake

Using a paired study, the individual (A), the donor, of each pair licked his thumb, allowed it to dry for either 5 or 30 minutes, and then placed it in the palm of the individual (B), the vector for a period of 1 minute of contact. Following the 1 minute handshake, the vector waited for either 5 or 30 minutes and then gripped a sterile 50 mL plastic tube for ten seconds. These samples were labeled as TA, TB, TC, and TD ("T" for thumb and "A-D" for the designated time interval)

Experiment 2: Handshake (atomizer used)

Experiment 1 was repeated, but in this experiment an atomizer (water spray bottle) was used to deliver a fine mist of water to the palm of the volunteers' hands in order to simulate sweaty palms. These samples were labeled as TSA, TSB, TSC, and TSD ("T" for thumb, "S" for sweat and "A-D" for the designated time interval).

Experiment 3: Holding a pen in mouth

A pen was used as a potential saliva transfer vector. Individual (A), the donor was asked to place a pen in his/her mouth for 2 minutes. After a period of 30 minutes, the pen was placed into the palm of the individual (B), the vector, and following periods of 5 and 30 minutes, the vector then held a tube for 10 seconds and the tube was swabbed for analysis. These samples were labeled as BA, BB, BC, and BD ("B" for biting pen, "A-D" for designated time interval). The design of this experiment is actually tertiary transfer instead of secondary transfer due to three transfer events that take place.

Experiment 4: Holding a pen in mouth (atomizer used)

Experiment 3 was repeated, but in this experiment, an atomizer (water spray bottle) was used to deliver a fine mist of water to the palm of the volunteers' hands in order to simulate

sweaty palms. These samples were labeled as BSA, BSB, BSC, and BSD ("B" for biting pen, "S" for sweat, and "A-D" for designated time interval).

Experiment 5: Licking thumb before turning pages

Volunteers were asked to lick their thumbs and using common computer paper, turn 4 pages, followed by allowing the thumb to dry for 5 minutes and then placing the thumb in the palm of individual (B), the vector, for 1 minute. Following a 5 and 30 minute time interval, individual (B), the vector, held a sterile tube for 10 seconds and the tube was swabbed for analysis. These samples were labeled as PA, PB, PC, and PD ("P" for page turning, "A-D" for designated time interval).

Experiment 6: Licking thumb before turning pages (used)

Experiment 5 was repeated, but in this experiment, an atomizer (water spray bottle) was used to deliver a fine mist of water to the palm of the volunteers' hands in order to simulate sweaty palms. These samples were labeled as PSA, PSB, PSC, and PSD ("P" for page turning, "S" for sweat, and "A-D" for designated time interval).

Donor and Vector reverse roles

For all experiment sets, the process was repeated by reversing the roles of the individuals in each pair. Therefore, each individual was the donor and the vector for each experiment. All subjects washed their hands immediately following the experiment under investigator's or investigator designee's supervision.

Sample processing

DNA was extracted using a QIAamp® DNA Mini Kit (Qiagen, Valencia, CA). The quantity of DNA was determined DNA using the Quantifiler™ Human DNA Quantification Kit DNA (Applied Biosystems, Foster City, CA). Autosomal STRs were typed using an

AmpFLSTR® Identifiler® PCR Amplification Kit (Applied Biosystems) at both 28 cycles and 34 cycles. DNA fragments were separated by capillary electrophoresis using an ABI prism® 3130*xl* Genetic Analyzer (Applied Biosystems). Autosomal STR data were compiled and analyzed using the GeneMapper® *ID* v3.2.1 software (Applied Biosystems).

CHAPTER III

RESULTS

The quantity of DNA detected during quantification ranged from 0 to 9 nanograms of total DNA recovered. The samples with the highest recovery were from experiments 3 and 4 (BSA, BSB, BB, and BSD from pairs 3-6). For typing, ten microliters of the extracted DNA (the final elution volume for each sample was 100 uL) were placed into a final reaction volume of twenty-five microliters for amplification. All of the samples were initially amplified using standard parameters at 28 cycles.

When using 28 cycles for amplification, ten of the samples (BB-P6, BC-P6, BD-P3, BSB-P3, BSB-P4, BSC-P2, BSC-P3, BSD-P3, TSA-P3, and TSA-P4) yielded at least one allele in the DNA profile (Table 2). After analyzing the ten DNA profiles, the samples that resulted in the most alleles (i.e., BSB-P4) as well as some samples that resulted in no alleles (i.e., BB-P5) were re-amplified using low copy number analyses at 34 cycles. The 12 samples that were re-amplified are BSB-P3-A, BSB-P3-B, BSB-P4-A, BSB-P4-B, BSB-P5-A, BSB-P5-B, BSB-P6-A, BSB-P6-B, BB-P5-A, BB-P5-B, BSD-P5-A, and BSD-P5-B. When 12 samples were amplified at 34 cycles more detectable results were obtained (Figure 2). The data presented in this report are from the subset of samples that were amplified with low copy parameters.

Table 2. Ten samples resulted in at least one allele when amplified with standard parameters at 28 cycles. The different colors correspond to different experiments. Height values are in relative fluorescent units (RFUs).

Sample Name	Marker	Allele 1	Height 1	Allele 2	Height 2
BB_P6	AMEL	X	106		
BC_P6	AMEL	X	55		
BD_P3	AMEL	Y	62		
TSA_P3	D8S1179	13	52		
TSA_P3	vWA	15	51		
TSA_P4	D8S1179	14	95		
BSB_P3	D8S1179	13	128		
BSB_P3	vWA	14	108	15	53
BSB_P3	AMEL	X	60	Y	71
BSB_P4	D8S1179	11	200	12	131
BSB_P4	D19S433	15	68		
BSB_P4	vWA	14	193	19	70
BSB_P4	TPOX	8	69		
BSB_P4	AMEL	X	199		
BSC_P2	D8S1179	16	61		
BSC_P3	D8S1179	13	76		
BSD_P3	D8S1179	13	52		

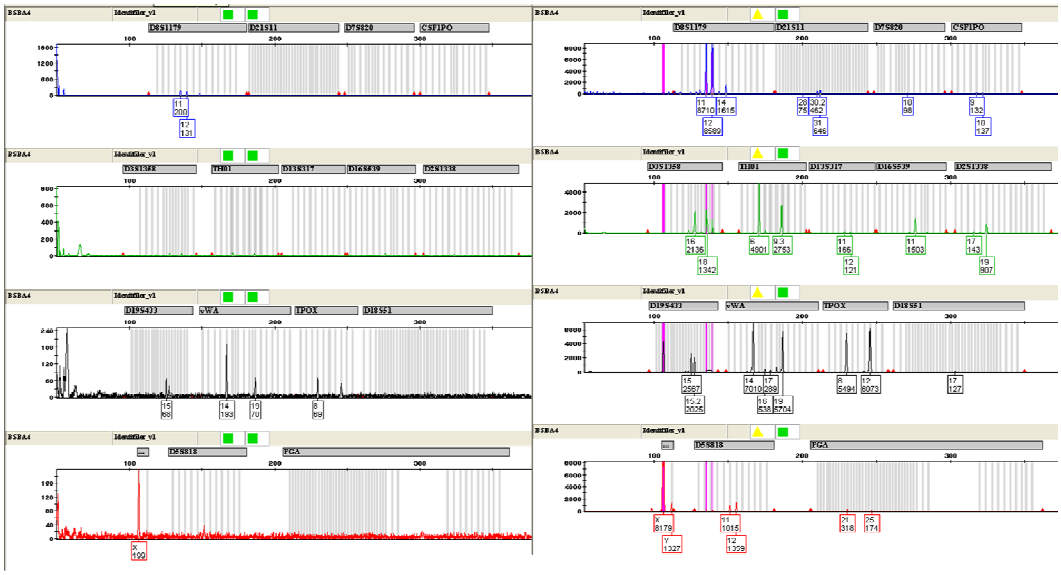

Figure 2. When the samples were amplified at 28 cycles they revealed limited results, as exemplified in the electropherogram of experiment BSB-P4-A on the left. The electropherogram on the right represents the results obtained at 34 cycles. A complete profile of BSB-P4-A was obtained at 34 cycles.

All samples resulted in mixtures except two, and those two pairings contained only the donor's profile. One of the 12 samples resulted in a complete profile while the rest were partial profiles. The non-shared allelic contributions (i.e., the alleles that the individuals do not have in common) were examined between the donors and vectors. An allele table for the subjects involved in the represented experiments is provided in Table 3. The trend observed in these experiments was that the donor contributed the majority of alleles in all experiments except one (Figure 3). For experiment BSB-P5-B, the vector of pair 5 contributed a greater number of alleles to the mixture DNA profile than the donor.

Table 3. Reference profiles of individuals in pairs 3-6. These are the profiles of the individuals that participated in the subset of re-amplified 12 experiments that were used for this study.

	Pair 3		Pair 4		Pair 5		Pair 6	
	Ref 5	Ref 6	Ref 7	Ref 8	Ref 9	Ref 10	Ref 11	Ref 12
D8S1179	15,17	13,13	14,14	11,12	12,15	11,13	14,15	12,13
D21S11	28,30	27,28	28,32.2	30.2,31	27,29	31,31.2	28,33.2	28,30.2
D7S820	9,9	10,10	11,11	10,10	8,10	10,11	8,11	10,10
CSF1PO	12,12	11,11	11,11	9,10	10,12	10,13	10,11	10,10
D3S1358	16,17	15,15	16,16	16,18	14,17	15,18	15,16	17,17
TH01	7,9.3	8,9	6,9.3	6,9.3	7,9	8,9	8,9	8,9.3
D13S317	9,11	8,14	12,12	11,12	11,13	8,13	11,12	12,13
D16S539	11,12	11,11	11,12	11,11	8,11	10,11	8,12	11,12
D2S1338	17,19	20,23	17,23	19,19	19,24	24,25	18,21	18,24
D19S433	14,14	12,13.2	15,15	15,15.2	12,12	14,15	12,16.2	13,14
VWA	16,17	14,15	16,17	14,19	17,17	15,18	14,17	15,18
TPOX	9,11	8,11	8,8	8,12	10,11	8,9	8,8	8,11
D18S51	13,18	14,17	12,12	17,17	13,17	15,18	17,18	12,18
D5S818	12,13	11,12	11,12	11,12	12,13	10,12	10,11	12,13
FGA	20,22	22,25	22,23	21,25	19,24	22,26	21,22	22,25
AMEL	X,Y	X,Y	X,Y	X,X	X,X	X,Y	X,X	X,X

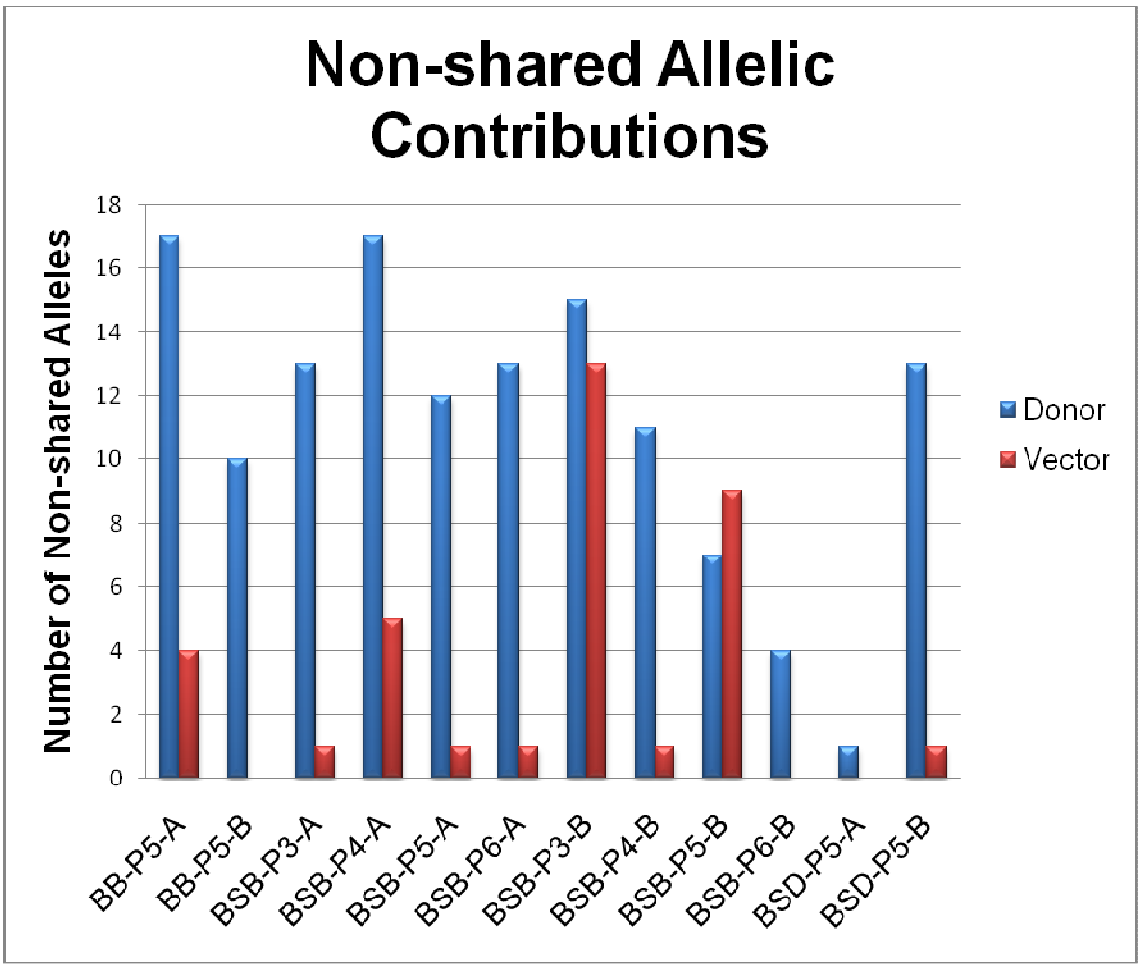

Figure 3. Non-shared Allelic Contributions. The number of non-shared alleles for the donors and vectors in all experiments. The red bars represent the vectors and the blue bars are the donors for each experiment.

