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Impact of the Post-deposition Interval on Male DNA Recovery from Female Skin in Forensic Investigations

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Abstract:

Purpose: Crime scene investigations are time-sensitive, and delays in evidence recovery can critically impact forensic outcomes. This study examines the effect of post-depositional time on the integrity of male salivary DNA recovered from female skin, simulating real-world delays in sexual assault evidence collection.

Methods: Saliva samples from 10 couples were collected at five intervals: one, three, six, twelve, and eighteen hours post-deposition (n=50). DNA was extracted using the MyPrep Forensic DNA Extraction Kit and profiled using the Ingenomics Y Profiler Kit targeting 38 Y-STR loci. Profile quality was assessed via total peak height and global colour balance, with statistical comparisons performed using the Kruskal-Wallis H test and Dunn's post hoc test with Bonferroni correction.

Results: Complete Y-STR profiles were obtained from all samples up to twelve hours, with no allele dropout. A statistically significant decline in profile quality was observed from six hours onward ($p=0.050$), becoming most pronounced at eighteen hours ($p < 0.001$, $\eta^2=0.53$). At eighteen hours, 80% of samples still yielded complete profiles, with dropout concentrated at medium and high amplicon loci.

Conclusion: Male Y-STR profiles can be successfully recovered from female skin up to twelve hours post-deposition, supporting the forensic utility of salivary DNA in delayed sexual assault reporting. Beyond twelve hours, progressive degradation reduces genotyping reliability, emphasizing the need for timely evidence collection.

K**eywords: Saliva, DNA extraction, Y-STR, Sexual assault investigation, DNA yield**

1. Introduction:

The study of DNA degradation on various surfaces has profound implications in forensic science, since the integrity of DNA is crucial for accurate identification and analysis. Degraded DNA often becomes unsuitable for analysis because fragmentation of DNA leads to a loss of critical information, resulting in incomplete profiles and unreliable statistical outcomes [1] [2]. Among the different sources of human DNA, saliva is frequently encountered in forensic investigations because of its common presence at crime scenes, such as bite marks, sexual assault cases, discarded items, or coughing or speaking [3-5]. However, when saliva is deposited on human skin, the environmental conditions and the nature of the skin itself constitute significant challenges to the preservation of DNA. Understanding the degradation dynamics of salivary

DNA on human skin is essential for improving the accuracy and reliability of forensic evidence [6].

Several factors influence the degradation process of salivary DNA, such as environmental exposure, temperature, humidity, and the biochemical properties of the skin. Additionally, the interaction between saliva and skin introduces additional variables, such as skin oils, microbial activity, and the inherent shedding of skin cells, all of which can accelerate DNA degradation [7-10]. Degradation leads to allele dropout, where true alleles in the DNA profile fail to produce peak heights sufficient to exceed the detection threshold [11]. Despite these challenges, there is a need to better understand the time-dependent degradation of salivary DNA on the skin, as this knowledge can significantly impact the interpretation of evidence and the determination of the time of deposition.

This research examines the impact of time on male salivary DNA recovered from female skin, with samples collected at five different intervals: one, three, six, twelve, and eighteen hours. The primary focus is on assessing key quality parameters such as peak height and global color balance, which reflect the strength and consistency of the DNA signal. By monitoring changes in these parameters, this study aims to evaluate how sample degradation affects the interpretability of DNA profiles, providing insights into the time-sensitive nature of forensic evidence.

2. Methodology:

Sample collection

A total of 10 couples in the age group 18-50 years were randomly selected for their participation in the study. The work was carried out after ethical clearance from the ethical committee, SGT University, vid letter no. SGTU/FOSC/EC/2021-22/949. Written informed consent was obtained from the volunteer couples prior to sample collection. A total of 50 saliva samples were collected, with the male partner transferring saliva by biting, sucking, or licking the female partner's forearm at three different sites. The deposition site was allowed to air dry for 10 minutes. The volunteers were instructed only to avoid touching the site or bathing and then resumed their normal daily activities to simulate real-life conditions. Samples were subsequently collected at intervals of 1, 3, 6, 12, and 18 hours via the double swabbing [12] method from Mantacc nylon oral swabs (cat. no. 93050D). The swabs were kept at 2-4°C until further processing.

Extraction of DNA

A total of 50 samples were collected from 10 pairs for each time interval (one, three, six, twelve and eighteen hours). For the DNA extraction method, a MyPrep forensic DNA extraction kit (Mygene Life Sciences, Delhi, India, cat. no. 44441352) was used with an AutoMate Express forensic DNA extraction system (Thermo Fischer, UK/USA, cat. no. 4441763). The procedure followed the manufacturer's guidelines.

Quantification and genotyping

The amplification of extracted DNA was carried out via the QiAamplifier 96 thermal cycler (QIAGEN, Germany) with the Ingenomics Y Profiler Kit, which targets 38 Y-STR markers. This kit utilizes six fluorescent dyes and enables multiplex amplification of additional loci, including rs2032678, DYS444, DYS460, DYS447, DYS596, DYS449, DYS518, DYF404S1, DYF387S1, DYS627, DYS527a/b, and DYS55 offering an expanded panel, compared with other commercially available kits. Genotyping was performed via a 3500 Genetic Analyzer (Thermo Fisher Scientific, Australia), which separates the amplified fragments by size. Data analysis was conducted via GeneMapper ID-X v1.6 software (Thermo Fisher Scientific) according to the manufacturer's guidelines. The negative controls were included, consisting of swabs collected from non-deposited sites on female volunteer and blank swabs processed through the full extraction pipeline, to assess background contamination.

Statistical Analysis

Peak height and global colour balance data across time intervals were compared using the Kruskal-Wallis H test, a non-parametric alternative to one-way ANOVA appropriate for small, non-normally distributed samples. Where the overall test was significant, pairwise comparisons were performed using Dunn's post hoc test with Bonferroni correction for multiple comparisons. Effect sizes were calculated as eta-squared (η^2). All analyses were performed using Python (SciPy v1.17.1). Statistical significance was set at $\alpha = 0.05$.

Per-sample median peak height was calculated across all 38 Y-STR markers for each individual sample, yielding a single representative value per sample per time point (n=10 per group). This approach was adopted to enable valid inferential statistical comparison across time intervals using the Kruskal-Wallis H test, as it reduces marker-level variability to a single biologically meaningful unit of analysis the individual donor sample. Descriptive summaries of peak height distributions across markers, as presented in the boxplot figures, reflect the within-time point variation across all markers and are reported separately as visual representations of profile consistency.

