Statement of Amanda Jane REEVES (née STORER)

I, **Amanda Jane REEVES (née STORER)** of [redacted] in the State of Queensland, state:

1. I have previously provided a statement to the Commission of Inquiry, declared by me on 27 October 2023. In that statement, I indicated that I did not have access, and thus not had an opportunity, to interrogate my emails and other documents relevant to the period from 2007 until 2016.

2. Upon hearing the evidence excerpted below, I had a different recollection to that given by the witnesses mentioned. This caused me to go back to my restored emails to which I have now been given access, and to specifically look for emails that were relevant to the "go-live" of the DNA IQ automation procedure. I started this exercise on Monday night. I hastily gathered the emails I believed to be relevant, although did not have an opportunity to review these. I have now further reviewed them, and reduced them down to those to which I now make reference in this statement.

Oral Evidence on Monday 30 October 2023

3. I was present during the hearing of the Commission of Inquiry on Monday 30 October 2023 and in particular for the evidence given by Ms Vanessa Ientile, Mr Thomas Nurthen, Dr Vojtech Hlinka and Mr Allan McNevin, in relation to the "go live" of the DNA IQ automation. The following passages from their evidence are now relevant to this my second statement, and to the emails that I have interrogated.

Transcript Evidence:

4. Monday 30 October 2023 transcript page 66, lines 4-7:

   Ms Ientile: "*In reviewing what was available to me, there was no indication that there was any - in terms of the go-live or following that, any indication that people had raised any concerns about that at the time.*"

5. Monday 30 October 2023 transcript page 78, lines 18-25:

THE COMMISSIONER: "*By which you mean no-one said, "Hang on a second, we're suddenly getting --*"

MR McNEVIN: "*That's right, and I don't recall any of the other sort of senior scientists at the time saying "Hey, should we be looking into this?" I don't recall any of that conversation happening.*""

Relevant Emails

6. An email from Justin Howes on 24 October 2007 at 1:02 pm, Reporting Senior Scientist in charge of the Sexual Assault sub-team of the Major Crime team, to me, Emma Caunt, Kylie Weller and Samantha Cave attaching a draft document titled "*Questions/Issues regarding DNAIQ*" which specifically asks among other queries, "*Where is the validation data located?*". Justin and I emailed between 1:28-1:39 pm that same day on these issues. Justin responded at 1:39 pm saying, "*not much – surprised?*" reflects my recollection of the sequestering of information and lack of open communication in existence at this time. Exhibit **AJR-1** is a copy of this email.

7. The email on 24 October 2007 at 9:34 am from Vanessa Ientile to Emma Caunt and Iman Muharam at paragraph 10 shows the factsheet of the DNA IQ automated method[1] being sent just 5 days before the go-live, thereby revealing the limited extent of any consultation with the reporting scientists in the lab, before the system was operationalised. Exhibit **AJR-2** is a copy of this email.

8. The email on 29 October 2007 at 3:40 pm from Justin Howes to the named recipients which include Messers McNevin and Nurthen, about the "*gamut of processes involved*" in the DNA IQ automation implementation, again illustrates the sequestration of information in that the lab reporting scientists had not been provided with any training with respect to the theory behind the new processes, or any involvement or consultation in the project work leading up to the implementing of DNA IQ until the "go live" date. Exhibit **AJR-3** is a copy of this email.

[1] The inadequacy of the factsheet was also raised in the evidence of Dr Hlinka, in which he described the factsheet as being "*slightly misleading*". See transcript from Tuesday 31 October p: 198, lines 19-32.

[redacted]

Signature

[redacted]

Witness

9. Furthermore, the email on 30 October 2009 at 9:18 am from Thomas Nurthen, the day after the "go live" of the automation implementation, attaches the DNA IQ protocols. From all the material that I have reviewed, this appears to be the first time that these protocols were sent to the other scientists in the lab, and is further evidence of the haste, and the lack of consultation and information sharing. Exhibit **AJR-4** is a copy of this email.

10. The email on 18 April 2008 at 4:24 pm from Vanessa Ientile to Shannon Merrick[2] reveals that a significant and urgent problem of an undetermined nature in the extraction of case work samples using the DNA IQ automated method had been identified. The email reveals that there was to be an urgent investigation, however, the email does not reveal any cessation of the use of the automated method on case work samples at that time. In my opinion, this is significant because the unknown impacts were on case work samples, which had the potential to impact on justice outcomes. Exhibit **AJR-5** is a copy of this email.