The peak heights were compared between the donors and vectors of each experiment in order to determine how much DNA each individual was contributing to each DNA profile. The sum of the relative fluorescent units (RFUs) was calculated for each individual at each marker in each experiment. When pairs 3 through 6 from experiment BSB were compared, it was obvious that the majority of donor alleles had higher peaks than the vectors (Table 4). However, in

experiments BSB-P3-B and BSB-P5-B, the vector contributed more DNA (greater peak heights) than the donor.

Table 4. In the BSB experiments, the peak heights of pairs 3-6 were compared between the donors and vectors at each marker of each experiment. The yellow indicates person A being the donor while person B was the vector. The purple represents when the individuals switched roles as the vector and the donor.

BSB	Pair 3		Pair 4		Pair 5		Pair 6		Pair 3		Pair 4		Pair 5		Pair 6	
	5	6	7	8	9	10	11	12	5	6	7	8	9	10	11	12
Marker	D	V	D	V	D	V	D	V	D	V	D	V	D	V	D	V
D8S1179	8694	146	17299	1615	808	0	2572	0	5470	5714	1091	0	694	2601	1365	0
D21S11	273	0	1108	75	0	0	75	0	128	372	728	56	58	0	0	0
D7S820	0	0	98	0	0	0	0	0	0	0	0	0	0	0	0	0
CSF1PO	0	0	269	0	0	0	0	0	0	50	128	0	0	0	0	0
D3S1358	439	0	1342	0	0	0	126	0	311	445	0	0	0	74	0	0
TH01	2843	0	0	0	112	0	344	0	1285	1445	0	0	115	66	0	0
D13S317	0	0	166	0	0	0	0	0	0	0	0	0	0	0	0	0
D16S539	0	0	0	0	268	0	60	0	91	0	457	0	0	0	0	0
D2S1338	305	0	907	143	0	0	94	0	261	101	1336	0	0	0	0	0
D19S433	960	0	2025	0	217	0	254	0	527	807	0	0	73	98	0	0
VWA	11955	0	12714	827	845	346	716	0	3437	5144	1898	0	1564	1195	413	0
TPOX	4132	0	6073	0	2294	0	836	0	1948	2071	0	0	846	1339	0	0
D18S51	0	0	127	0	73	0	0	0	0	0	225	0	0	0	0	0
D5S818	178	0	0	0	257	0	65	54	85	109	0	0	0	0	0	0
FGA	0	0	492	0	54	0	0	0	0	0	136	0	0	0	0	0

A marker-by-marker comparison was performed between the donor and vector peak heights for all experiments (Figures 4-18). When comparing each marker, D7S820, CSF1PO, D13S317, and FGA had fewer alleles than the rest of the markers. D13S317, D16S539, D18S51, FGA, and D7S820 did not have any alleles from the vector. D8S1179, VWA , and TPOX resulted in the highest peaks among the markers. There was no consistent pattern to these observations; but generally larger sized amplicon loci showed fewer alleles than smaller sized amplicon loci as expected when processing low template DNA.

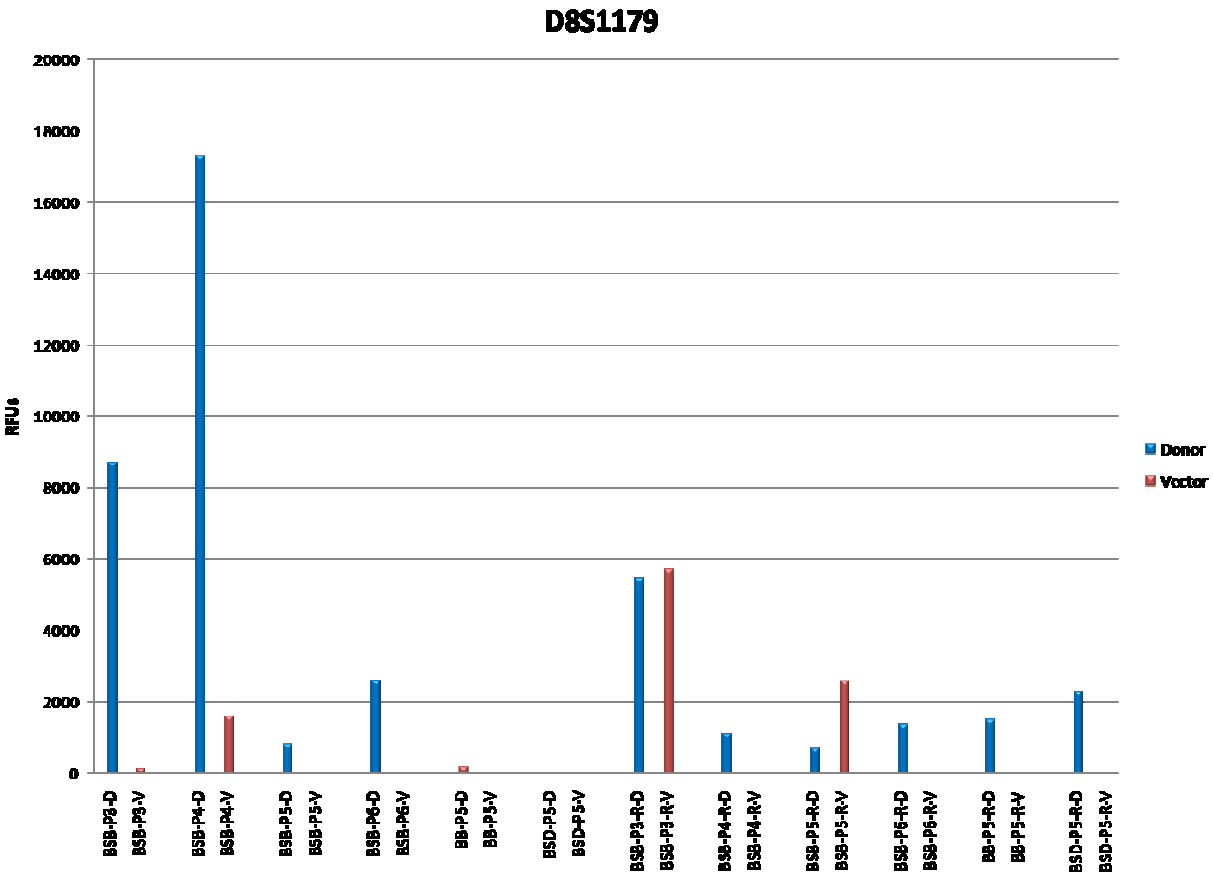

Figure 4. Peaks observed at marker D8S1179. The blue bars represent donor peaks and the red bars are vector peaks.

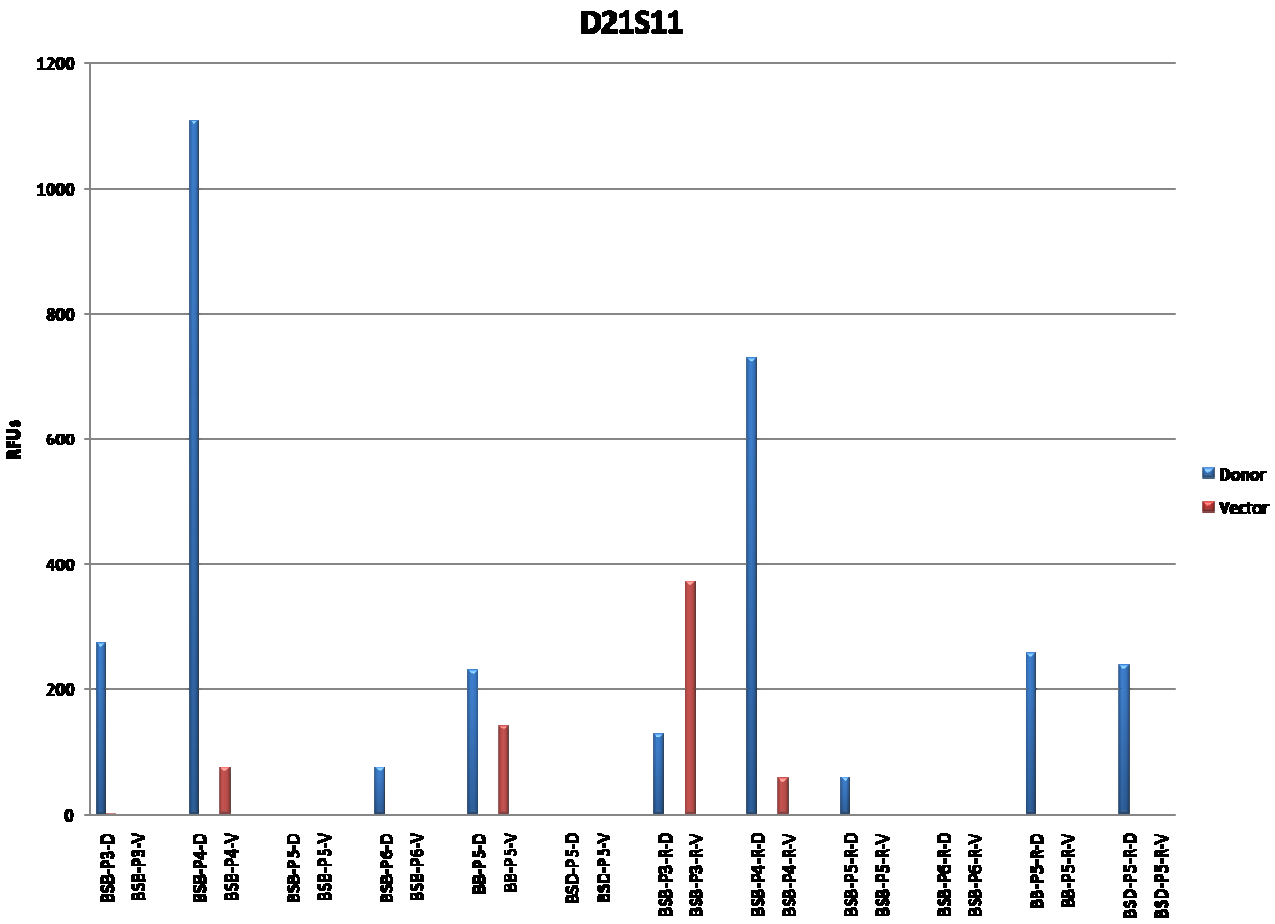

Figure 5. Peaks observed at marker D21S11. The blue bars represent donor peaks and the red bars are vector peaks.

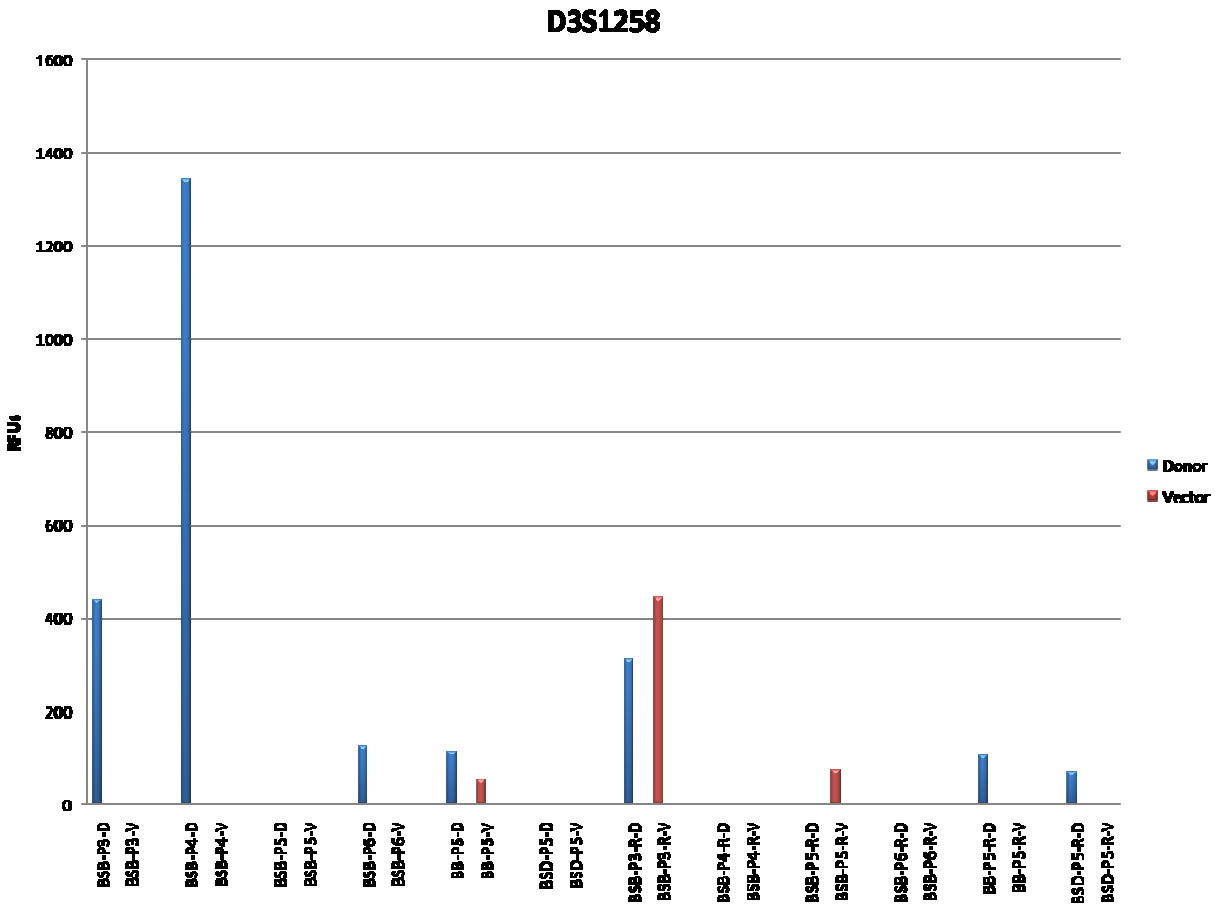

Figure 6. Peaks observed at marker D3S1258. The blue bars represent donor peaks and the red bars are vector peaks.