3. Results:

The MyPrep DNA Extraction Kit uses magnetic beads for DNA extraction, and the method was applied for all time intervals. The extraction procedure followed the manufacturer's guidelines for optimal DNA yield. The present study focused on Y-STR profile quality as the primary outcome measure, as profile completeness and allele integrity are of direct forensic relevance; DNA quantification data are not reported accordingly. The full Y-STR profiles were successfully obtained from all samples collected at 1-hour to 12-hour time points, with no observed allele dropout, indicating minimal degradation during this early post-deposition period. However, indications of DNA degradation became apparent in the samples collected at 18 hours, with minor allelic dropout observed, typically involving the loss of fewer than 50% of alleles. Of the 10 samples collected at 18 hours, 8 yielded a complete profile, while 2 exhibited partial profiles with allele dropout. The alleles that were depleted after 18 hours were observed to be of medium amplicon size, such as DYS447, Y GATA H4, and DYS449, and high amplicon sizes, such as DYS557, DYS444, and DYS518. Statistical analysis confirmed a significant effect of post-deposition time on both peak height ($H = 27.66$, $df = 4$, $p < 0.001$, $\eta^2 = 0.53$) and global colour balance ($H = 27.58$, $df = 4$, $p < 0.001$, $\eta^2 = 0.52$). Dunn's post hoc test with Bonferroni correction revealed that peak height at 1 hour was significantly higher than at 6 hours ($p = 0.050$), 12 hours ($p = 0.0004$), and 18 hours ($p < 0.001$). Similarly, GCB at 1 hour differed significantly from values at 6 hours ($p = 0.011$), 12 hours ($p = 0.0003$), and 18 hours ($p < 0.001$). No significant differences were detected between the 3-hour and any other time point after correction, nor between the 12-hour and 18-hour intervals, do suggesting the most marked decline in profile quality occur between 6 and 12 hours post-deposition.

4. Profile Quality:

The DNA profile quality of all samples exhibiting successful amplification at all 38 Y-STR markers, or demonstrating less than 50% allele loss, was assessed via two key parameters: total peak height (RFU) and global colour balance (GCB). These measures were used to evaluate the consistency and overall integrity of the DNA profiles across the five post-deposition time intervals.

At 1 hour, the median peak height across samples was 12,041 RFU (IQR: 11,040-13,980), with the highest recorded GCB values, indicating strong and balanced signal intensity across all dye channels (Fig. 5). At 3 hours, a decline in median peak height to 7,666 RFU (IQR: 5,257-8,669) was observed, though profiles remained complete with no allele dropout (Fig. 6). At 6 hours, the

median peak height was 10,065 RFU (IQR: 749-10,243); however, considerable inter-sample variability was noted at this time point, with a subset of samples exhibiting near-complete signal loss while others retained peak heights comparable to earlier intervals, likely reflecting inter-individual biological differences in skin microenvironment (Fig. 7). At 12 hours, median peak height declined markedly to 1,959 RFU (IQR: 730-4,504), accompanied by a reduction in GCB, suggesting progressive signal deterioration (Fig. 8). At 18 hours, the lowest median peak height of 868 RFU (IQR: 488-1,889) was recorded alongside the greatest reduction in GCB, indicating substantial DNA degradation and profile quality loss (Fig. 9).

Statistical analysis confirmed a significant effect of post-deposition time on both peak height ($H = 27.66$, $df = 4$, $p < 0.001$, $\eta^2 = 0.53$) and global colour balance ($H = 27.58$, $df = 4$, $p < 0.001$, $\eta^2 = 0.52$). Dunn's post hoc test with Bonferroni correction revealed that peak height at 1 hour was significantly higher than at 6 hours ($p = 0.050$), 12 hours ($p = 0.0004$), and 18 hours ($p < 0.001$). No significant differences were detected between the 3-hour and any other time point after correction, nor between the 12-hour and 18-hour intervals, do suggesting the most marked decline in profile quality occur between 6 and 12 hours post-deposition.

5. Discussion:

The study investigated the time-dependent degradation of salivary DNA on human skin. Environmental factors such as temperature, humidity, and UV exposure were not systematically controlled or recorded in this study. However, volunteers resumed normal daily activities between collection intervals, during which incidental exposure to sunlight, humidity, sweat, and physical activity occurred. These environmental conditions are known to affect DNA stability and recovery [14]. It addresses forensic challenges in delayed sexual assault reporting, where saliva is often the primary source of biological evidence and where degradation can hinder DNA profiling [6]. Despite prolonged surface exposure, complete male DNA profiles were successfully obtained from trace saliva samples, demonstrating the viability of genetic analysis via multi-locus amplification. However, allelic dropouts are more common at medium- and high-molecular-weight loci, which are more prone to degradation under suboptimal conditions [15]. Previous studies have shown that elevated temperature, humidity, and UV exposure accelerate DNA degradation and reduce amplification success [10] [16]. This finding correlates with our study, where after eighteen hours, a significant drop in alleles was observed. Exposure to real-world conditions likely contributed to the observed variability in DNA yield and resulting DNA profile.

The Y-STR markers are identified on the basis of their mutation rates. Markers with high mutation rates, such as DYS481, DYS576, and DYS549, are on the higher density side. Similarly, markers such as DYS533 and DYS643 have medium density, and DYS19 and DYS448 have low mutation rates [17-19]. A study performed by Alketbi et al. [14] revealed that DNA on skin is affected by many environmental factors as well as the shedding status of individuals. The DNA yield was greater at 1, 3, 6, and 12 hours post-deposition than at subsequent extractions performed after 18 hours. At 18 hours, 8 of 10 samples (80%) yielded complete profiles, while the remaining 2 exhibited partial profiles with dropout at medium and high amplicon loci, consistent with time-dependent fragmentation of longer DNA strands.

Salivary DNA, which is more prone to degradation due to its composition and exposure to the external environment, demands immediate attention for optimal recovery. The volunteers were taken back to their normal schedule between the collection intervals, during which they were exposed to sunlight, humid weather conditions, sweat and physical activity. This, however, in turn led to either absolute degradation or loss of DNA upon UV exposure, and increased microbial activity led to significant destruction of DNA [20]. Tvedebrink et al. reported that in degraded DNA samples, the signal intensities of STR fragments decrease with increasing fragment length, as longer fragments are more prone to degradation than shorter fragments. As a result, alleles corresponding to the longest fragments are often absent.

