# AQ-01

**Alicia Quartermain**

**From:** Alicia Quartermain
**Sent:** Friday, 4 December 2020 6:45 AM
**To:** Kylie Rika; Emma Caunt; Angelina Keller; Josie Entwistle; Tegan Dwyer; Claire Gallagher; Deborah Nicoletti; Ingrid Moeller; Penelope Taylor
**Subject:** RE: TAT and lists - another follow-up email

Good morning Team and Happy Friday!

Please see below for the response I received from Cathie. I don't feel as though any of my questions/suggestions were actually addressed, but it is a response nonetheless!

[redacted]

Alicia

Hi Alicia

Thanks for your feedback on this -- it's really appreciated.

If staff feel that there are issues between teams, it would be great if they could highlight this to their line manager so that each team can discuss it, and ways to be proactive about the work we undertake. Ultimately, we can't get a profile on the database without the help of all staff members in Forensic DNA Analysis to get it there. If you hear anyone discussing a possible divide or feeling that there's a divide, it would be great if you could encourage them to have a chat with their line manager or team leader about it.

I am working on some things with the QPS and had planned to provide an update to the team when I'd completed that work, but your email has made me rethink that approach. I'm not sure what I'll do yet, but thanks again for your email.

Cheers
Cathie

**From:** Alicia Quartermain
**Sent:** Thursday, 3 December 2020 2:15 PM
**To:** Kylie Rika <[redacted]>; Emma Caunt <[redacted]>; Angelina Keller <[redacted]>; Josie Entwistle <[redacted]>; Tegan Dwyer <[redacted]>; Claire Gallagher <[redacted]>; Deborah Nicoletti <[redacted]>; Ingrid Moeller <[redacted]>; Penelope Taylor <[redacted]>
**Subject:** RE: TAT and lists - another follow-up email

Hi RT2,

Please see below for the email I have just sent to Cathie. I will let you all know when I hear back from her. Or not, if it's after about 3pm tomorrow!!

Alicia

Hi Cathie,

I was wondering whether you might agree that it is a good idea to send an email to FDNA clarifying the actual amount of outstanding results, in light of our email discussion around results/lines within results/lists/TATs? I know there have been quite a few conversations happening around staff being concerned after the email you sent out about outstanding results and TATs. It has caused somewhat of a divide between departments as we all try to work out where the bottleneck is and where the bulk of the outstanding work actually sits. Are you able to provide some clarification around this to everyone?

Perhaps you could give the individual figures and note what lists they are on so staff can look at them?

Another thought – given the QPS TAT is based mostly on P3 samples involved in cold links, we could potentially be prioritising P3 samples with NCIDD uploads. I would expect that this would reduce the QPS TAT fairly substantially.

Thank you Cathie.

Kind regards,
Alicia

**From:** Alicia Quartermain
**Sent:** Friday, 27 November 2020 7:12 AM
**To:** Kylie Rika [redacted]; Emma Caunt [redacted] Angelina Keller [redacted]; Josie Entwistle <[redacted]; Tegan Dwyer <[redacted] Claire Gallagher [redacted]; Deborah Nicoletti <[redacted]; Ingrid Moeller <[redacted] Penelope Taylor [redacted]
**Subject:** FW: TAT and lists

Good morning everyone,

Please find below a response from Cathie. Maybe my reply to her email will bring it back to my original question.... So Christmas Eve.....??!

Have a lovely Friday!

Alicia

**From:** Cathie Allen [redacted]
**Sent:** Thursday, 26 November 2020 5:39 PM
**To:** Alicia Quartermain <[redacted]
**Subject:** RE: TAT and lists

Hi Alicia

The QPS measure the Receipt to Cold Link metric as this is where DNA analysis is most useful to them in solving crime. For most major crime cases, they usually have a suspect and DNA analysis results are essentially confirming the scene that they have processed. So we're most useful to them when we're able to solve crimes that they haven't been able to solve in other ways, such as fingerprints, CCTV etc. When we aren't able to rapidly solve these types of crimes, we lose our value to them, as the offender has had the opportunity to commit another crime during that period. So doubling the TAT from 10 days to 24 days means the offender has had so many more opportunities to crime further crimes, and also possibly escalate in crime class as well. So I can understand why that metric is important for them, and also for us.

Moving forward with an MOU with the QPS, it would be our expectation that the TAT would be based on all samples that have been submitted. The QPS may wish to continue monitoring the Receipt to Cold Link metric, given this is a high priority area for them. FSS may also agree that this is a metric we'd like to keep at 10 days (for example) as well, but we're still a way off getting an MOU signed with the QPS.

Thanks for letting me know about the tally counting – I can see now that you would count the 'profile review' code. The FR makes all of this so much easier for tracking your work, and not having to keep a manual count.

Justin and I have had a few discussions regarding the metrics within the FR and how we can make them better. Including ensuring that particular lists don't 'overlap' with the same profiles. Justin has previously requested an enhancement regarding some of the samples on lists, but I've put in another enhancement to try and remove samples from the outstanding that shouldn't be there (some on the list have been reported but are still on the list). Unfortunately, the FR Tender process took over 18 months to complete and this has meant that we've stagnated and haven't had some of the things that we'd like. Good metrics are essential to seeing where the bottlenecks are and for accurate assessment of how much work is there to be done (or how much we've completed) – as Statements can sometimes be underestimated, especially when the QPS forward 17 Statement requests in one day!

I've found the length of the FR Tender process very frustrating (and actually disheartening), as we previously were able to give enhancements to staff every 2 weeks. This was great as we could regularly prioritise the enhancements and each work unit had an opportunity to get something new (SSLU, FPP, For Chem and For DNA Analysis). The process taking so long has meant that we're all unhappy, as we can't move forward with streamlining processes, which helps both us and the QPS. I really want the batch functionality for Forensic Chemistry, as they don't have that and it would be a huge benefit to them. They would be able to track consumables and equipment use, have instrument data available to them in the FR for when they are interpreting and reviewing drugs found (data is manually added to each sample, rather than batch of samples) and for keeping an eye on standards that they use and when they may need to re-run them. They don't have very many metrics in the FR for them (they have less than FDA). So getting some of that for them to track bottlenecks would be great as well.

Thanks for your email, I appreciate that you've thought about this and sought some information on this to help clarify it for you. Please let me know if there's anything else I can help with.

Cheers
Cathie

**Cathie Allen**
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 15 Sept 2022

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**From:** Alicia Quartermain <[redacted]>
**Sent:** Thursday, 26 November 2020 3:20 PM
**To:** Cathie Allen <[redacted]>
**Subject:** TAT and lists

Hi Cathie,

Thanks again for your email.

The fact that QPS as basing their 'doubled' TAT on just samples that have a cold link reported back is a bit of a problem from my perspective, and somewhat of a surprise. Given there are so many samples that are either 'No DNA detected', 'DNA insufficient for further processing' or 'Single source matching to a reference sample', it seems that they are using a very small data set to set a standard TAT for us. Why wouldn't they use all available data, do you know? I wonder why they just choose such a small sample set to gauge TAT?

Also, it's my understanding that the worklist called 'Awaiting Review' contains all of the samples that already occupy the 'Pending Review – result' list. They are duplicates of one another and each currently sits at 929. This list appears to show all of the 'result lines' that need to be reviewed, rather than the number of outstanding results. For example, on page one of this list, sample [redacted] has 7 outstanding 'lines' to be reviewed, however they all form part of the one 'result'.

The way the reporters count tallies is based on how many 'Profile review' codes you order or review. One ordered counts as 1 x tally for PDA, one reviewed counts as 1 x tally for review. There may be (as in the example above) 7 result lines that are checked by the reviewer, but we only count this as one tally because only one 'Profile review' code is actually reviewed. These tallies are recorded in the FR, which is where my line manager views how many samples I have PDA'd and how many samples I have reviewed for the week. We don't manually keep track of these anymore.

As you mention, the FR enhancements that have been applied for will be of great benefit.

Kind regards,

Alicia

Hi Alicia

Thanks for your email.

The KPI that the QPS are measuring is Receipt of the Item to Cold Link received and the advice they gave was that this had almost doubled. So this metric doesn't include everything – just the ones that have Cold Links on them.

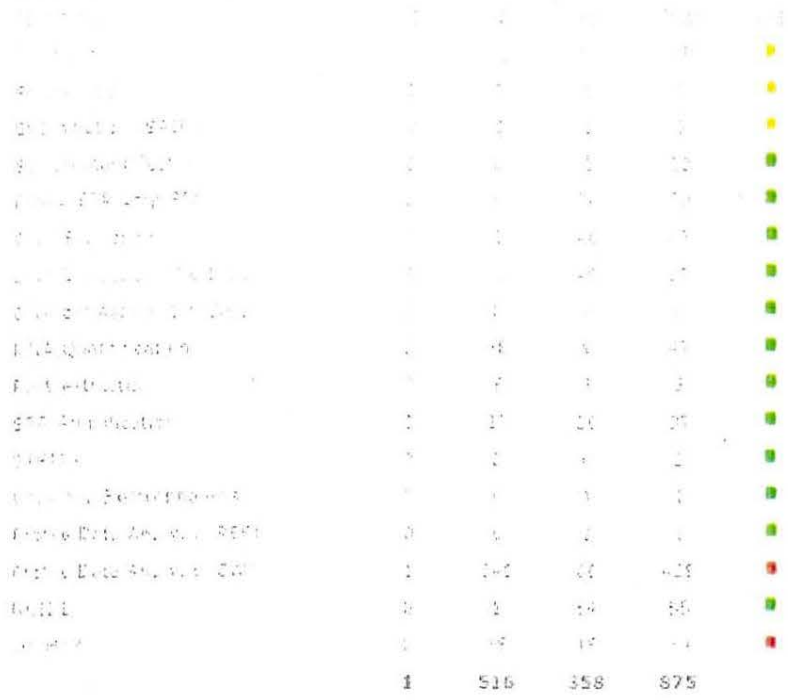
There are some stats that we're able to access in the FR that help to show where the samples are sitting. Below is the 'Current QHSS Auslab Case Status @ 20/11/2020' and this shows as at today, there are 3781 samples that have been started but not finalised. The Table has the old name against it but still captures current data that's outstanding. There could be some 'samples' on that list that we've finalised but the FR doesn't recognise that as a final result line, however I don't anticipate this to be in the hundreds, more likely to be a handful. We have put forward an enhancement to have those result lines recognised as final so that they won't be counted. I provided the list of the outstanding samples to Kylie, but I'm not sure what's become of that list (ie who's working on it etc).

Current QHSS Auslab Case Status @ 20/11/2020

| Status | Crime Type | Cases | Sar |
|---|---|---|---|
| RECEIVED | MAJOR | 3 | 3 |
| STARTED | MAJOR | 1466 | 31' |
| STARTED | VOLUME | 509 | 63( |

Also below is the Worklist Summary and it shows that there's 47 items that are with ER, 70 Refs with OO's, 243 samples progressing through Analytical, 429 samples at PDA and 1,528 samples that require a result (of some description). Also on the worklist called 'Awaiting Review' – there's 844 samples that are awaiting a result (of some description, excludes ER and Analytical results). These 3 places add up to 3,247 samples. Which is close to what's outstanding (although there's about 500 unaccounted for and I'm not sure where they are, I haven't had the time to trawl through everything to find that out I'm afraid).

Worklist Summary

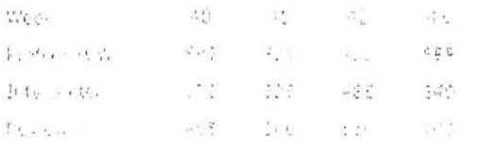


| | | | | |
|---|---|---|---|---|
| | 1 | 516 | 358 | 875 |

Pending Review

| | | |
|---|---|---|
| | 2 | 18 |

Profile Data Analysis



The KPIs that reporters put forward to their line managers are the number of lines of results that they've completed (aren't they? They used to be so I could be wrong on this bit). So the number of lines being reported may have increased, but that doesn't necessarily correlate to the number of items being reported. We could issue 4 lines for one item (as it's complex etc). As we're doing 4 person mixtures now, the increase in number of lines reported could be due to that (or other factors).

The metrics that are captured have been set up in the FR so the QPS get their data directly from the FR and as far as I'm aware, they don't have to manually get the numbers. So the figures for the Receipt to Cold Link are mostly likely to be accurate. This is a metric that they have set up to calculate on a regular basis.

We've put in a number of enhancements regarding statistics for our teams (both Forensic DNA Analysis and Forensic Chemistry). At the moment, we haven't been able to get these enhancements done, but we're hoping that once the meetings regarding the operation of the contract for the FR have been done, we'll be able to prioritise those enhancements and move forward with this. We may look at team specific metrics or process specific metrics so that we can see where the bottlenecks are.

For me, I'm really looking forward to getting enhancements that helps both my teams to streamline their processes. I know that staff are working hard, but we don't have visibility of where we might need to put more or less effort. I've had FR enhancements on my monthly report to John Doherty since he started with FSS, so I'm pretty sure he knows how important it is to me and my teams.

Hope you have a great weekend too.

Cheers
Cathie

**Cathie Allen**
Managing Scientist

Social Chair, Organising Committee for 25th International Symposium of the
Australian and New Zealand Forensic Science Society (ANZFSS), Brisbane, 11 – 16 Sept 2022

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*Please note that I may be working from a different location during the COVID-19 pandemic. The best contact method is via email.*

No DNA Detected (NDNA)

| Barcode | Case priority/ case type | Initial Quant value | Quant value after microon | Single source (SS) / Mixed DNA profile (Mix) | Alleles Present | Final Interpretation | Description of profile | Potential Intelligence Interpretation possible? |
|---|---|---|---|---|---|---|---|---|
| [redacted] | P2 Rape | 0.00067669 | 0.000819033 | SS | Y | SS | 14 alleles matching to reference sample (known contributor) | N/A |
| | P2 Rape | 0.000593529 | N/A | Mix | Y | CMPU | 1 x sub-threshold peak makes it non-interpretable (it would otherwise be SS) | Y |
| | P3 Burglary | 0.000450739 | 0.001338829 | Mix | Y | PU | Unable to interpret - low level | N |
| | P2 Drugs | 0.000367879 | N/A | Mix | Y | CMPU | 2P mix low level DNA profile | N |
| | P2 Robbery | 0.000865592 | 0.00094415 | Mix | Y | CMPU | 3P mix low level DNA profile | N |
| | P2 Wounding | 0 | N/A | Mix | Y | PU | 2P mix low level DNA profile | N |
| | P2 Rape | 0.00038033 | 0.002201065 | SS | Y | SS | 23 alleles match to suspect LR>100 billion favouring contribution | N/A |
| | P2 Rape | 0.000365777 | N/A | SS | Y | SS | 18 alleles matching to a reference sample (known contributor) | N/A |
| | P2 Wilful Damage | 0.000776552 | N/A | Mix | Y | CMPU | 2P mix low level DNA profile | Y |
| | P2 Rape | 6.70627E-05 | N/A | Mix | Y | CMPU | 1 x extra peak makes it non-interpretable (it would otherwise be SS) | Y |
| | P2 Drugs | 0.000601177 | N/A | SS | Y | SS | 8 alleles UKF1 | Y |
| | P1 Murder | 0.000276482 | N/A | SS | Y | PU | 6 alleles | Y (has been requested by QPS) |
| | P1 Murder | 0.000508813 | N/A | SS | Y | PU | 5 alleles | Y (has been requested by QPS) |
| | P2 Rape | 0 | 0.001408356 | SS | Y | SS | 11 alleles UKM1 | Y |

DNA Insufficient for further processing (DIFP)

| Barcode | Case priority/case type | Initial Quant value | Quant value after microon | Single source (SS) / Mixed DNA profile (Mix) | Alleles Present | Final Interpretation | Description of profile | Potential Intelligence Interpretation possible? |
|---|---|---|---|---|---|---|---|---|
| [redacted] | P2 Wounding | 0.001092311 | 0.003507354 | Mix | Y | 2P mix | 2P mix DNA profile, complainant and defendant. | N/A |
| | P2 Rape | 0.006118513 | 0.010889843 | Mix | Y | 3P mix | 3P mixed DNA profile | N/A |
| | P3 Robbery | 0.006664042 | 0.02207155 | Mix | Y | 2P mix | 2P mix, UKM1 uploaded to NCIDD resulting in a link | N/A |
| | P2 Murder | 0.006455632 | N/A | Mix | Y | 2P mix | 2P mix, Deceased LR>100B favouring contribution | N/A |
| | P3 Burglary | 0.002910232 | N/A | Mix | Y | 2P mix | 2P mix, UKM1 uploaded to NCIDD | N/A |

NB: Generally, samples that are microconned to full are not quanted (to save sample)

NB: A full DNA profile has 40 alleles

| | |
|---|---|
| SS | Single Source DNA profile |
| CMPU | Complex mixed profile unsuitable for Interpretation or Comparison |
| PU | Partial DNA profile unsuitable for comparison purposes |
| UKM1 | Uknown Male 1 |
| UKF1 | Unknown Female 1 |
| 2P mix | 2 Person mixed DNA profile |

3P mix

NCIDD

3 Person mixed DNA profile

National Criminal Investigation DNA Database

# AQ-03

Project: CCE20220808-02

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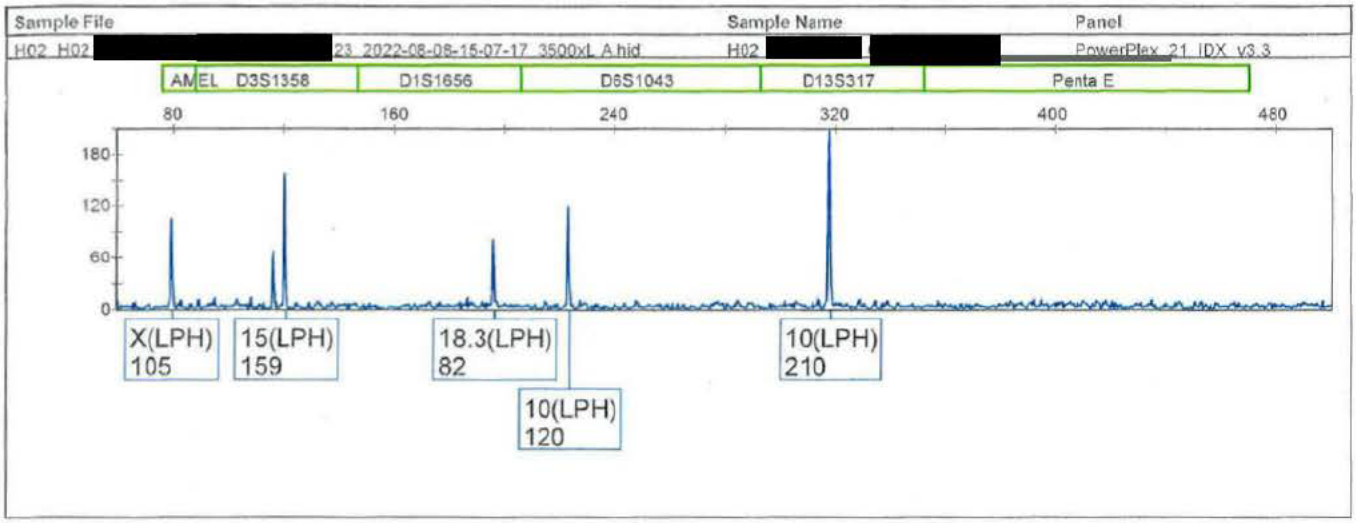


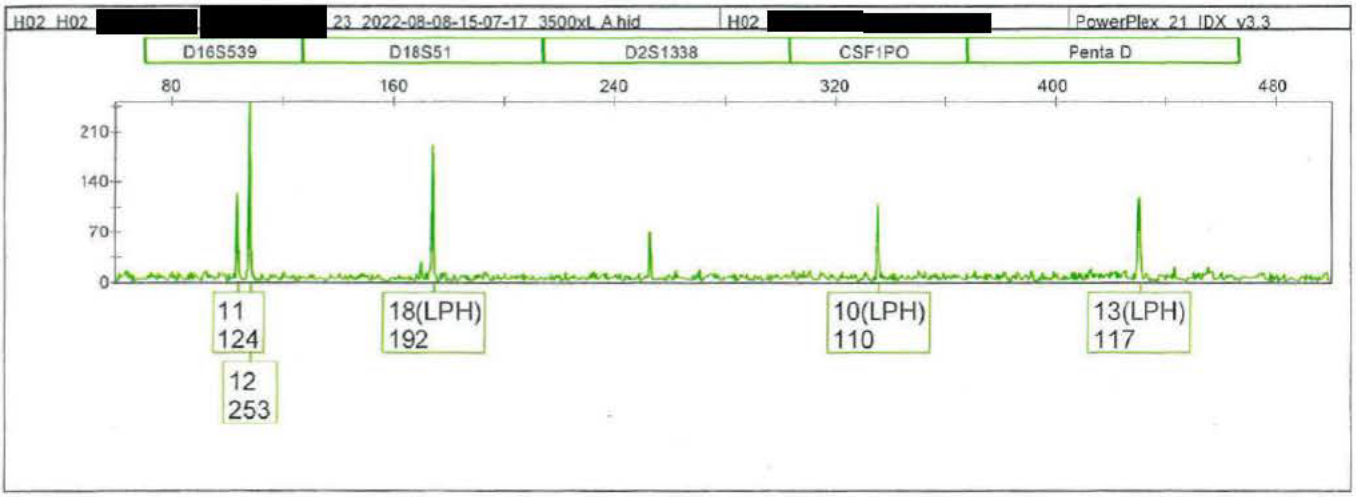


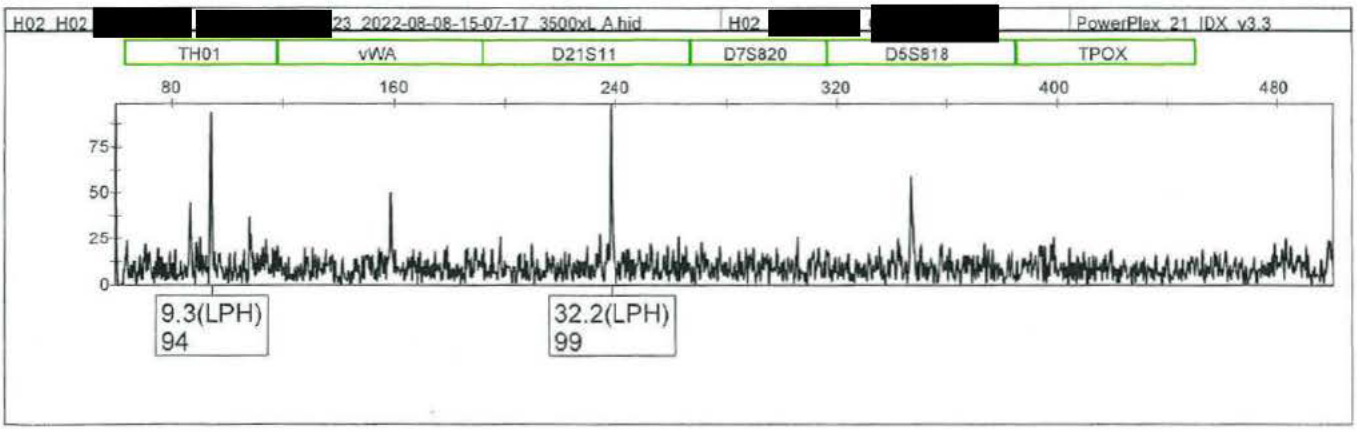

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Project: CCE20220808-02

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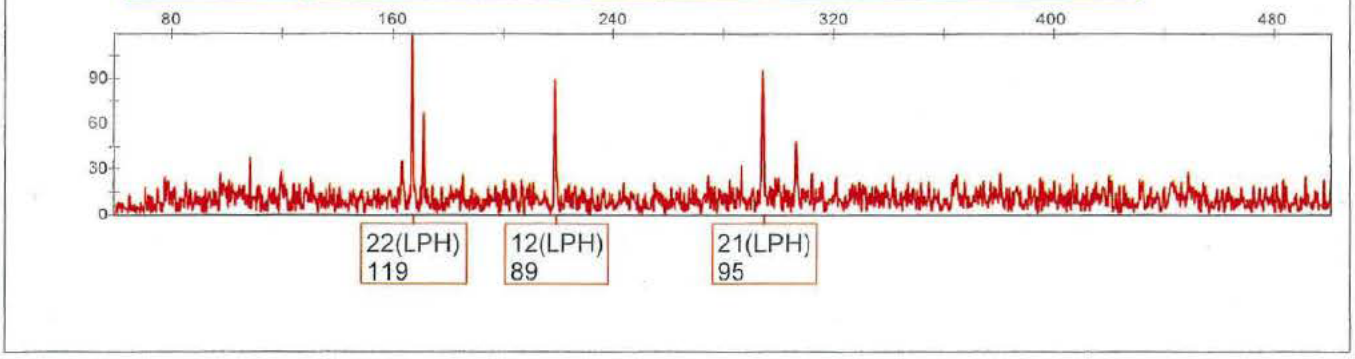

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Project: CCE20220811-01

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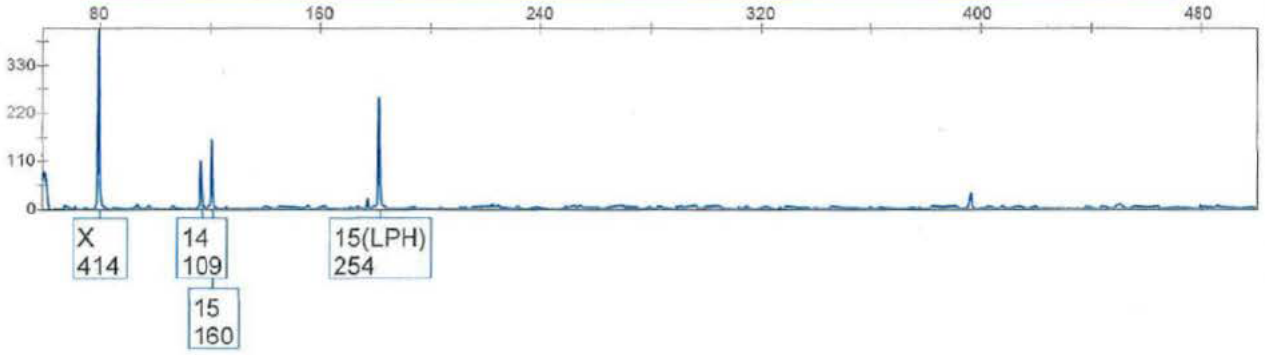


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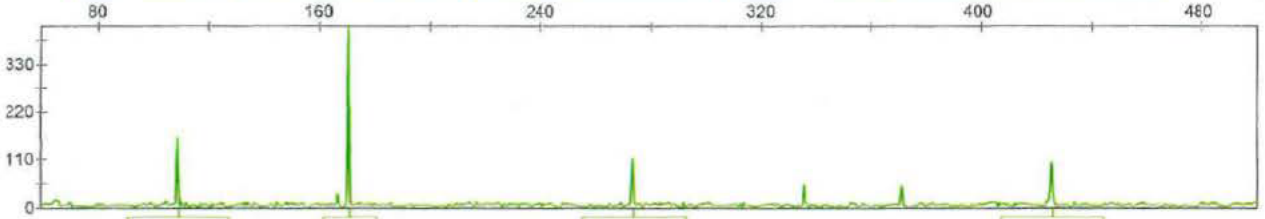


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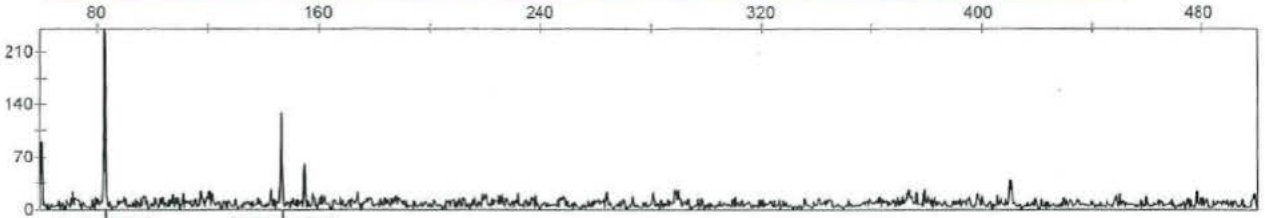

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Project: CCE20220811-01

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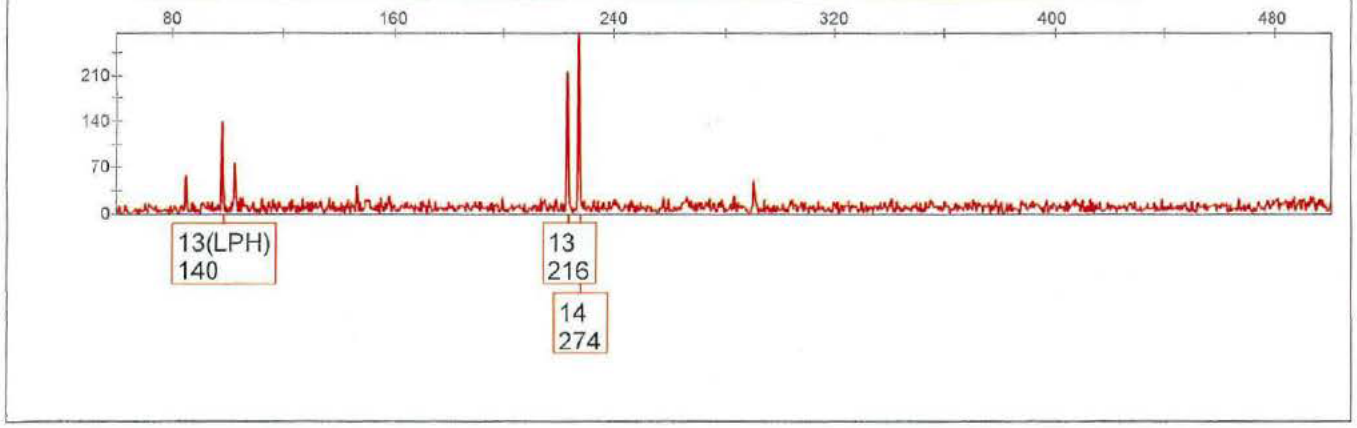