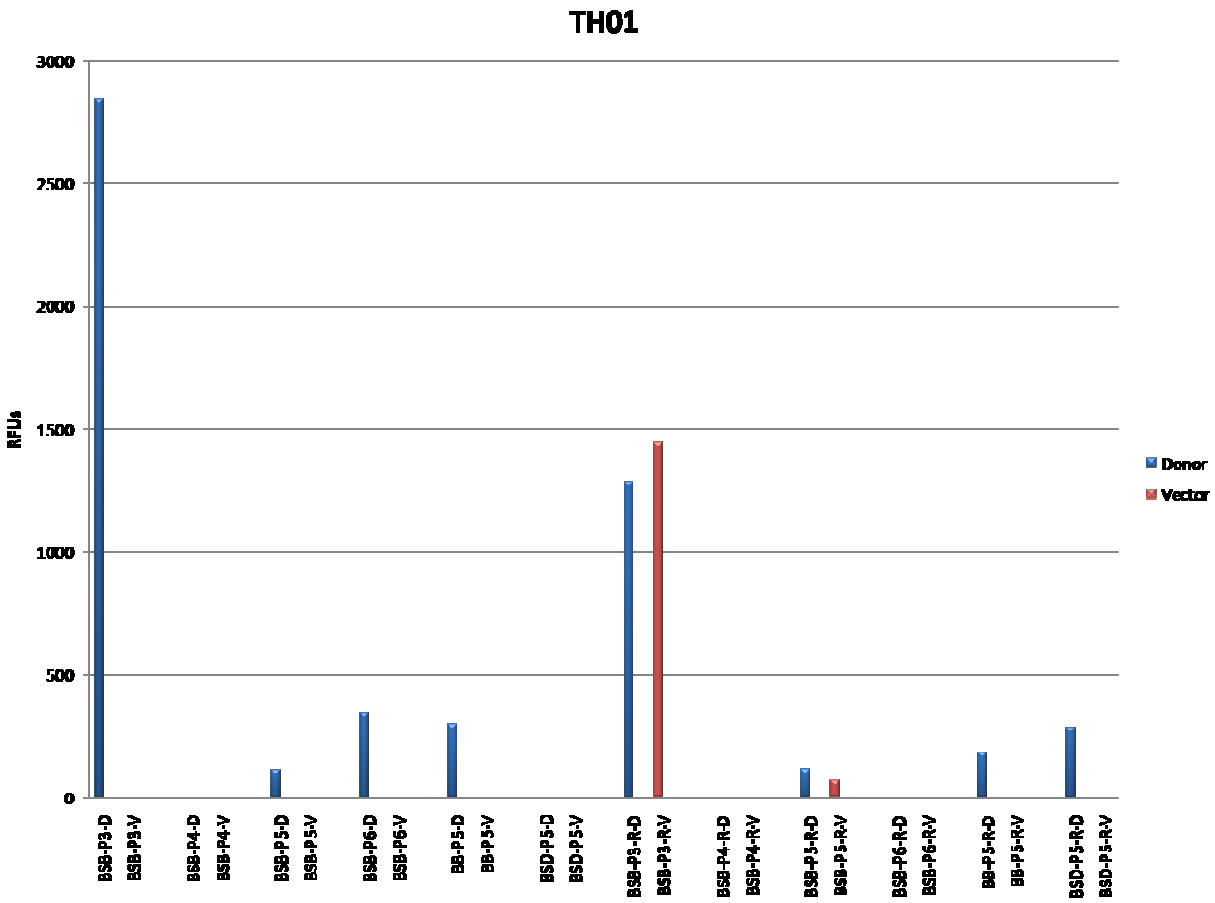

Figure 7. Peaks observed at marker TH01. The blue bars represent donor peaks and the red bars are vector peaks.

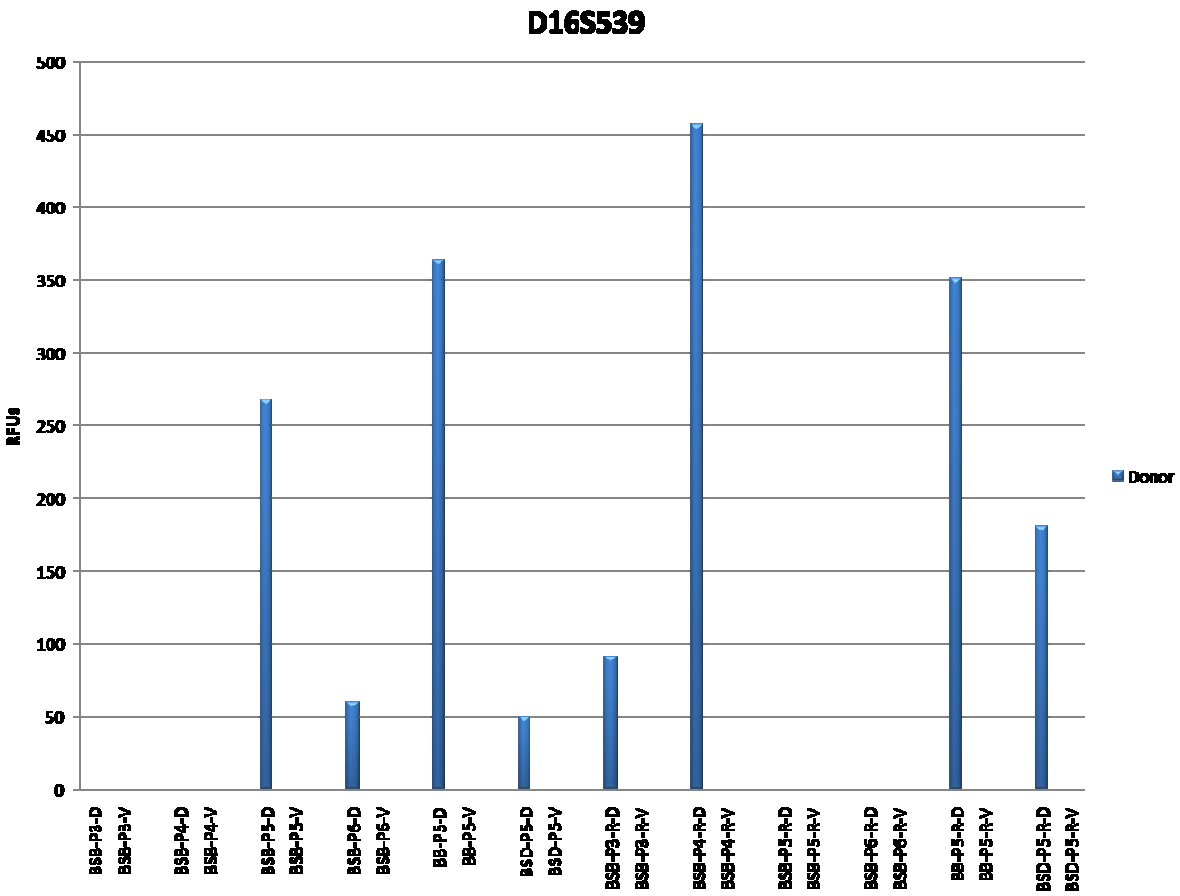

Figure 8. Peaks observed at marker D16S539. The blue bars represent donor peaks. There were no vectors present at this marker.

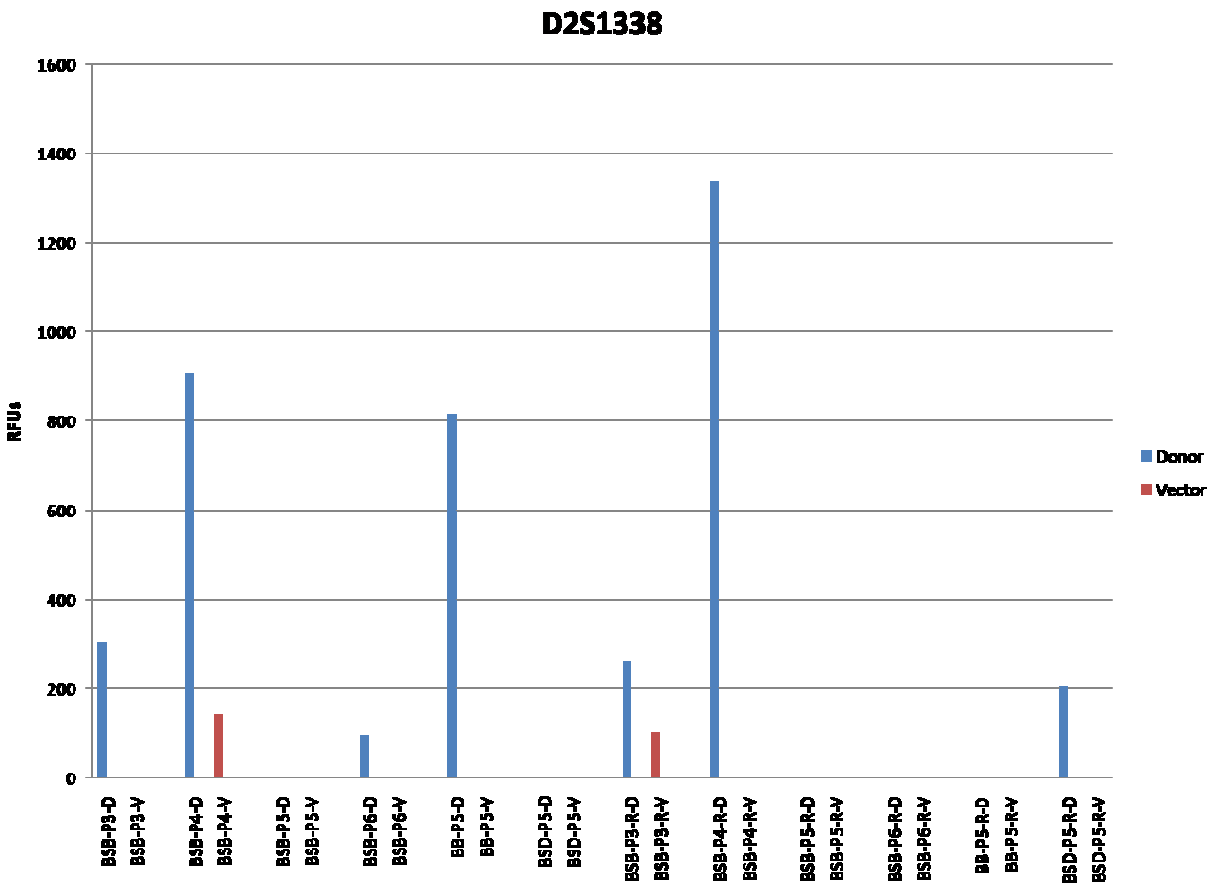

Figure 9. Peaks observed at marker D2S1338. The blue bars represent donor peaks and the red bars are vector peaks.

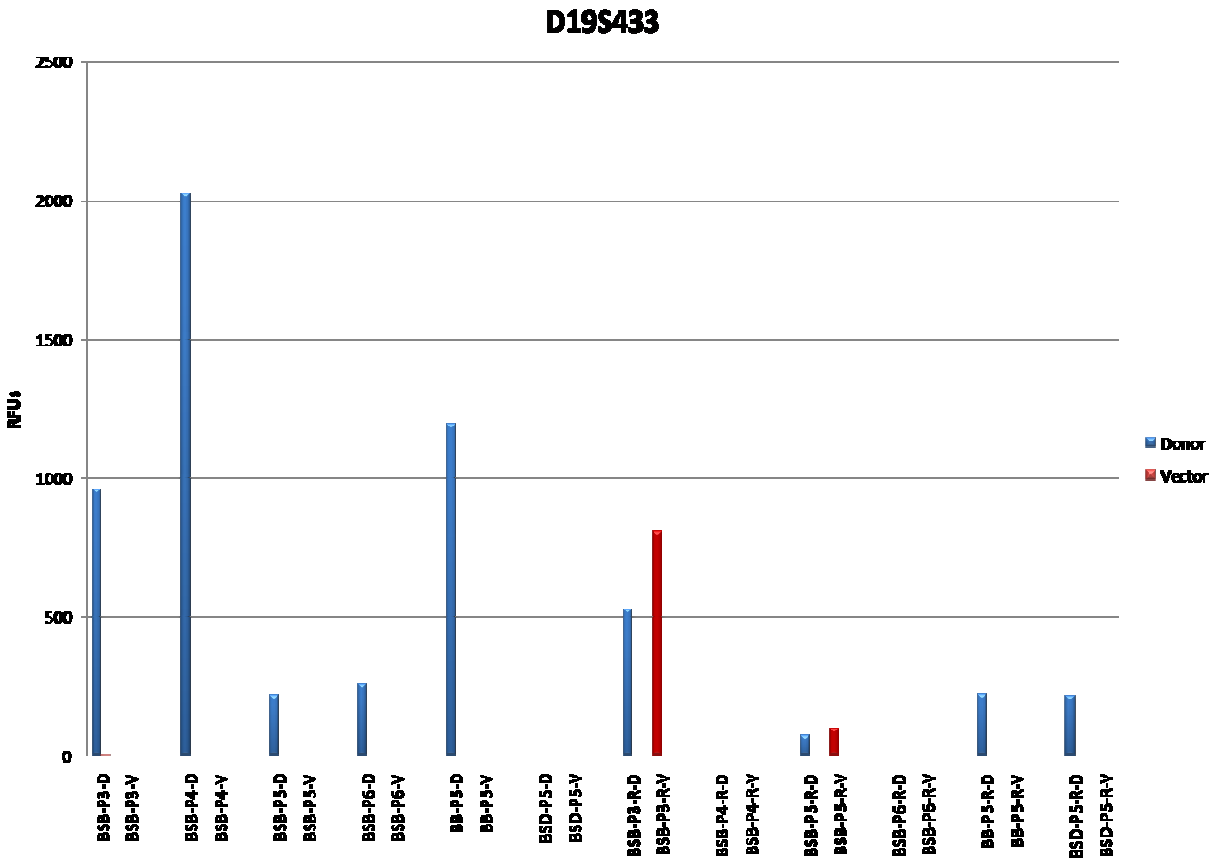

Figure 10. Peaks observed at marker D19S433. The blue bars represent donor peaks and the red bars are vector peaks.