These observations align with the findings of our study, where complete DNA profiles were obtained at all-time intervals. Peak heights consistently remained above the analytical threshold of 150 RFU, indicating efficient amplification and reliable profile quality. At one and three hours, the profiles exhibited very high signal strength, enabling accurate genotyping (Figures 5 and 6). Peak heights at these intervals were well above the threshold and the highest among all time points, suggesting that the DNA had not yet undergone degradation, thereby allowing successful amplification across all loci without allelic dropout.

At the 6-hour time point, some samples showed a sharp drop in signal while others performed similarly to the 1-hour and 3-hour samples (Figure 7). This variation between donors was unexpected and is likely due to differences in individual skin characteristics, such as sweat levels, skin acidity, and natural microbial activity, all of which can affect how long DNA survives on the skin surface. This kind of donor-to-donor variation is commonly seen in forensic trace evidence research and is difficult to control for, particularly with a small sample size. Including more donors in future studies would help clarify whether this variability follows a consistent biological pattern or reflects random individual differences.

By 12 hours, a noticeable reduction in peak height was evident, reflecting sub-optimal signal intensity. Despite initial signs of degradation, complete profiles were still generated, and the quality parameters remained within acceptable limits, which is particularly advantageous when working with low-template DNA (Figure 8).

At 18 hours, a significant decline in peak height was observed, indicating the onset of progressive DNA degradation (Figure 9). Nevertheless, peak heights remained above 150 RFU in most cases, and complete profiles were still achievable for some samples. Although compromised, the DNA at this stage was still capable of producing partial profiles with low but consistent signal intensity. These findings align with Swango et al., who reported that in degraded DNA samples, amplification efficiency is influenced by the size of the amplified target. A qPCR assay targeting a short fragment (~62 bp) detected more DNA than assays targeting longer regions (170–190 bp), consistent with the minor allele dropout trends observed in our study at the 18-hour time point [21].

Statistical analysis confirmed a significant effect of post-deposition time on both peak height ($H = 27.66$, $df = 4$, $p < 0.001$, $\eta^2 = 0.53$) and global colour balance ($H = 27.58$, $df = 4$, $p < 0.001$, $\eta^2 = 0.52$). Dunn's post hoc test with Bonferroni correction revealed significant differences between the 1-hour time point and 6 hours ($p = 0.050$), 12 hours ($p = 0.0004$), and 18 hours ($p < 0.001$). Notably, no significant difference was detected between the 12-hour and 18-hour intervals ($p = 1.00$), suggesting that once degradation reaches a critical threshold around 12 hours, further temporal progression does not produce statistically distinguishable deterioration at this sample size.

Some studies have analyzed male DNA from female skin but have focused mainly on sample collection and extraction methods [22-26]. As shown in our study, male saliva remains on female skin even after eighteen hours of deposition. The saliva sample was directly deposited on the female skin, unlike other studies where a propylene tube was used to obtain a good amount of saliva from males, which was then deposited on specific sites via swabs. This control could lead to less contamination and better salivary content composition. Sweet et al. [12] and Banaschak et al. [27] performed similar studies in which they used propylene tubes before depositing on the skin, ensuring higher DNA quality with minimal contamination.

This progressive pattern of allele loss over time clearly reflects the impact of time-dependent DNA degradation. The observed dropout events, particularly at later time intervals, underscore the vulnerability of genetic material to environmental and biological factors that accelerate

degradation on skin surfaces. These findings demonstrate a direct correlation between an increased post-deposition interval and reduced genotyping success, highlighting the critical importance of timely sample collection in forensic investigations.

This study opens the door for further research in an area that has not been extensively explored. The use of 10 couples per time point was adequate to reveal meaningful and statistically significant differences across time intervals; though a larger group of volunteers in future studies would allow these findings to be applied more broadly. The volunteers went about their normal daily routines between sample collections, which while not a strictly controlled setting, actually mirrors the real conditions encountered in forensic casework more closely than a laboratory environment would. Future studies that also record environmental conditions such as temperature and humidity alongside this real-world approach would add another layer of detail to these findings. Including swabs from non-deposited sites as additional controls in future work would further strengthen confidence in the extraction process, building on the reliable profiling results this study has already demonstrated.

6. Conclusion:

This study underscores the critical impact of post-depositional time and environmental exposure on the recovery and integrity of male salivary DNA from female skin. By analyzing samples across multiple time intervals under real-world conditions, this research simulates authentic forensic scenarios, particularly in delayed reporting of sexual assault cases where saliva may be the primary biological evidence.

The findings revealed a clear pattern of time-dependent DNA degradation. Complete male DNA profiles were successfully obtained at all-time points up to 12 hours, with no allele dropout, demonstrating the reliability of Y-STR profiling within this window. Statistically significant decline in profile quality was observed from 6 hours onward ($p=0.050$), becoming most pronounced between 12 and 18 hours post-deposition ($p < 0.001$). At 18 hours, 8 of 10 samples still yielded complete profiles, while the remaining 2 exhibited partial profiles with dropout concentrated at medium and high amplicon loci. High-amplicon STR markers were more susceptible to degradation, supporting prior evidence that longer DNA fragments are less likely to be amplified in compromised samples. Environmental factors such as UV exposure, humidity, and physical activity further contributed to DNA loss, highlighting their role in post-depositional degradation.

These findings emphasize the need for prompt evidence recovery, improved field protocols, and strategic marker selection to ensure genotyping success in forensic investigations involving salivary DNA.

7. Abbreviation

1. DNA: Deoxy ribonucleic acid
2. PCI: phenol:chloroform:isoamyl
3. MCT: microcentrifuge tube
4. Ng: nanogram
5. RFU: relative-flouroscence unit.

8. Declaration

Ethics approval and consent to participate

Written consent was obtained from the volunteers after ethical approval was obtained from the committee of the Faculty of Science, SGT University, Gurugram, Haryana, India. The process and purpose of the study were also well explained to the volunteers. The ethical certificate reference number is SGTU/FOSC/EC/2021-22/949.

Consent for publication

Not applicable.

Availability of data and material

All the data generated or analyzed during this study are included in this published article.

Competing interests

The author declares that they have no competing interests.