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Project: CCE20220809-03

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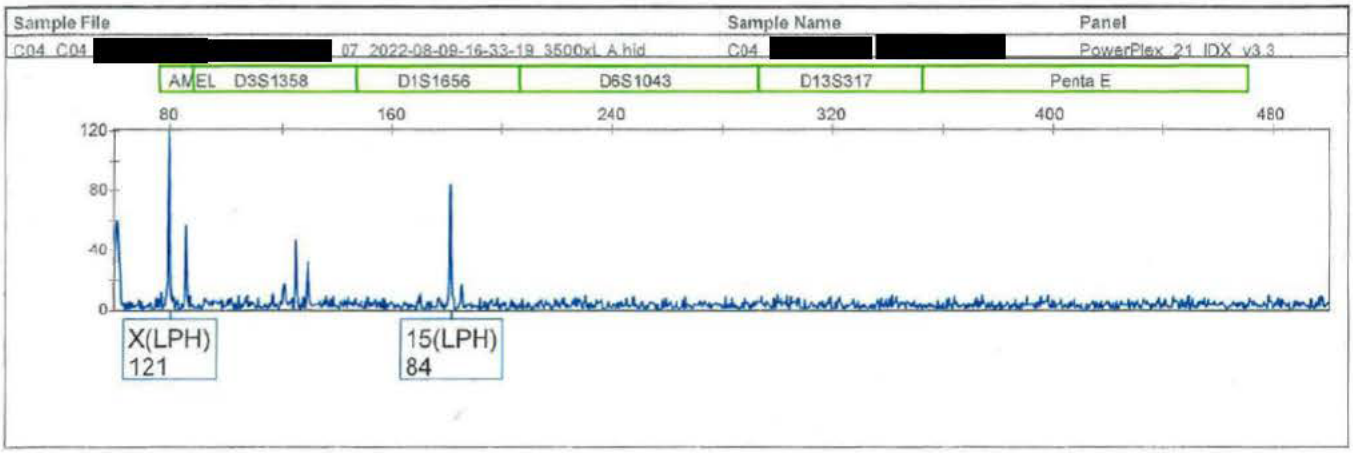


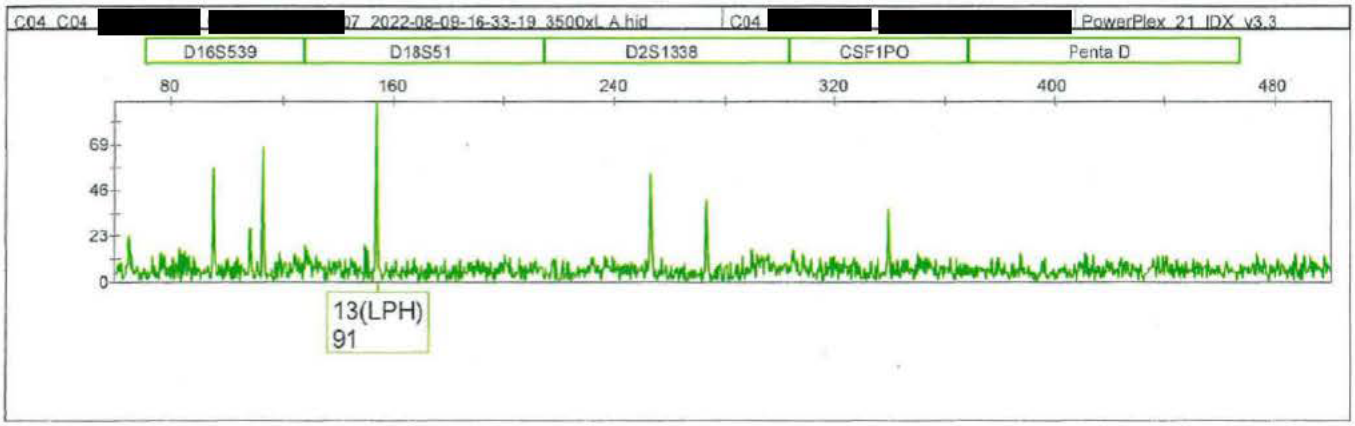


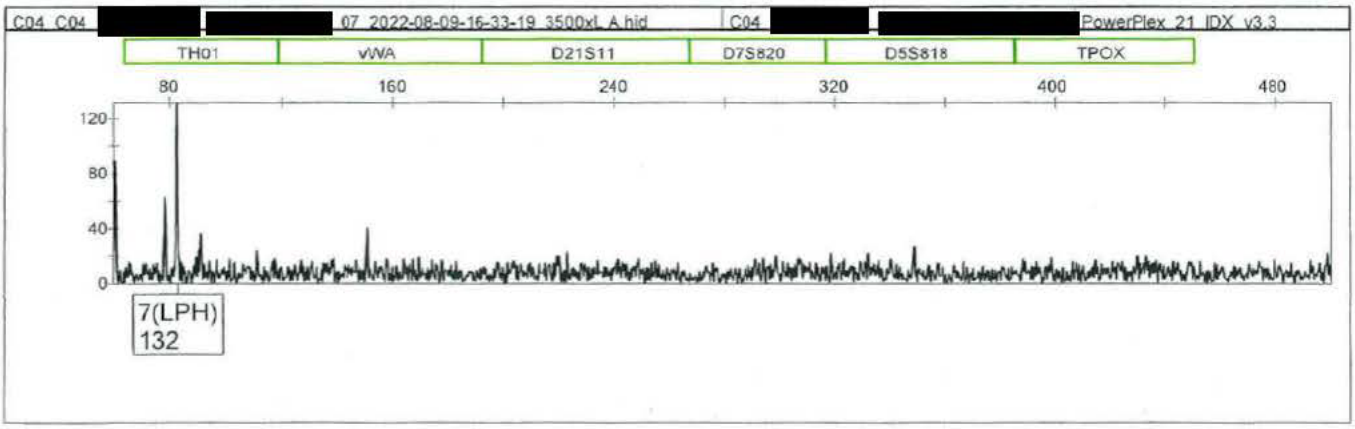


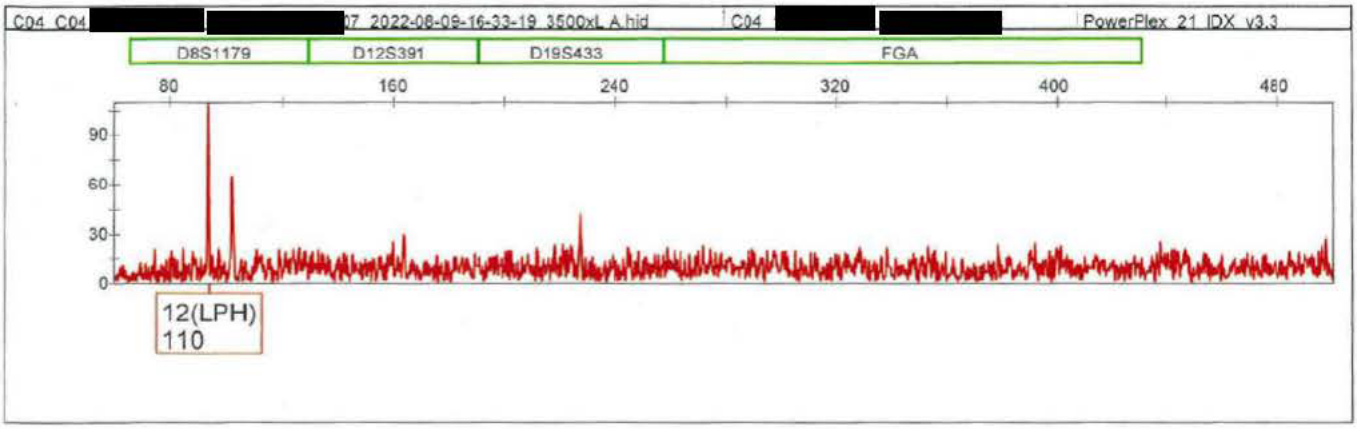

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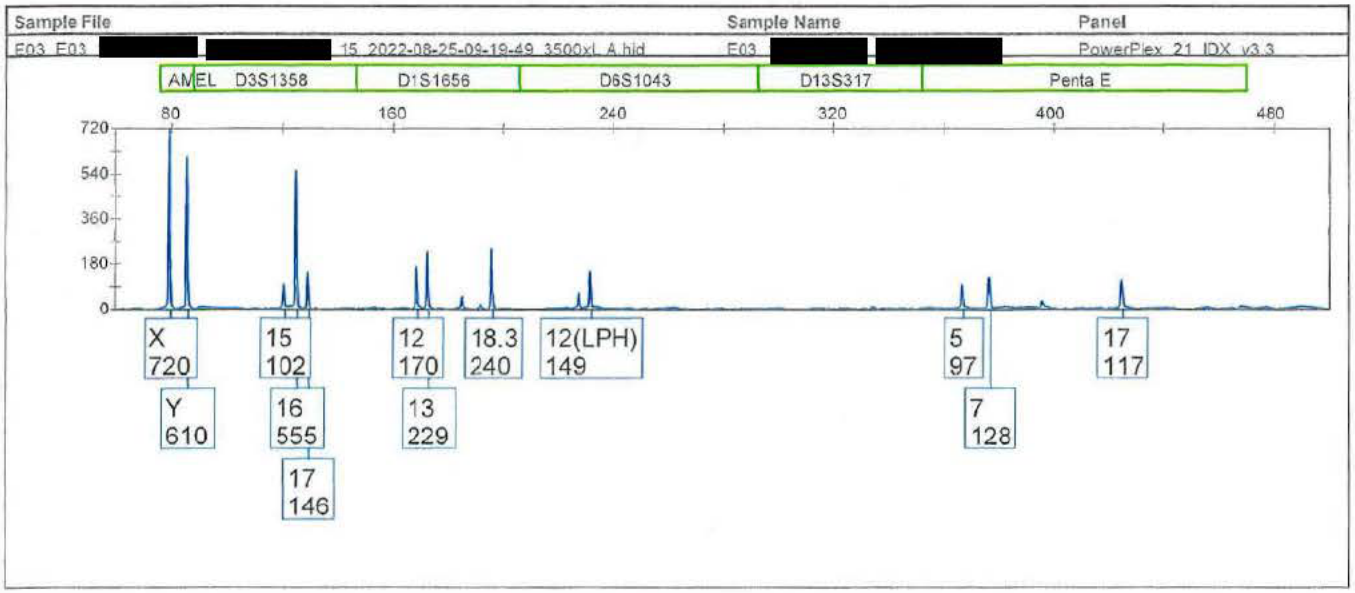
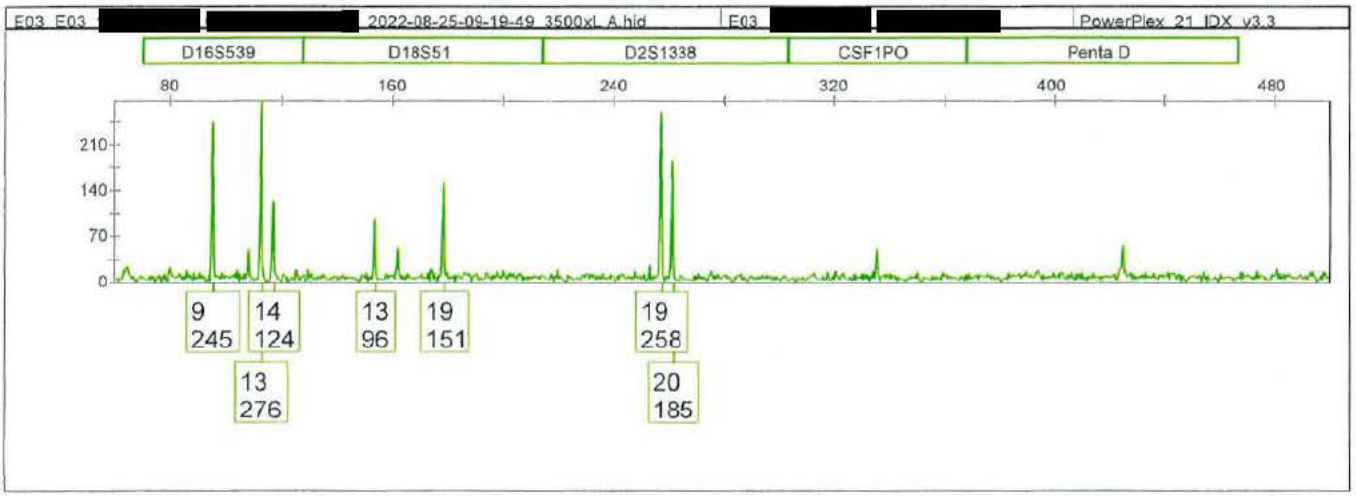
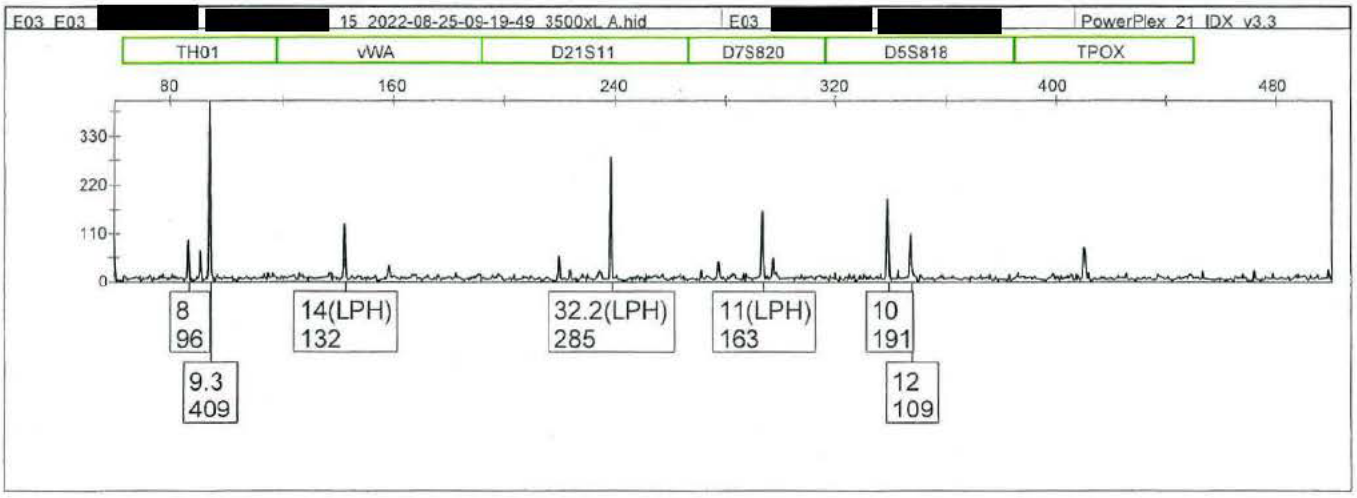
Project: CCE20220825-01

GeneMapper™ ID-X 1.6



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Project: CCE20220825-01

GeneMapper™ ID-X 1.6

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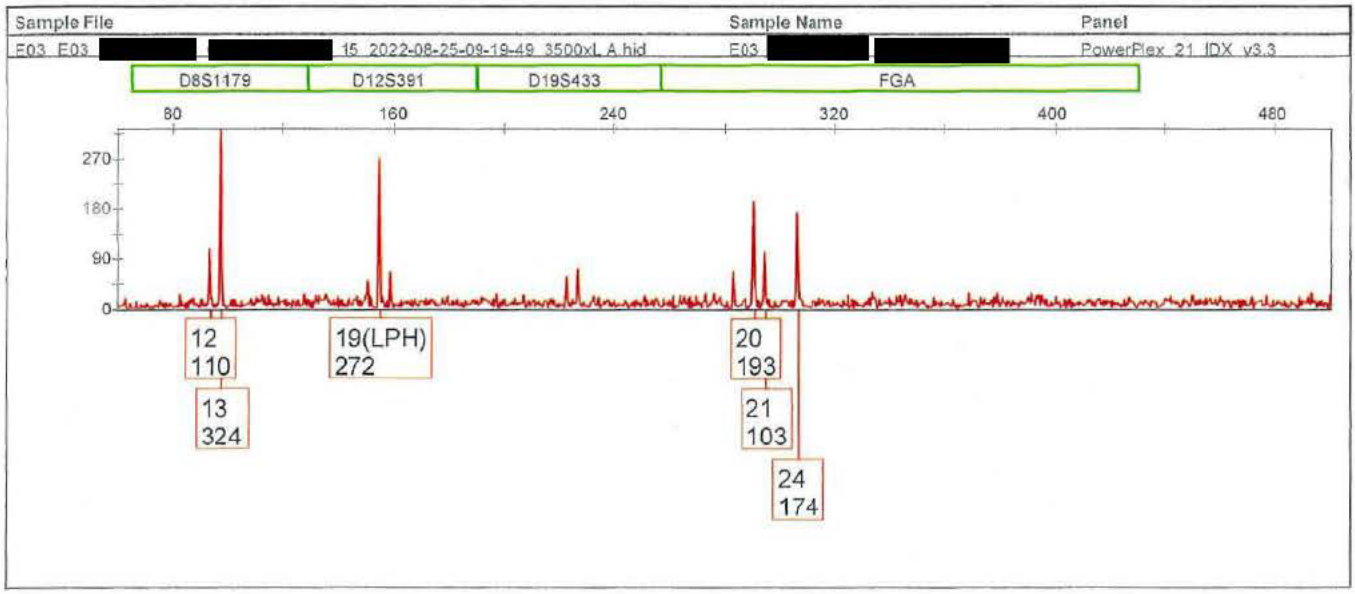

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Project: CCE20220816-02

GeneMapper™ ID-X 1.6

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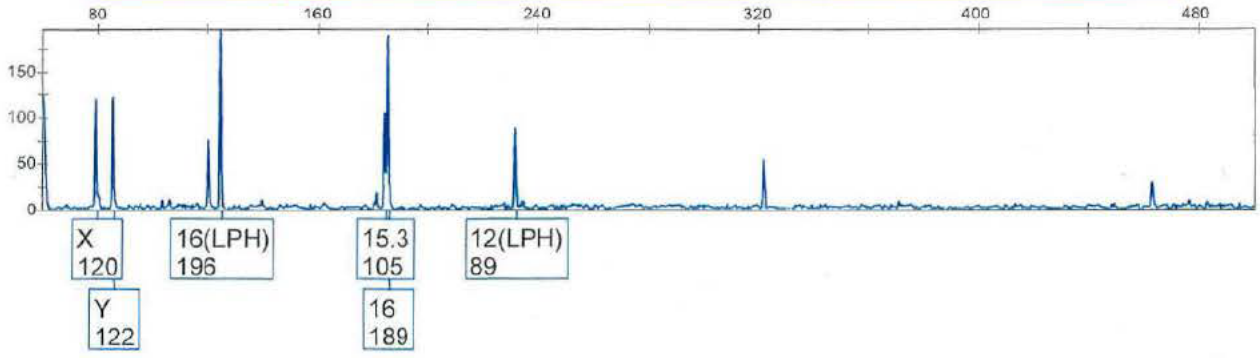
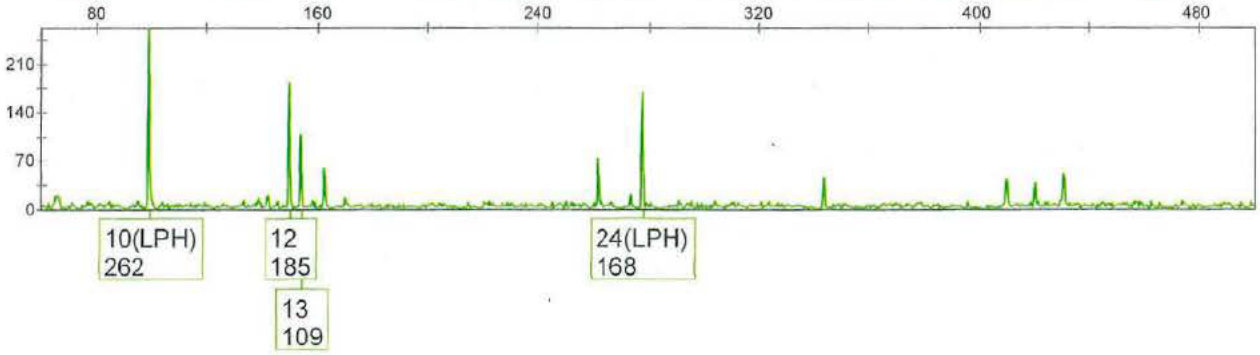


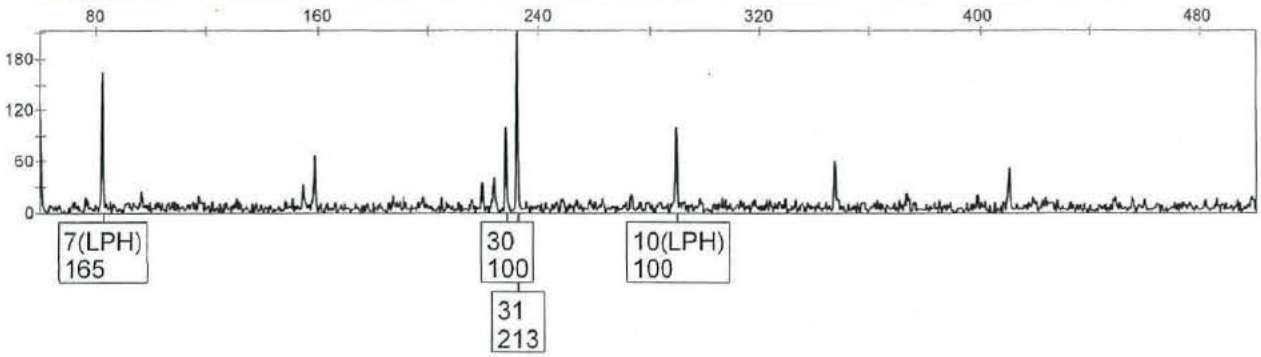

D01_D01 [redacted] 10_2022-08-16-10-25-21_3500xL_A.hid | D01 [redacted] | PowerPlex_21_IDX_v3.3

D16S539 | D18S51 | D2S1338 | CSF1PO | Penta D




D01_D01 [redacted] 10_2022-08-16-10-25-21_3500xL_A.hid | D01 [redacted] | PowerPlex_21_IDX_v3.3

TH01 | vWA | D21S11 | D7S820 | D5S818 | TPOX

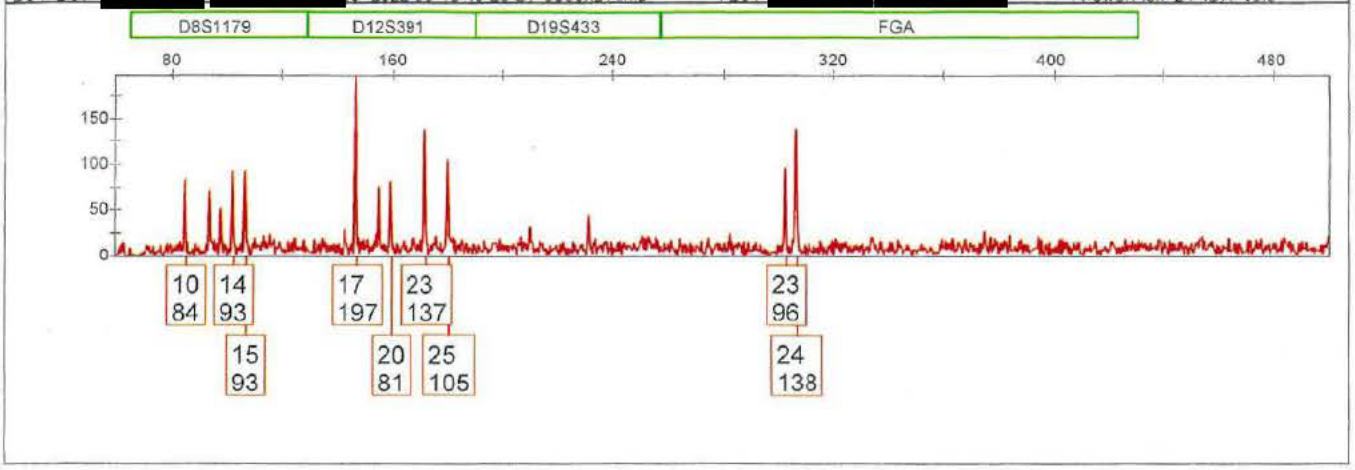


applied biosystems

Project: CCE20220816-02

GeneMapper™ ID-X 1.6

| Sample File | Sample Name | Panel |
|---|---|---|
| D01_D01 [redacted] 0_2022-08-16-10-25-21_3500xL_A.hid | D01 [redacted] | PowerPlex_21_IDX_v3.3 |



applied biosystems

Project: CCE20220825-01

GeneMapper™ ID-X 1.6

| Sample File | Sample Name | Panel |
|---|---|---|
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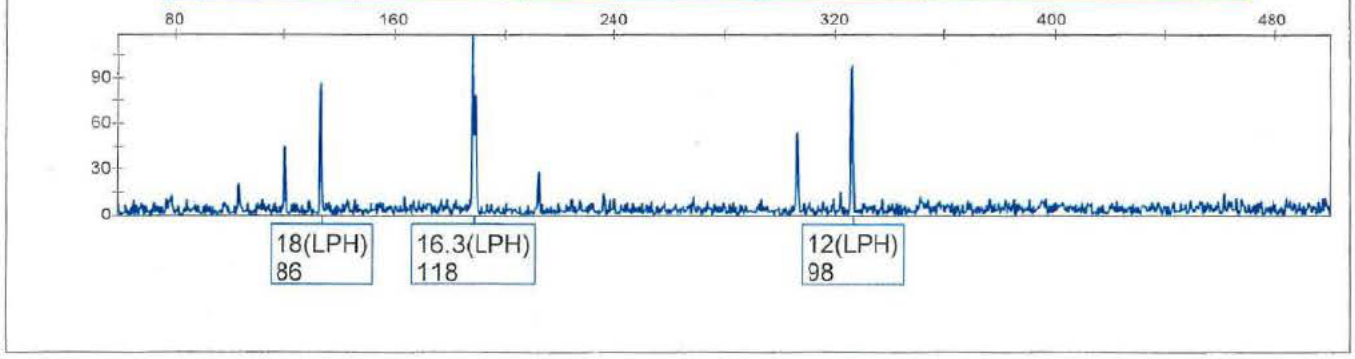
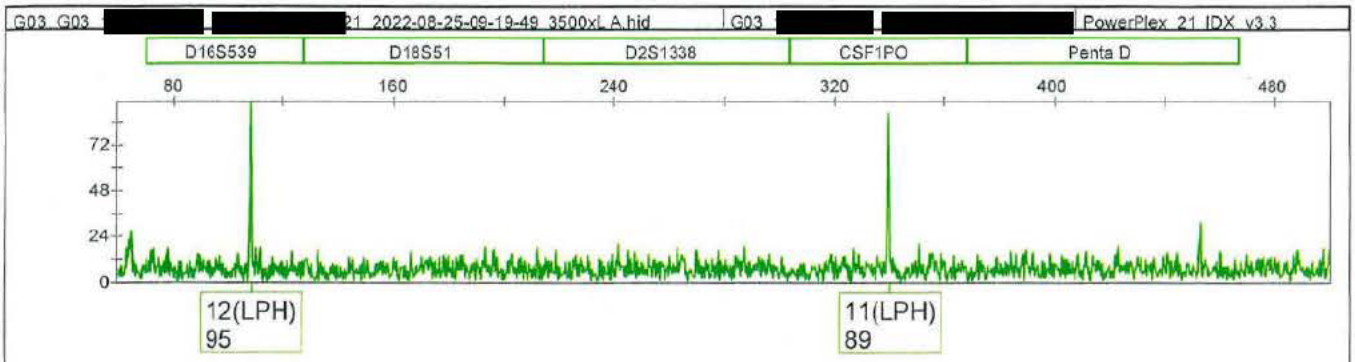
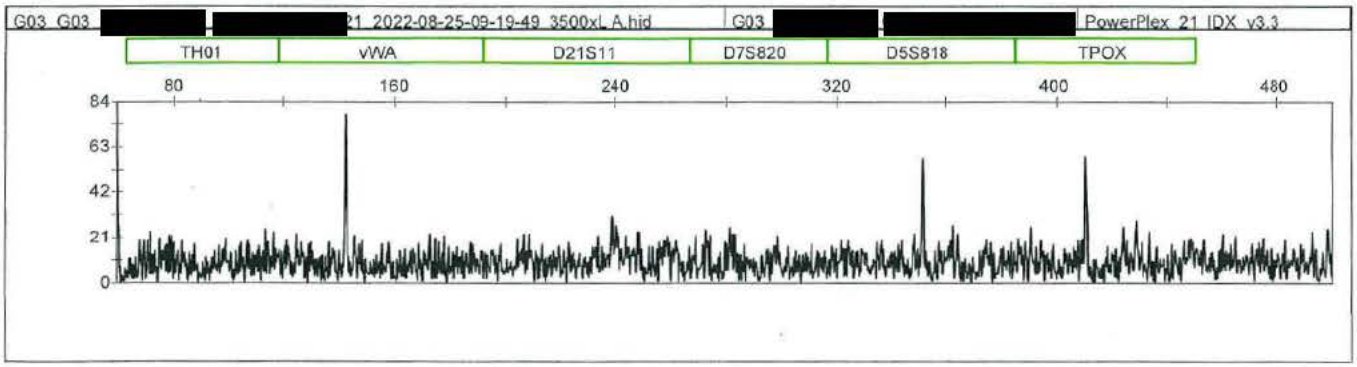


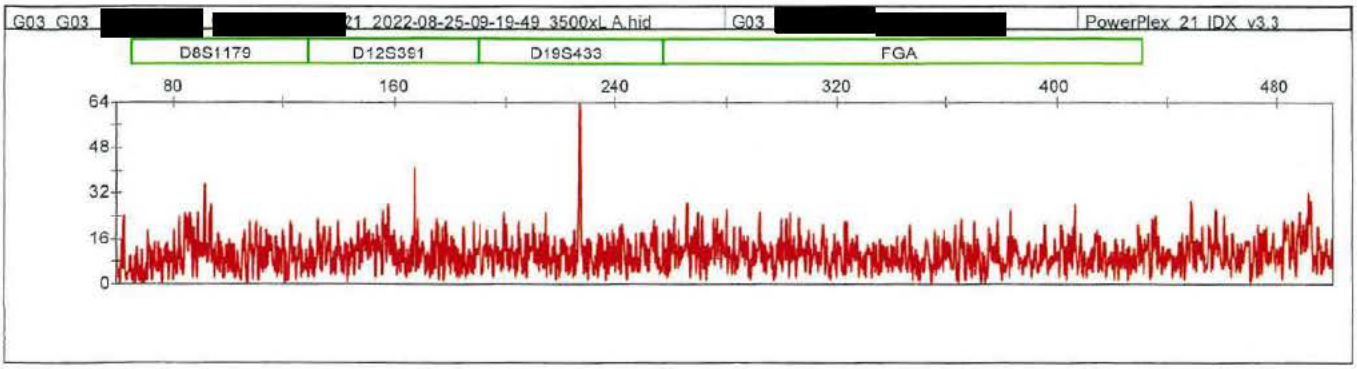

| Sample File | Sample Name | Panel |
|---|---|---|
| G03_G03 [redacted] 21_2022-08-25-09-19-49_3500xL_A.hid | G03 [redacted] | PowerPlex_21_IDX_v3.3 |




| Sample File | Sample Name | Panel |
|---|---|---|
| G03_G03 [redacted] 21_2022-08-25-09-19-49_3500xL_A.hid | G03 [redacted] | PowerPlex_21_IDX_v3.3 |