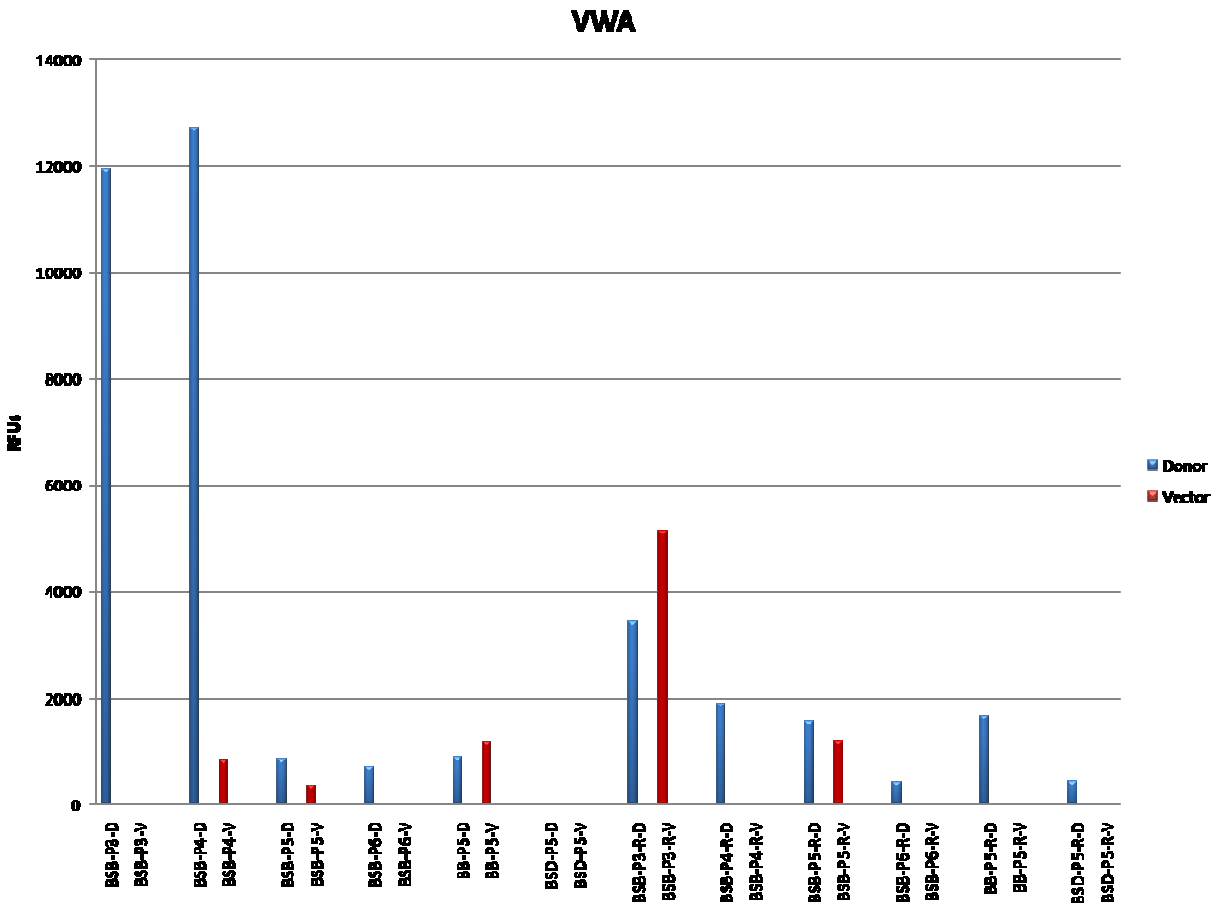

Figure 11. Peaks observed at marker VWA. The blue bars represent donor peaks and the red bars are vector peaks.

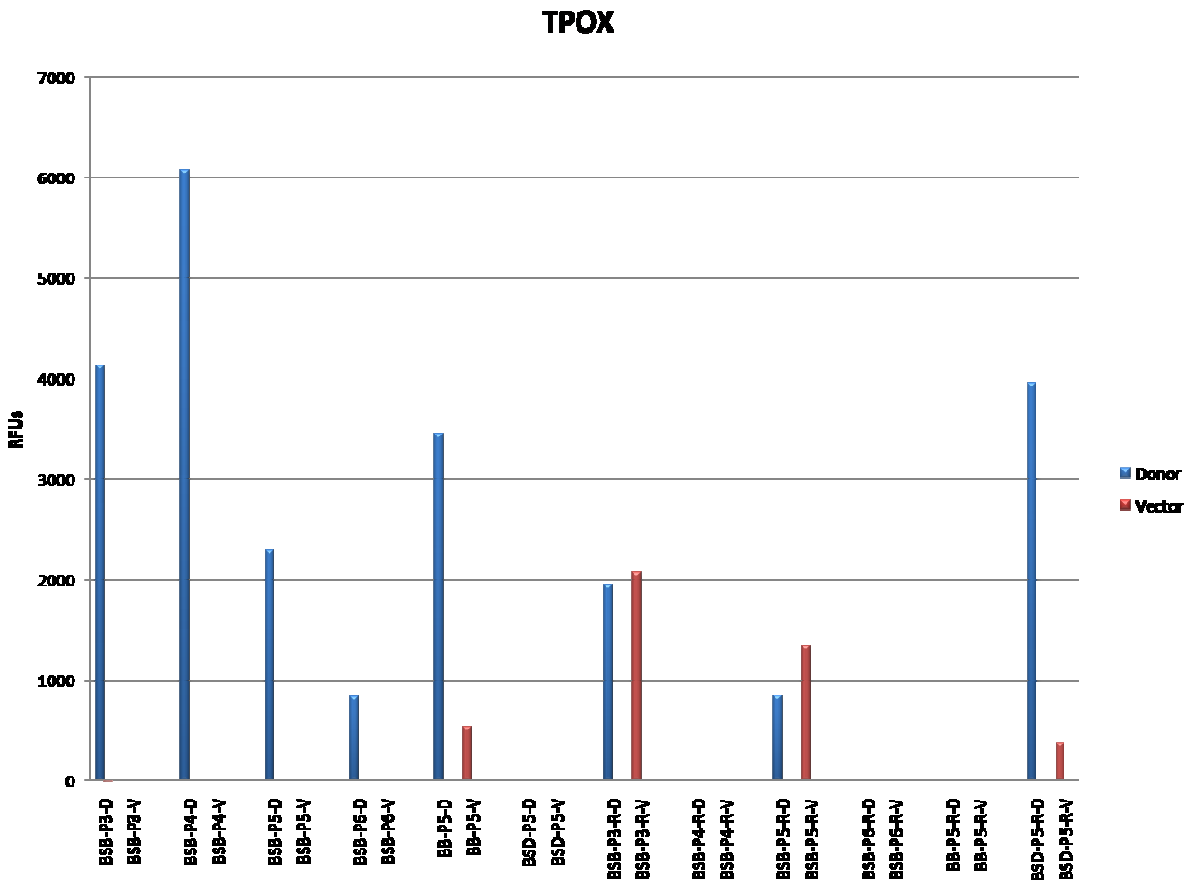

Figure 12. Peaks observed at marker TPOX. The blue bars represent donor peaks and the red bars are vector peaks.

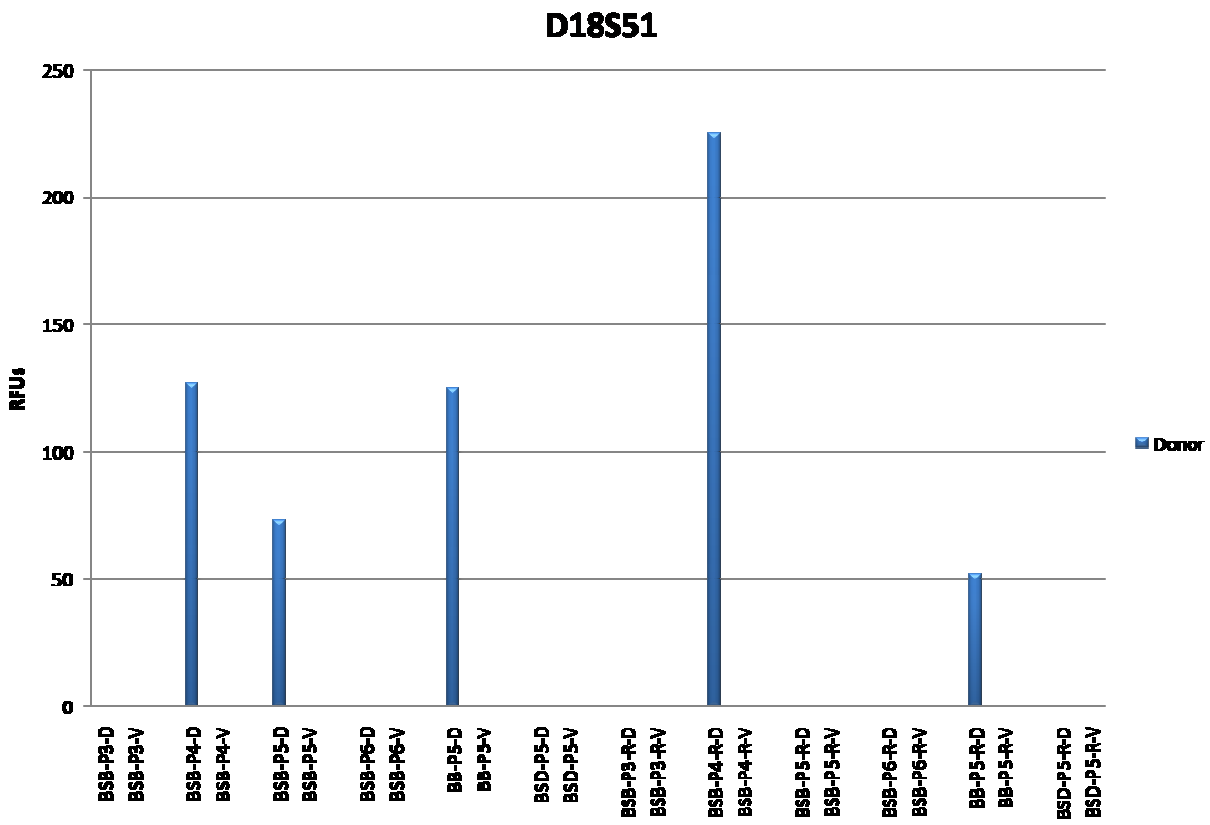

Figure 13. Peaks observed at marker D18S51. The blue bars represent donor peaks. There were no vectors present at this marker.

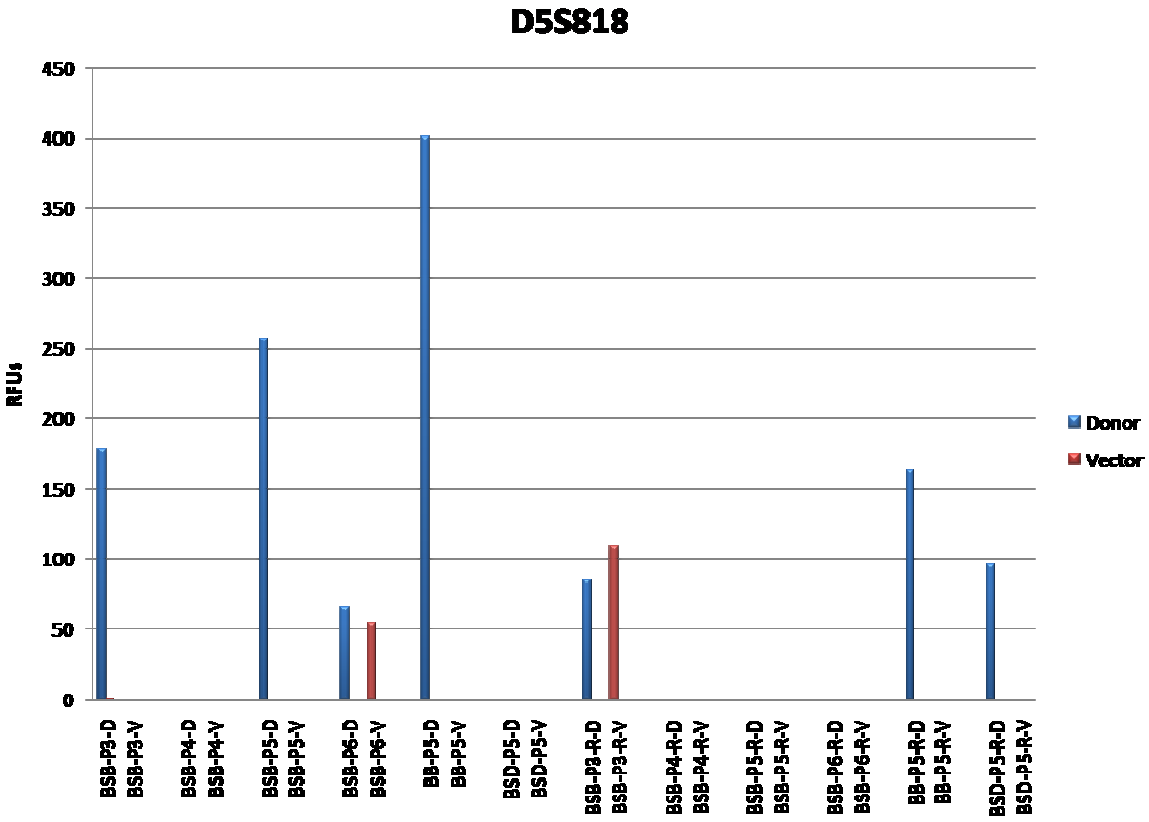

Figure 14. Peaks observed at marker D5S818. The blue bars represent donor peaks and the red bars are vector peaks.