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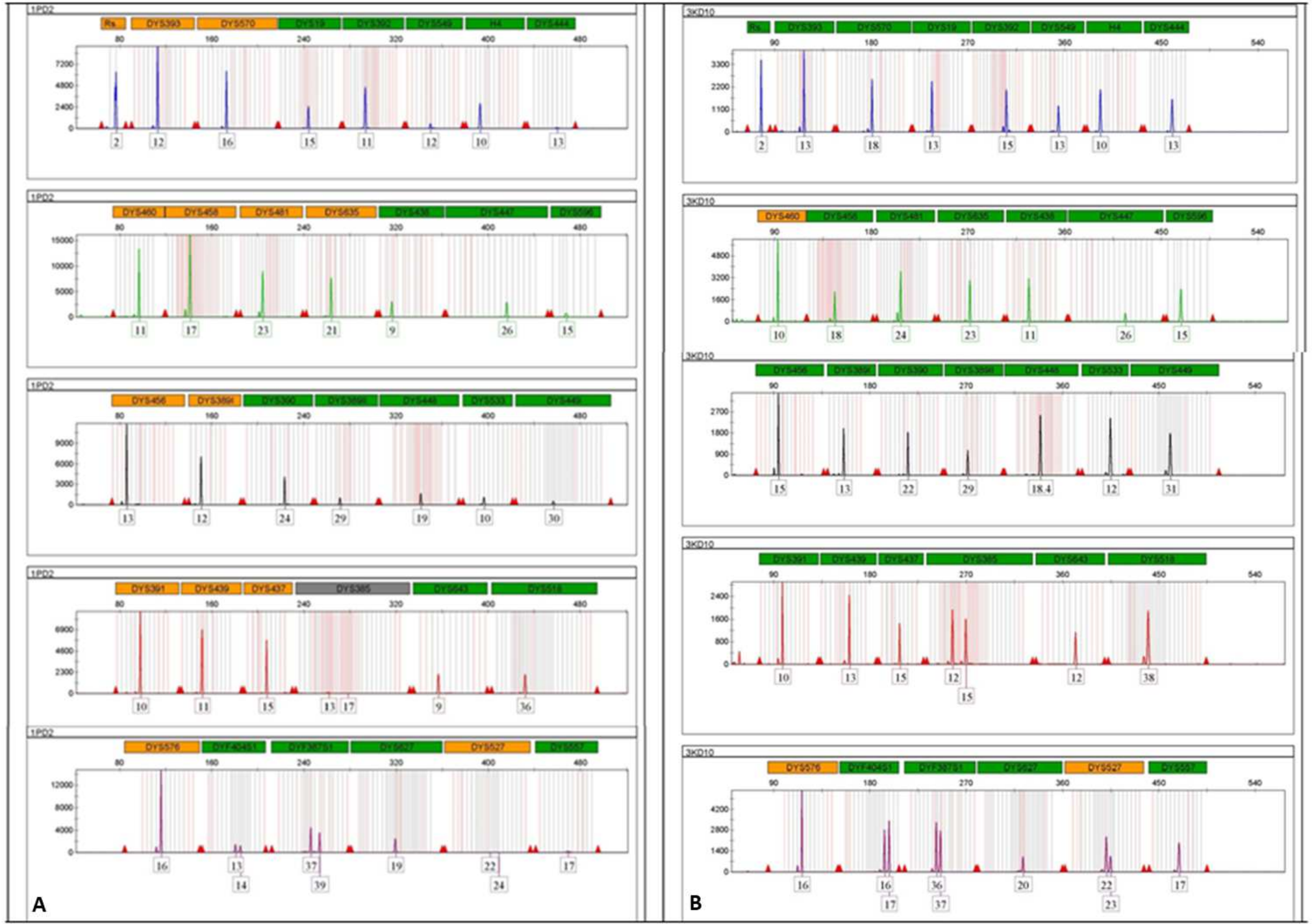
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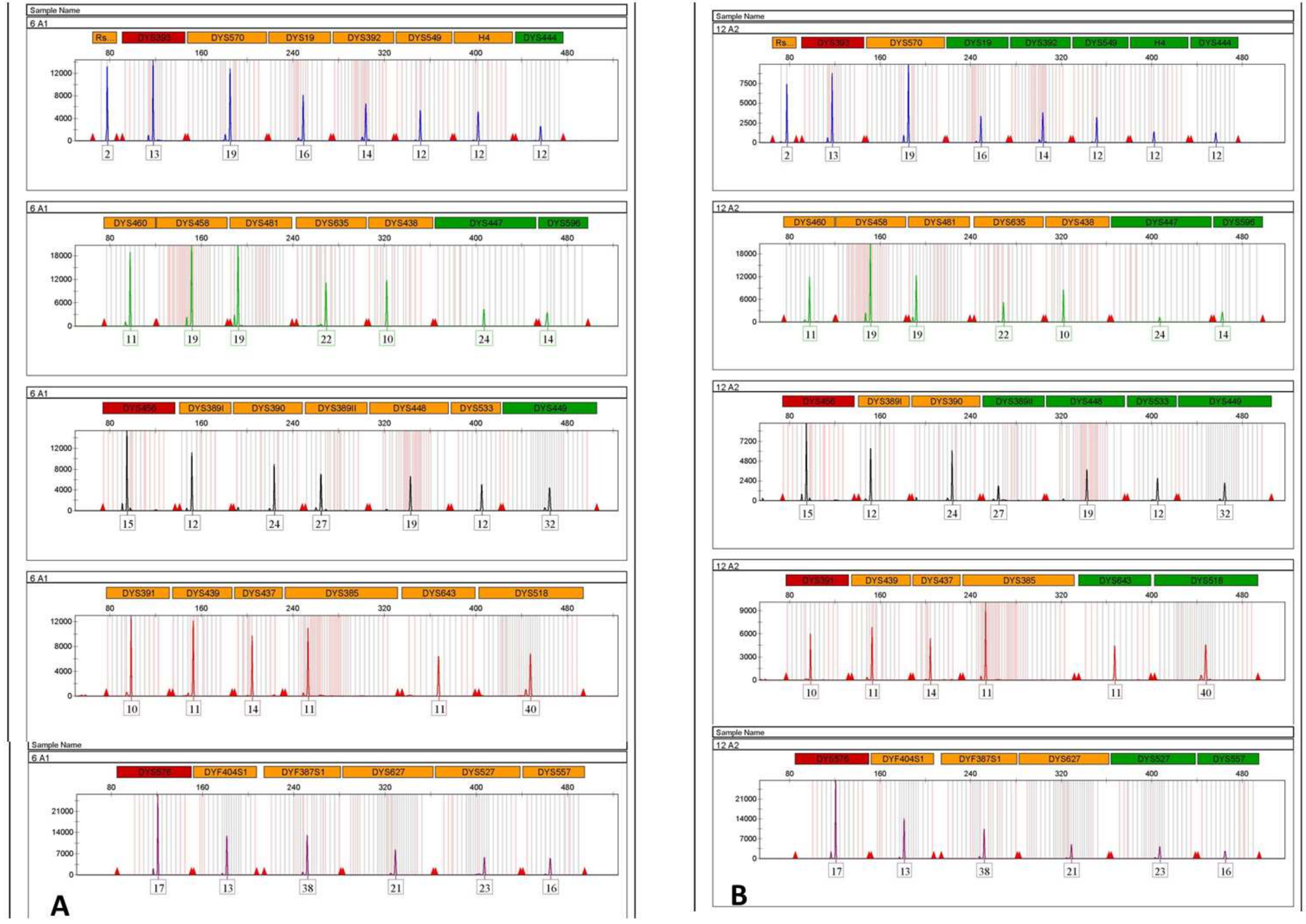
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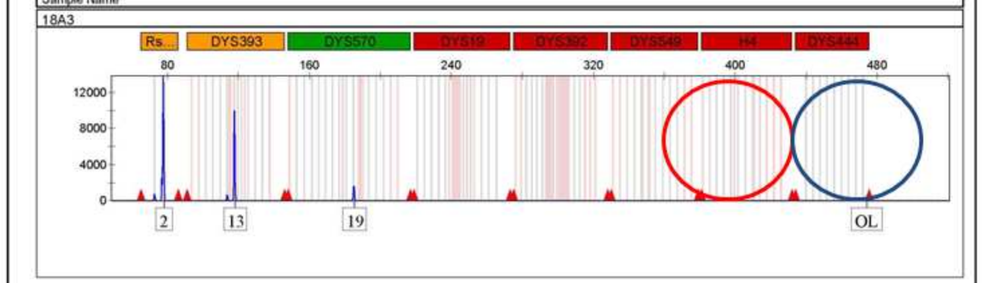
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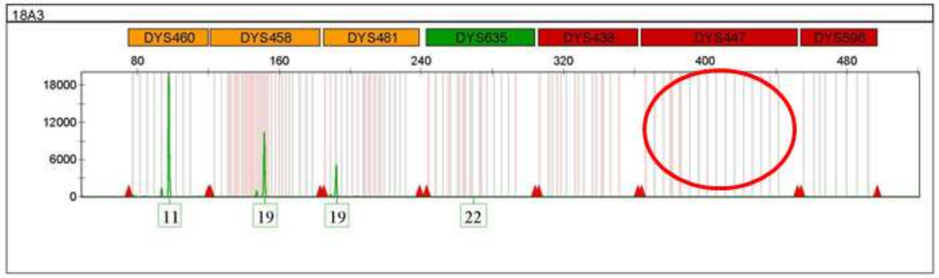
- **Figure 1: Deposition site of saliva on female arms by a) the licking b) biting c) sucking method**
- **Figure 2: Electropherogram of samples taken after A- one hour and B- three hours.**
- **Figure 3: Electropherogram of samples taken after A- six hours and B- twelve hours.**
- **Figure 4: Electropherogram of samples taken after eighteen hours. A-Full profile; B-partial profile.**
- **Fig. 5: Profile parameters after one hour. (a) Peak height and (b) global balance**
- **Fig. 6: Profile parameters after three hours. (a) Peak height (b) Global balance.**
- **Fig. 7: Profile parameters after six hours. (a) Peak height and (b) global balance.**
- **Fig. 8: Profile parameters after twelve hours. (a) Peak height and (b) global balance.**
- **Fig. 9: Profile parameters after eighteen hours. (a) Peak height and (b) global balance.**