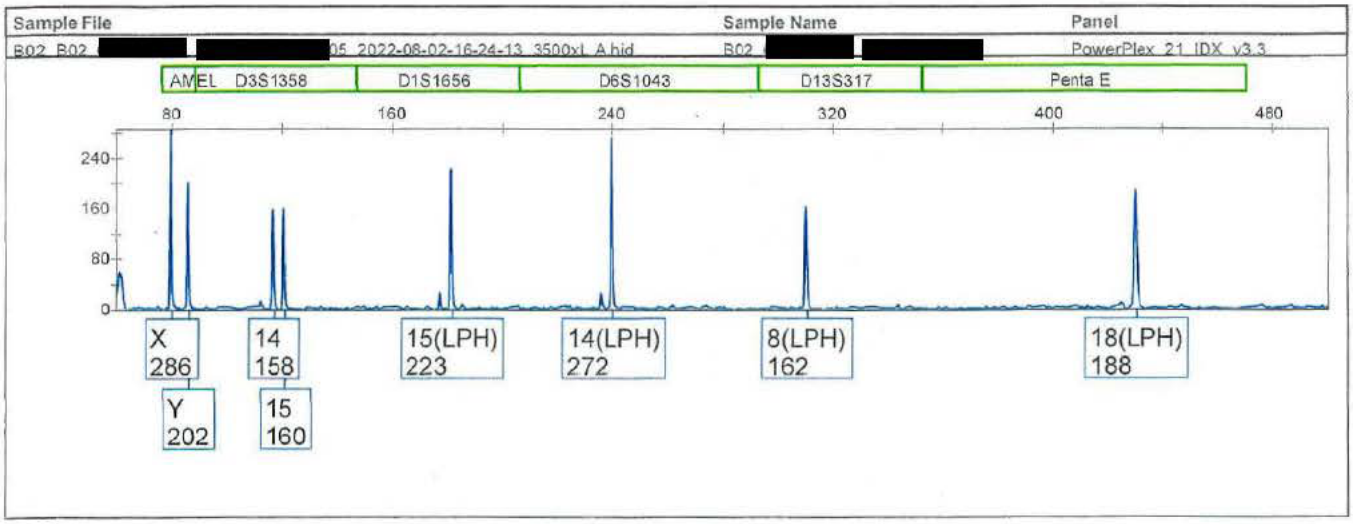

| Sample File | Sample Name | Panel |
|---|---|---|
| G03_G03 [redacted] 21_2022-08-25-09-19-49_3500xL_A.hid | G03 [redacted] | PowerPlex_21_IDX_v3.3 |

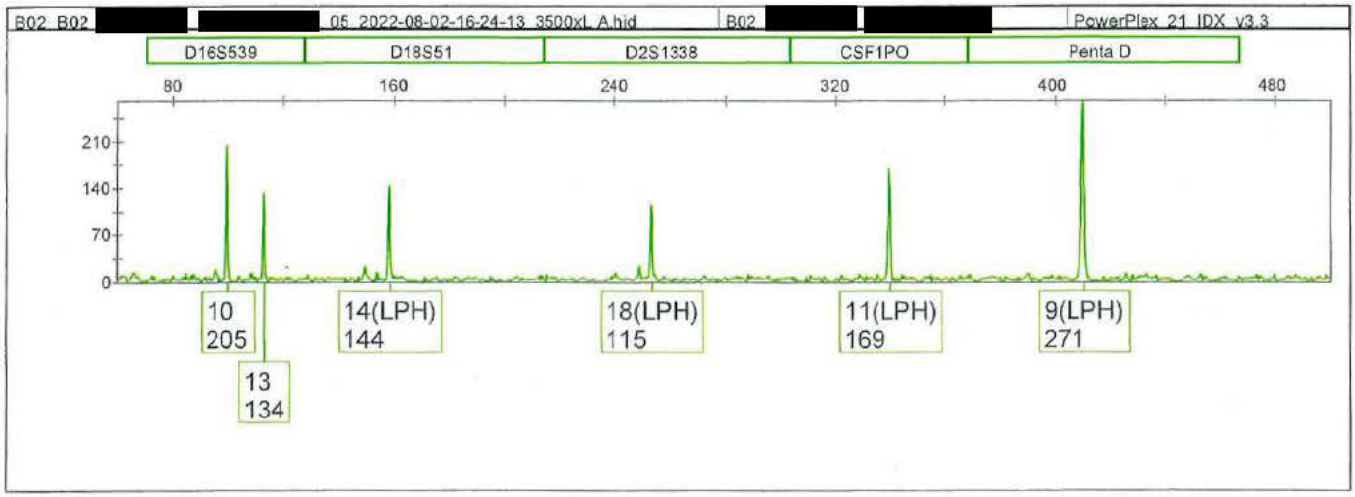


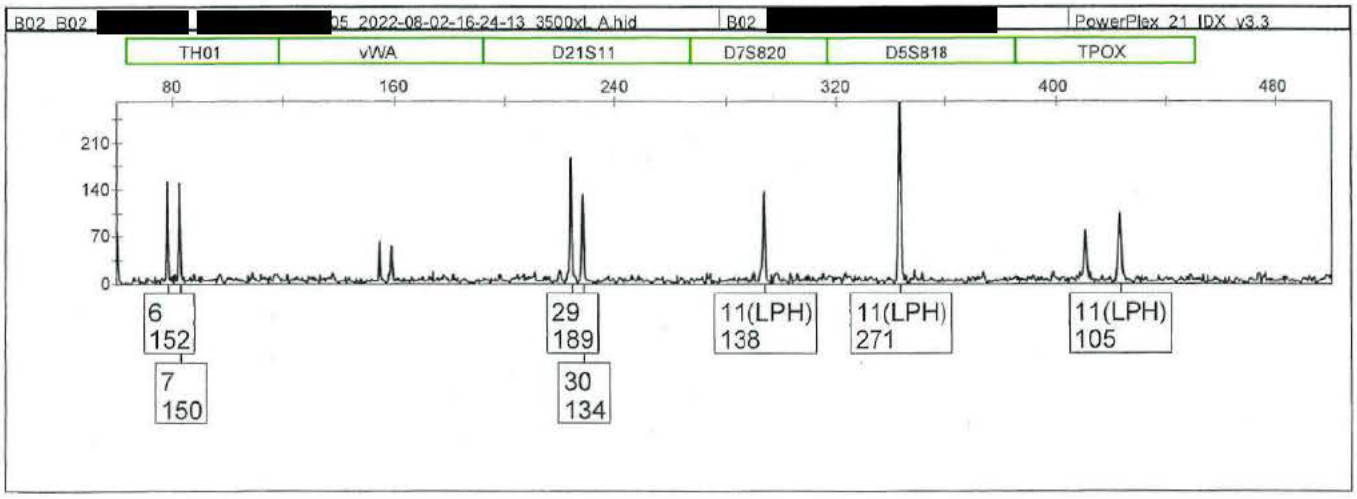
appliedbiosystems

Project: CCE20220802-04

GeneMapper™ ID-X 1.6



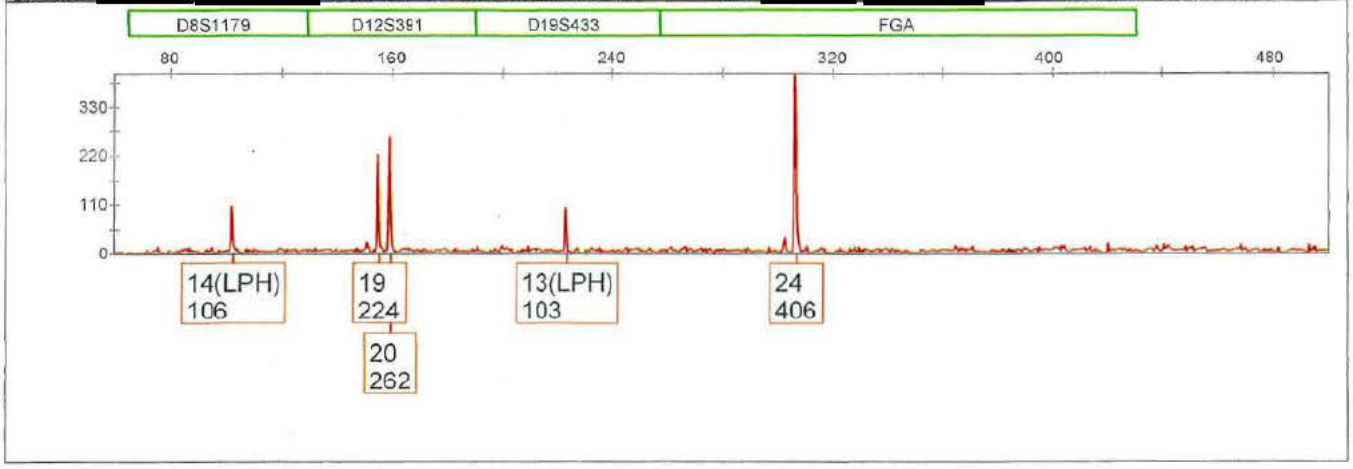



applied biosystems

Project: CCE20220802-04

GeneMapper™ ID-X 1.6

| Sample File | Sample Name | Panel |
|---|---|---|
| B02_B02 [redacted] 05_2022-08-02-16-24-13_3500xL_A.hid | B02 [redacted] | PowerPlex_21_IDX_v3.3 |



applied biosystems

Project: CCE20220825-02

GeneMapper™ ID-X 1.6

| Sample File | Sample Name | Panel |
|---|---|---|
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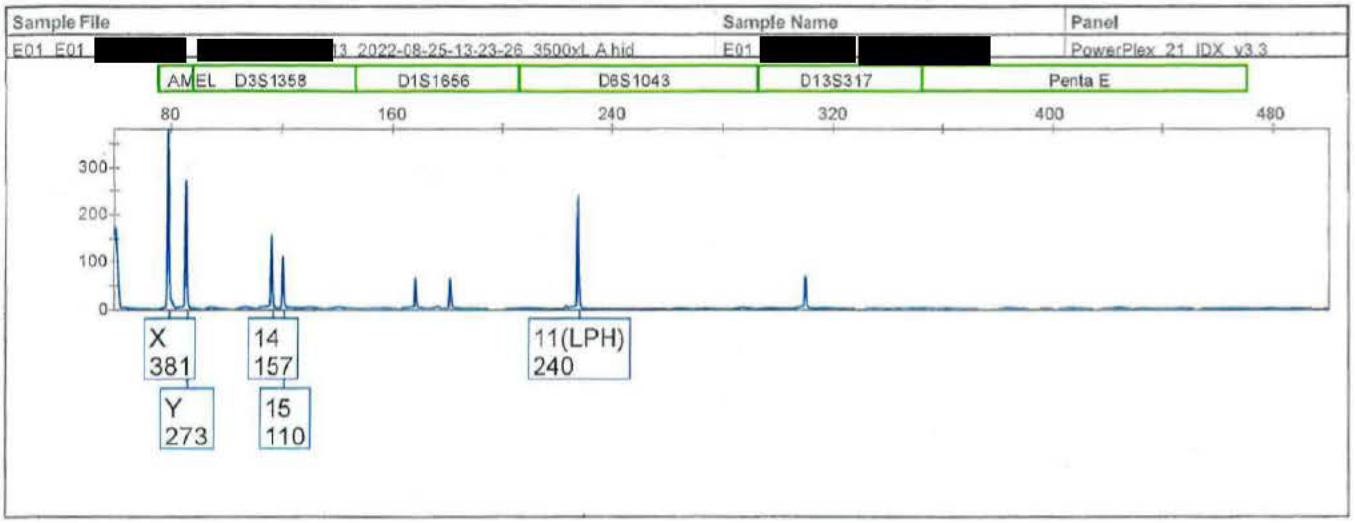
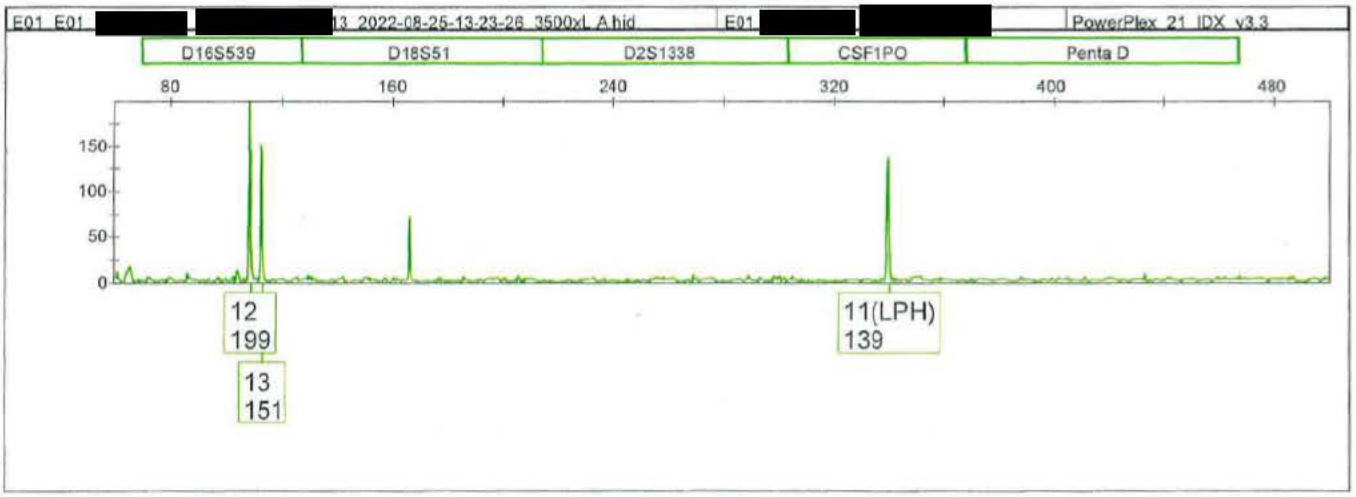
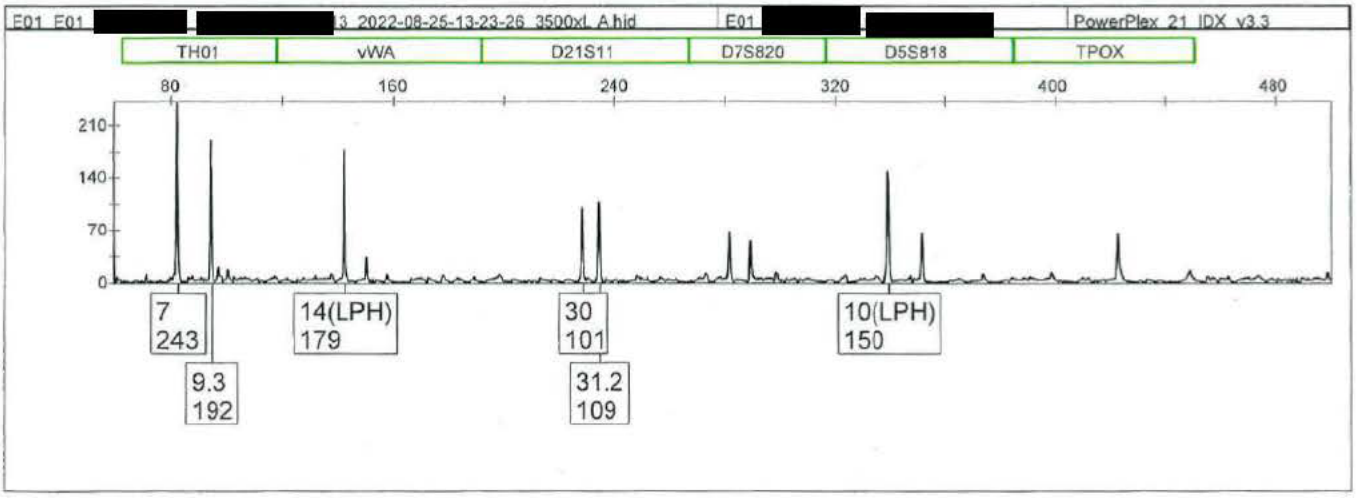



| E01_E01 [redacted] 13_2022-08-25-13-23-26_3500xL_A.hid | E01 [redacted] | PowerPlex_21_IDX_v3.3 |
|---|---|---|




| E01_E01 [redacted] 13_2022-08-25-13-23-26_3500xL_A.hid | E01 [redacted] | PowerPlex_21_IDX_v3.3 |
|---|---|---|

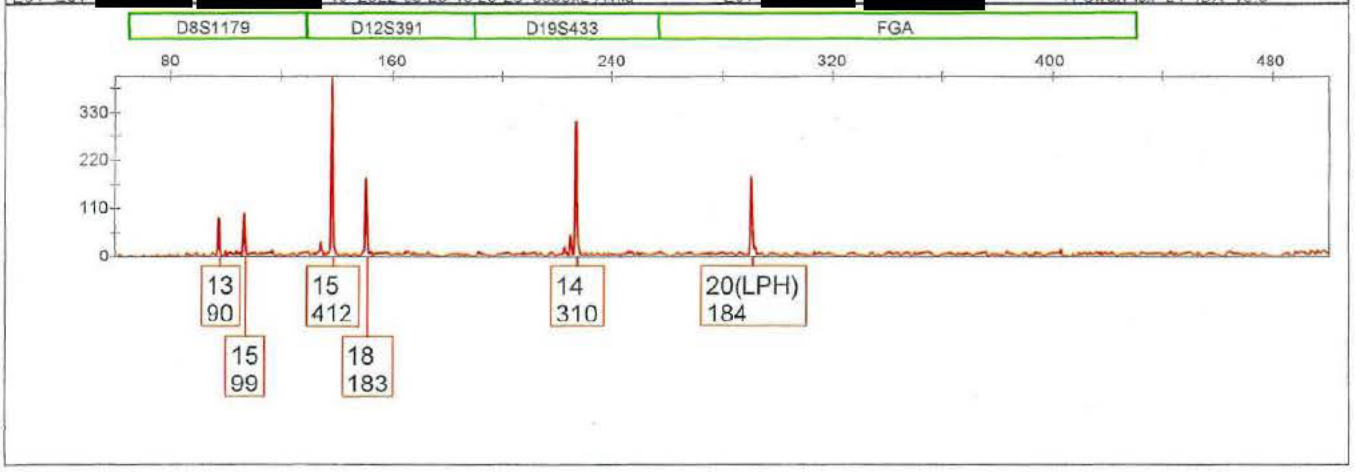


appliedbiosystems

Project: CCE20220825-02

GeneMapper™ ID-X 1.6

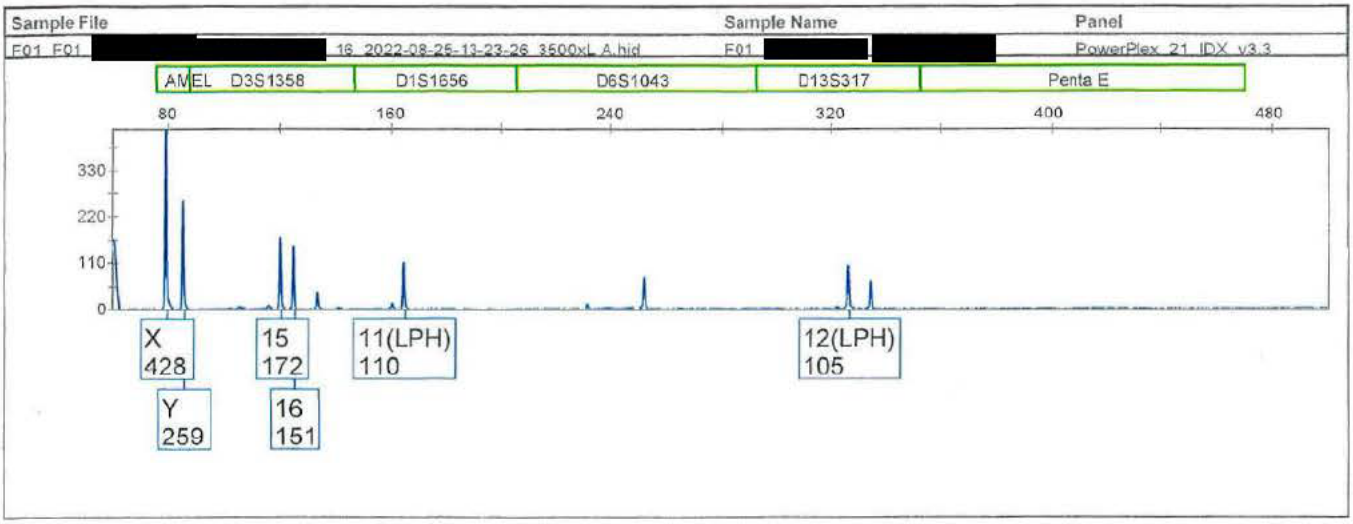
| Sample File | Sample Name | Panel |
|---|---|---|
| E01_E01 [redacted] 13_2022-08-25-13-23-26_3500xL_A.hid | E01 [redacted] | PowerPlex_21_IDX_v3.3 |

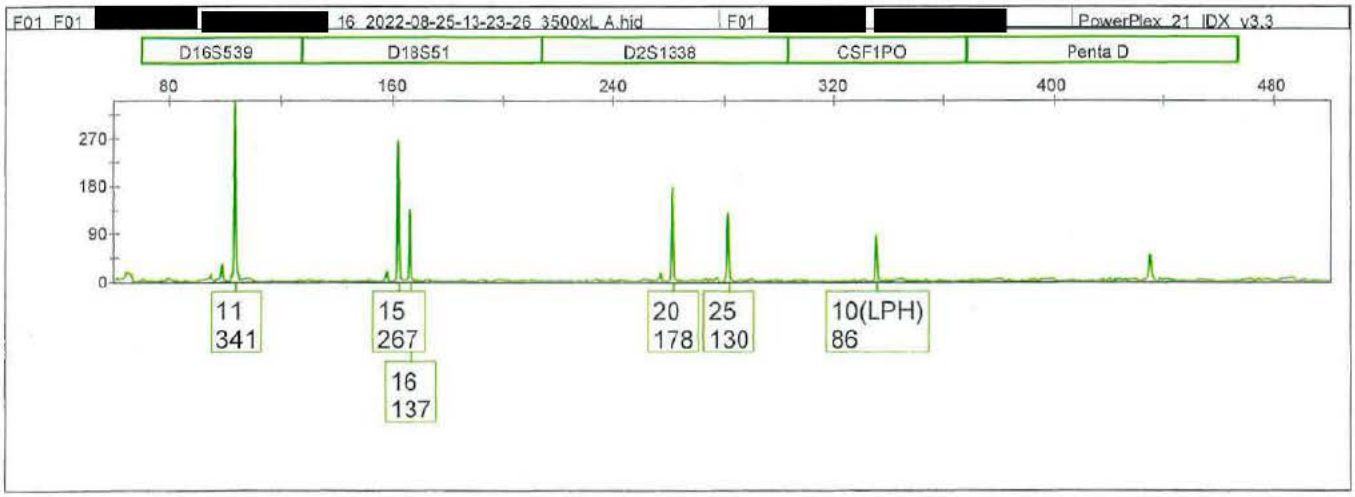


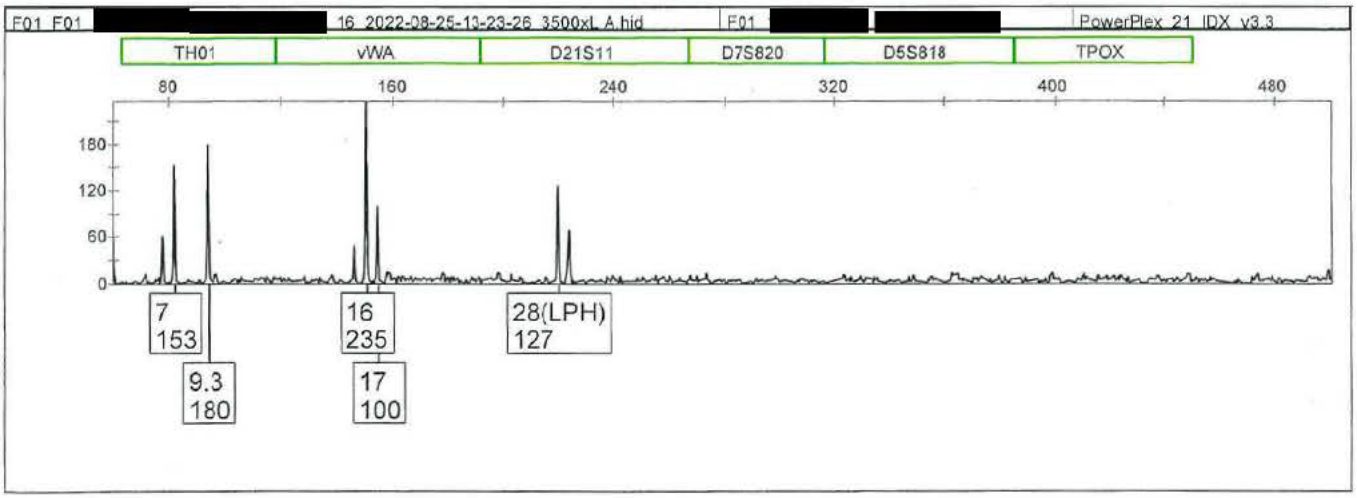
applied biosystems

Project: CCE20220825-02

GeneMapper™ ID-X 1.6



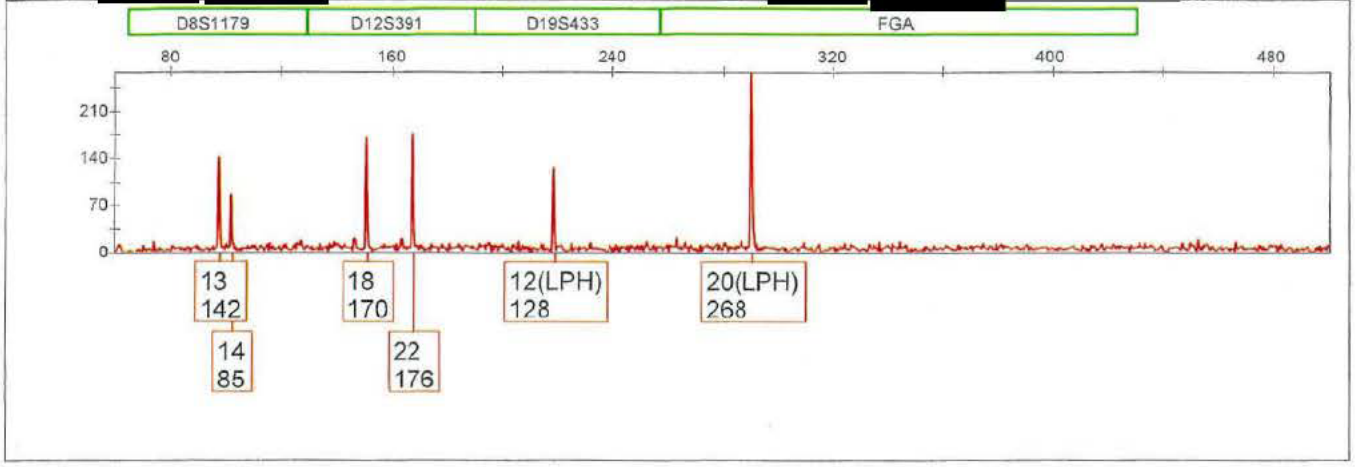



appliedbiosystems

Project: CCE20220825-02

GeneMapper™ ID-X 1.6

| Sample File | Sample Name | Panel |
|---|---|---|
| F01_F01 [redacted] 16_2022-08-25-13-23-26_3500xL_A.hid | F01 [redacted] | PowerPlex_21_IDX_v3.3 |