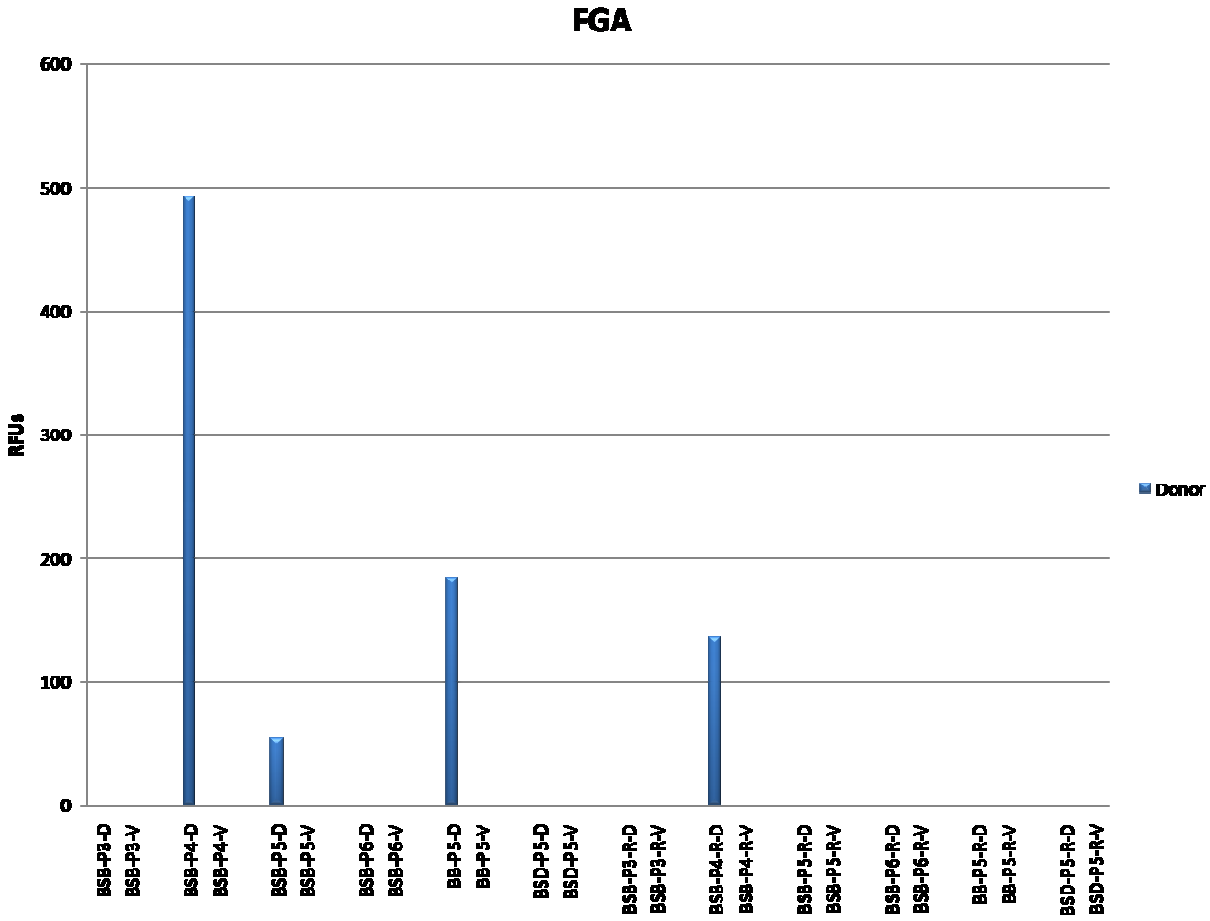

Figure 15. Peaks observed at marker FGA. The blue bars represent donor peaks. There were no vectors present at this marker.

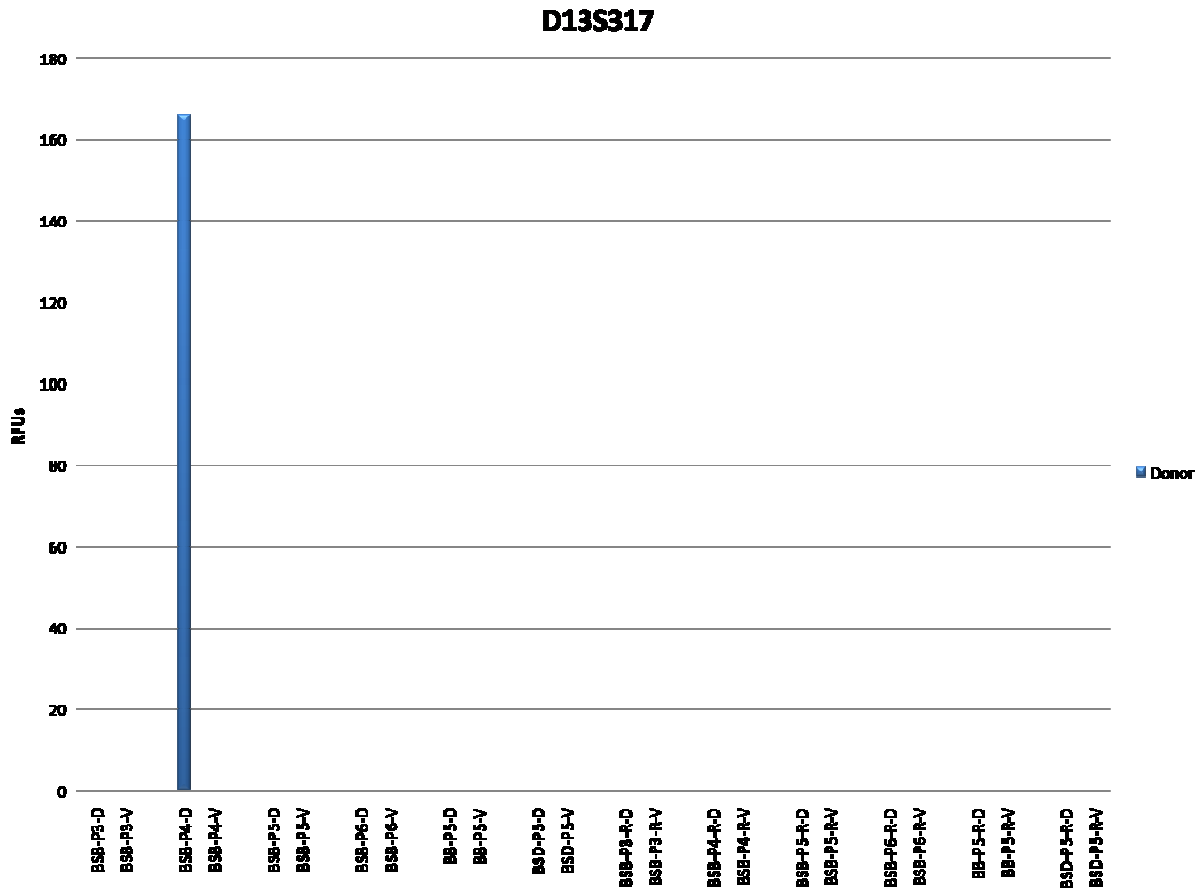

Figure 16. Peaks observed at marker D13S317. The blue bar represents the donor peak. There were no vectors present at this marker.

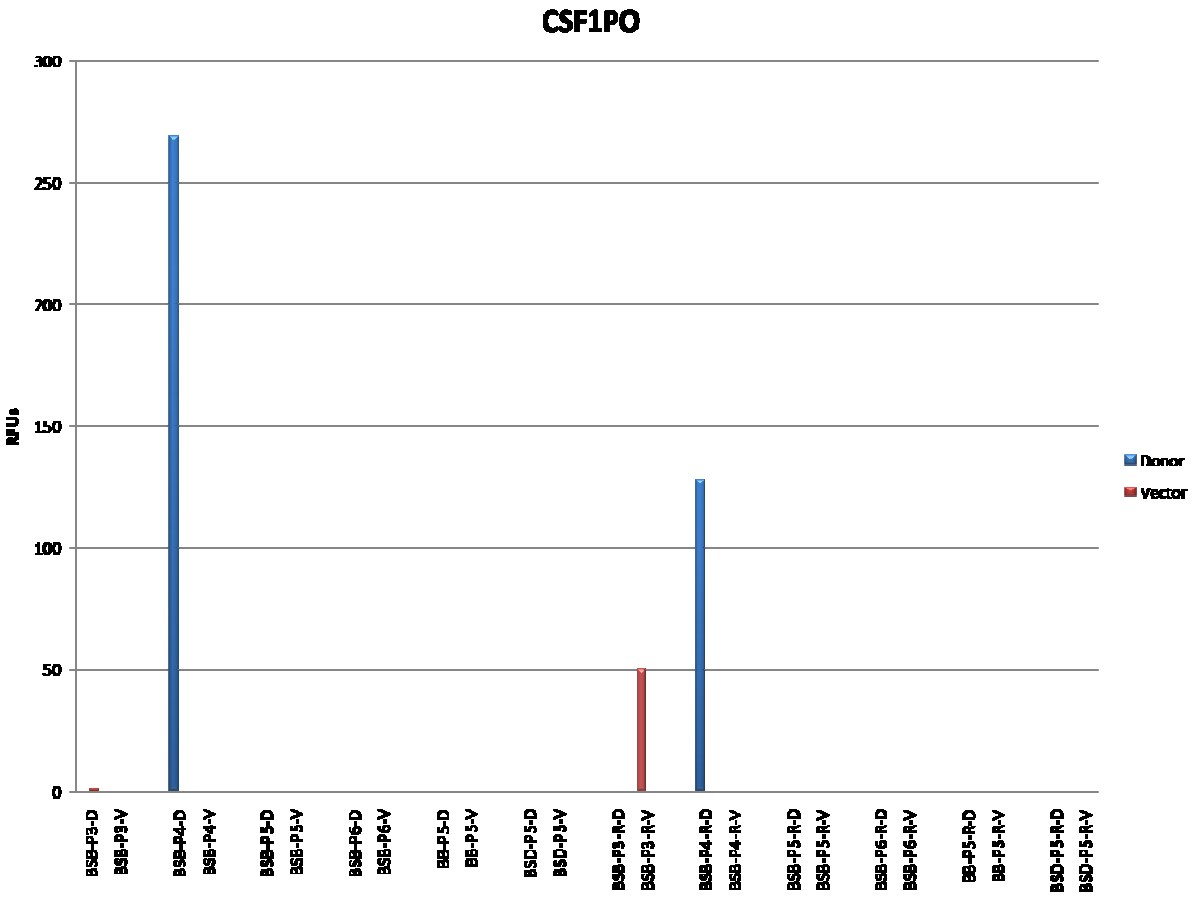

Figure 17. Peaks observed at marker CSF1PO. The blue bars represent donor peaks and the red bars are vector peaks.

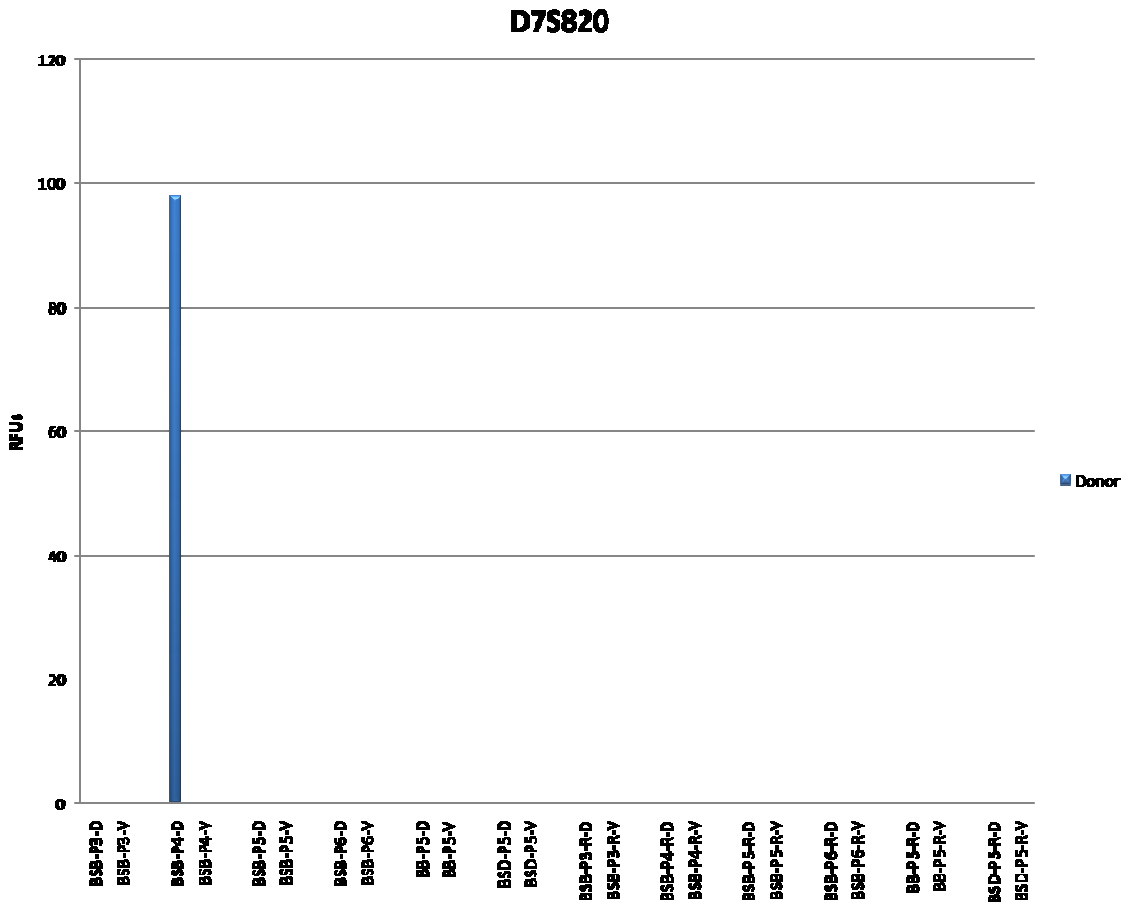

Figure 18. Peaks observed at marker D7S820. The blue bar represents the donor peak. There were no vectors present at this marker.