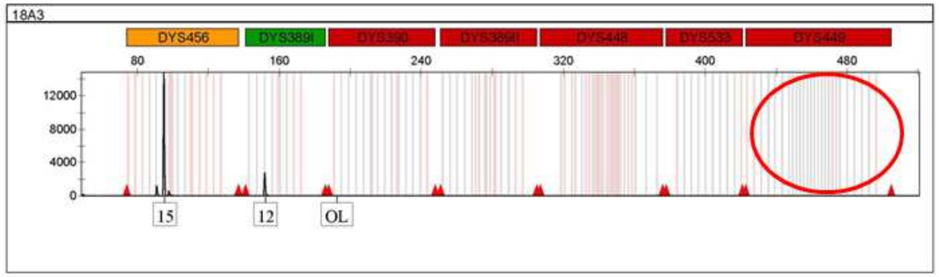

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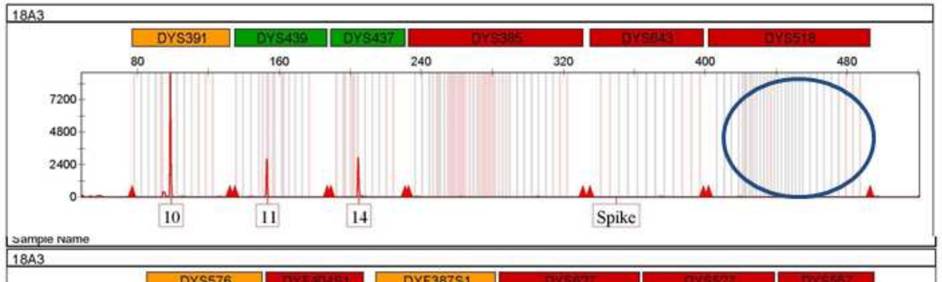

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15 13 22 29 18.4 12 31
10 13 15 12 15 12 38
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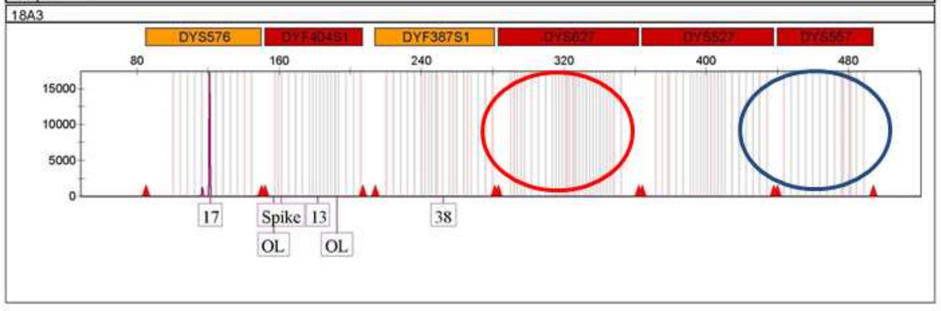