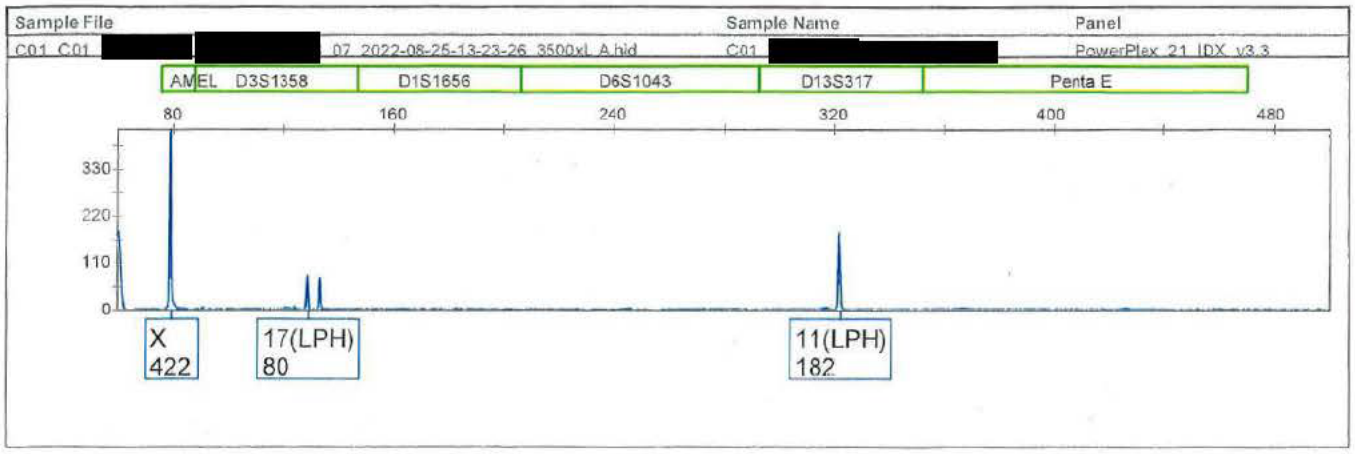


appliedbiosystems

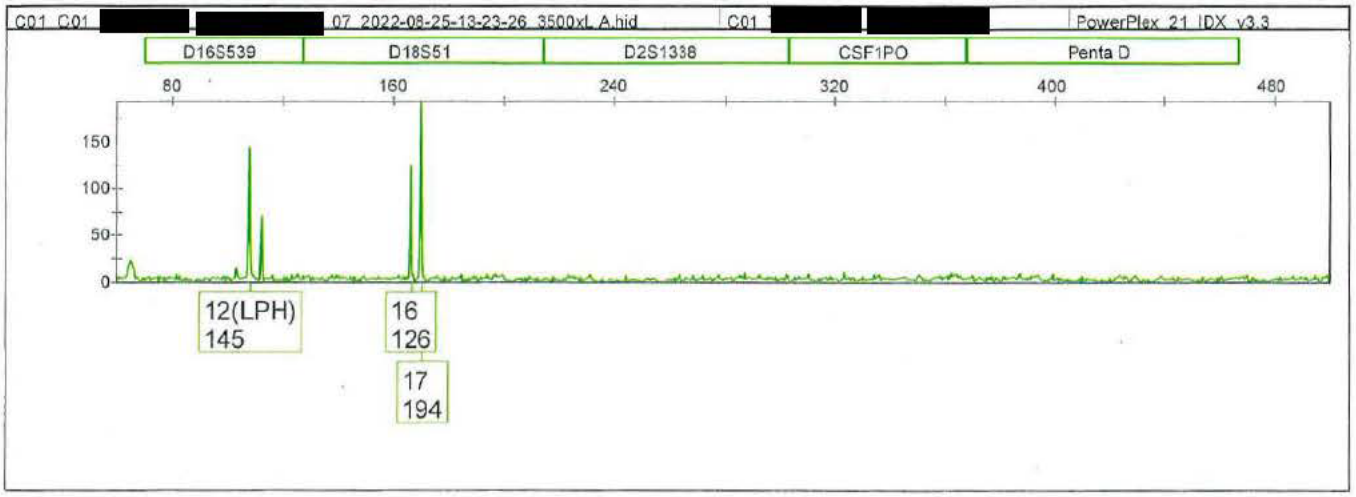
Project: CCE20220825-02

GeneMapper™ ID-X 1.6

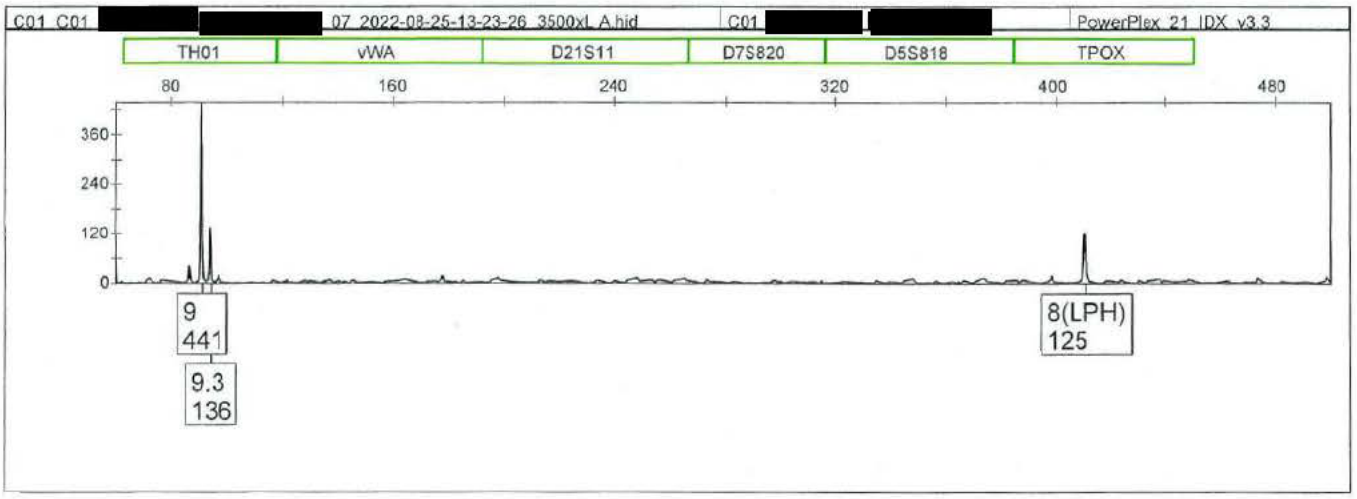
| Sample File | Sample Name | Panel |
|---|---|---|
| C01 C01 [redacted] 07 2022-08-25-13-23-26 3500xL A.hid | C01 [redacted] | PowerPlex 21 IDX v3.3 |




C01 C01 [redacted] 07 2022-08-25-13-23-26 3500xL A.hid C01 [redacted] PowerPlex 21 IDX v3.3




C01 C01 [redacted] 07 2022-08-25-13-23-26 3500xL A.hid C01 [redacted] PowerPlex 21 IDX v3.3

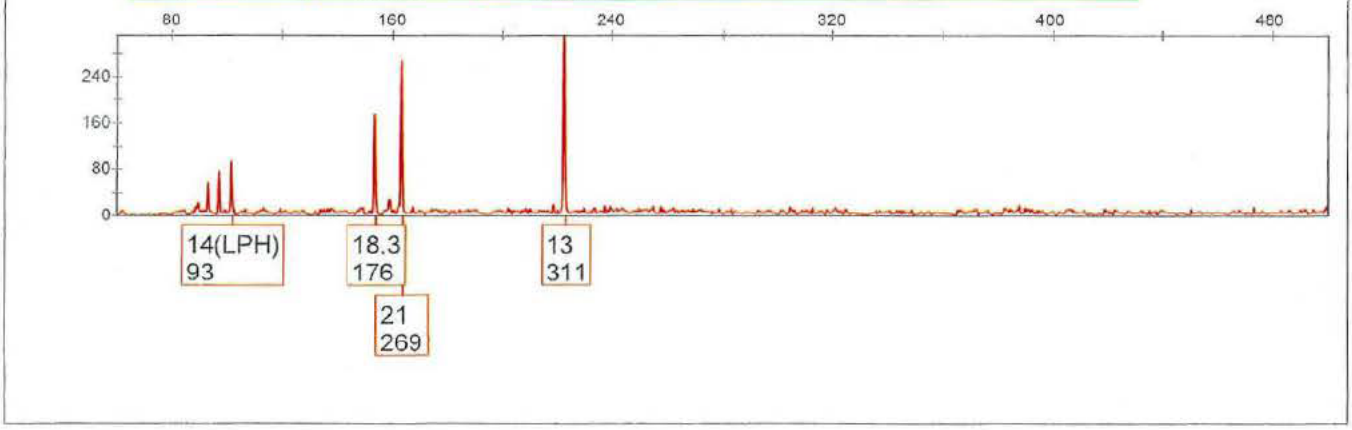


appliedbiosystems

Project: CCE20220825-02

GeneMapper™ ID-X 1.6

| Sample File | Sample Name | Panel |
|---|---|---|
| C01_C01 [redacted] 07_2022-08-25-13-23-26_3500xL_A.hid | C01 [redacted] | PowerPlex_21_IDX_v3.3 |



appliedbiosystems

Project: CCE20220829-06

GeneMapper™ ID-X 1.6

| Sample File | Sample Name | Panel |
|---|---|---|
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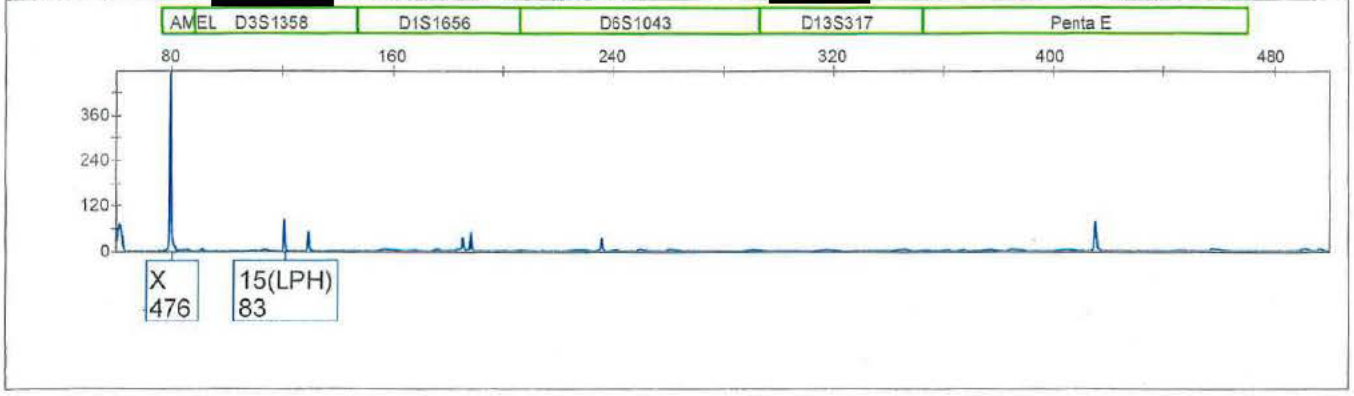
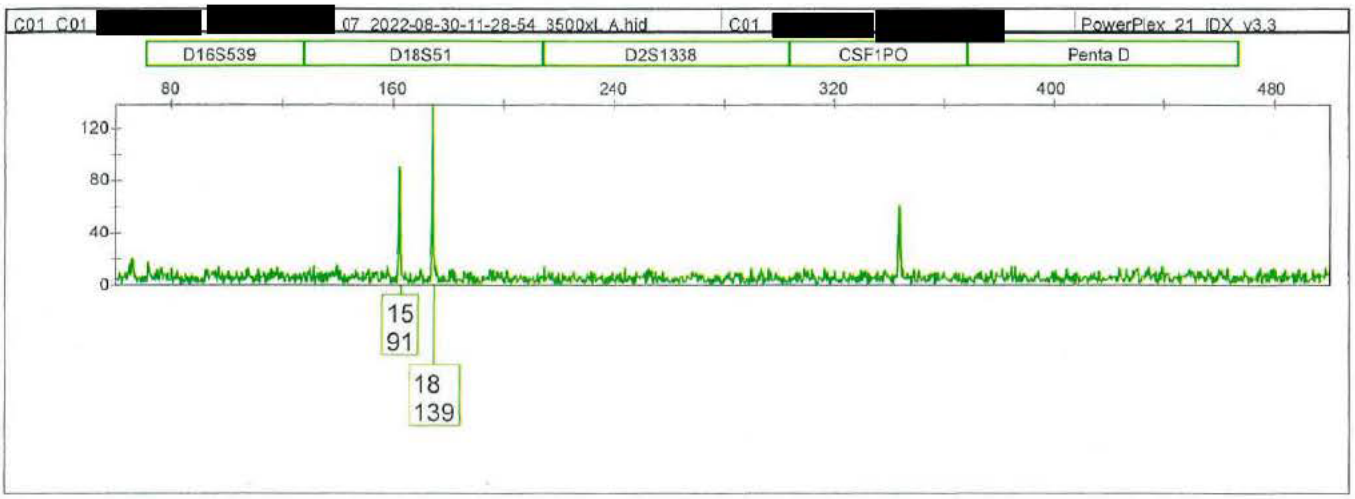
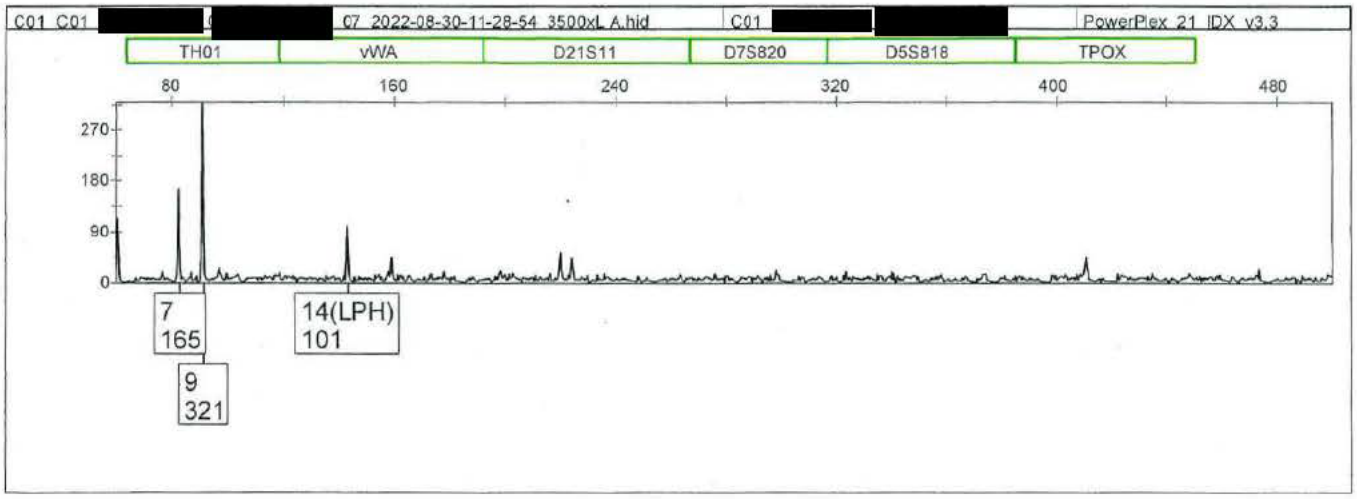



C01 C01 [redacted] 07 2022-08-30-11-28-54 3500xL A.hid C01 [redacted] PowerPlex 21 IDX v3.3




C01 C01 [redacted] 07 2022-08-30-11-28-54 3500xL A.hid C01 [redacted] PowerPlex 21 IDX v3.3



appliedbiosystems

Project: CCE20220829-06

GeneMapper™ ID-X 1.6

| Sample File | Sample Name | Panel |
|---|---|---|
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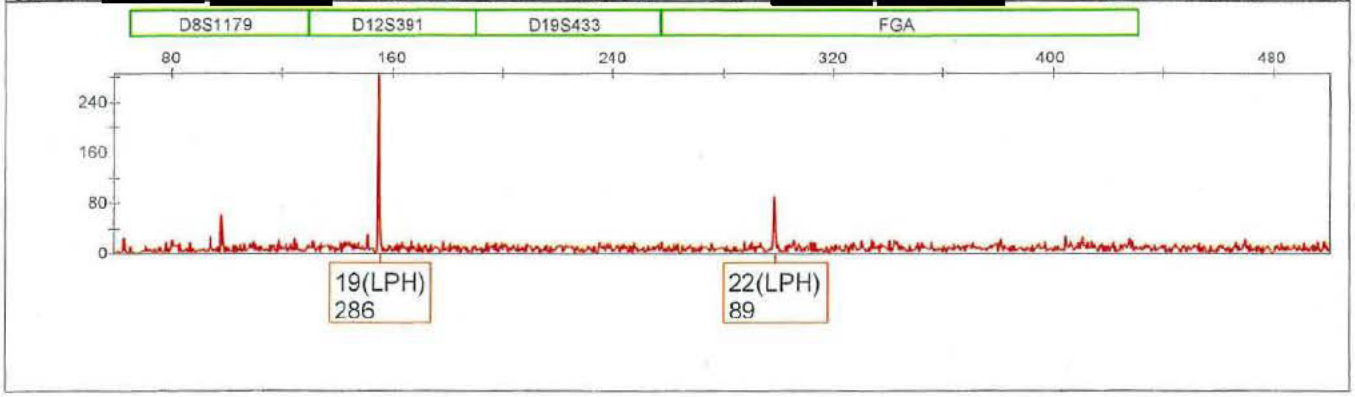

appliedbiosystems

Project: CCE20220812-03

GeneMapper™ ID-X 1.6

| Sample File | Sample Name | Panel |
|---|---|---|
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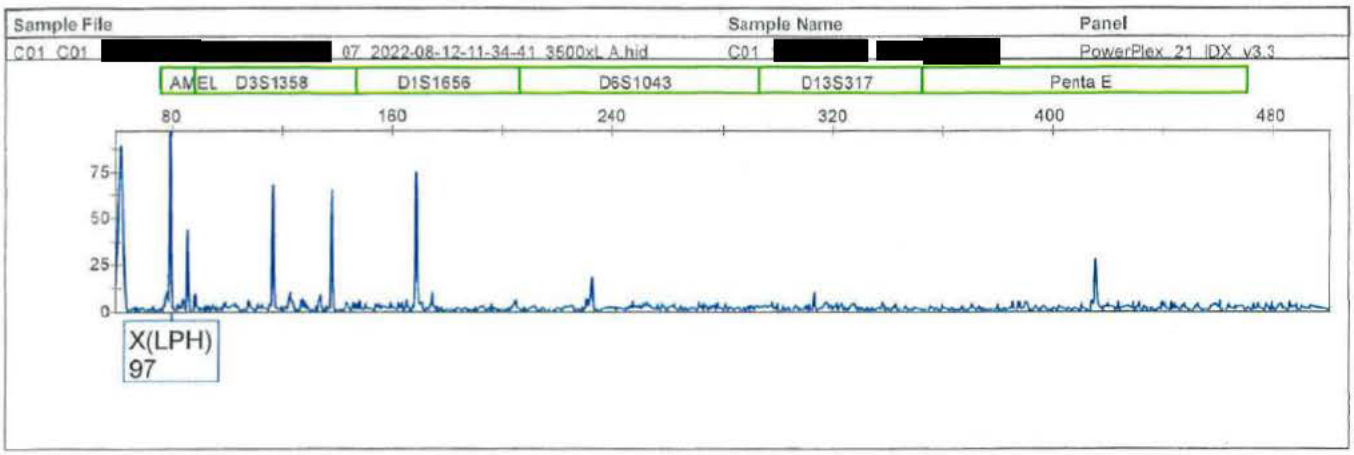
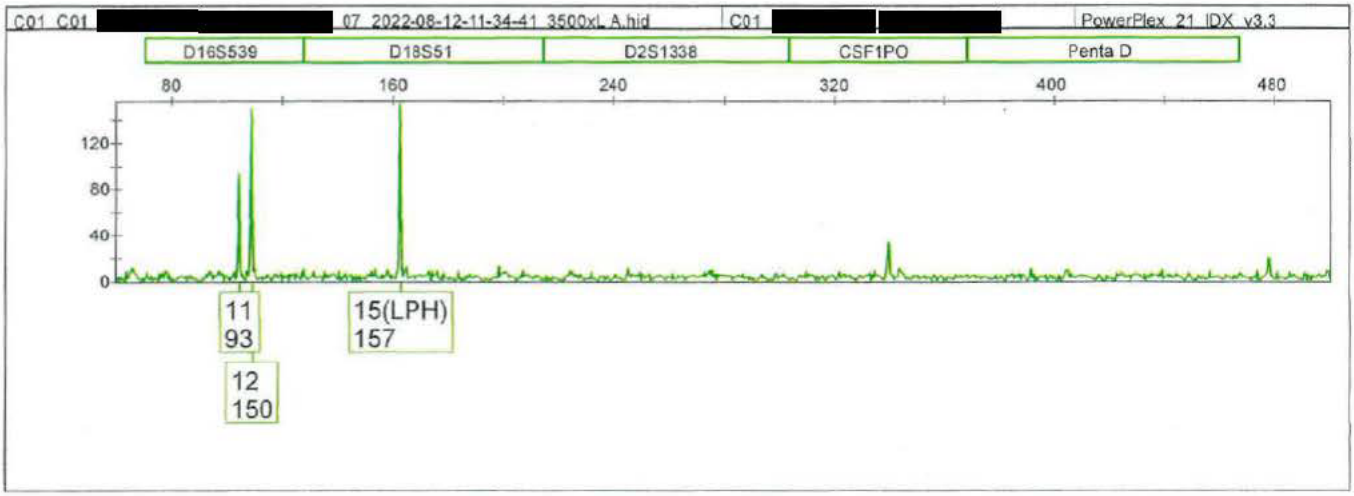
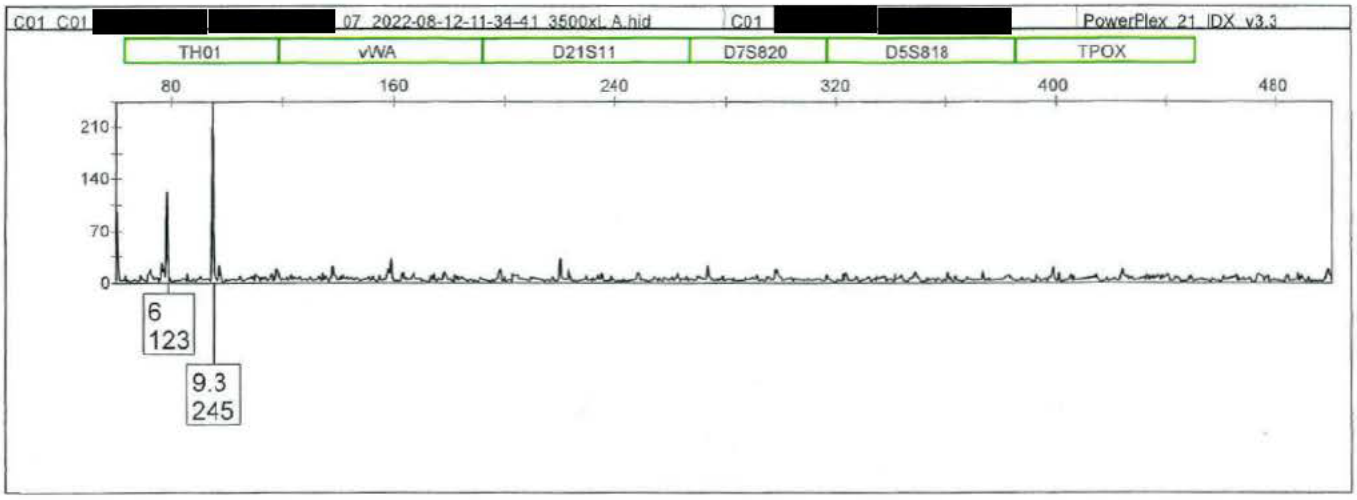



| Sample File | Sample Name | Panel |
|---|---|---|
| C01 C01 [redacted] 07_2022-08-12-11-34-41_3500xL_A.hid | C01 [redacted] | PowerPlex_21_IDX_v3.3 |




| Sample File | Sample Name | Panel |
|---|---|---|
| C01 C01 [redacted] 07_2022-08-12-11-34-41_3500xL_A.hid | C01 [redacted] | PowerPlex_21_IDX_v3.3 |



applied biosystems

Project: CCE20220812-03

GeneMapper™ ID-X 1.6

| Sample File | Sample Name | Panel |
|---|---|---|
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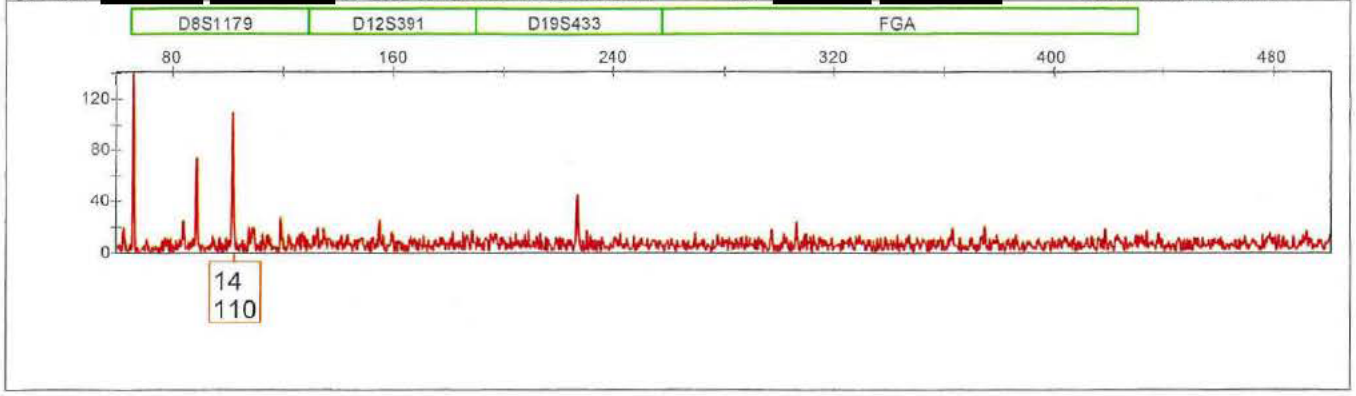

applied biosystems

Project: CCE20220812-03

GeneMapper™ ID-X 1.6

| Sample File | Sample Name | Panel |
|---|---|---|
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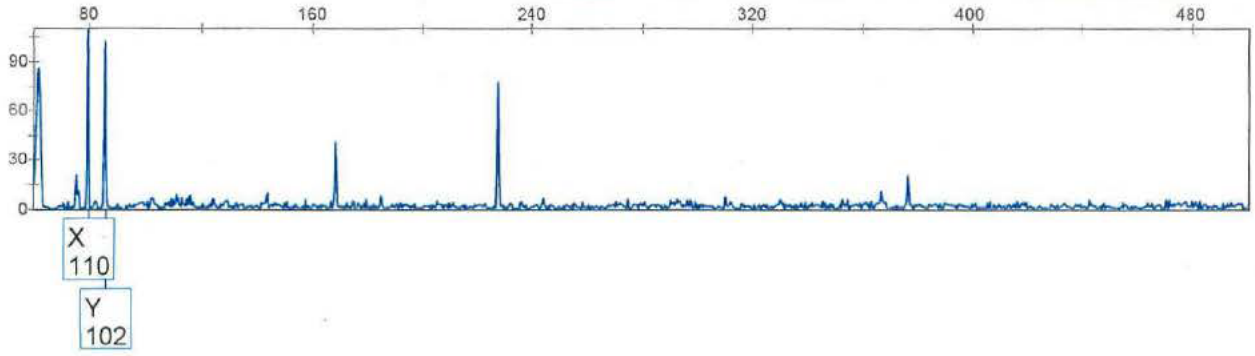
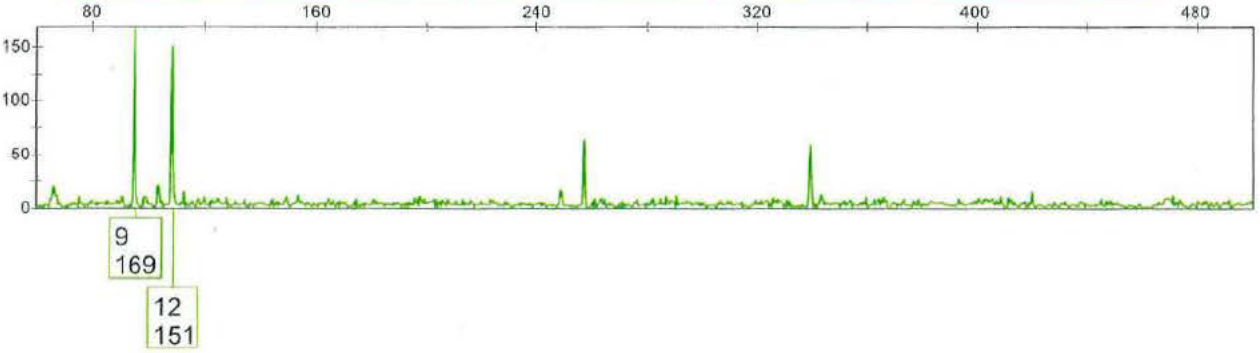
AMEL | D3S1358 | D1S1656 | D6S1043 | D13S317 | Penta E



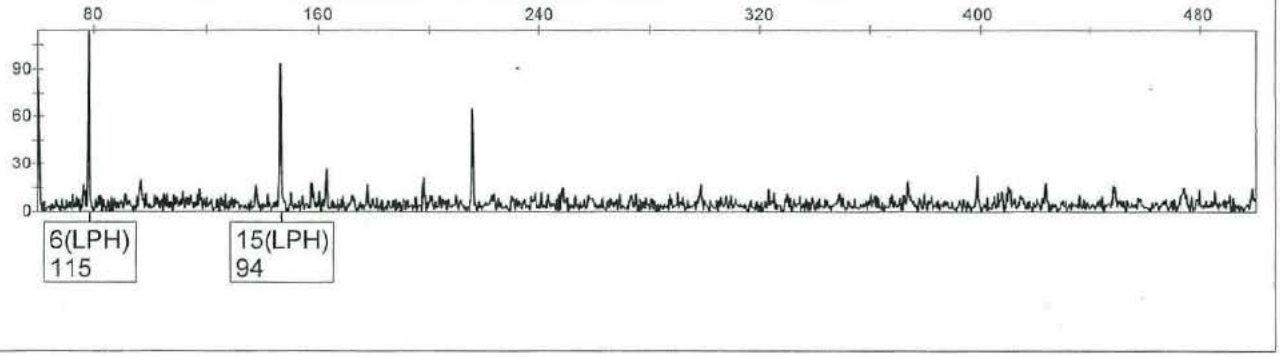

E01_E01 [redacted] 13_2022-08-12-11-34-41_3500xL_A.hid | E01 [redacted] | PowerPlex_21_IDX_v3.3

D16S539 | D18S51 | D2S1338 | CSF1PO | Penta D




E01_E01 [redacted] 13_2022-08-12-11-34-41_3500xL_A.hid | E01 [redacted] | PowerPlex_21_IDX_v3.3

TH01 | vWA | D21S11 | D7S820 | D5S818 | TPOX

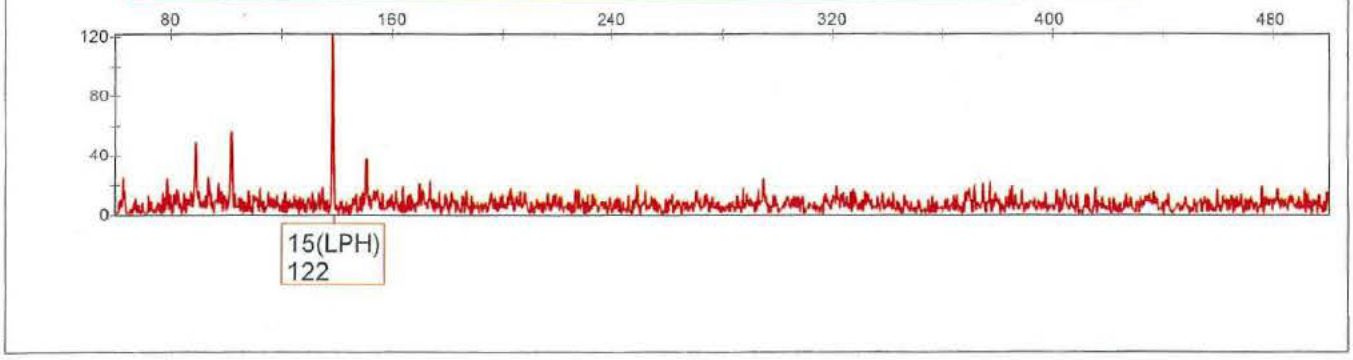


appliedbiosystems

Project: CCE20220812-03

GeneMapper™ ID-X 1.6

| Sample File | Sample Name | Panel |
|---|---|---|
| E01_E01 [redacted] 13_2022-08-12-11-34-41_3500xL A.hid | E01 [redacted] | PowerPlex_21_IDX_v3.3 |