11. The email on 26 October 2007 at 8:28 am from Justin Howes to me, Samantha Cave, Emma Caunt, Kylie Weller, 3 days before "go live" of the DNA IQ automation, highlights the lack of open communication and consultation when Reporting Scientists tried to raise issues with the automation implementation with management. Exhibit **AJR-6** is a copy of this email.

Transcript Evidence:

12. Monday 30 October 2023 transcript page 68, lines 9-12:

    Allan McNevin: "*I was just going to say I don't recall, and over the years I did do various data mining exercises. I don't recall doing that at the time and I also don't recall anyone else raising it as something that would be a worthwhile study.*"

Relevant Emails

13. An email from Allan McNevin on 26 November 2007 at 12:19 pm shows that consultation and consideration for statistic project ideas to obtain data, forwarding on from an email from

[2] I believe this email was also sent to other recipient as it begins "*Hi guys*" however any other recipients are not showing.

[redacted] [redacted]

Signature Witness

Paula Taylor, Senior Scientist in Volume Crime[3] noted that other scientists raised the comparison be undertaken between the pre-DNA IQ success rates of initial profiles to the normal Chelex success rates. This shows that the other recipients to the email were aware that other scientists wanted data on comparing the success rates between Chelex and the DNA IQ automated method. Exhibit **AJR-7** is a copy of this email.

Transcript Evidence

14. Monday 30 October 2023 transcript page 81, lines 38-45:

> MR HOLT: "*And again in terms of the significance of go-live, and, Dr Nurthen, you might recall this, but I think it's clear from the memorandum that Ms Ientile sent at the time to all staff, that initially it was only to be that the automated DNA IQ system was to be used for high-volume backlog cases, not everything across the board?*"
>
> MR NURTHEN: "*That's my understanding.*"

Relevant Emails

15. The email on 24 October 2007 at 11:42 am from Vanessa Ientile at paragraph 10 evidences a practice that is directly contrary to Ms Veth's testimony on Tuesday 31 October 2023[4] to the effect that *reference* samples should have been processed through the new DNA IQ automation system before any use with case work, yet the lab did the opposite. Exhibit **AJR-8** is a copy of this email.

Transcript Evidence

16. Monday 30 October 2023 transcript page 57, lines 1- 21:

> MR McNEVIN: "*So I guess from my perspective at the time, the lab had a massive backlog of work and so if we had just continued down a fully manual method, we would have been irresponsible, because a lot of work wouldn't have just got done. So, you know, I see that it was necessary for us to implement technologies that would enable us to actually process the samples required. If we'd have just continued down*

[3] I am not certain this was Ms Taylor's exact title; this is to the best of my recollection.
[4] Transcript Tuesday 31 October 2023 pg 162 lines 44 – 47 and page 163, lines 1-7 and Dr Budowle's corroborating evidence on page 163, lines 16-27.

[redacted] [redacted]

Signature Witness

doing low numbers of samples in a very laborious way, the laboratory wouldn't have needed any other liquid handling platforms because we wouldn't have had the volume of work to feed them from the extraction process. So in order for us to actually get on with the business of doing DNA profiling, we needed to automate. So was it irresponsible to persist with validating an automated method? No, I think that was the remit we were given and it was what we set out to do. It seemed to me that that was a necessary - we needed to move the laboratory forward. We needed to implement technologies which enabled us to actually get through the volume of work that the laboratory was being supplied with."

Relevant Emails

17. The emails on 3 December 2007 at 12:24pm and 14 April 2008 12:16pm from Allan McNevin to the recipients highlighting the record number of extractions being completed. In my opinion, this evidences the priority placed on throughput. Exhibit **AJR-9** is a copy of these emails.

Signed by:
Amanda Jane Reeves ..[redacted]
At Brisbane 1 November 2023

Before me:
Caitlyn Alyce Wessels .....
Lawyer 1 November 2023
Macpherson Kelley

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Exhibit	**Document**	**Page no.**
AJR-01	Email from Justin Howes on 24 October 2007 at 1:02 pm to me, Emma Caunt, Kylie Weller and Samantha Cove attaching a draft document titled "*Questions/Issues regarding DNAIQ*"	1-3
AJR-02	Email on 24 October 2007 at 9:34 am from Vanessa Ientile to Emma Caunt and Iman Muharam	4
AJR-03	Email on 29 October 2007 at 3:40 pm from Justin Howes	5
AJR-04	Email on 30 October 2009 at 9:18 am from Thomas Nurthen	6
AJR-05	Email on 18 April 2008 at 4:24 pm from Vanessa Ientile to Shannon Merrick	7
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AJR-07	Email from Allan McNevin on 26 November 2007 at 12:19 pm	9-11
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AJR-09	Emails on 3 December 2007 at 12:24pm and 14 April 2008 12:16pm from Allan McNevin	12-14