Sample Name
6 A1
Rs...
DYS393
DYS570
DYS19
DYS392
DYS549
H4
DYS444
2
13
19
16
14
12
12
12
6 A1
DYS460
DYS458
DYS481
DYS635
DYS438
DYS447
DYS596
11
19
19
22
10
24
14
6 A1
DYS456
DYS389I
DYS390
DYS389II
DYS448
DYS533
DYS449
15
12
24
27
19
12
32
6 A1
DYS391
DYS439
DYS437
DYS385
DYS643
DYS518
10
11
14
11
11
40
Sample Name
6 A1
DYS576
DYF404S1
DYF387S1
DYS627
DYS527
DYS557
17
13
38
21
23
16
A
Sample Name
12 A2
Rs...
DYS393
DYS570
DYS19
DYS392
DYS549
H4
DYS444
2
13
19
16
14
12
12
12
12 A2
DYS460
DYS458
DYS481
DYS635
DYS438
DYS447
DYS596
11
19
19
22
10
24
14
12 A2
DYS456
DYS389I
DYS390
DYS389II
DYS448
DYS533
DYS449
15
12
24
27
19
12
32
12 A2
DYS391
DYS439
DYS437
DYS385
DYS643
DYS518
10
11
14
11
11
40
Sample Name
12 A2
DYS576
DYF404S1
DYF387S1
DYS627
DYS527
DYS557
17
13
38
21
23
16
B