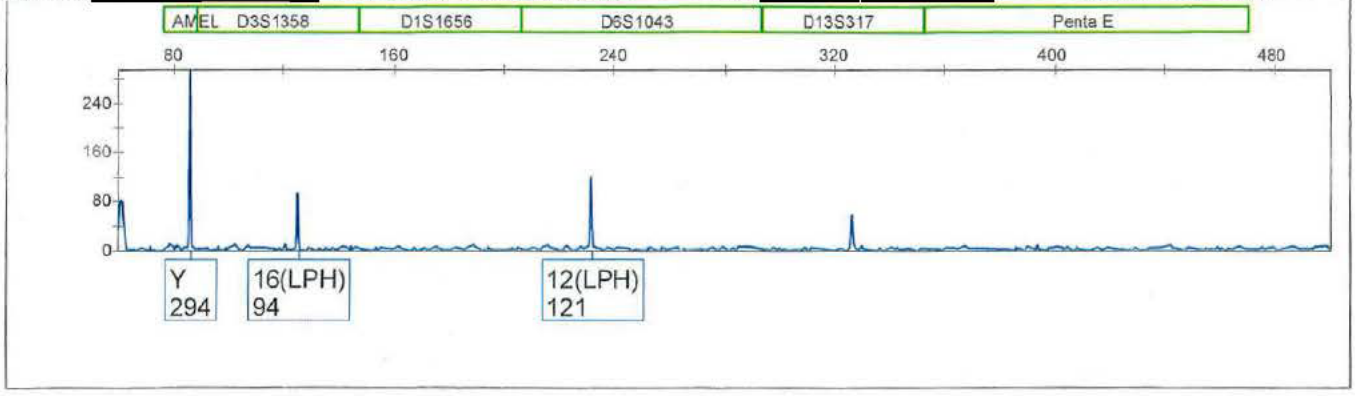


appliedbiosystems

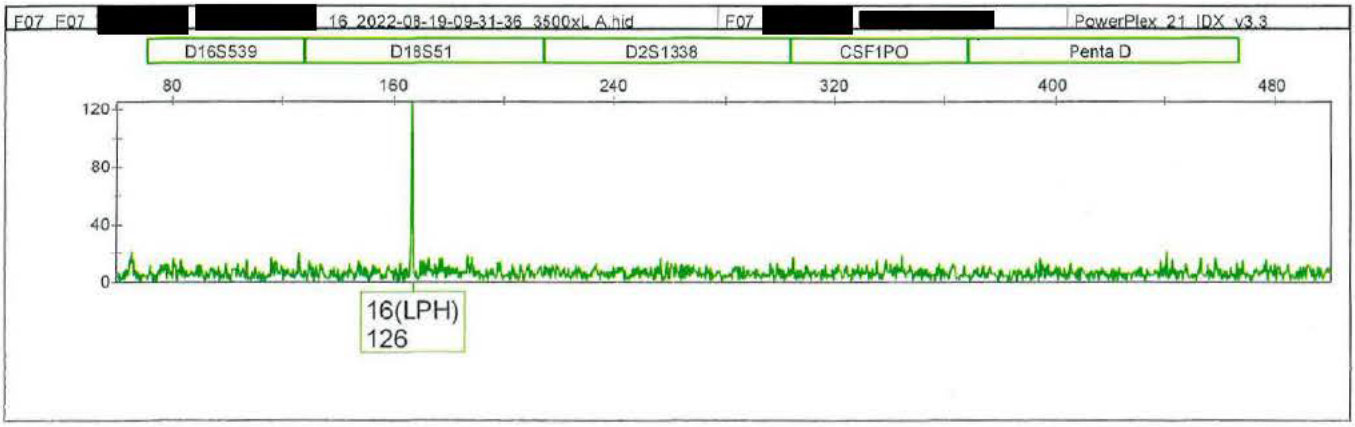
Project: CCE20220819-02

GeneMapper™ ID-X 1.6

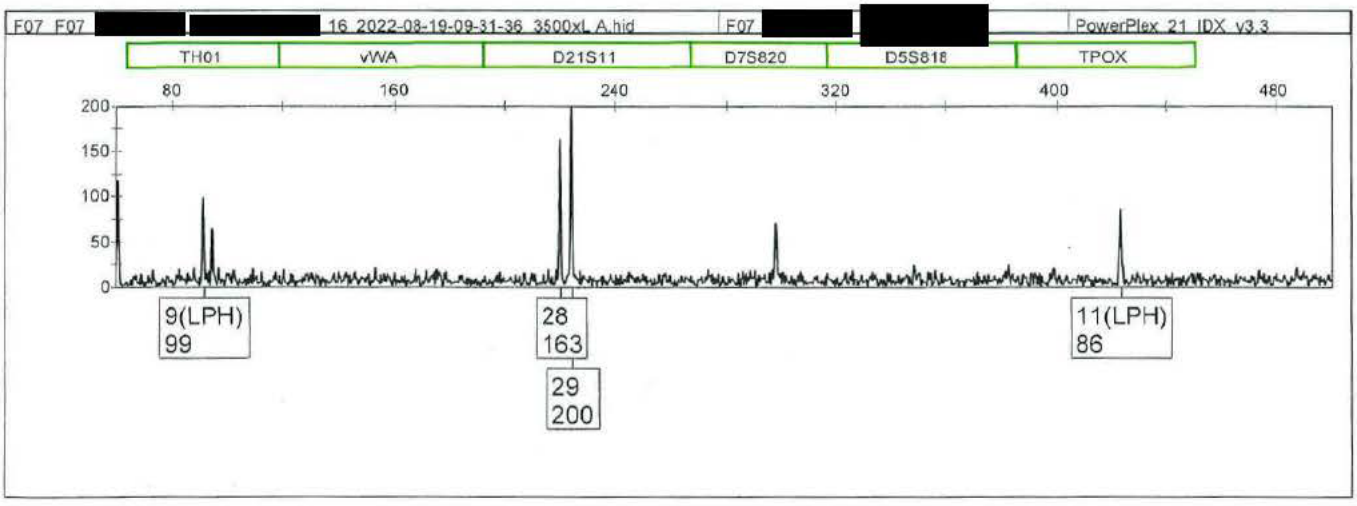
| Sample File | Sample Name | Panel |
|---|---|---|
| F07_F07 [redacted] 16_2022-08-19-09-31-36_3500xL_A.hid | F07 [redacted] | PowerPlex_21_IDX_v3.3 |



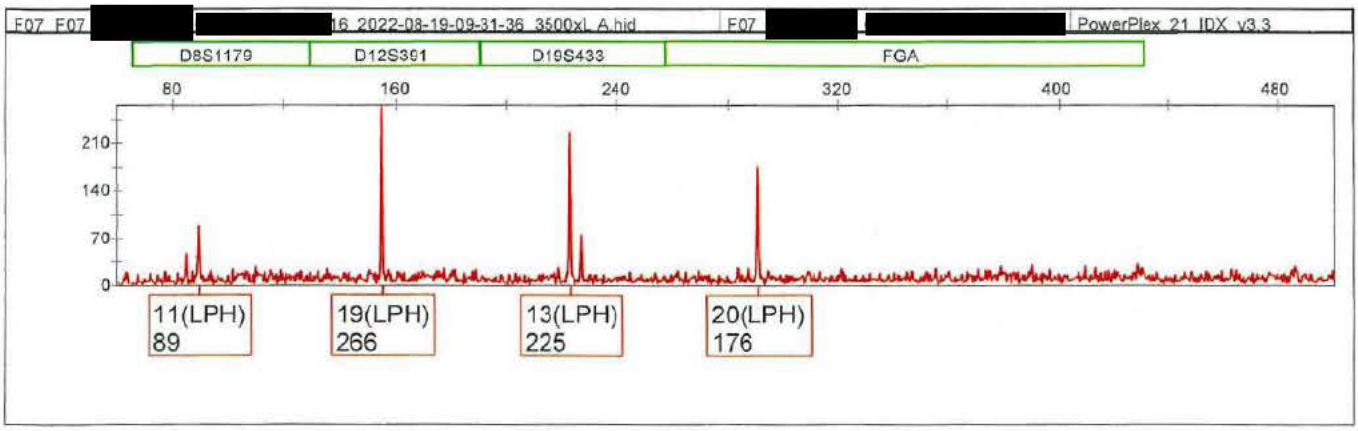

| Sample File | Sample Name | Panel |
|---|---|---|
| F07_F07 [redacted] 16_2022-08-19-09-31-36_3500xL_A.hid | F07 [redacted] | PowerPlex_21_IDX_v3.3 |




| Sample File | Sample Name | Panel |
|---|---|---|
| F07_F07 [redacted] 16_2022-08-19-09-31-36_3500xL_A.hid | F07 [redacted] | PowerPlex_21_IDX_v3.3 |




| Sample File | Sample Name | Panel |
|---|---|---|
| F07_F07 [redacted] 16_2022-08-19-09-31-36_3500xL_A.hid | F07 [redacted] | PowerPlex_21_IDX_v3.3 |



appliedbiosystems

Project: CCE20220714-04

GeneMapper™ ID-X 1.6

| Sample File | Sample Name | Panel |
|---|---|---|
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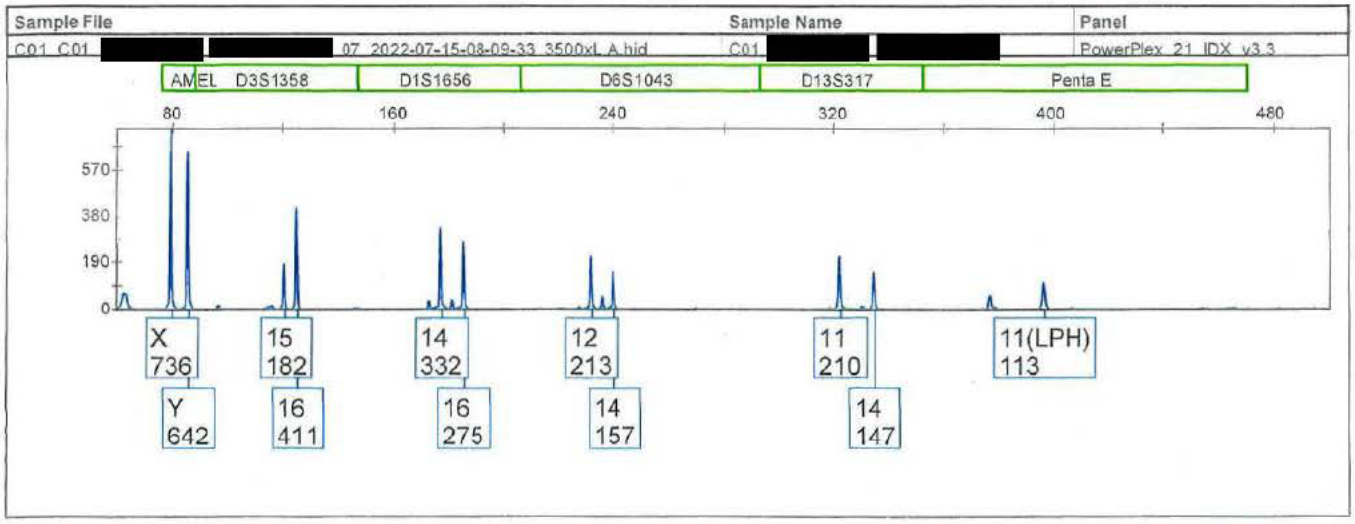


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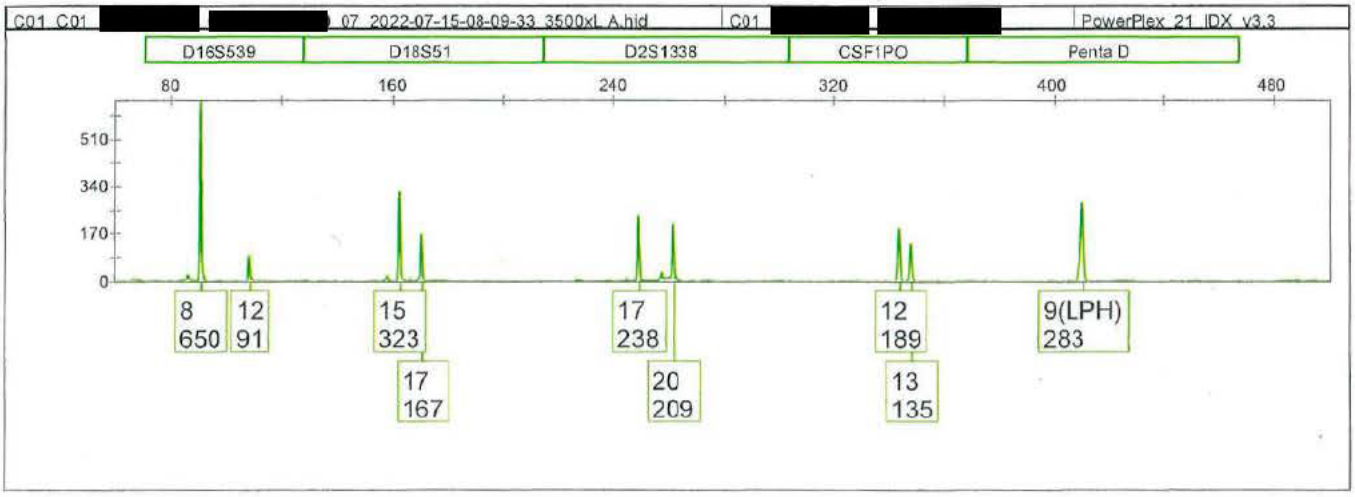
|---|---|---|

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|---|---|---|

applied biosystems

Project: CCE20220714-04

GeneMapper™ ID-X 1.6

| Sample File | Sample Name | Panel |
|---|---|---|
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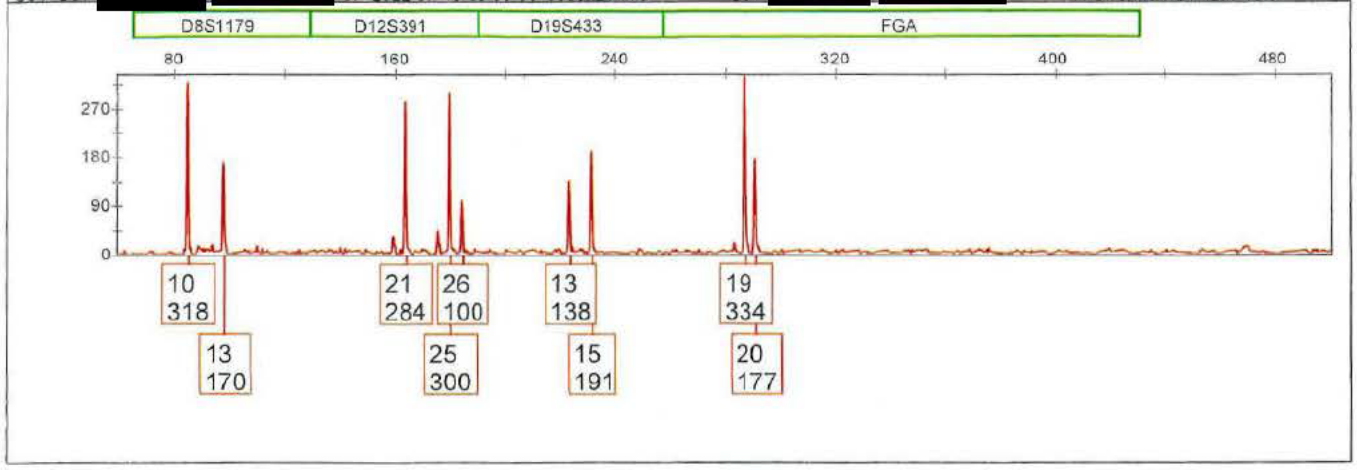
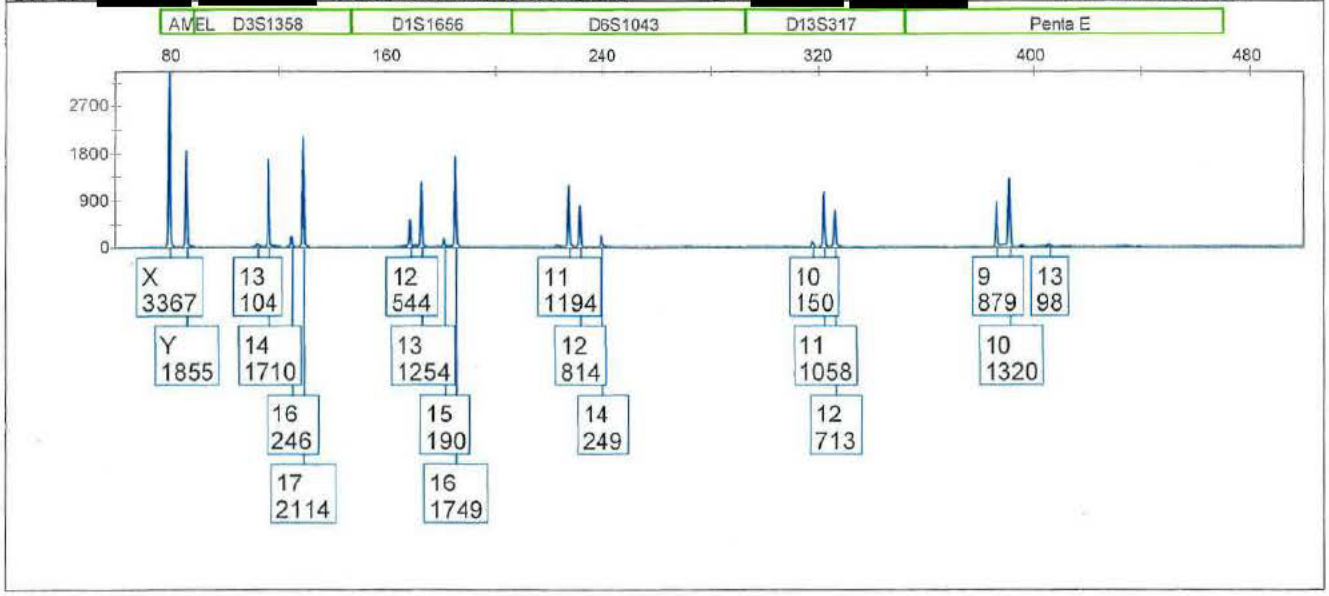


appliedbiosystems

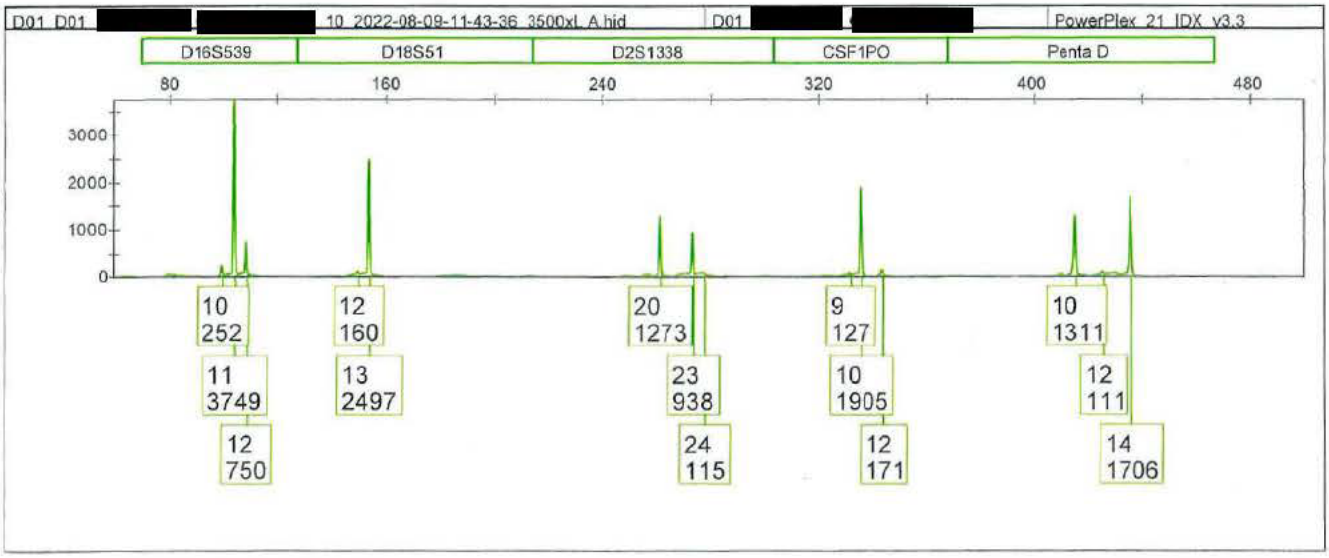
Project: CCE20220809-01

GeneMapper™ ID-X 1.6

| Sample File | Sample Name | Panel |
|---|---|---|
| D01_D01 [redacted] 10_2022-08-09-11-43-36_3500xL_A.hid | D01 [redacted] | PowerPlex_21_IDX_v3.3 |



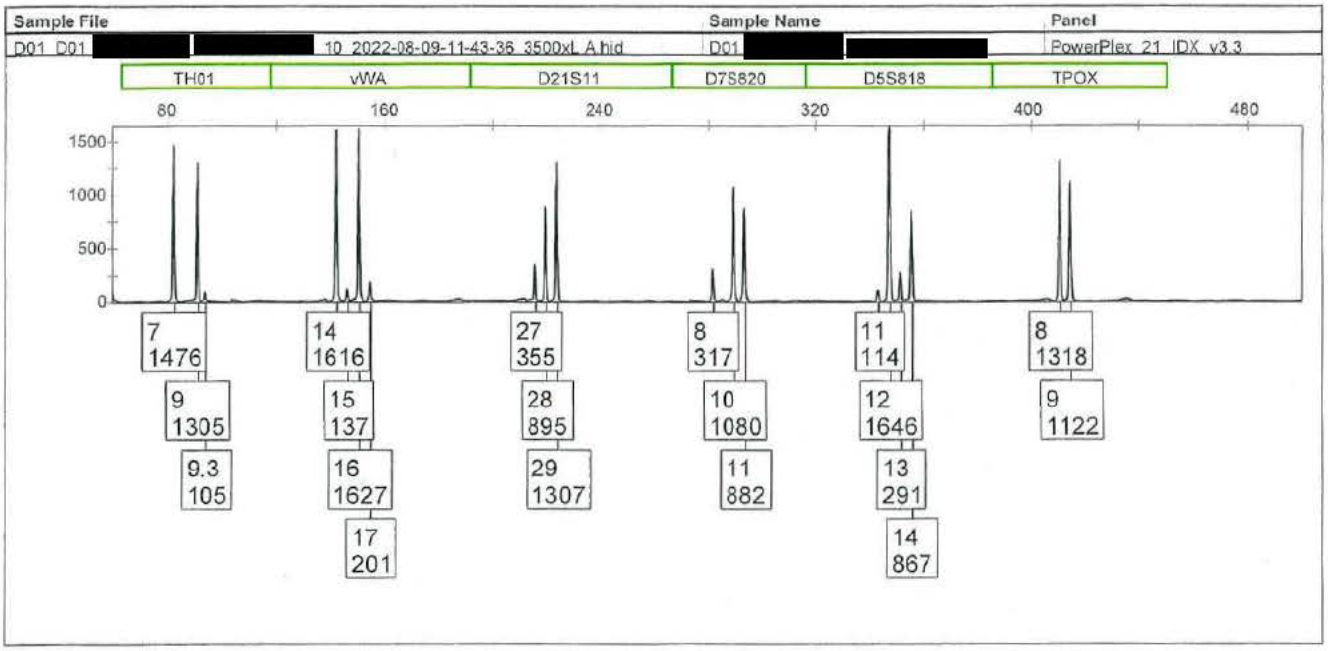

| D01_D01 [redacted] 10_2022-08-09-11-43-36_3500xL_A.hid | D01 [redacted] | PowerPlex_21_IDX_v3.3 |
|---|---|---|