[redacted] [redacted]

Signature Witness

DNAIQ

Justin Howes <[redacted]>

Wed 24/10/2007 1:02 PM

Cc:Amanda Storer <[redacted]>;Emma Caunt <[redacted]>;Kylie Weller <[redacted]>;Samantha Cave <[redacted]>

1 attachments (25 KB)

Questions re DNAIQ.doc;

Hello
I have started the doc as discussed. Please read it and add to it if you have something by COB today!!!
It is stored in the G: YT folder. Change this master copy if you have additions and send an email to all that something has been added.
I have attached the starting version for your pleasure.
ta
JAH

Questions/Issues regarding DNAIQ

- In reference to tapelifts, as these are not for DNAIQ, what do the samplers request ie. NUCC?
  - What are the implications in the cases where supernatant is to be retained and this is not poss with NUCC??
- Where is the validation data located?
- Why not listed in change management? If it is, where is it to be found?
- In reference to swabs for cells, what do we do when the swab is wet and the outer casing is therefore not dry to cut off? (eg. AP tested vulval swab)
- Wet/dry swabs - are we going to have to pool (with 'phantom' barcodes) these in the future? Complicates case management and creates more room for error.
- Is there any literature to show that within the outer casing of swabs there is no DNA? Can we be certain if outer casing only is to be cut that the cells are trapped only there?
- How is the workflow to be organised? Who does the wiping of storstar and are the environmental studies as part of the investigations able to be viewed? It is best practice to have disposable forceps for each sample. Can all reporting scientists observe the process of transferring from sampling tubes to SlicPrep?
- What will the process be for fingernails/scrapings - these can be very fiddly and will be difficult to transfer to SlicPrep?
- What is the future for hairs?
- What is the future for DLYS?
-

Questions prepared by
Justin Ahuja

Re: DNAIQ

Justin Howes <[redacted]>
Wed 24/10/2007 1:39 PM
To:Amanda Storer <[redacted]>

not much - surprised???
RJP is adding more stuff to doc at the moment. What about wet/dry breast swabs and pooling post-extraction due to sample size - what if supt testing gives pos and neg etc...

>>> Amanda Storer Wednesday, 24 October 2007 1:29:20 pm >>>
true? what has been said about that?

>>> Justin Howes 10/24/07 1:26 pm >>>
right -o. Looks like the end of supernatant testing...

>>> Amanda Storer Wednesday, 24 October 2007 1:26:12 pm >>>
this looks good mate, just would change wording a bit regarding the swabs.... perhaps use outer layer and inner layer of swab head rather than outer casing??? i found this confusing at first, because i initially thought you meant the sheath, which didn't amke sense. also, on the 6th dot point, i think you mean to say 'no DNA in the inner layers of the swab head', rather than 'Is there any literature to show that within the outer casing of swabs there is no DNA?'

hope this made sense, :|

>>> Justin Howes 10/24/07 1:02 pm >>>
Hello
I have started the doc as discussed. Please read it and add to it if you have something by COB today!!!
It is stored in the G: YT folder. Change this master copy if you have additions and send an email to all that something has been added.
I have attached the starting version for your pleasure.
ta
JAH

not entirely sure who else received this but likely MCT seniors to go to Sam Cave
KDR (MCT Lead)
AJR
EJC (?)
indicates how little info we were being given in advance of implementat" (29/10/2007)

4

Automation Go Live

Vanessa Ientile <[redacted]>
Wed 24/10/2007 9:34 AM
To:Emma Caunt <[redacted]>
Cc:Iman Muharam <[redacted]>

Hi guys

Just wanted to provide some clarification around the Go Live strategy with automation and also some actions that will be occurring in the next few weeks.

We'll follow this up with a bit of discussion on Thursday at the management meeting if that's ok with everyone.

First of all, the date for commencing the use of the platforms has been set to the 24th October and both extraction platforms will be used to run casework samples from this date.

Plates will be prepared using the backlog samples prepared by Volume and part of the process will be the transfer of samples from tubes to plates using StarStar. Allan has asked his team to develop the transfer protocol taking any quality issues into account.
The automation team will start the ball rolling next week and run the instruments and start the training of the analytical staff.

We will be ramping up slowly over the next few months so I don't expect the instruments to hit full capacity until the new year.