18A3
Rs...
DYS393
DYS570
DYS519
DYS392
DYS549
H4
DYS444
80
160
240
320
400
480
12000
8000
4000
0
2
13
19
OL

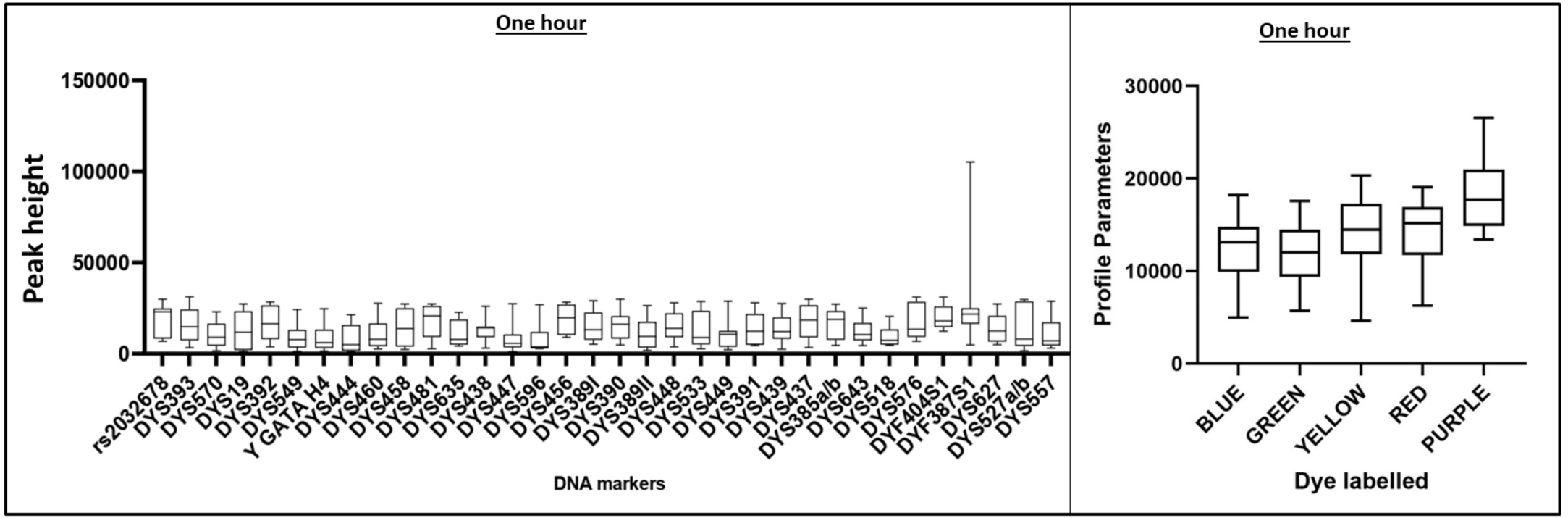

18A3
DYS460
DYS458
DYS481
DYS635
DYS438
DYS347
DYS596
80
160
240
320
400
480
18000
12000
6000
0
11
19
19
22

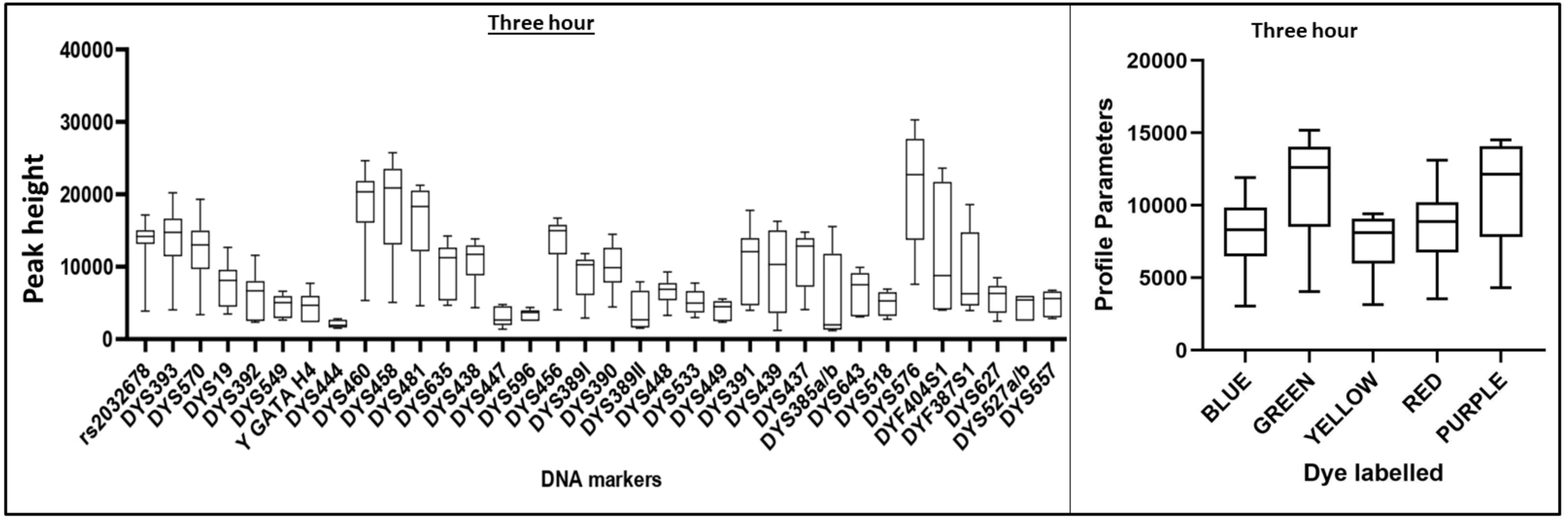

18A3
DYS456
DYS389I
DYS390
DYS389II
DYS448
DYS533
DYS449
80
160
240
320
400
480
12000
8000
4000
0
15
12
OL

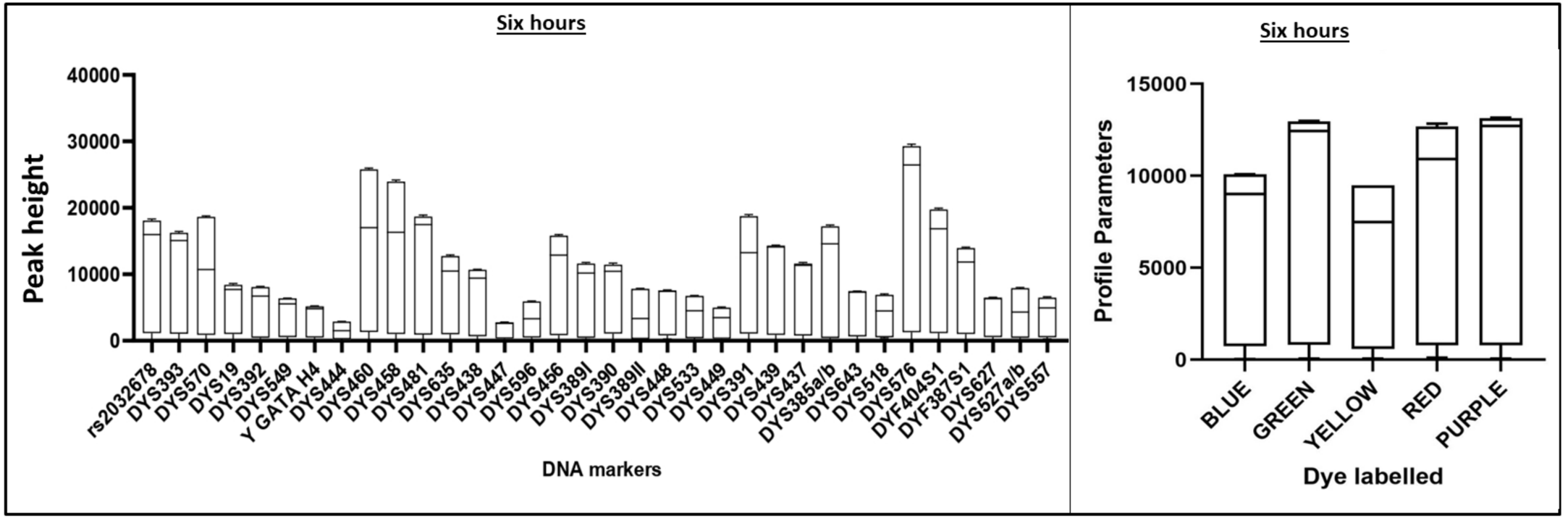

18A3
DYS391
DYS439
DYS437
DYS385
DYS643
DYS518
80
160
240
320
400
480
7200
4800
2400
0
10
11
14
Spike

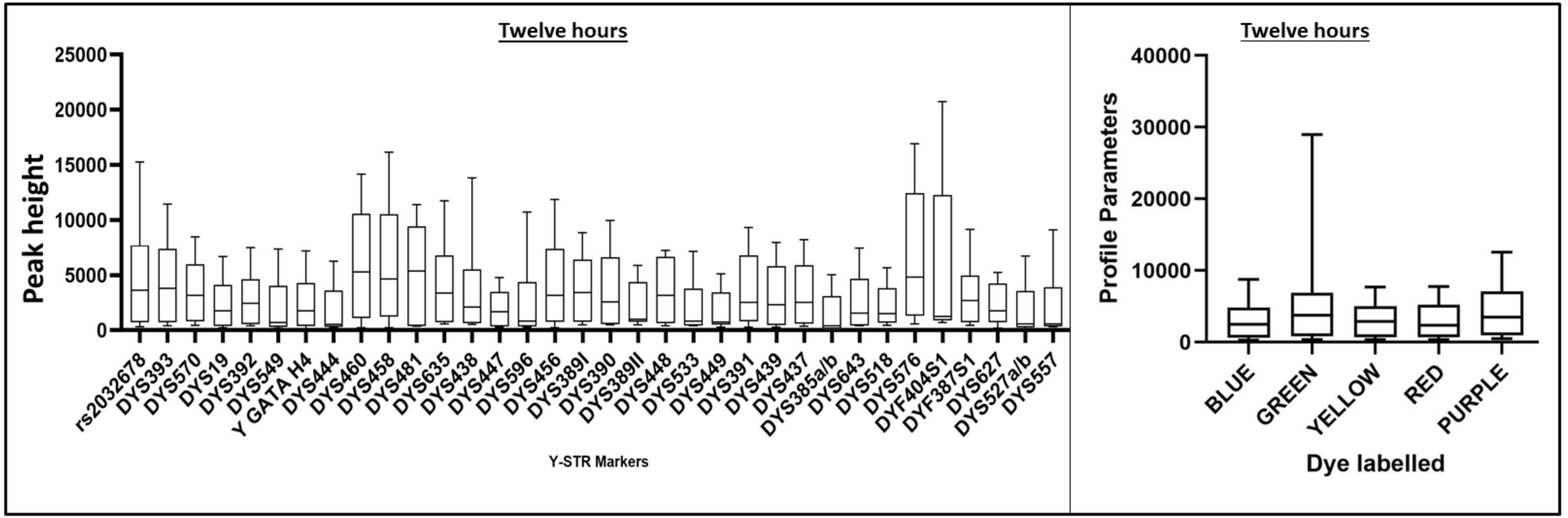

Sample Name
18A3
DYS576
DYF404S1
DYF387S1
DYS627
DYS527
DYS567
80
160
240
320
400
480
15000
10000
5000
0
17
Spike
13
38
OL
OL