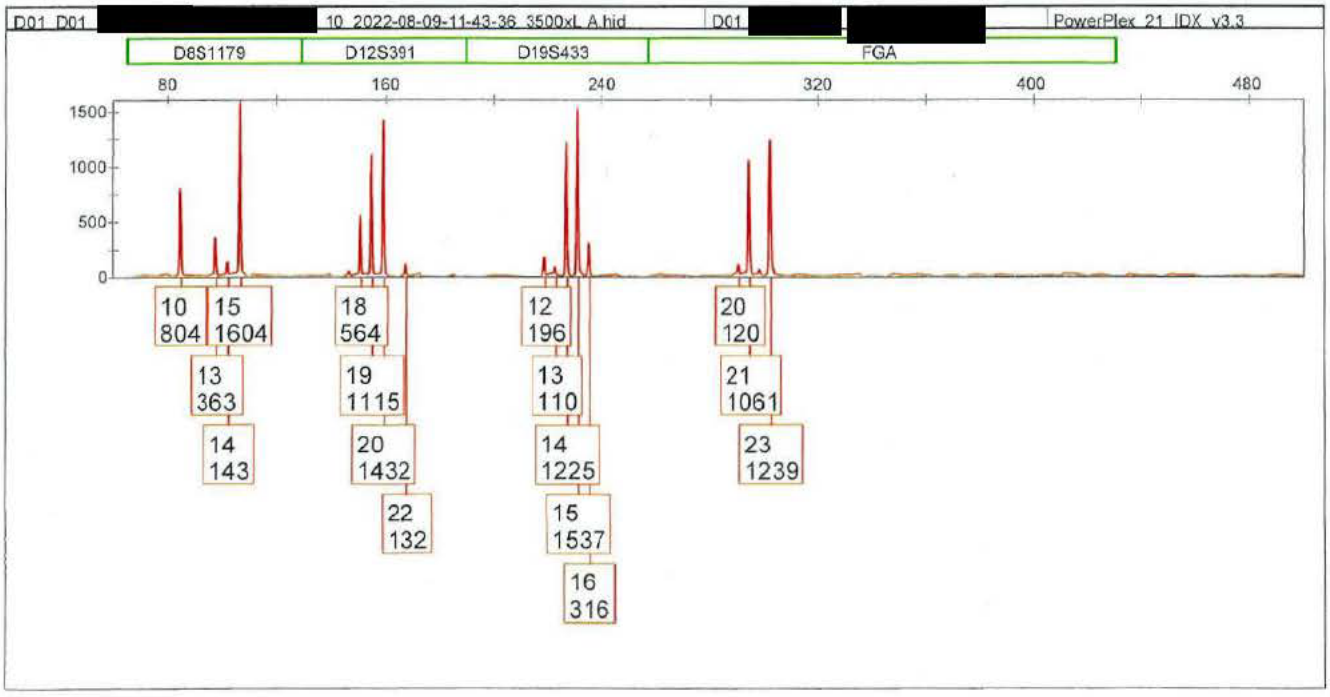


applied biosystems

Project: CCE20220809-01

GeneMapper™ ID-X 1.6



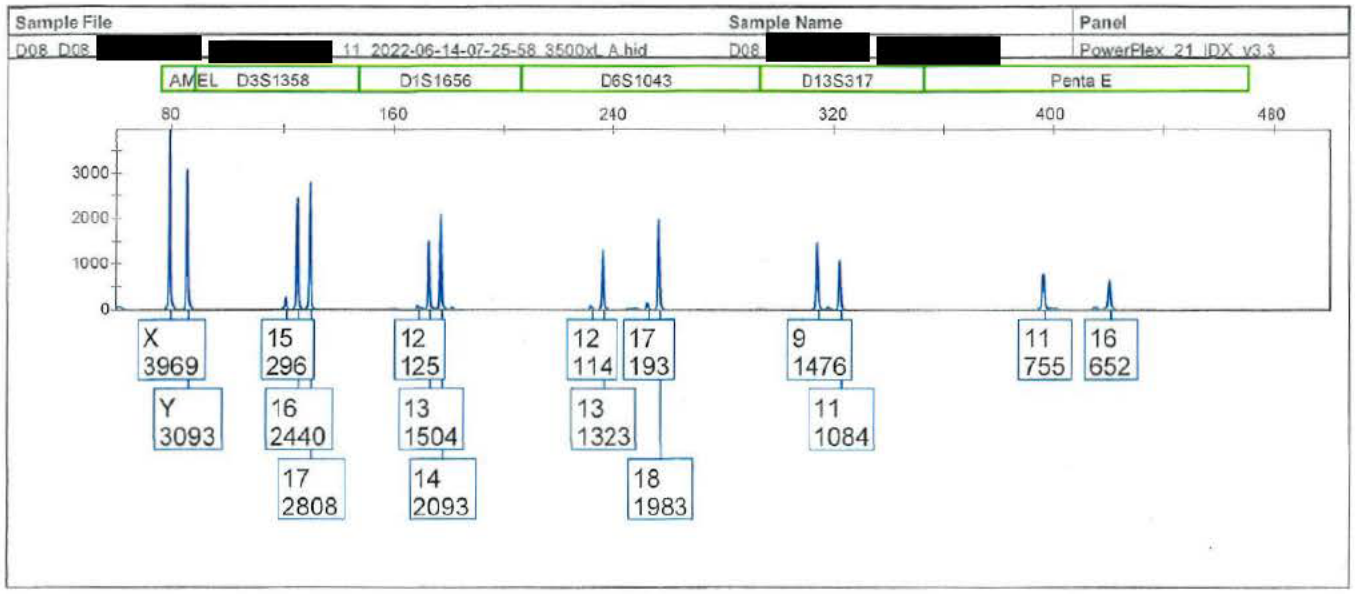



appliedbiosystems

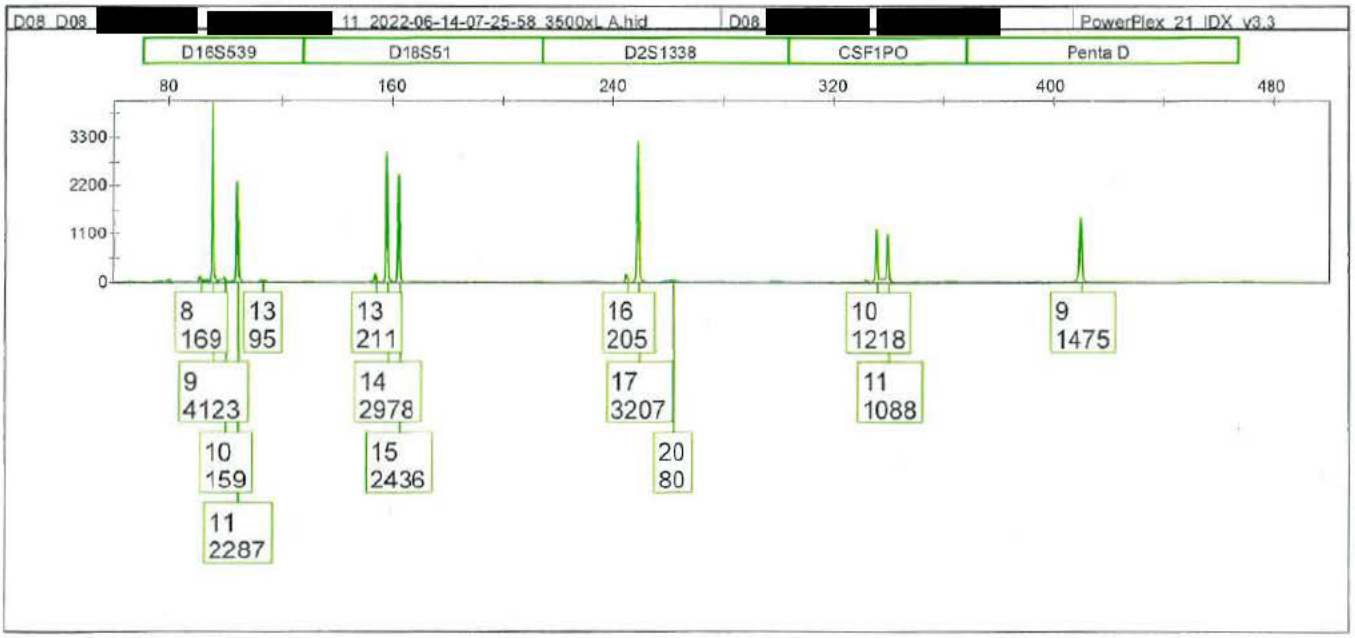
Project: CCE20220613-05

GeneMapper™ ID-X 1.6

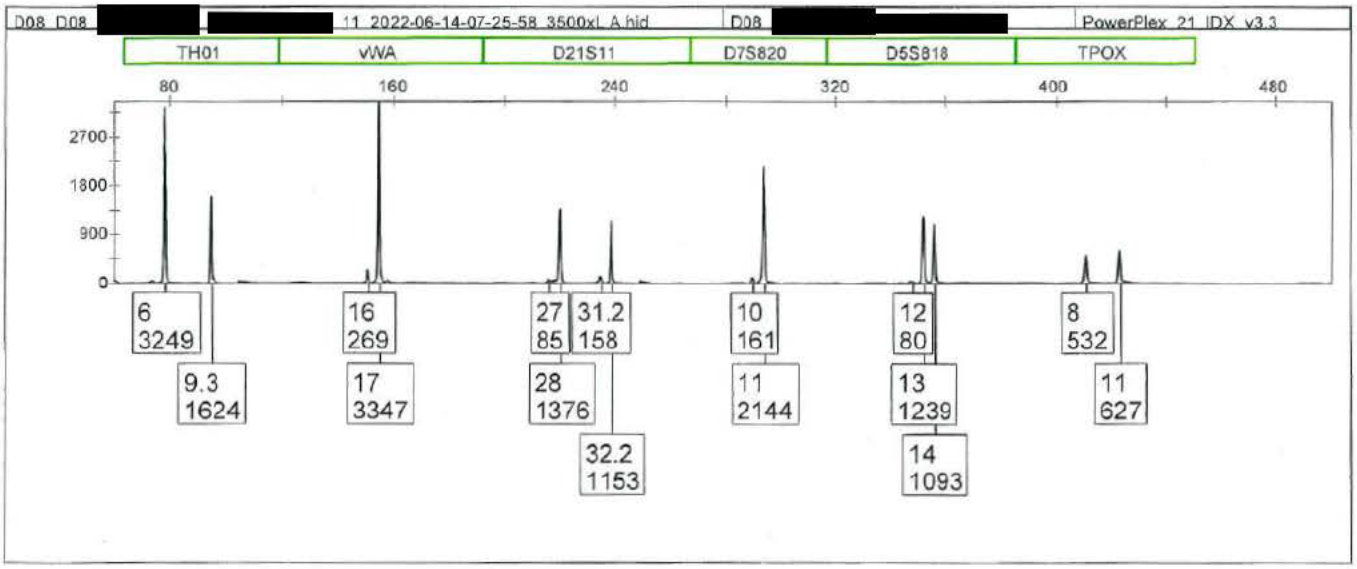
| Sample File | Sample Name | Panel |
|---|---|---|
| D08_D08 [redacted] 11_2022-06-14-07-25-58_3500xL_A.hid | D08 [redacted] | PowerPlex_21_IDX_v3.3 |




| D08_D08 [redacted] 11_2022-06-14-07-25-58_3500xL_A.hid | D08 [redacted] | PowerPlex_21_IDX_v3.3 |
|---|---|---|




| D08_D08 [redacted] 11_2022-06-14-07-25-58_3500xL_A.hid | D08 [redacted] | PowerPlex_21_IDX_v3.3 |
|---|---|---|

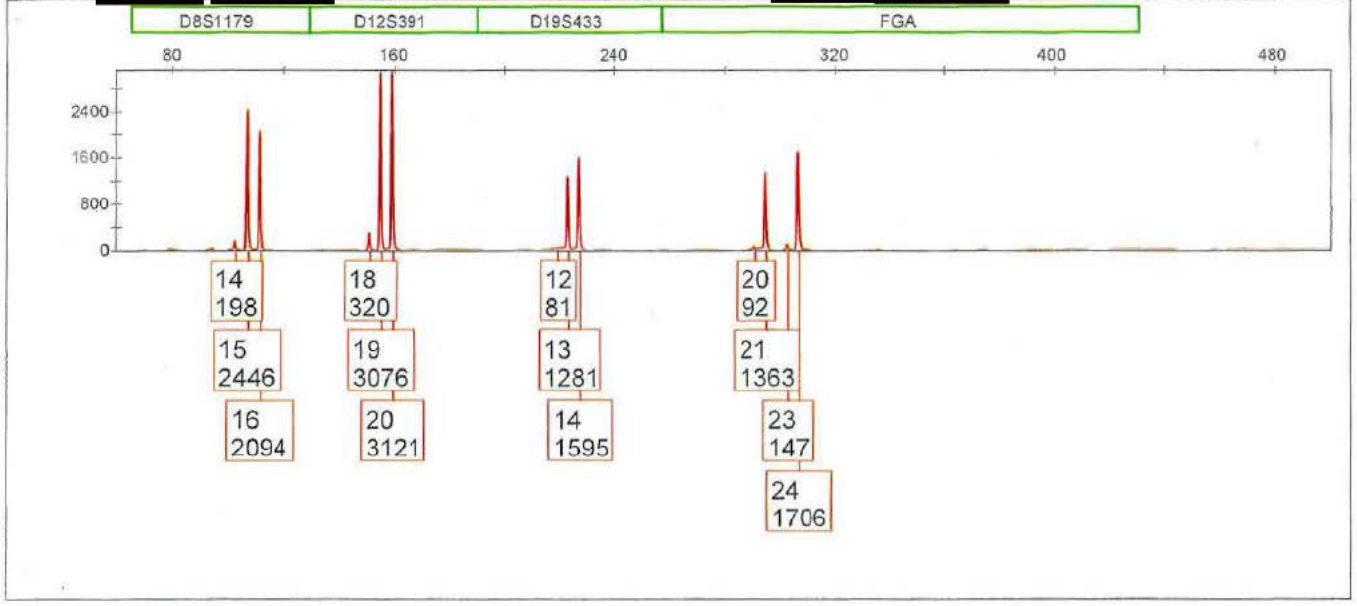


applied biosystems

Project: CCE20220613-05

GeneMapper™ ID-X 1.6

| Sample File | Sample Name | Panel |
|---|---|---|
| D08_D08 [redacted] 11_2022-06-14-07-25-58_3500xL_A.hid | D08 [redacted] | PowerPlex_21_IDX_v3.3 |

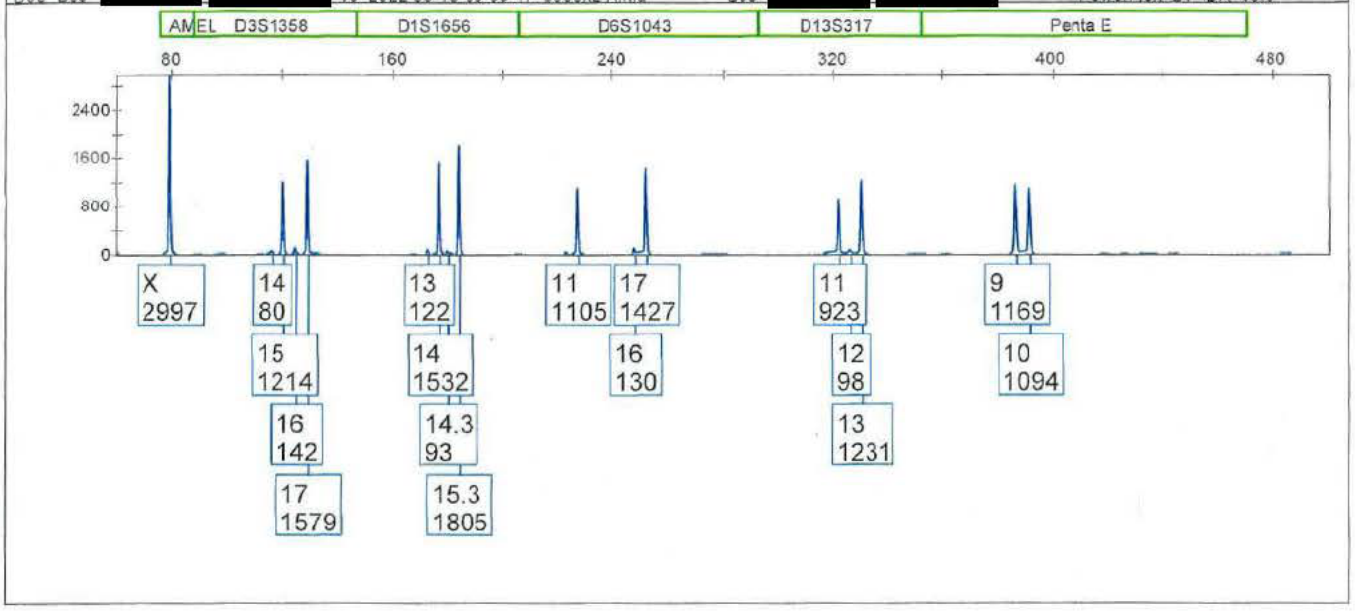


applied biosystems

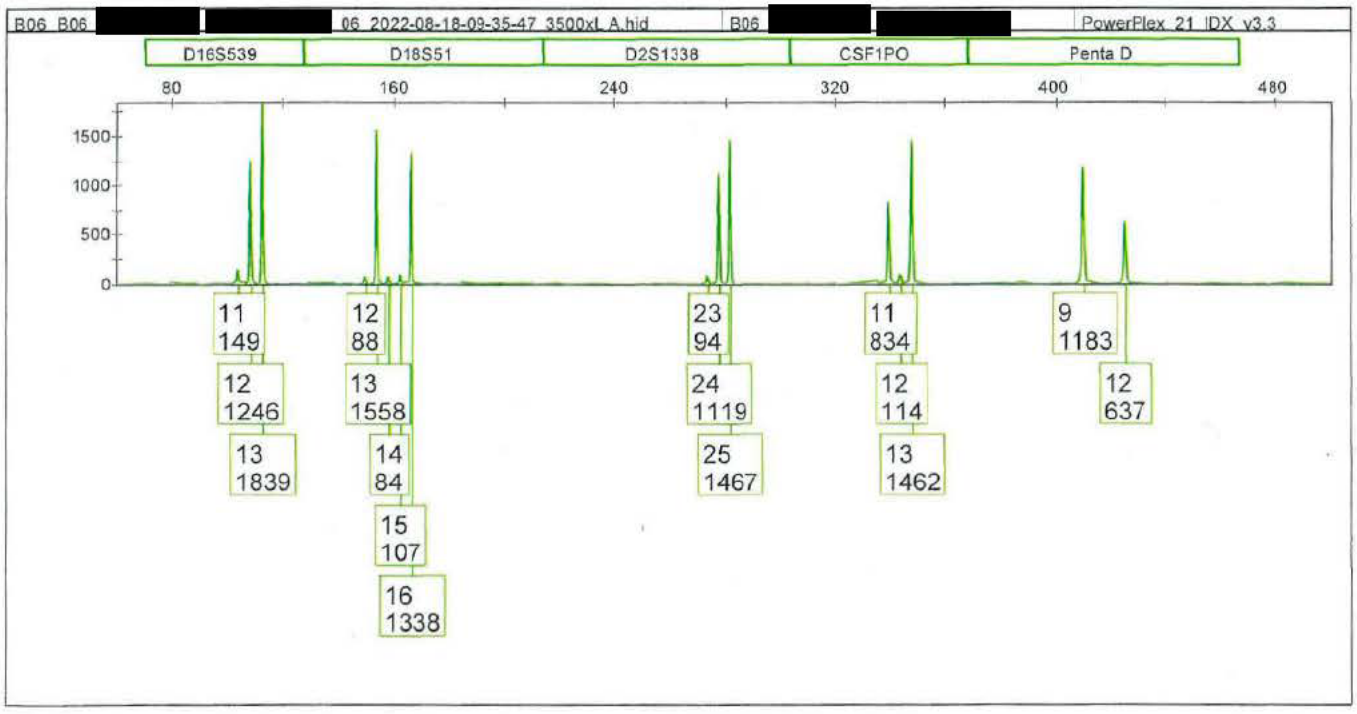
Project: CCE20220818-02

GeneMapper™ ID-X 1.6

| Sample File | Sample Name | Panel |
|---|---|---|
| B06_B06 [redacted] 06_2022-08-18-09-35-47_3500xL_A.hid | B06 [redacted] | PowerPlex_21_IDX_v3.3 |



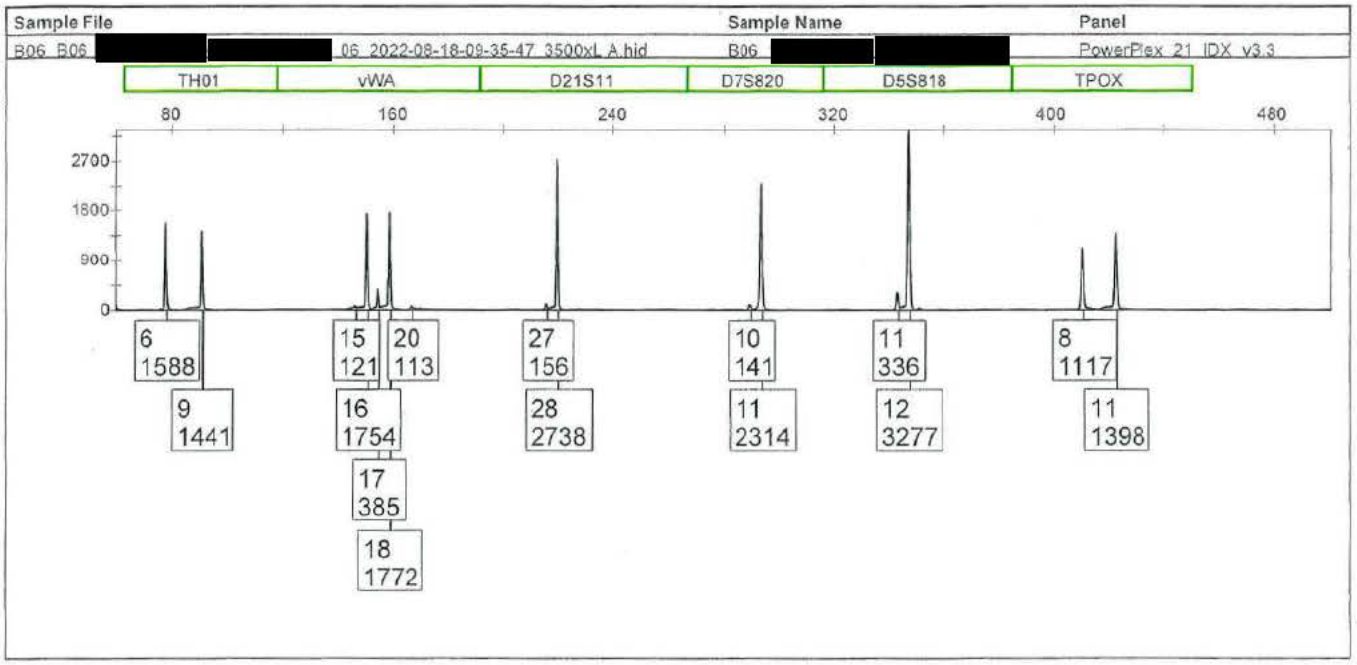

| B06_B06 [redacted] 06_2022-08-18-09-35-47_3500xL_A.hid | B06 [redacted] | PowerPlex_21_IDX_v3.3 |
|---|---|---|

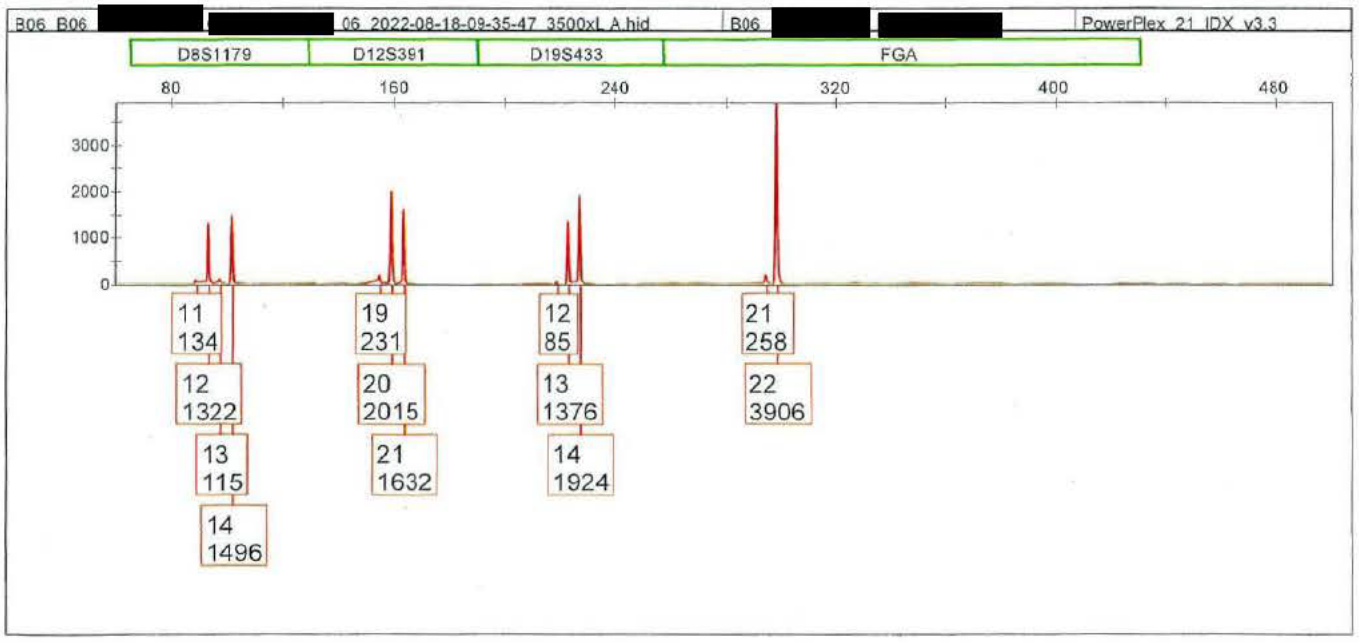


appliedbiosystems

Project: CCE20220818-02

GeneMapper™ ID-X 1.6



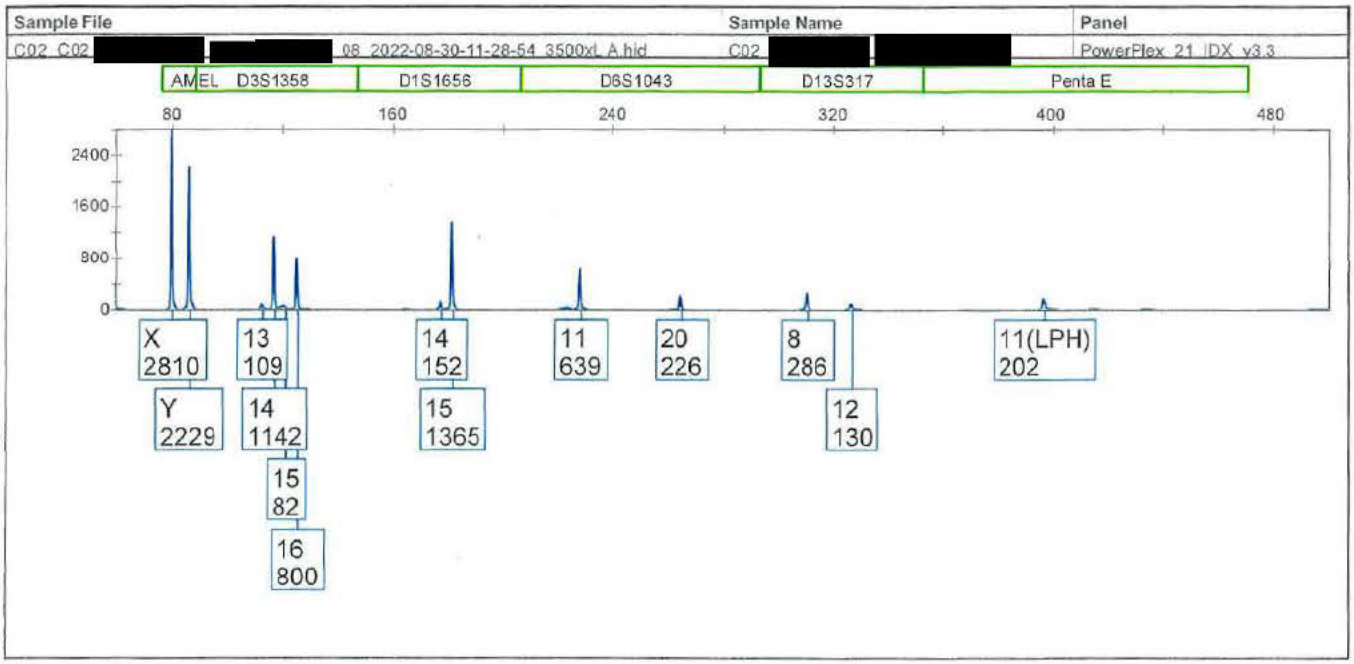



appliedbiosystems

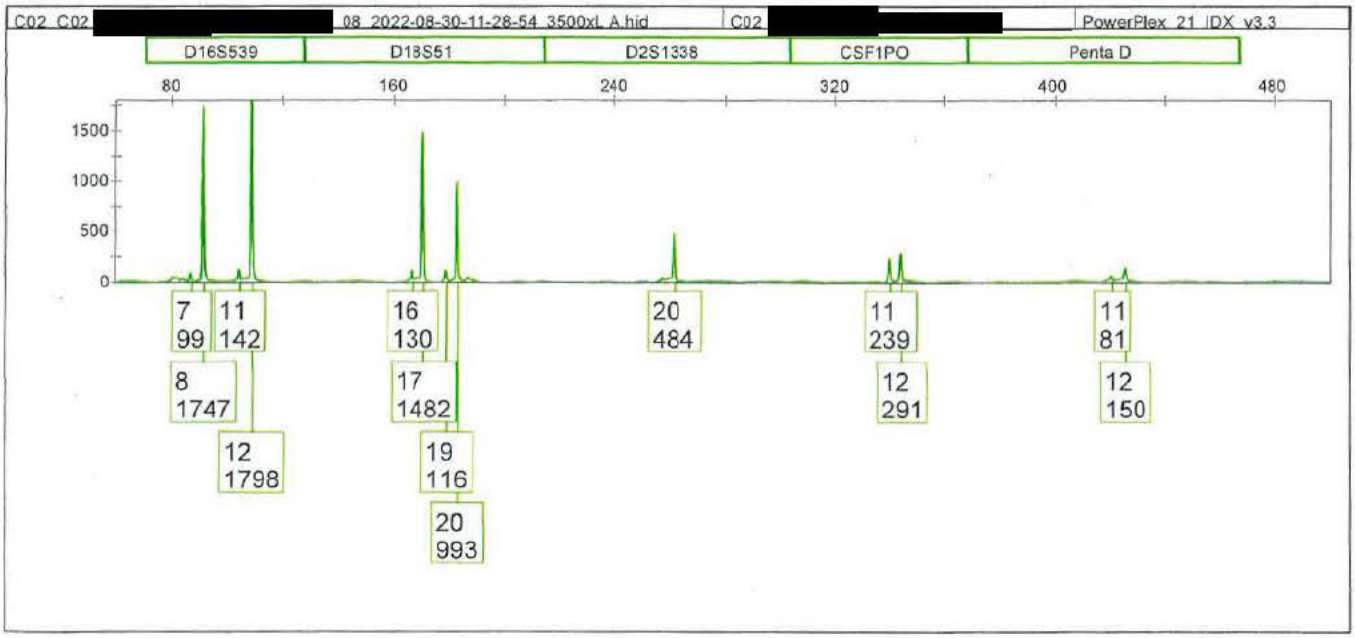
Project: CCE20220829-06

GeneMapper™ ID-X 1.6

| Sample File | Sample Name | Panel |
|---|---|---|
| C02_C02 [redacted] 08_2022-08-30-11-28-54_3500xL A.hid | C02 [redacted] | PowerPlex_21_IDX_v3.3 |



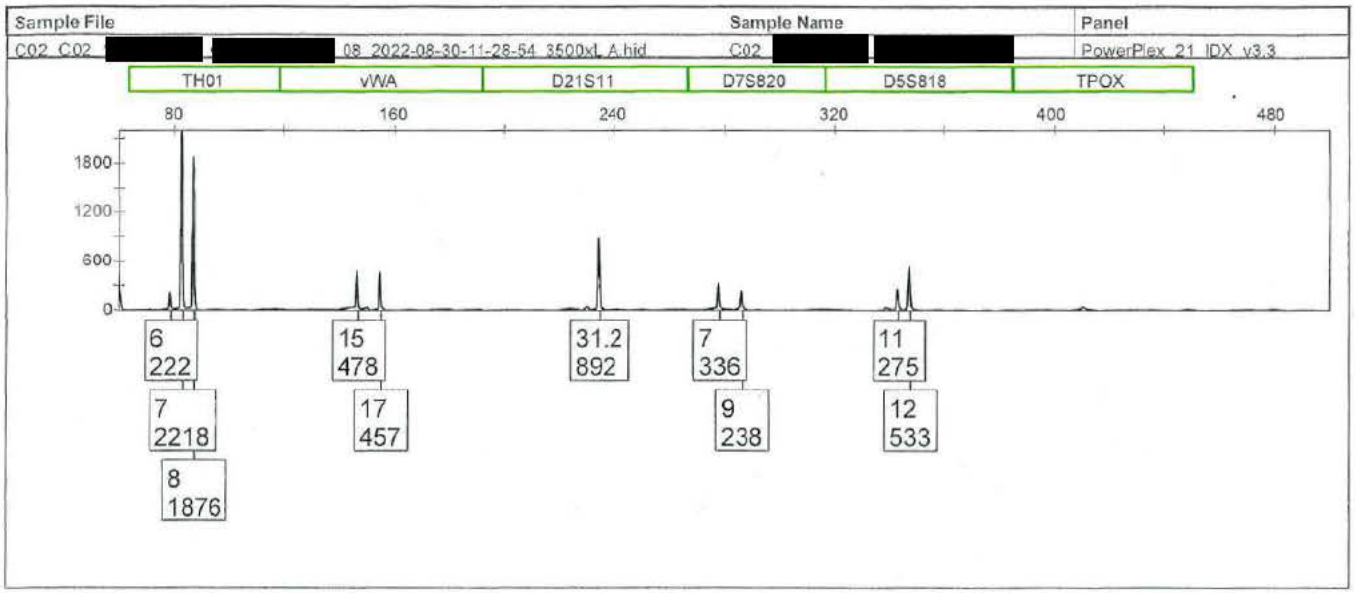

| C02_C02 [redacted] 08_2022-08-30-11-28-54_3500xL A.hid | C02 [redacted] | PowerPlex_21_IDX_v3.3 |
|---|---|---|