Experiment BSB-P4-B resulted in a partial profile. In this experiment, the donor was reference 7 and the vector was reference 8. There was little evidence of a mixture of both the donor and the vector after the tertiary transfer event (Figure 19). The donor contributed more alleles with higher peaks than the vector at non-shared alleles. A comparison of donor and vector is shown in Figures 21-23.

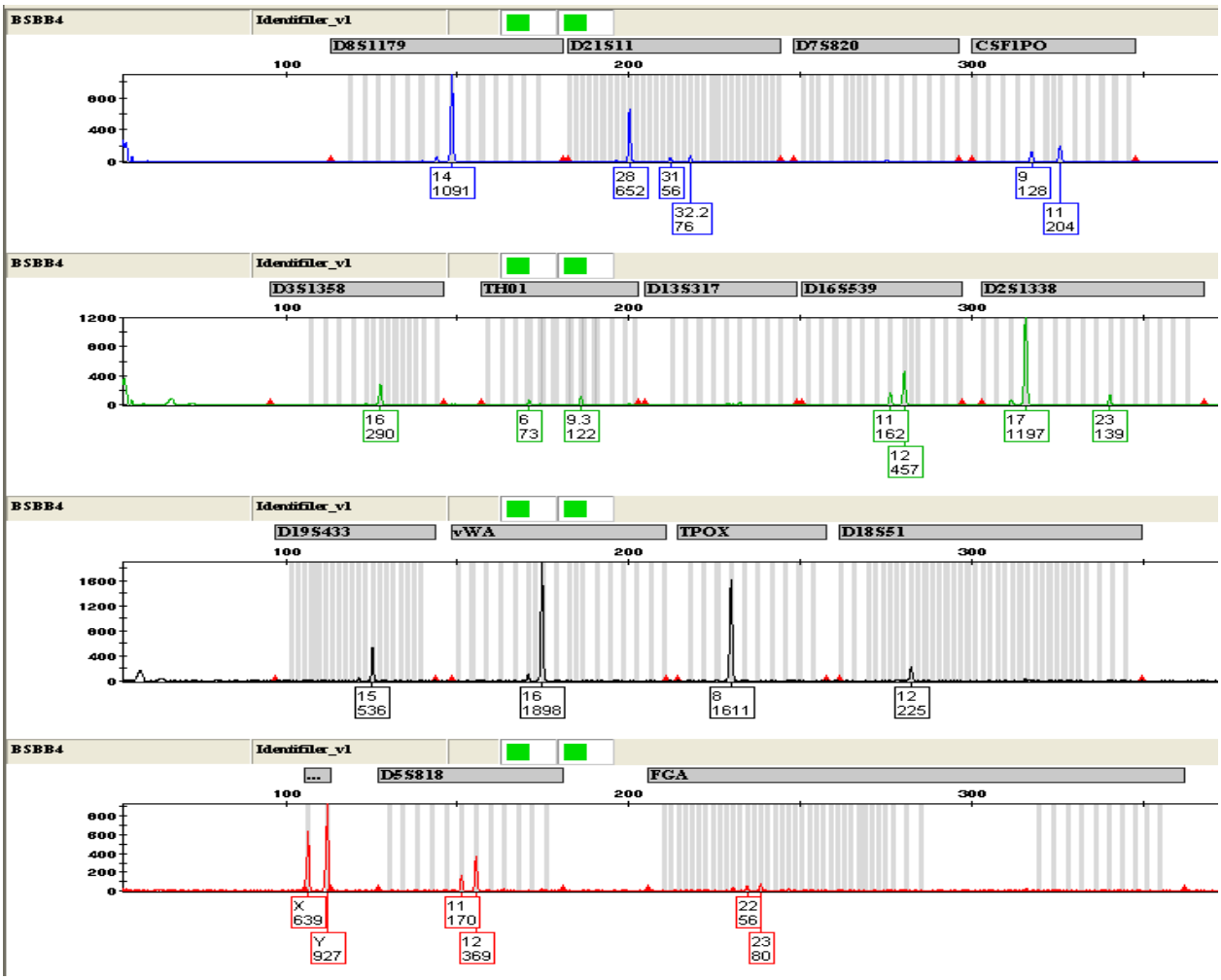

Figure 19. Experiment BSB-P4-B. DNA profile of donor and vector recovered from plastic tube after tertiary transfer.

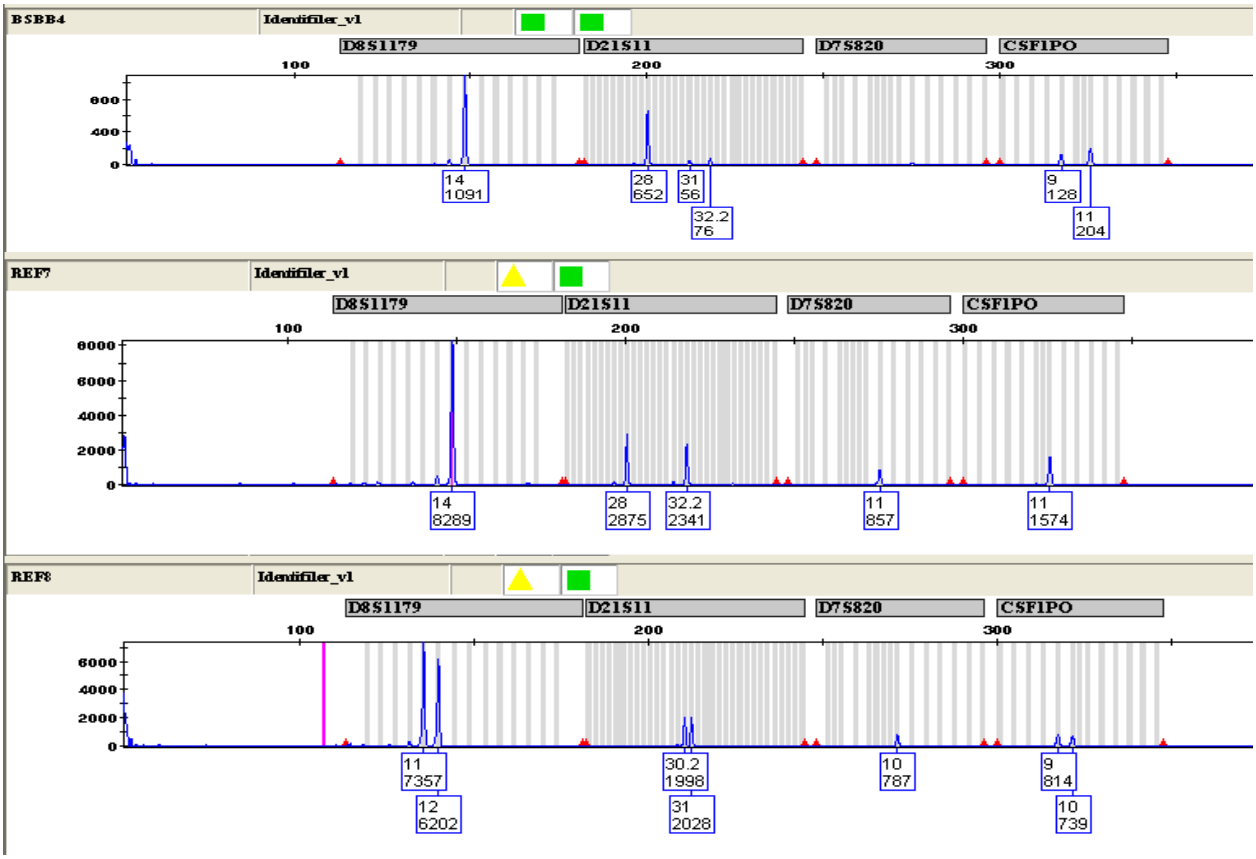

Figure 20. Comparison of blue (6-FAM™) dye labeled loci. The top is experiment BSB-P4-B, the middle is Reference 7 (donor) and the bottom is Reference 8 (vector).

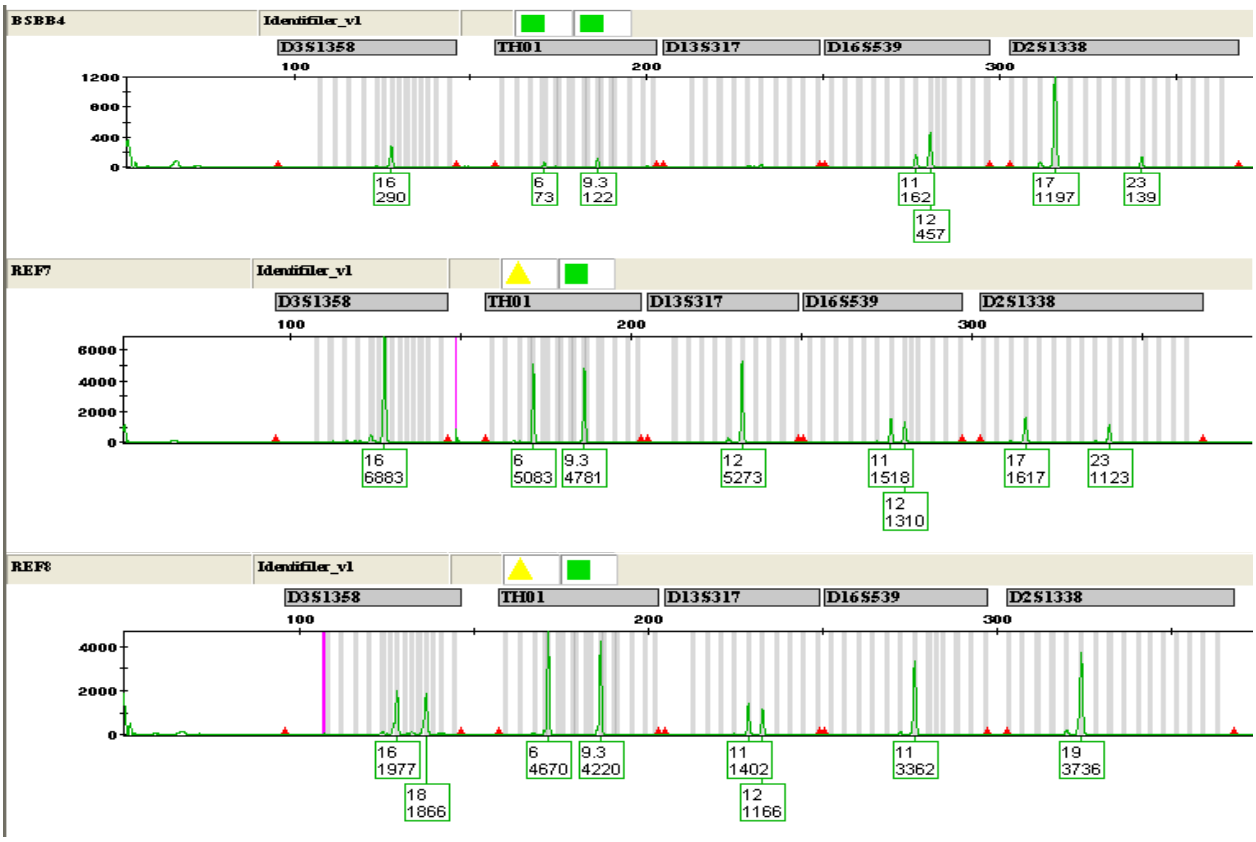

Figure 21. Comparison of green (VIC™) dye labeled loci. The top is experiment BSB-P4-B, the middle is Reference 7 (donor) and the bottom is Reference 8 (vector).

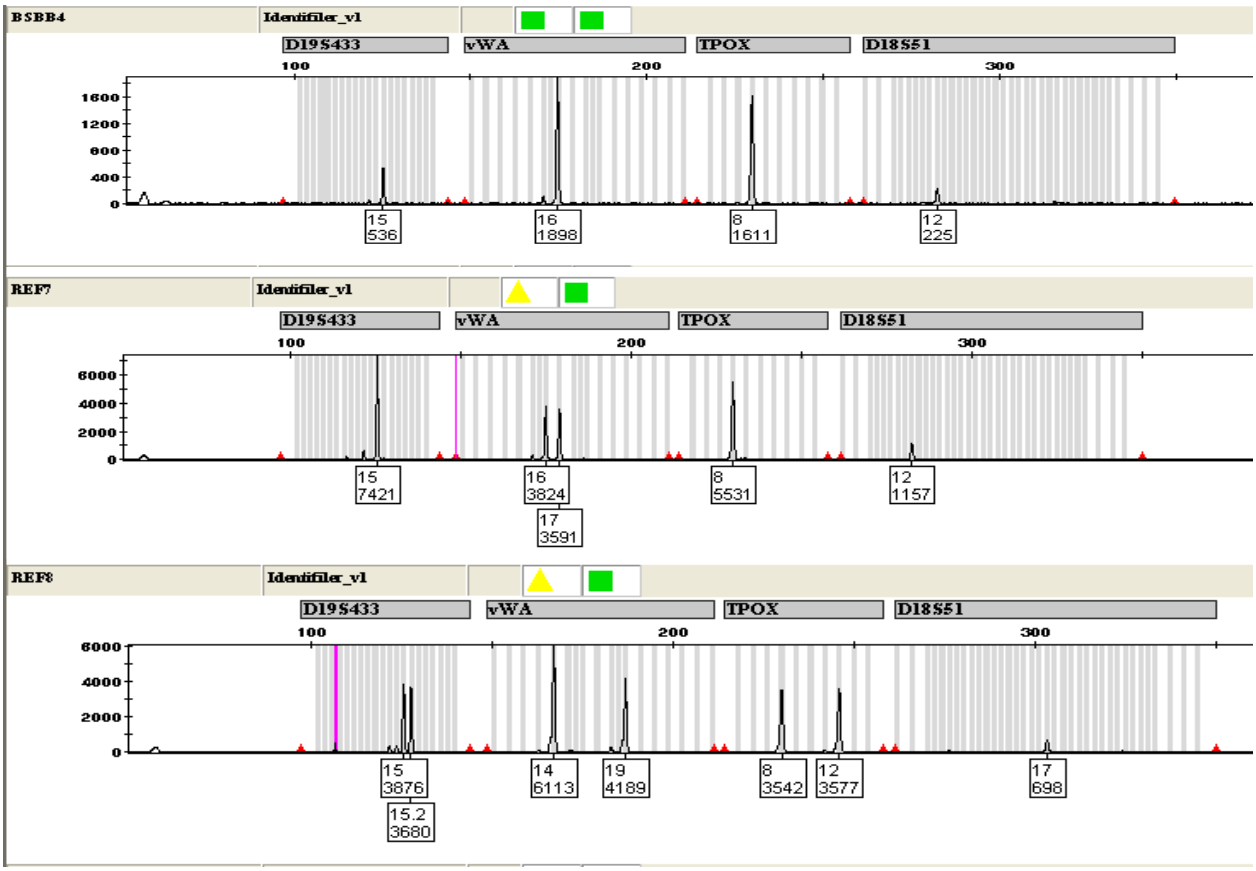

Figure 22. Comparison of yellow (NED™) dye labeled loci. The top is experiment BSB-P4-B, the middle is Reference 7 (donor) and the bottom is Reference 8 (vector).