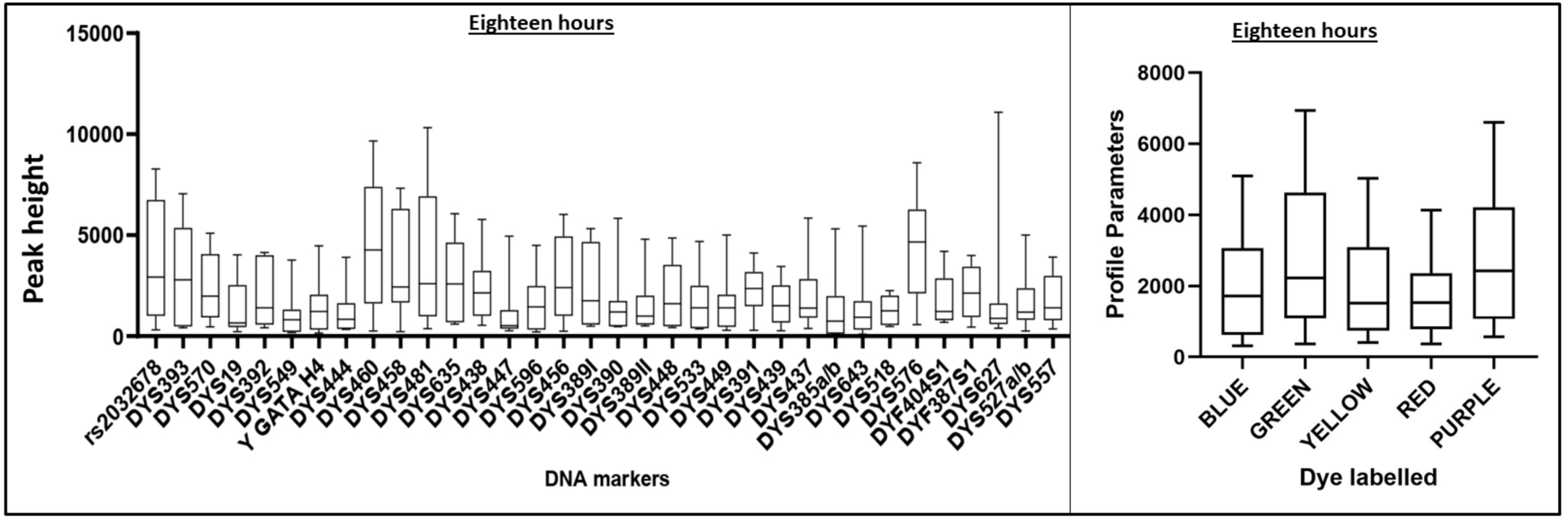

High Density
Medium Density


One hour
Peak height
150000
100000
50000
0
rs2032678
DYS393
DYS570
DYS19
DYS392
DYS549
Y GATA H4
DYS444
DYS460
DYS458
DYS481
DYS635
DYS438
DYS447
DYS596
DYS456
DYS389I
DYS390
DYS389II
DYS448
DYS533
DYS449
DYS391
DYS439
DYS437
DYS385a/b
DYS643
DYS518
DYS576
DYF404S1
DYF387S1
DYS627
DYS527a/b
DYS557
DNA markers
One hour
Profile Parameters
30000
20000
10000
0
BLUE
GREEN
YELLOW
RED
PURPLE
Dye labelled


Three hour
Peak height
40000
30000
20000
10000
0
rs2032678
DYS393
DYS570
DYS19
DYS392
DYS549
Y GATA H4
DYS444
DYS460
DYS458
DYS481
DYS635
DYS438
DYS447
DYS596
DYS456
DYS389I
DYS390
DYS389II
DYS448
DYS533
DYS449
DYS391
DYS439
DYS437
DYS385a/b
DYS643
DYS518
DYS576
DYF404S1
DYF387S1
DYS627
DYS527a/b
DYS557
DNA markers
Three hour
Profile Parameters
20000
15000
10000
5000
0
BLUE
GREEN
YELLOW
RED
PURPLE
Dye labelled


Six hours
Peak height
40000
30000
20000
10000
0
rs2032678
DYS393
DYS570
DYS19
DYS392
DYS549
Y GATA H4
DYS444
DYS460
DYS458
DYS481
DYS635
DYS438
DYS447
DYS596
DYS456
DYS389I
DYS390
DYS389II
DYS448
DYS533
DYS449
DYS391
DYS439
DYS437
DYS385a/b
DYS643
DYS518
DYS576
DYF404S1
DYF387S1
DYS627
DYS527a/b
DYS557
DNA markers
Six hours
Profile Parameters
15000
10000
5000
0
BLUE
GREEN
YELLOW
RED
PURPLE
Dye labelled


Twelve hours
Peak height
25000
20000
15000
10000
5000
0
rs2032678
DYS393
DYS570
DYS19
DYS392
DYS549
Y GATA H4
DYS444
DYS460
DYS458
DYS481
DYS635
DYS438
DYS447
DYS596
DYS456
DYS389I
DYS390
DYS389II
DYS448
DYS533
DYS449
DYS391
DYS439
DYS437
DYS385a/b
DYS643
DYS518
DYS576
DYF404S1
DYF387S1
DYS627
DYS527a/b
DYS557
Y-STR Markers
Twelve hours
Profile Parameters
40000
30000
20000
10000
0
BLUE
GREEN
YELLOW
RED
PURPLE
Dye labelled


Eighteen hours
Peak height
15000
10000
5000
0
rs2032678
DYS393
DYS570
DYS19
DYS392
DYS549
Y GATA H4
DYS444
DYS460
DYS458
DYS481
DYS635
DYS438
DYS447
DYS596
DYS456
DYS389I
DYS390
DYS389II
DYS448
DYS533
DYS449
DYS391
DYS439
DYS437
DYS385a/b
DYS643
DYS518
DYS576
DYF404S1
DYF387S1
DYS627
DYS527a/b
DYS557
DNA markers
Eighteen hours
Profile Parameters
8000
6000
4000
2000
0
BLUE
GREEN
YELLOW
RED
PURPLE
Dye labelled