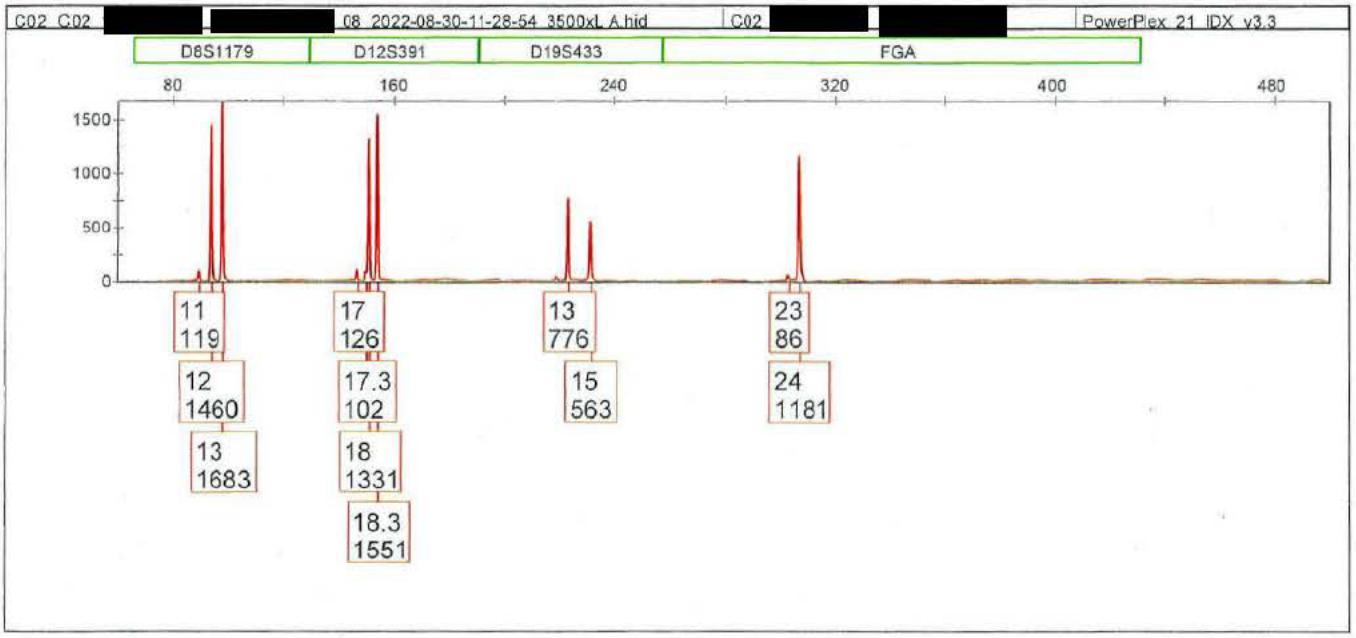


applied biosystems

Project: CCE20220829-06

GeneMapper™ ID-X 1.6

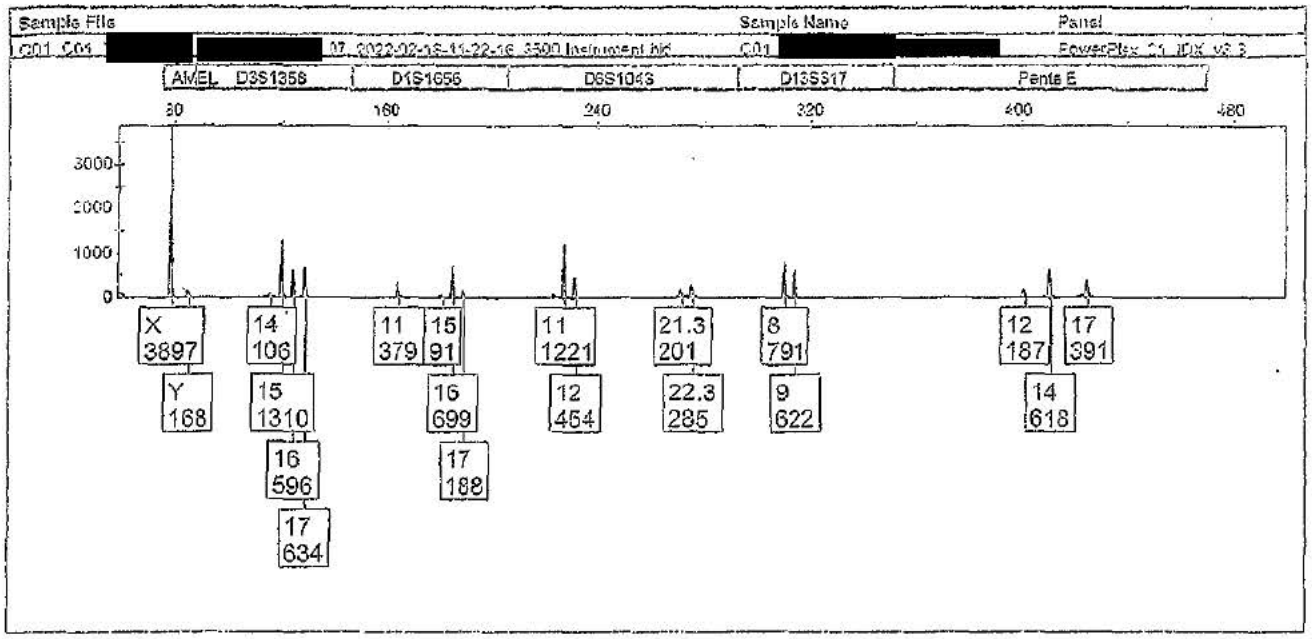


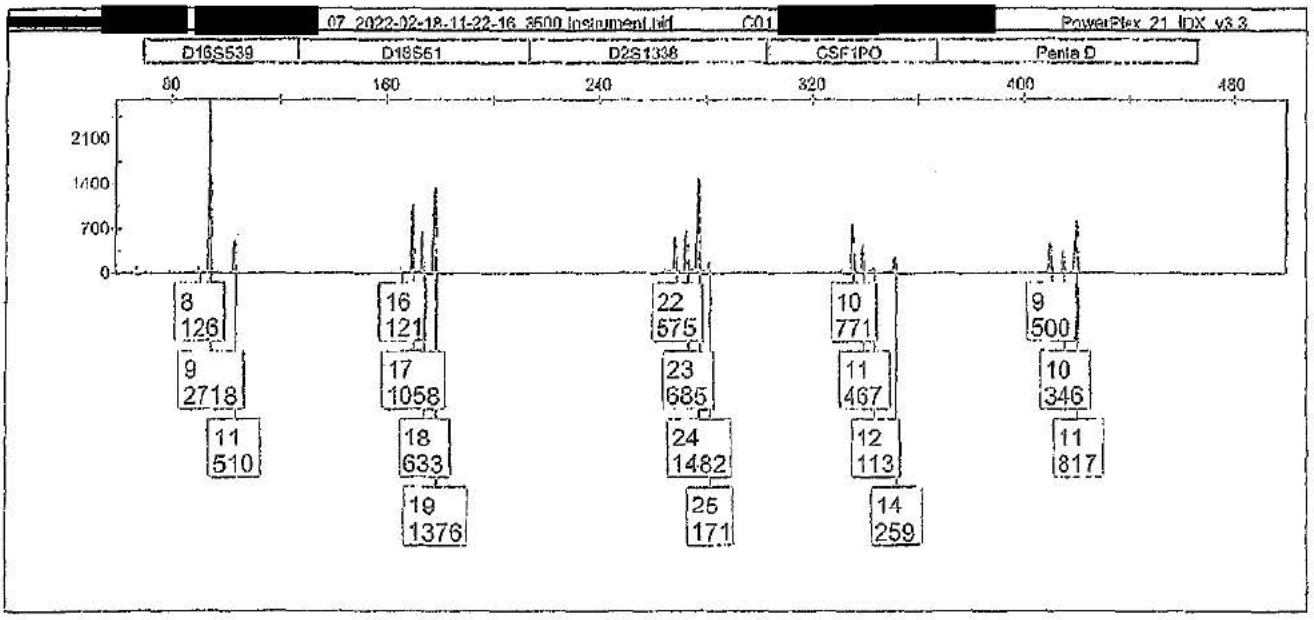



appliedbiosystems

Project: CCE20220218-02

GeneMapper™ ID-X 1.6

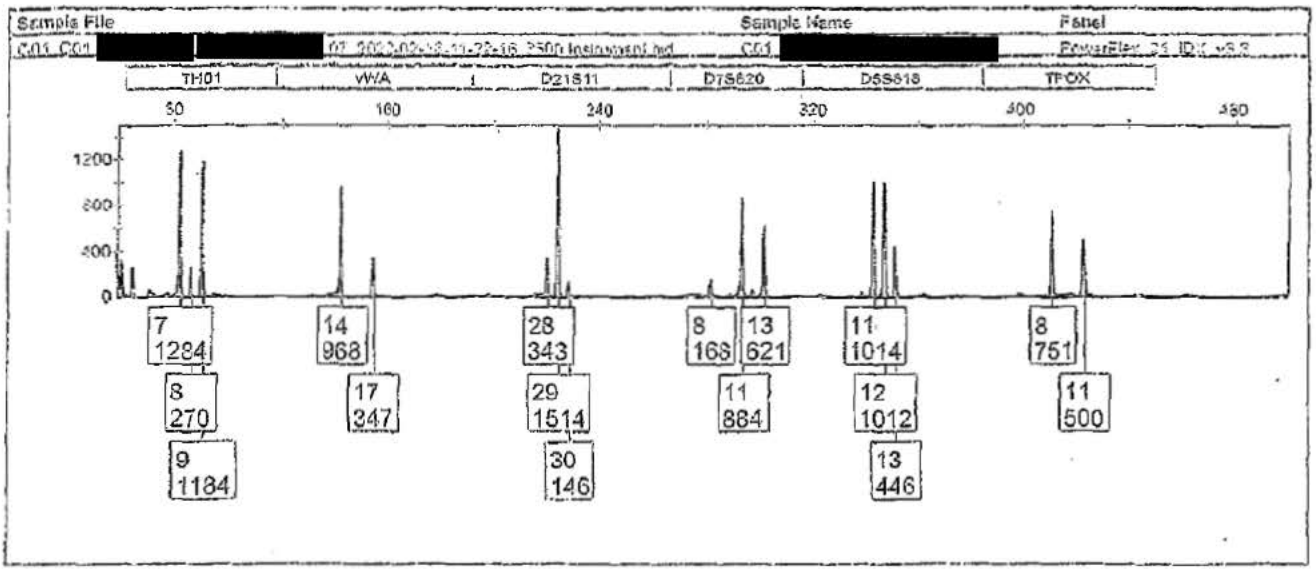


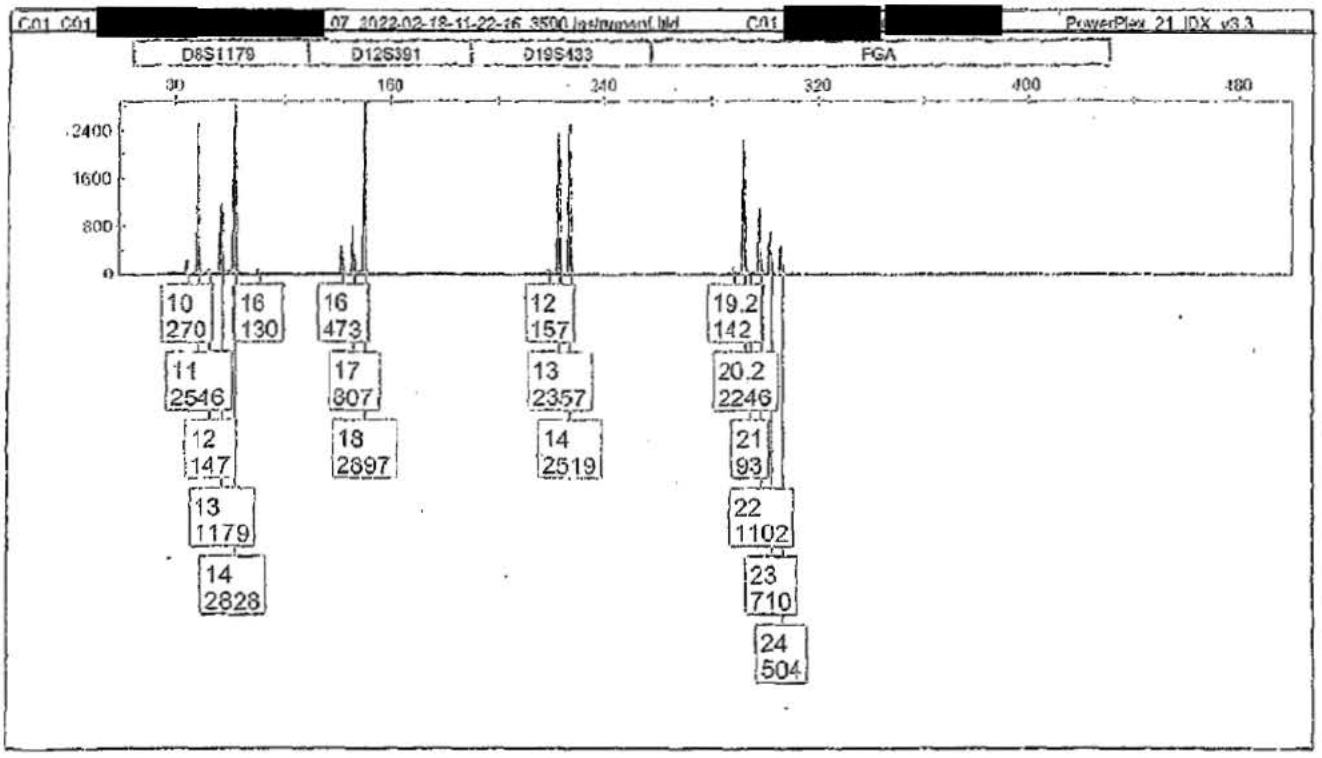



appliedbiosystems

Project: CCE20220218-02

GeneMapper™ ID-X 1.6



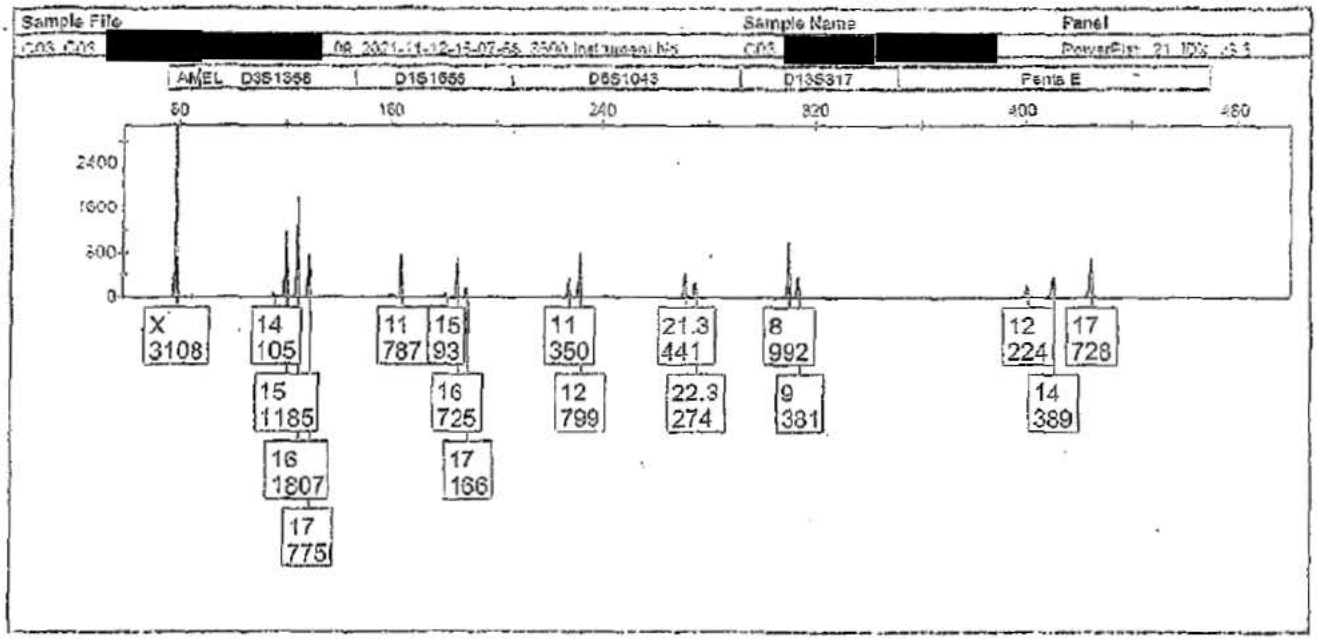



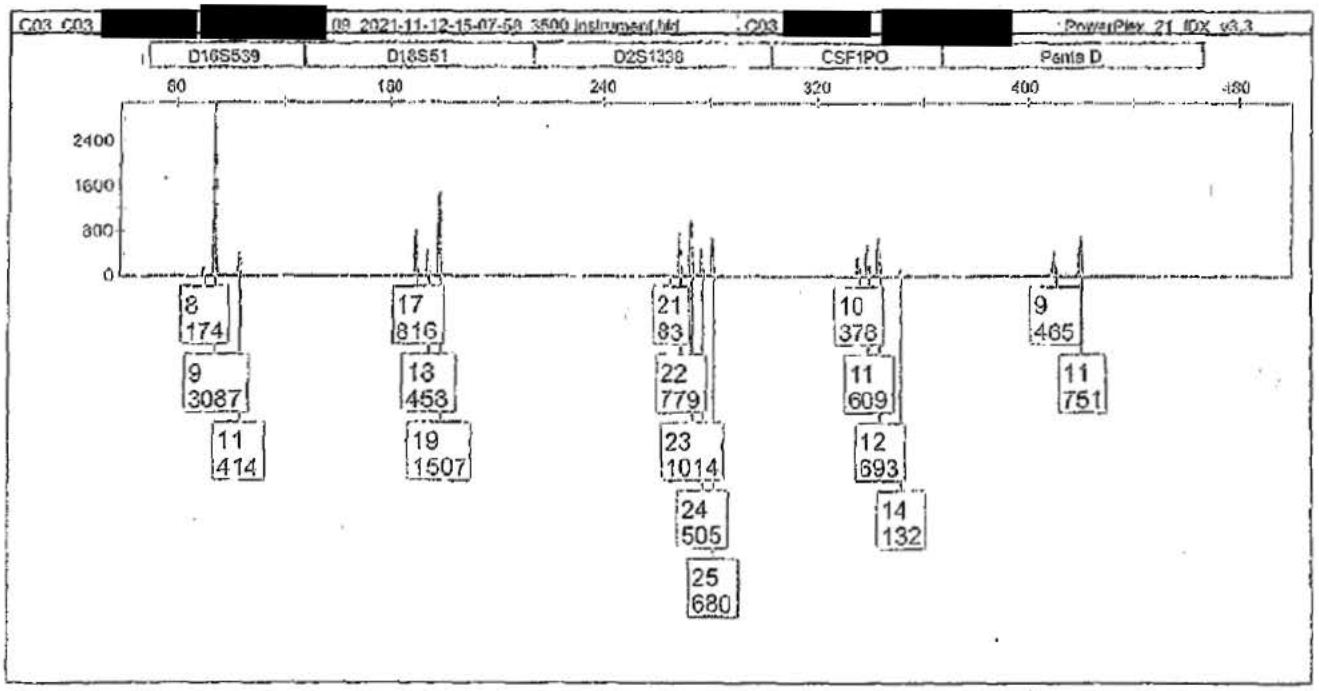
applied biosystems

GeneMapper™ ID-X 1.6

Project: CCE20211112-02

Sheet 2

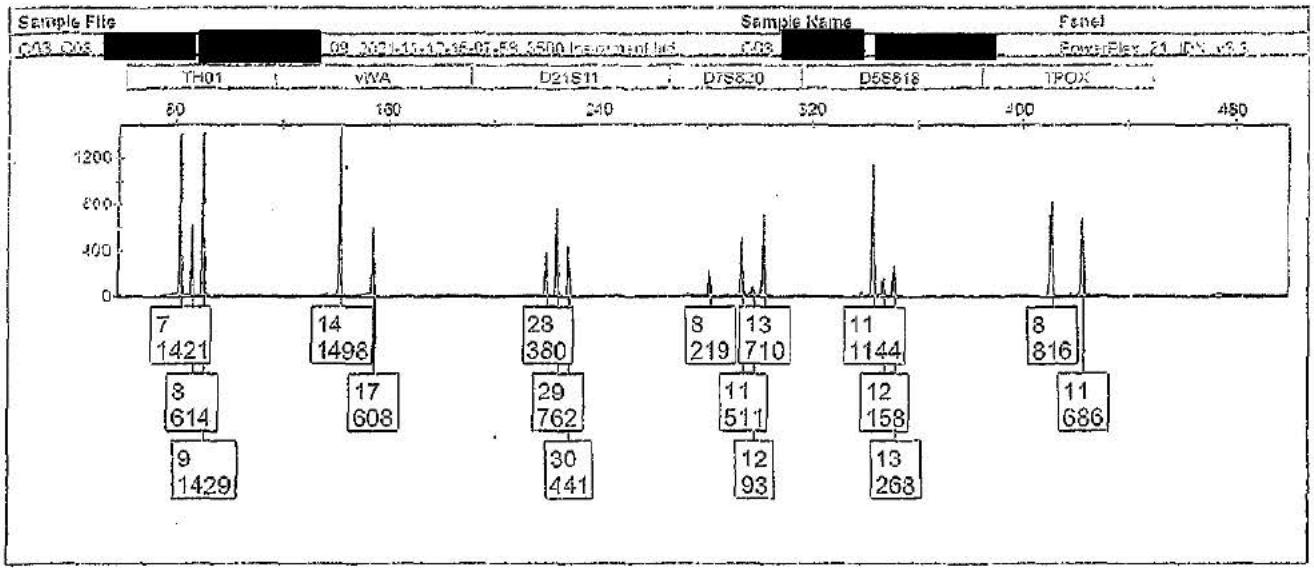


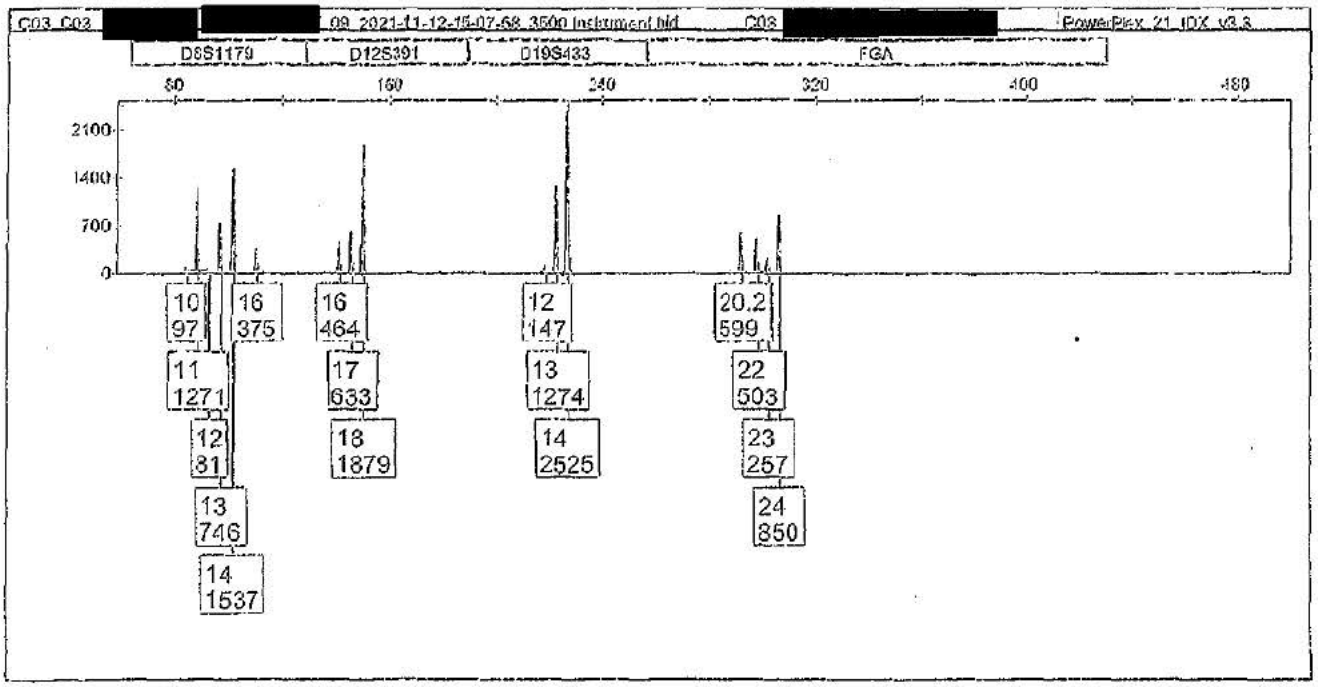



applied biosystems

Project: CCE20211112-02

GeneMapper™ ID-X 1.6



STATEMENT OF WITNESS Client Reference : [redacted]

1 x dropsheet – examined

Spermatozoa were microscopically observed on slides prepared from the low vaginal swabs posterior fornix swabs and the labia minora swabs. The fluid in speculum swab tested positive for the possible presence of blood and possible presence of seminal fluid.

The dropsheet was observed to contain apparent dirt and hair. This item was not examined further.

*DNA Analysis Results*

Low vagina swab 1 – Spermatozoa fraction
Low vagina swab 2 – Spermatozoa fraction
Posterior fornix swab 1 – Spermatozoa fraction
Posterior fornix swab 2 – Spermatozoa fraction
Labia minora swab 2 – Spermatozoa fraction [redacted]

The swabs listed above are currently undergoing DNA Analysis, the results of which will be reported in an addendum statement.

Labia minora swab 1 – Spermatozoa fraction

A mixed DNA profile was obtained from this sample indicating the presence of DNA from two contributors. Given this sample is said to have been taken from [redacted], the finding of DNA that could have originated from her would not be unexpected.

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from two contributors, one of whom is [redacted].

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with [redacted]

Based on statistical analysis, the results are as follows:

It is estimated that the mixed DNA profile obtained is approximately 4.9 million times more likely to have occurred if [redacted] had contributed DNA rather than if he had not.

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had not contributed DNA rather than if she had.

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

Labia minora swab 1 – Epithelial fraction

A mixed DNA profile was obtained from this sample indicating the presence of DNA from two contributors. Given this sample is said to have been taken from [redacted] the finding of DNA that could have originated from her would not be unexpected.



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Phone [redacted]

AQ-05

Queensland Government

Forensic and Scientific Services

# STATEMENT OF WITNESS

Peer Reviewed.....Yes/ No

Case Analyst.....

Peer Analyst.....

Date Issued.....

Client Reference : [redacted]
Report Number :

QUEENSLAND)
TO WIT)

**I, Alicia Ann QUARTERMAIN, of Brisbane in the State of Queensland, do solemnly and sincerely declare that:-**

1. I am employed by Queensland Health Forensic and Scientific Services (QHFSS) at Coopers Plains, Brisbane.

2. I hold the position of scientist in the Forensic DNA Analysis laboratory of QHFSS.

3. I was awarded a Bachelor of Health Science from Griffith University.
   I was awarded a Master of Science (Forensic Science) from Griffith University.

4. I am a member of the Australian and New Zealand Forensic Science Society.

5. This is a replacement statement in relation to the alleged offence that Occurrence Number [redacted] refers. This statement supersedes my original Statement of Witness issued on 10 November 2021. This statement has been issued after receiving additional sample information provided by PCSC James ADAMS (Queensland Police). This statement also details results from testing of additional samples. The defendant in this matter is [redacted]. The complainant in this matter is [redacted].



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[redacted]

**STATEMENT OF WITNESS** Client Reference : [redacted]

6 Laboratory records show that on 10 May 2021, Australia Post delivered the following 3 items:

[redacted]

7. Laboratory records show that on 24 June 2021, S/CONST GRANT THOMAS WATKINS delivered the following 2 items:

[redacted]

8. Laboratory records show that on 6 July 2021, SGT IAN ROGER HAYDEN delivered the following 2 items:

[redacted]

9. Laboratory records show that on 21 May 2021, CAROLYN PALMER delivered the following reference samples:

[redacted]

10. Laboratory records show that on 25 May 2021, S/CONST PAUL JAMES MCPHEE delivered the following reference sample:

[redacted]

11. The results of the scientific examinations conducted in the laboratory are as follows:

**Reference Samples**

[redacted]

A DNA profile was obtained from each of these reference samples.

**Exhibits**

[redacted] - **JA3 NIL VISIBLE MATERIAL - SKIN [TRACE] from neck of** [redacted]

A mixed DNA profile was obtained from this sample indicating the presence of DNA from three contributors. Given this sample is said to have been taken from [redacted], the finding of DNA that could have originated from her would not be unexpected.

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from three contributors, one of whom is [redacted].

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with [redacted].

Based on statistical analysis, the results are as follows:

STATEMENT OF WITNESS Client Reference : [redacted]

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had contributed DNA rather than if he had not.

It is estimated that the mixed DNA profile obtained is approximately 2000 times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

It is estimated that the mixed DNA profile obtained is approximately 5300 times more likely to have occurred if [redacted] had not contributed DNA rather than if she had.

It is estimated that the mixed DNA profile obtained is approximately 17000 times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

[redacted] **NIL VISIBLE MATERIAL - FABRIC [TRACE] from black beanie in a refuse bin on** [redacted]

A mixed DNA profile was obtained from this sample indicating the presence of DNA from four contributors. Therefore, an assumption of DNA from four contributors has been made for statistical analysis.

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA.

Based on statistical analysis, the results are as follows:

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had contributed DNA rather than if he had not.

It is estimated that the mixed DNA profile obtained is approximately 1200 times more likely to have occurred if [redacted] had contributed DNA rather than if she had not.

It is estimated that the mixed DNA profile obtained is approximately 16 million times more likely to have occurred if [redacted] had not contributed DNA rather than if she had.

It is estimated that the mixed DNA profile obtained is approximately 20 billion times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

[redacted] **- JA7. NIL VISIBLE MATERIAL - FABRIC [TRACE] from black jacket in a refuse bin on** [redacted]

A mixed DNA profile was obtained from this sample indicating the presence of DNA from three contributors. Therefore, an assumption of DNA from three contributors has been made for statistical analysis.

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA.

Based on statistical analysis, the results are as follows:

**STATEMENT OF WITNESS** Client Reference : [redacted]

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had contributed DNA rather than if he had not.

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had contributed DNA rather than if she had not.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

**[redacted] Sexual Assault Investigation Kit (SAIK) - [redacted]**

*Item examined by Forensic DNA Analysis*

This SAIK contained the following items:

1 x coronal sulcus (wet) swab – examined
1 x coronal sulcus (dry) swab – examined
1 x glans penis (wet) swab – examined
1 x glans penis (dry) swab – examined
1 x shaft penis (wet) swab – examined
1 x shaft penis (dry) swab – examined
1 x base penis (wet) swab – examined
1 x base penis (dry) swab – examined

*DNA Analysis Results*

Coronal sulcus (wet) swab

This swab tested positive for the possible presence of blood and was submitted for DNA analysis.

A mixed DNA profile was obtained from this sample indicating the presence of DNA from two contributors. Given this sample is said to have been taken from [redacted], the finding of DNA that could have originated from him would not be unexpected.

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from two contributors, one of whom is [redacted].

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with [redacted].

Based on statistical analysis, the results are as follows:

It is estimated that the mixed DNA profile obtained is approximately 6 times more likely to have occurred if [redacted] had contributed DNA rather than if she had not.

It is estimated that the mixed DNA profile obtained is approximately 99 times more likely to have occurred if [redacted] had not contributed DNA rather than if she had.

STATEMENT OF WITNESS Client Reference : [redacted]

It is estimated that the mixed DNA profile obtained is approximately 41000 times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

It is estimated that the mixed DNA profile obtained is approximately 120000 times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

Coronal sulcus (dry) swab

This swab was submitted for DNA analysis.

A mixed DNA profile was obtained from this sample indicating the presence of DNA from two contributors. Given this sample is said to have been taken from [redacted] the finding of DNA that could have originated from him would not be unexpected.

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from two contributors, one of whom is [redacted].