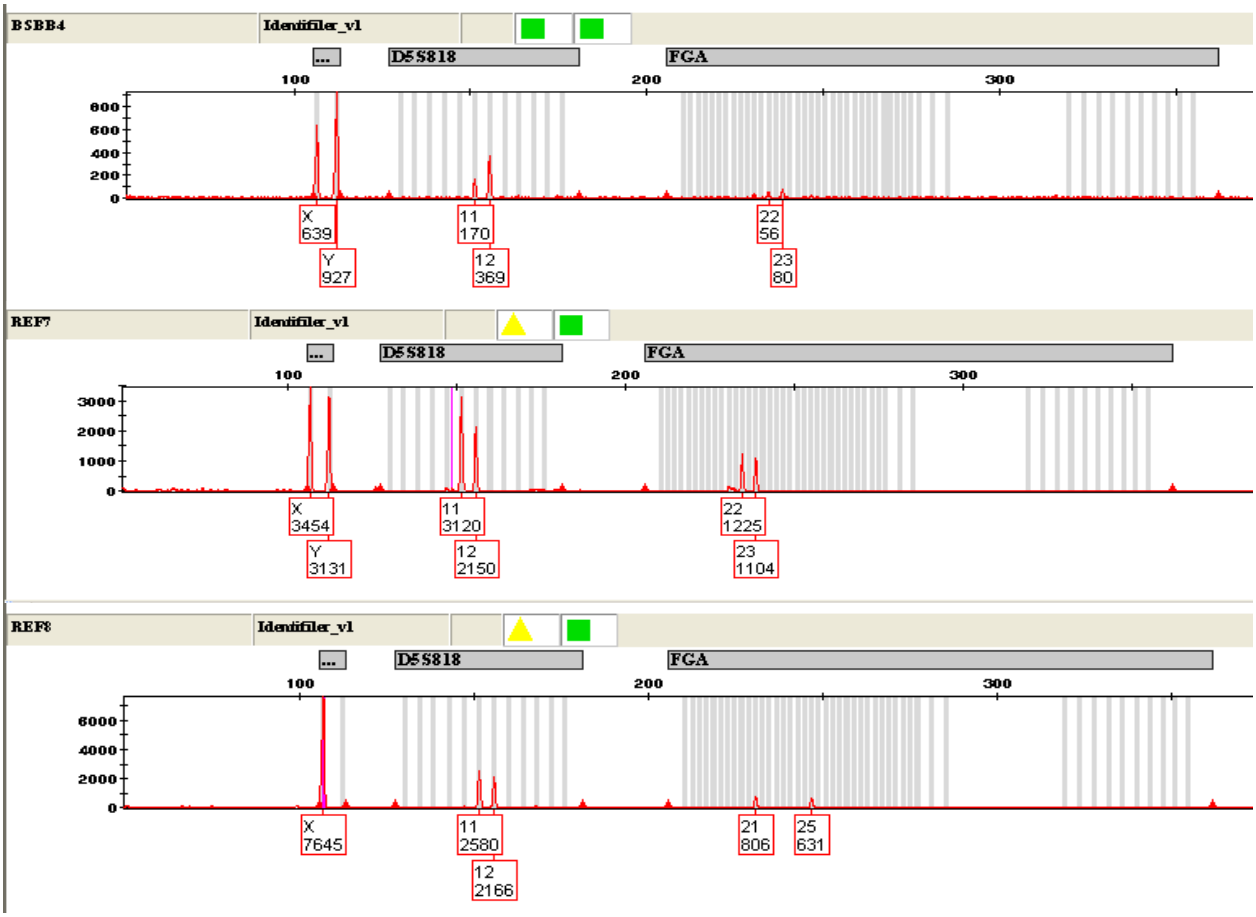

Figure 23. Comparison of red (PET™) dye labeled loci. The top is experiment BSB-P4-B, the middle is Reference 7 (donor) and the bottom is Reference 8 (vector).

Experiment BSB-P3-B resulted in a partial profile. An obvious mixture of both the donor and the vector was obtained from the plastic tube after tertiary transfer (Figure 24). In this experiment, the donor was reference 5 and the vector was reference 6. A comparison of donor and vector is shown in Figures 25-28. Contrary to the majority of the results, the vector contributed more alleles with slightly higher peaks than the donor at most non-shared alleles.

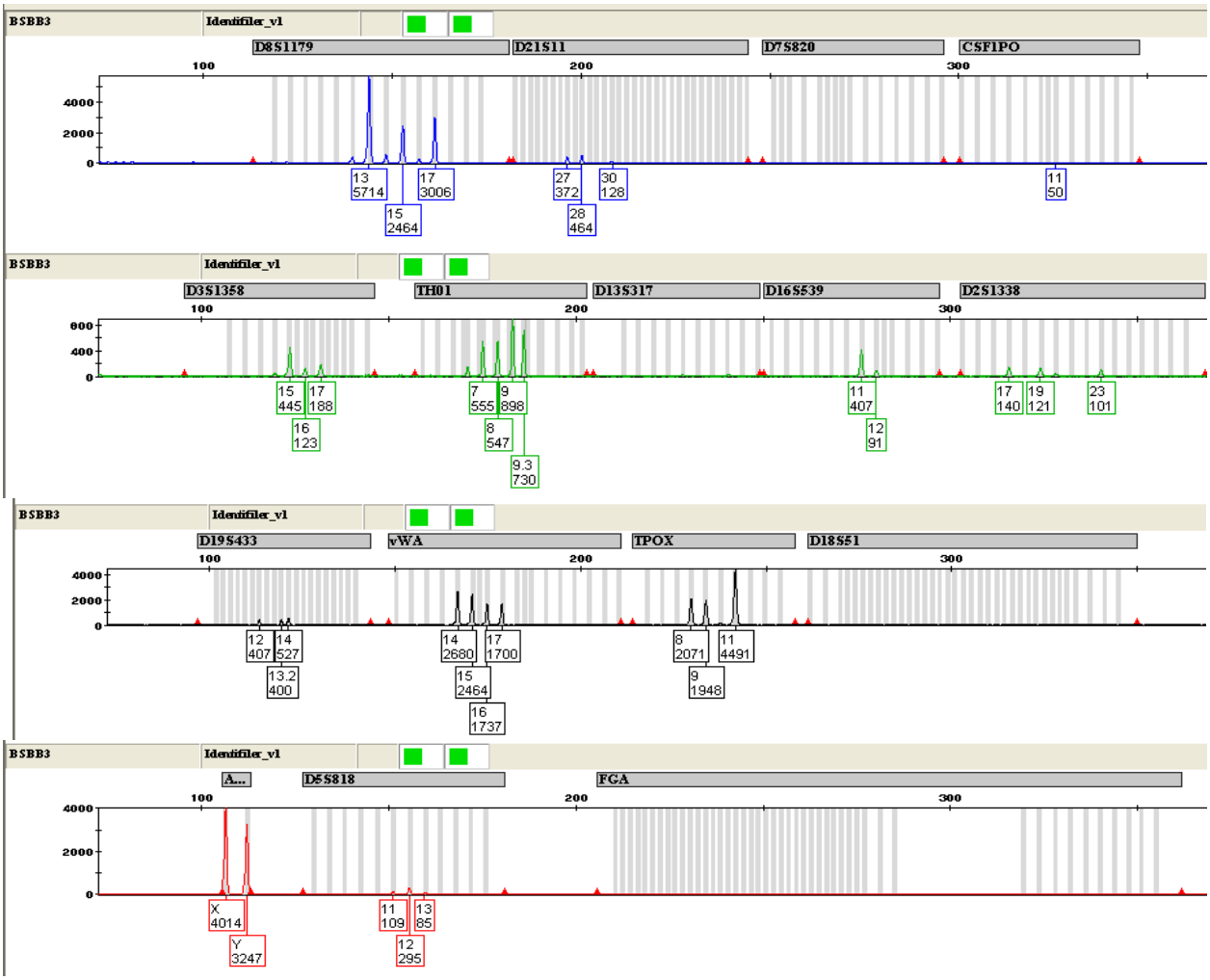

Figure 24. Experiment BSB-P3-B. Mixture DNA profile of donor and vector recovered from plastic tube after tertiary transfer.

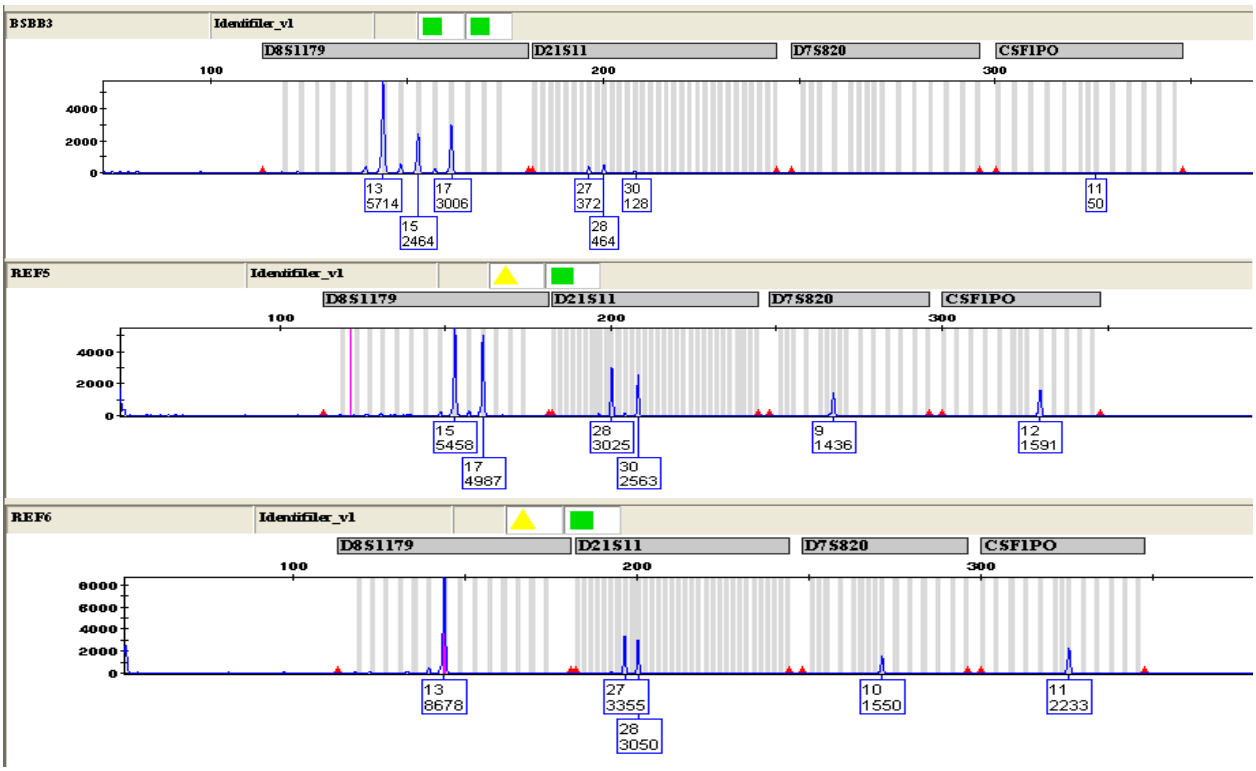

Figure 25. Comparison of blue (6-FAM™) dye labeled loci. The top is experiment BSB-P3-B, the middle is Reference 5 (donor) and the bottom is Reference 6 (vector).