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with [redacted].

Based on statistical analysis, the results are as follows:

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had contributed DNA rather than if she had not.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

Glans penis (wet) swab

This swab was submitted for DNA analysis.

A mixed DNA profile was obtained from this sample indicating the presence of DNA from three contributors. Given this sample is said to have been taken from [redacted], the finding of DNA that could have originated from him would not be unexpected.

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from three contributors, one of whom is [redacted].

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with [redacted]

Based on statistical analysis, the results are as follows:

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had contributed DNA rather than if she had not.



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P [redacted]
F
E

STATEMENT OF WITNESS Client Reference : [redacted]

It is estimated that the mixed DNA profile obtained is approximately 800000 times more likely to have occurred if [redacted] had not contributed DNA rather than if she had

It is estimated that the mixed DNA profile obtained is approximately 34000 times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

It is estimated that the mixed DNA profile obtained is approximately 19000 times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

Glans penis (dry) swab

This swab was submitted for DNA analysis.

A mixed DNA profile was obtained from this sample indicating the presence of DNA from three contributors. Given this sample is said to have been taken from [redacted] the finding of DNA that could have originated from him would not be unexpected.

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from three contributors, one of whom is [redacted].

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with [redacted]

Based on statistical analysis, the results are as follows:

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had contributed DNA rather than if she had not.

It is estimated that the mixed DNA profile obtained is approximately 6900 times more likely to have occurred if [redacted] had not contributed DNA rather than if she had.

It is estimated that the mixed DNA profile obtained is approximately 53000 times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

It is estimated that the mixed DNA profile obtained is approximately 11000 times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

Shaft penis (wet) swab

This swab was submitted for DNA analysis.

A mixed DNA profile was obtained from this sample indicating the presence of DNA from three contributors. Given this sample is said to have been taken from [redacted] the finding of DNA that could have originated from him would not be unexpected.

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from three contributors, one of whom is [redacted].

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with [redacted]

Based on statistical analysis, the results are as follows:

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had contributed DNA rather than if she had not.

It is estimated that the mixed DNA profile obtained is approximately 12000 times more likely to have occurred if [redacted] had not contributed DNA rather than if she had.

It is estimated that the mixed DNA profile obtained is approximately 21000 times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

It is estimated that the mixed DNA profile obtained is approximately 3000 times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

Shaft penis (dry) swab

This swab was submitted for DNA analysis.

A mixed DNA profile was obtained from this sample indicating the presence of DNA from two contributors. Given this sample is said to have been taken from [redacted] the finding of DNA that could have originated from him would not be unexpected.

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from two contributors, one of whom is [redacted].

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with [redacted]

Based on statistical analysis, the results are as follows:

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had contributed DNA rather than if she had not.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

Base penis (wet) swab

This swab tested positive for the possible presence of blood and was submitted for DNA analysis.

A mixed DNA profile was obtained from this sample indicating the presence of DNA from two contributors. Given this sample is said to have been taken from [redacted] the finding of DNA that could have originated from him would not be unexpected.

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from two contributors, one of whom is [redacted].

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with [redacted].
Based on statistical analysis, the results are as follows:

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It is estimated that the mixed DNA profile obtained is approximately 1.1 billion times more likely to have occurred if [redacted] had contributed DNA rather than if she had not.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

Base penis (dry) swab

This swab was submitted for DNA analysis.

A mixed DNA profile was obtained from this sample indicating the presence of DNA from three contributors. Given this sample is said to have been taken from [redacted] the finding of DNA that could have originated from him would not be unexpected.

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from three contributors, one of whom is [redacted]

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with [redacted]

Based on statistical analysis, the results are as follows:

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had contributed DNA rather than if she had not.

It is estimated that the mixed DNA profile obtained is approximately 4000 times more likely to have occurred if [redacted] had not contributed DNA rather than if she had.

It is estimated that the mixed DNA profile obtained is approximately 6500 times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

It is estimated that the mixed DNA profile obtained is approximately 1500 times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

[redacted] **Sexual Assault Investigation Kit (SAIK) -** [redacted]

*Item examined by Forensic DNA Analysis*

This SAIK contained the following items:
2 x low vaginal swabs – examined
2 x posterior fornix swabs – examined
2 x labia minora swabs – examined
1 x fluid in speculum swab – examined
1 x pre surfaces swab – not examined
1 x post surfaces swab – not examined
1 x dropsheet – examined



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[redacted]

**STATEMENT OF WITNESS** Client Reference : [redacted]

Spermatozoa were microscopically observed on slides prepared from the low vaginal swabs, posterior fornix swabs and the labia minora swabs. The fluid in speculum swab tested positive for the possible presence of blood and possible presence of seminal fluid.

The dropsheet was observed to contain apparent dirt and hair. This item was not examined further.

*DNA Analysis Results*

Labia minora swab 1 – Spermatozoa fraction

A mixed DNA profile was obtained from this sample indicating the presence of DNA from two contributors. Given this sample is said to have been taken from [redacted] the finding of DNA that could have originated from her would not be unexpected.

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from two contributors, one of whom is [redacted].

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with [redacted]

Based on statistical analysis, the results are as follows:

It is estimated that the mixed DNA profile obtained is approximately 4.9 million times more likely to have occurred if [redacted] had contributed DNA rather than if he had not.

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had not contributed DNA rather than if she had.

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

Labia minora swab 1 – Epithelial fraction

A mixed DNA profile was obtained from this sample indicating the presence of DNA from two contributors. Given this sample is said to have been taken from [redacted], the finding of DNA that could have originated from her would not be unexpected.

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from two contributors, one of whom is [redacted].

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with [redacted].

Based on statistical analysis, the results are as follows:

It is estimated that the mixed DNA profile obtained is approximately 45 times more likely to have occurred if [redacted] had contributed DNA rather than if he had not.



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T [redacted]

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It is estimated that the mixed DNA profile obtained is approximately 11 times more likely to have occurred if [redacted] had contributed DNA rather than if she had not.

It is estimated that the mixed DNA profile obtained is approximately 24 times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

It is estimated that the mixed DNA profile obtained is approximately 360 times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

Labia minora swab 2 – Spermatozoa fraction

A mixed DNA profile was obtained from this sample. Due to the complex nature of this DNA profile, including uncertainty as to the number of contributors, in my opinion this DNA profile is not suitable for meaningful interpretation.

Labia minora swab 2 – Epithelial fraction

A mixed DNA profile was obtained from this sample indicating the presence of DNA from two contributors. Given this sample is said to have been taken from [redacted], the finding of DNA that could have originated from her would not be unexpected.

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from two contributors, one of whom is [redacted].

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with [redacted].

Based on statistical analysis, the results are as follows:

It is estimated that the mixed DNA profile obtained is approximately 18 times more likely to have occurred if [redacted] had contributed DNA rather than if he had not.

It is estimated that the mixed DNA profile obtained is approximately 1.4 million times more likely to have occurred if [redacted] had not contributed DNA rather than if she had.

It is estimated that the mixed DNA profile obtained is approximately 32 million times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

It is estimated that the mixed DNA profile obtained is approximately 33 million times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

Low vagina swab 1 – Spermatozoa fraction

A mixed DNA profile was obtained from this sample. Due to the complex nature of this DNA profile, including uncertainty as to the number of contributors, in my opinion this DNA profile is not suitable for meaningful interpretation.

STATEMENT OF WITNESS Client Reference : [redacted]

Low vagina swab 2 – Spermatozoa fraction

A mixed DNA profile was obtained from this sample. Due to the complex nature of this DNA profile, including uncertainty as to the number of contributors, in my opinion this DNA profile is not suitable for meaningful interpretation.

Posterior fornix swab 1 – Spermatozoa fraction

A mixed DNA profile was obtained from this sample indicating the presence of DNA from two contributors. Given this sample is said to have been taken from [redacted] the finding of DNA that could have originated from her would not be unexpected.

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from two contributors, one of whom is [redacted]

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with [redacted].

Based on statistical analysis, the results are as follows:

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had contributed DNA rather than if he had not.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

Posterior fornix swab 2 – Spermatozoa fraction

A mixed DNA profile was obtained from this sample indicating the presence of DNA from two contributors. Given this sample is said to have been taken from [redacted] the finding of DNA that could have originated from her would not be unexpected.

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from two contributors, one of whom is [redacted]

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with [redacted]

Based on statistical analysis, the results are as follows:

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had contributed DNA rather than if he had not.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.



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[redacted]

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Fluid in speculum swab – Spermatozoa fraction

A mixed DNA profile was obtained from this sample indicating the presence of DNA from two contributors. Given this sample is said to have been taken from [redacted], the finding of DNA that could have originated from her would not be unexpected.

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from two contributors, one of whom is [redacted]

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with [redacted]

Based on statistical analysis, the results are as follows:

It is estimated that the mixed DNA profile obtained is approximately 10 times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

It is estimated that the mixed DNA profile obtained is approximately 1700 times more likely to have occurred if [redacted] had not contributed DNA rather than if she had.

It is estimated that the mixed DNA profile obtained is approximately 1800 times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

It is estimated that the mixed DNA profile obtained is approximately 260 times more likely to have occurred if [redacted] had not contributed DNA rather than if he had.

Fluid in speculum swab – Epithelial fraction

A DNA profile was obtained from this sample indicating the presence of DNA from a single contributor. This DNA profile matches the reference DNA profile of [redacted]

Given this sample is said to have been taken from [redacted], the finding of DNA that could have originated from her would not be unexpected and as such, statistical analysis has not been conducted.

**[redacted] - D – Fingernail scraping, right hand – [redacted]**

This sample tested positive for the possible presence of blood and was submitted for DNA analysis.

A DNA profile was obtained from this sample indicating the presence of DNA from a single contributor. This DNA profile matches the reference DNA profile of [redacted]. Given this sample is said to have been taken from [redacted] the finding of DNA that could have originated from her would not be unexpected and as such, statistical analysis has not been conducted.

**[redacted] - C - Fingernail scraping, left hand – [redacted]**

This sample was submitted for DNA analysis.

A mixed DNA profile was obtained from this sample indicating the presence of DNA from two contributors. Given this sample is said to have been taken from [redacted] the finding of DNA that could have originated from her would not be unexpected.

**STATEMENT OF WITNESS** Client Reference : [redacted]

Therefore, in order to interpret this mixed DNA profile, I have assumed the presence of DNA from two contributors, one of whom is [redacted].

The reference DNA profiles associated with this matter have been compared to this mixed DNA profile separately, in an attempt to determine whether or not any of them may have contributed DNA, along with [redacted]

Based on statistical analysis, the results are as follows:

It is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if [redacted] had contributed DNA rather than if he had not.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.

[redacted] can be excluded as having contributed DNA to this mixed DNA profile.



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[redacted]

**STATEMENT OF WITNESS** Client Reference : [redacted]

APPENDIX

**Procedural and technical overview of DNA profiling at Forensic DNA Analysis, Forensic and Scientific Services**

### Forensic Biologist

It is a forensic biologist's role to:

1. Report on the examination of items submitted in relation to a case for the presence of possible biological material. If identified, a sample of the biological material is analysed in an attempt to obtain a DNA profile.

2. Report on the DNA profiles obtained from samples submitted by the Queensland Police Service (QPS) in relation to a case.

Any DNA profiles that are obtained from these samples are compared with the DNA profile obtained from an individual's reference sample to assess whether or not the individual may be a contributor of DNA. Where multiple reference DNA profiles are analysed for a case, they are all genetically different to each other unless otherwise specified. That is, they all possess differing allelic designations – see the *DNA Profiling* section below.

### Examinations

Unless otherwise stated, the examinations of items for biological material were conducted by staff within the QPS. Sub-samples from these items were forwarded to Forensic and Scientific Services (FSS), for the purposes of conducting DNA analysis.

The descriptions of items and/or samples submitted to Forensic DNA Analysis by the QPS, and listed within this Statement, are derived from the descriptions entered by the QPS into the Forensic Register.

Receipt details are listed for items reported in this statement, including reference samples where relevant. The period of testing on these items is from the date of the first submission, to the date of this Statement. Details of specific dates of testing are retained within the Laboratory Information Management System (LIMS). Where relevant, any items that are still in progress at the time of issuing this Statement are identified and final results will be reported in an addendum Statement.

Forensic DNA Analysis operates under the agreement that the QPS are responsible for item prioritisation, sample selection, selection of screening/sampling methods, anti-contamination procedures and the application of Standard Operating Procedures (SOPs) on work undertaken on the items/samples prior to submission to the Forensic DNA Analysis laboratory. As such, forensic biologists may not be able to provide information or opinion on possible biological origin of DNA profiles that may be obtained from these samples.

At the discretion of the QPS, some items may be submitted to this laboratory for the purposes of both examination and DNA profiling. These examinations are performed in accordance with the SOPs of this laboratory. For these items, contemporaneous notes are made during the examination by the examining scientist and these notes form part of the casefile.

Forensic DNA Analysis casefiles and any samples remaining are available for independent examination and / or testing upon request.

As a representative of the laboratory, I am only able to comment on the processes performed within Forensic DNA Analysis.

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### Chain of Custody

All Forensic DNA Analysis case files and exhibits are electronically tracked, monitored, and securely stored to ensure that appropriate chain of custody and continuity measures are maintained. The QPS case number and sample submission information is provided from the QPS via an electronic interface to FSS, and this information is cross-checked against labelling on the exhibit packaging prior to processing.

Entry into Forensic DNA Analysis is restricted to authorised persons only, via electronic proximity access cards. Forensic DNA Analysis forms part of a Queensland Health campus site wherein access is controlled and monitored by a security team. Records of visitors to Forensic DNA Analysis are retained.

### Accreditation

Forensic DNA Analysis first achieved accreditation by the National Association of Testing Authorities (NATA) to conduct forensic DNA analyses in 1998, and has continuously maintained NATA accreditation since this date. NATA ensures continued compliance with the accreditation requirements through routine reassessment (every 3 years) and an intermediate surveillance visit (at approximately 18 months between reassessment surveys).

NATA accredited facilities are assessed against best international practices based on the ISO/IEC 17025 standard. Laboratories are deemed able to competently perform testing and analysis activities if the laboratory demonstrates that it meets compliance with the standard within the scope of their accreditation.

The parameters assessed during accreditation include:

- Organisation and management
- Quality management system
- Personnel
- Evidence management
- Methods and procedures
- Quality control and Proficiency Testing
- Equipment
- Reporting of results
- Procurement of services and supplies
- Accommodation and safety
- Security and access

For details of the current ISO/IEC 17025 Standard, refer to *Standards Australia*.

http://www.nata.com.au

### DNA Profiling

Deoxyribonucleic acid (DNA) is a complex chemical found in almost all cells of the human body. It carries genetic information that determines the physical and chemical characteristics of a person. Forensic DNA Analysis uses two main systems for the generation of DNA profiling results. In this case, the PowerPlex® 21 System was used, which examines 21 regions (loci) of DNA, 20 of which contain highly variable short tandem repeats (STRs). The 21st region gives an indication as to the genotypic sex of the donor (for details see Table 1). The generation of a DNA profile involves a method known as the polymerase chain reaction (PCR), which is used to produce numerous copies of these specific regions of the DNA. In this way, minimal

amounts of DNA isolated from small or degraded samples can be increased to a level where the DNA can be detected, profiled, and compared with DNA profiles from other samples.

The individual components (alleles) of a DNA profile are represented by a series of peaks on a graph that are measured and given a designation, using standard sizing ladders. A person will have two alleles (represented graphically as peaks) for each locus, one inherited from the biological mother and one inherited from the biological father. However, if the same allele is inherited from both parents, only one peak will be graphically represented at that locus

A DNA profile obtained from biological material such as blood, semen, saliva, hair or cellular material (eg. touch DNA) can be compared with the DNA profile obtained from the reference sample from any person.

*Table 1: PowerPlex® 21 system, list of loci*

| Abbreviated Name | Scientific Name | Chromosomal Name |
|---|---|---|
| Amel | AMELOGENIN | Sex (X and Y) |
| D3 | D3S1358 | 3 |
| D1 | D1S1656 | 1 |
| D6 | D6S1043 | 6 |
| D13 | D13S317 | 13 |
| Penta E | Penta E | 15 |
| D16 | D16S539 | 16 |
| D18 | D18S51 | 18 |
| D2 | D2S1338 | 2 |
| CSF | CSF1PO | 5 |
| Penta D | Penta D | 21 |
| TH01 | TH01 | 11 |
| vWA | HUMVWAFA31/A | 12 |
| D21 | D21S11 | 21 |
| D7 | D7S820 | 7 |
| D5 | D5S818 | 5 |
| TPOX | TPOX | 2 |
| D8 | D8S1179 | 8 |
| D12 | D12S391 | 12 |
| D19 | D19S433 | 19 |
| FGA | HUMFIBRA | 4 |

**Statistical Analysis of DNA Profiles**

STRmix™ is an expert statistical DNA profile analysis system developed and validated in Australia and New Zealand. Forensic DNA Analysis uses the STRmix™ software to assist in the interpretation of DNA profiles and the calculation of likelihood ratios for DNA profiles generated using the PowerPlex® 21 system.

DNA profiles are initially assessed to determine the number of contributors. This value will be the minimum number of people that are required to reasonably explain the observed profile, however, it is noted that there is always the possibility that the profile is a result of a different number of contributors.

As such, if there is no indication of a contribution by more than one person, then a DNA profile is described as being from a "single contributor". If less than 40 alleles are present in a DNA profile, this is referred to as a "partial" or "incomplete" DNA profile. If there are indications of two or more contributors, then a DNA profile is described as being a "mixed" DNA profile.

DNA Profiles Assumed To Originate From One Person (Single Source)

A person can be excluded as a possible source of the biological material if the alleles of the crime-scene DNA profile are different from the corresponding alleles of the person's reference DNA profile. If the corresponding alleles of the crime-scene DNA profile contain the same information, then that person, along with any other person who has the same corresponding alleles as the crime-scene DNA profile, can be considered as a potential contributor of the DNA.

The evidential significance of such a finding is assessed by considering two competing propositions:

Proposition 1: The crime-scene DNA originated from the person of interest.

Proposition 2: The crime-scene DNA originated from someone other than, and unrelated to, the person of interest.

The resultant figure (termed the 'Likelihood Ratio') compares the two opposing propositions. The likelihood ratio describes how likely the DNA profile obtained from the biological material is to have occurred if Proposition 1 were true (the DNA originated from the person of interest) rather than if Proposition 2 were true (the DNA originated from someone other than, and unrelated to, the person of interest).

The likelihood ratio is calculated by taking into account the characteristics of the DNA profile and the frequency of occurrence of the individual alleles that make up the DNA profile.

If less than the 20 STR regions of DNA are observed in a DNA profile, the likelihood ratio will be smaller than the likelihood ratio calculated for a full DNA profile obtained from the same individual. In other words, the more incomplete a DNA profile is, the greater the likelihood that the obtained DNA profile could have come from someone other than, and unrelated to the person of interest.

DNA Profiles Assumed To Originate From More Than One Person (Mixed DNA Profiles)

In order to assess whether a person may or may not have contributed to a mixed DNA profile, a set of competing propositions (similar to the single source DNA profile example) are considered. For example, for a two-person mixture:

Proposition 1: The crime-scene DNA originated from the person of interest and an unknown person, unrelated to the person of interest.

Proposition 2: The crime-scene DNA originated from two unknown people, both unrelated to the person of interest.

The likelihood ratio provides a statistical assessment of the possibility that the DNA profile obtained was the result of a DNA contribution by the person of interest.

The likelihood ratio will not always favour Proposition 1 (the DNA originated from the person of interest and an unknown person unrelated to the person of interest). The likelihood ratio could favour Proposition 2 (the DNA originated from two unknown people unrelated to the person of interest).

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In certain circumstances, if the ownership of an item is established or if the sample was collected from an identified person's body, then it is possible to make the reasonable assumption that the identified person has contributed DNA to the resultant mixed DNA profile. In these cases, a mixed DNA profile can be 'conditioned' on the DNA profile of the assumed contributor, such that the presence of the alleles corresponding with the assumed contributor's reference DNA profile can be factored into the statistical interpretation. This may facilitate a more meaningful statistical analysis of potential second and/or third contributors to the DNA profile. In this situation, the likelihood ratio is based on the following propositions:

Proposition 1: the DNA has originated from the assumed contributor and the person of interest.

Proposition 2: the DNA has originated from the assumed contributor and an unknown individual, unrelated to the person of interest.

DNA profiles with an uncertain number of contributors

Forensic DNA Analysis is currently validated for the interpretation of DNA profiles with 1-4 contributors. Once the assessment of the number of contributors has been made, this information is used in the STRmix™ analysis.

When a DNA profile is deemed unsuitable for interpretation it may be described as 'complex'. This can occur under the following circumstances:

- When a DNA profile could have a large number of contributors and therefore it is difficult to exclude individuals and/or determine whether a person could be a potential contributor to the DNA profile
- When there is very limited information available and/or the quality of the profile is poor.

It is important to note that should further information be received that renders the assumptions used in an analysis invalid, the DNA profile will require additional statistical interpretation.

Datasets Used in Statistical Analyses

Three validated datasets consisting of DNA profiles obtained from individuals of the Australian Caucasian, Aboriginal, and South-East Asian populations are used to calculate the likelihood ratio. A population correction factor, θ (theta), is applied to all likelihood ratio calculations in order to correct for the common genetic ancestry of people within a particular population (sharing of DNA components inherited from a common ancestor). In Forensic DNA Analysis, a likelihood ratio that represents a stratified population statistic is reported irrespective of whether the DNA profile of interest is single source or a mixed DNA profile.

The likelihood ratio is calculated using all three datasets and the relative proportions of each ethnic grouping in the overall Australian population based on data sourced from the Australian Bureau of Statistics. This calculation, which is known as stratification, allows for the possibility that a random unknown person, unrelated to the person of interest, from anywhere in Australia could have contributed to the DNA profile obtained. Therefore, the likelihood ratio is not dependent on the ethnicity of the person of interest, but it is representative of the relative proportion of the person of interest's ethnic population within the larger Australian population.

Theta cannot account for close blood relatives. Closely related people, such as siblings, will have a greater chance of sharing similar components within their DNA profiles. However, due to the nature of parental DNA recombination during conception, the probability that two siblings would share the same 40 alleles would be very small. As this relationship becomes more distant, the probability of two relatives having the same DNA profile becomes smaller still. If it were thought that a close blood relative might have been a contributor of DNA, the most meaningful approach to interpretation would be to submit the reference sample from the relative in question for DNA analysis and subsequent direct comparison to the crime-scene DNA profile.

Often the calculated likelihood ratio produces numbers of thousands (1000s) or even millions (1000.000s) of billions. To avoid the use of potentially confusing mathematical terminology, a "ceiling figure" for the likelihood ratio of 100 billion is used (this is called "truncation"). For example, a calculated likelihood ratio of "150 000 billion times more likely", would be reported as "greater than 100 billion times more likely". The actual calculated figure can be provided upon request.

### Touch DNA / Transfer of DNA

When a person touches a surface, it is possible for their DNA to be transferred onto that surface. This transferred DNA can often be recovered (sampled) by a swab, tape lift, or excision depending upon the nature of the surface in question, and the sample can then be subjected to DNA profiling.

This transferred DNA can originate from cells or cellular material within sweat and/or oils on the skin. The generation of a DNA profile will depend on many factors. These include the amount of DNA transferred, the nature of the surface being touched, and the amount of genetic material available for transfer. The persistence of any transferred genetic material to a surface will depend largely upon the nature of the surface and the conditions the surface has been subjected to in the time between deposition and recovery of the DNA. For example, DNA could be lost from the surface by washing or mechanical action such as abrasion.

It therefore follows that the inability to obtain a DNA profile from a touched surface does not necessarily mean that a person has not had contact with the surface. It is possible for a person to contact a surface without a detectable amount of their DNA being transferred or subsequently recovered for analysis.

### Blood Stains

Potential bloodstains are located in the laboratory by means of their visual appearance and the use of a presumptive chemical test (Tetramethylbenzidine – TMB). A positive result with this test is a good indication that blood may be present, however it does not provide proof as other substances are known to give the same result.

### Semen Stains

Semen is the collective name for the mixture of spermatozoa (sperm) and seminal fluid. The presence of semen on an item can be indicated by using a presumptive chemical test that detects a major constituent of seminal fluid, namely Prostate Specific Antigen (PSA / p30). This constituent may exist in other body fluids, such as urine, faecal material, sweat, breast milk and blood, albeit usually at much lower concentrations.

The location or presence of possible semen on items may also be indicated by using a presumptive chemical test that detects another major constituent of seminal fluid (Acid Phosphatase – AP). This constituent exists in other body fluids, such as vaginal secretions, albeit usually at much lower concentrations.

The presence of semen can be confirmed via the microscopic identification of spermatozoa.

Samples where semen may be present undergo a differential lysis extraction process that aims to separate spermatozoa and epithelial cells into separate fractions. This separation is not always completely effective, and a mixing of fractions can occur. This is often referred to as cellular carryover.

The current practice within Forensic DNA Analysis is for epithelial fractions from internal female sexual assault investigation kit (SAIK) samples to be stored following a differential lysis extraction process. This is because when these fractions are profiled, they are generally found to be a single contributor match to the person from whom the sample was taken. Given the nature of these samples, this finding is not unexpected. These epithelial fractions are stored indefinitely, and can be sent for DNA profiling at a future date if required.

**STATEMENT OF WITNESS** Client Reference : [redacted]

Semen Staining on Items

The presence of semen on an item is normally the result of either direct ejaculation or contact with an item wet with semen (transfer). Any semen that may have been transferred / deposited can subsequently be lost by actions such as washing.

Persistence of Semen in the Vagina

The presence of semen in the vagina is normally the result of vaginal intercourse with internal ejaculation. The chance of detecting semen on a vaginal swab depends upon a number of factors such as:

- the effectiveness of the sampling process;
- the delay between deposition of the semen and sampling during the medical examination;
- the biochemical conditions within the vagina;
- any physiological factors that may affect semen production in the donor.

The greater the delay between deposition and sampling, the less chance there is of finding semen. Although highly variable, semen is likely to be found on vaginal swabs if they were taken 1-2 days after the act of vaginal intercourse. Semen is sometimes found on swabs taken between 2-7 days afterwards, but it is unlikely to be detected after 7 days. This is due to a number of factors that can include the following:

- drainage of semen from the vagina;
- loss of semen by bathing or washing (especially on external sites);
- degradation of the spermatozoa and seminal fluid constituents.

**JUSTICES ACT 1886**

I acknowledge by virtue of Section 110A (6C) (c) of the Justices Act 1886 that:

(i) This written statement by me dated 28 July 2022 and contained in the pages numbered 1 to 20 is true to the best of my knowledge and belief; and

(ii) I make it knowing that, I would be liable to prosecution for stating anything that I know is false.

.....

Alicia Ann QUARTERMAIN

Signed at BRISBANE on 28 July 2022



NATA Accredited Laboratory 41 Accredited for compliance with ISO/IEC 17025 - Testing

39 Kessels Road
Coopers Plains QLD 4108
AUSTRALIA

PO Box 594
Archerfield QLD 4108
AUSTRALIA

[redacted]

**From:** Justin Howes <[redacted]>
**Sent:** Friday, 30 April 2021 8:47 AM
**To:** Alicia Quartermain <[redacted]>
**Subject:** RE: DNA Insuff. for further processing

Hi, happy for you to come and talk about this. It seems there are some things that require further clarification.

I am available most of the day.

Justin

**Justin Howes**
Team Leader - Forensic Reporting and Intelligence Team

**Forensic DNA Analysis, Police Services Stream**
Forensic & Scientific Services, Health Support Queensland, Queensland Health

*Please note that I may be working from a different location during the COVID-19 Pandemic. The best contact method is via email.*

p [redacted] m [redacted]
a 39 Kessels Road, Coopers Plains, QLD 4108
e [redacted] w www.health.qld.gov.au/hsq/support/businesses/forensic-and-scientific-services


*Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and emerging.*

**From:** Alicia Quartermain <[redacted]>
**Sent:** Thursday, 29 April 2021 3:52 PM
**To:** Justin Howes <[redacted]>
**Subject:** DNA Insuff. for further processing

Hi Justin,

In the past I had noticed some samples which had originally been called DIFF, were subsequently processed on the 3130, resulting in some decent profiles. Even if these profiles were low level, if the number of contributors was only one or two, then they were still interpretable. For example, light combur-pos stains or SAIK samples.

With the introduction of the 3500, I am seeing the same thing happening, except the peaks are much higher due to the sensitivity of the instrument. I feel that reporting these samples as DIFP is technically incorrect. I strongly feel that we should be processing a lot of these samples these days, especially ones that may have a quant value close to the cut-off range.

I don't see how data-mining around this can happen yet, as there would not be many samples that fall into this category. I would, however, be prepared to do the research. Are we able to get authorisation to put through Analytical any combur-pos or SAIK samples that fall within this category (samples with any quant) for a set period of time to see what happens? I would be happy to take this work on if you get the right person to say yes to my proposal.

Kind regards,
Alicia

**Alicia Quartermain BHSc MSc (forensic science)**
Scientist – Forensic Reporting and Intelligence Team

**Forensic DNA Analysis | Police Services Stream | Forensic & Scientific Services**
Health Support Queensland, Queensland Health

[redacted]
39 Kessels rd, Coopers Plains, Q 4108

[redacted] www.health.qld.gov.au/healthsupport

*Please note that I may be working from a different location during the COVID-19 pandemic. The best contact method is via email*

AQ-07

**Laura Reece**

**From:** Alicia Quartermain <[redacted]>
**Sent:** Wednesday, 21 September 2022 3:40 PM
**To:** Laura Reece
**Subject:** MS teams form

# DNA Rework Authorisations

Hi, Alicia. When you submit this form, the owner will see your name and email address.
Required

1.Barcode

2.DNA Priority

P1
P2
P3

3.Original Result (no mnemonics)

4.Type of Rework Requested

Reamp
Re-CE

5.Likely outcome of rework

6.Risk of undertaking the rework (eg. NCIDD removal)

7.Date for result release

Submit

**Alicia Quartermain BHSc MSc (forensic science)**
Scientist – Forensic Reporting and Intelligence Team

**Forensic DNA Analysis | Police Services Stream | Forensic & Scientific Services**
Prevention Division, Queensland Health

p [redacted]
a 39 Kessels rd, Coopers Plains, Q 4108

e [redacted] w www.health.qld.gov.au/fss

*Please note that I may be working from a different location during the COVID-19 pandemic. The best contact method is via email.*

Integrity | Customers and patients first | Accountability | Respect | Engagement

*Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and emerging.*