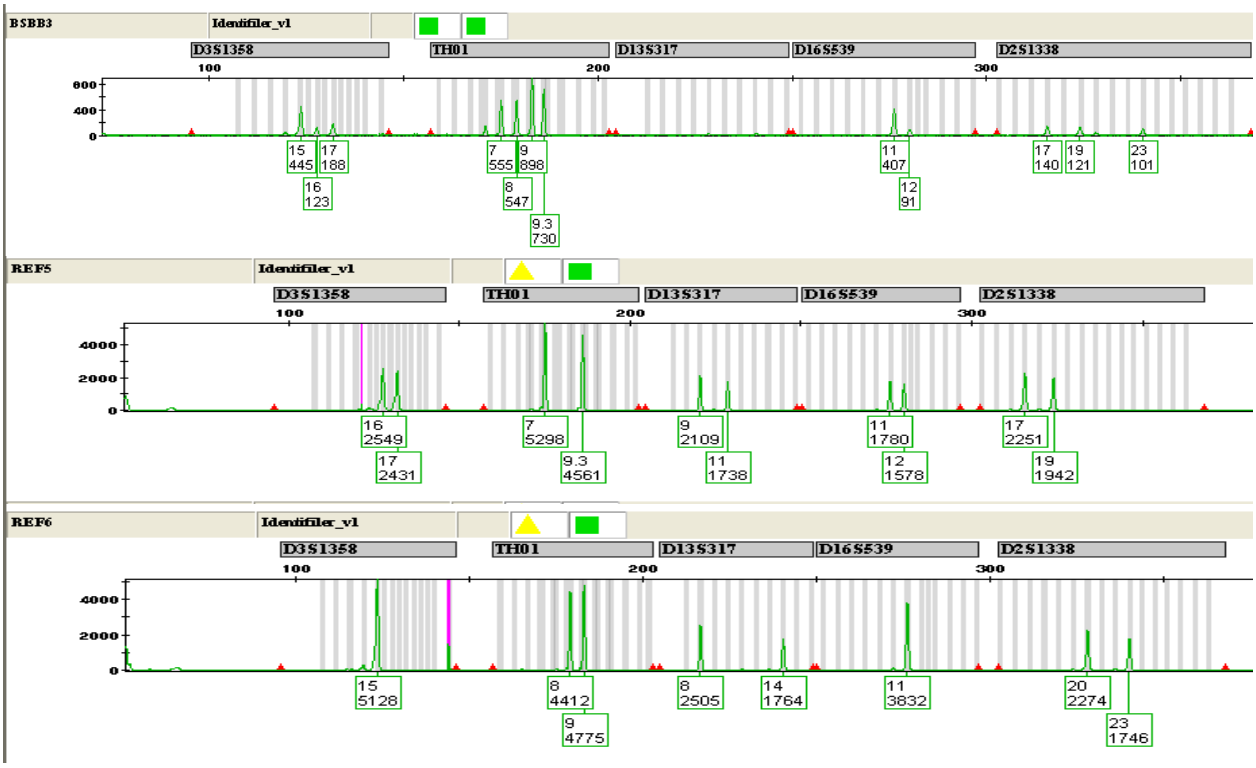

Figure 26. Comparison of green (VIC™) dye labeled loci. The top is experiment BSB-P3-B, the middle is Reference 5 (donor) and the bottom is Reference 6 (vector).

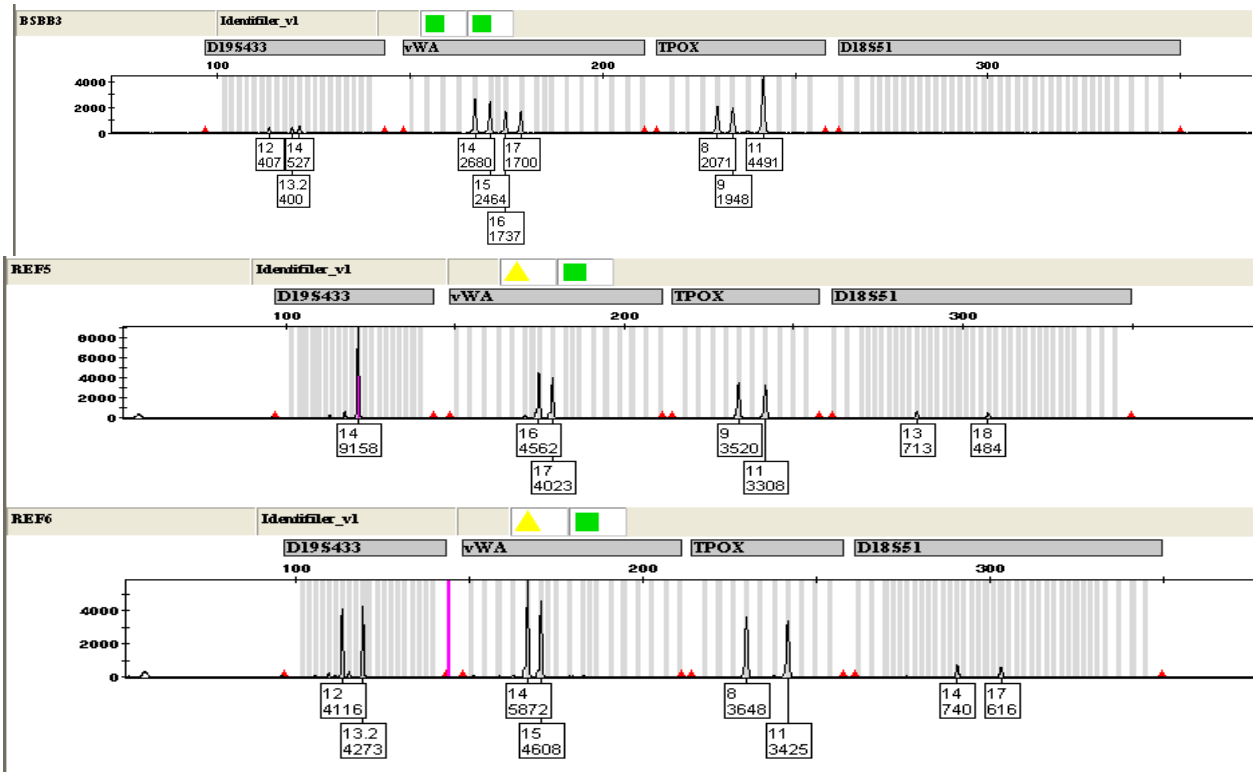

Figure 27. Comparison of yellow (NED™) dye labeled loci. The top is experiment BSB-P3-B, the middle is Reference 5 (donor) and the bottom is Reference 6 (vector).

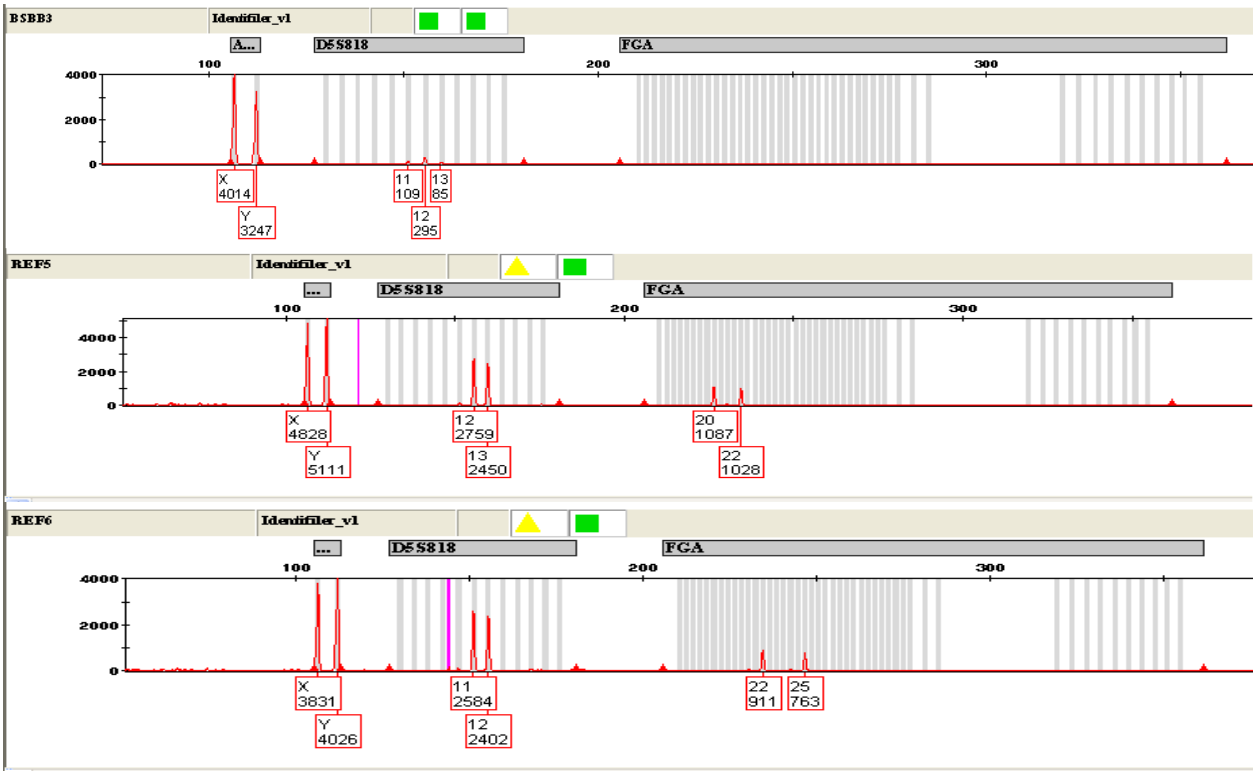

Figure 28. Comparison of red (PET™) dye labeled loci. The top is experiment BSB-P3-B, the middle is Reference 5 (donor) and the bottom is Reference 6 (vector).

In experiment BB-P5-B, a partial profile was obtained. The donor contributed all of the non-shared alleles. The DNA profile resembles a partial single source profile of the donor because all of the alleles present in the sample profile can be attributed to the donor (Figure 29).

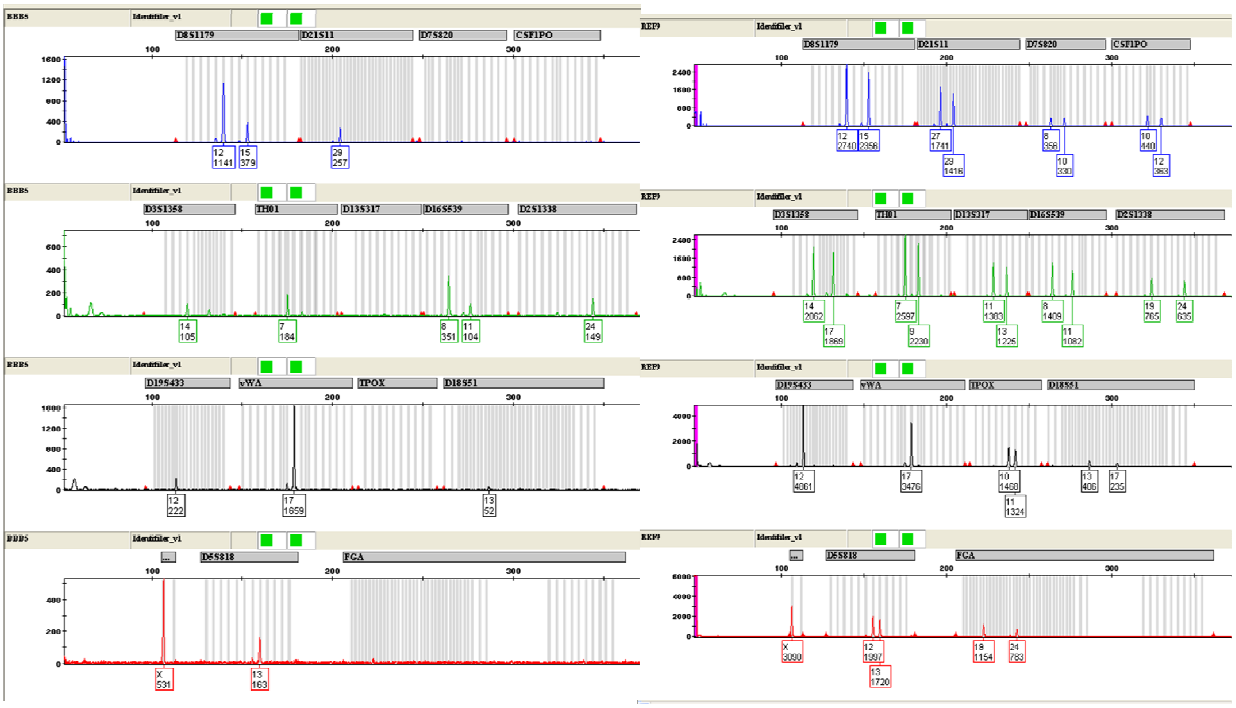

Figure 29. Comparison of BB-P5-B and reference 9 (donor). The electropherogram on the left is the profile from experiment BB-P5-B. The electropherogram on the right is the DNA profile from the donor in experiment BB-P5-B.

CHAPTER IV

CONCLUSIONS

The amount of DNA recovered was low in these sets of experiments. Therefore, using standard parameters at 28 cycles of amplification, very limited profile data were observed. However, when increasing the cycle number to 34 cycles, to simulate LCN typing conditions, allelic data were observed in the DNA profiles due to the increase in sensitivity of detection. No contamination was observed during these experiments and although not the primary focus of this study stutter artifacts were increased.

Through secondary and tertiary transfer, DNA profiles are obtainable. There was variation in the peaks among the markers. Some markers produced fewer alleles than other markers. The reason for the difference in allele yield among markers is likely correlated to some degree with amplicon size and partially due to stochastic effects.

The majority of experiments produced a greater number of alleles contributed by the donor rather than the vector. When the donor contributed more alleles, the vector allele peak heights (in RFUs) were either very low compared with those of the donor or seemingly non-existent in the DNA profile. There were two (out of 12) experiments that demonstrated the vector contributing a slightly greater amount of DNA (based on allele peak heights). Although the vector had slightly higher peaks in these two experiments, there was a clear mixture of two individuals.

As stated earlier, previous studies have demonstrated the DNA profile that was obtained was typically from the individual who last handled item. Since the primary contributor to the DNA profiles obtained in the majority of these experiments were from the individual who never touched the item, the results in this study suggest that there may be situations where the donor and vector may appear as a mixture, the donor may contribute DNA through secondary transfer and the contribution will result in the donor being the major portion of the mixture, or the donor may appear as the sole contributor to the sample. Thus, caution should be exercised regarding inference about the mode of primary and secondary transfer based solely on profile interpretation. One cannot exclude the possibility of a donor producing overwhelmingly more DNA to a DNA profile than a vector during secondary and tertiary transfer.

Further studies will be undertaken to investigate DNA transfer events. These experiments will explore DNA transfer involving routine behavior while individuals resume their daily activities. Saline solution will also be utilized to better mimic sweaty palms. Also, the persistence of DNA on a variation of handled items will also be undertaken.

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