I've had some feedback regarding concerns on the start date and the request to have Major Crime start sampling in the new format/size based on the information provided by Tom at the team meeting last week. It's my understanding also that people have concerns about not fully understanding the new extraction procedure and therefore being concerned about reporting these cases. Please correct me if I have misunderstood.

I would be happy to push the Major crime sampling size change start date back a week or two but really no more, I don't see this is a major change.

So onto the future, how do we as the senior scientists ensure all our staff have the appropriate level of knowledge for this process to proceed?

First of all, to address the knowledge gap concerns.

The automation team have prepared a fact sheet (attached) outlining the process, the evaluation and the changes. Iman has done an excellent job of putting this together and this will be sent out today. Please make sure it is discussed amongst your teams.
There is an SOP and Training module in QIS for this procedure. Once these have been approved and activated this week they will be sent out to everyone. I expect at the minimum that all reporting scientists must complete the Part B assessment.
We will need to set a timeframe for this and also ensure that we have appropriate sign off by members of the automation team who are the super users.

I have also asked Tom to organise a session once the validation reports have been signed off for all reporting scientists (mandatory attendance) and anyone else who is interested. At this session, we will be going through the entire validation process and report including the method evaluation phase, manual validation, automated protocol development and testing, anti-contamination tests and results in detail.

demos for MC (major crime)

Justin Howes <[redacted]>
Mon 29/10/2007 3:40 PM

To:Thomas Nurthen <[redacted]>
Cc:Allan McNevin <[redacted]>;Amanda Storer <[redacted]>;
Emma Caunt <[redacted]>;Samantha Cave <[redacted]>;Wendy
Harmer <[redacted]>

Hey
I have 9 groups to tour through - only 4 groups are a priority (reporting scientists). These groups have three people in each - two of the non-priority groups have 2 people.
If you have some times, I can ask Wendy and the admin staff to do busy searches and pick the groups.
I don't think more than 30 mins is required - as long as the gamut of processes involved are covered.

Thanks
JAH

on day of implementation

MCT started tours to try & understand how this would work

DNA IQ protocols

Thomas Nurthen <[redacted]>

Tue 30/10/2007 9:18 AM

3 attachments (728 KB)

DNA IQ Casework Isolation Guide.pdf; DNAiQ_SmallCW_tb296.pdf; Thomas Nurthen.vcf;

Hi Guys,

Attached are the electronic versions of the DNA IQ protocols.

Regards

Tom Nurthen BSc(Hons)
Project Manager
Automation & LIMS Implementation
Forensic Biology
Forensic and Scientific Services
Phone: [redacted]

protocols provided
day after implementation

DNA IQ update

Vanessa Ientile <[redacted]>
Fri 18/04/2008 4:24 PM
To:Shannon Merrick <[redacted]>

Hi guys

After our previous conversations about DNA IQ performance at the last management meeting, some information has come to light from ongoing investigations. At this stage we are not sure exactly what the issue is.

We need to work out exactly what is happening and therefore there will be a few impacts on work from next Monday.

We will still be extracting but part of the process will be moved to a manual process so therefore we will be reducing the number of extractions per day.

People will also be dedicated to investigating the method urgently.

After discussions with Tom, Cathie and Al we think this is the best course of action at this stage.

The purpose of this email is to let you know what is happening although we'll make sure that more information is given to you when we have it.

What I need from you guys is support for Tom and Al and their teams as they dedicate time and resources to this.

Regards

Vanessa

Vanessa Ientile
Managing Scientist
DNA Analysis
Queensland Health
Forensic and Scientific Services
[redacted]
COOPERS PLAINS QLD 4108

Telephone: [redacted]
Fax: [redacted]
Email: [redacted]

1. Know there is an issue
2. don't know nature / extent of issue
3. ~~urge~~ serious enough to warrant urgent investigating
4. decision-making restricted to Tom, VKI, Cathie, Al
5. process not stopped di~~keep~~ Kept processing
6. effect of last statement in my view is to dissuade causing further 'issues' → support them

Re: DNAIQ

Justin Howes <[redacted]>

Fri 26/10/2007 8:28 AM

To:Amanda Storer <[redacted]>;Samantha Cave <[redacted]>
Cc:Emma Caunt <[redacted]>;Kylie Weller <[redacted]>

We discussed it in the mgt meeting but Tom wasn't there and it was difficult to get points across. It was added as an action item though. But in answer to your qn - yes please! AAP in from Wed so anytime after that for the YT (two groups ideal for 5 people in total).
ta
JAH

>>> Samantha Cave Friday, 26 October 2007 7:59:56 am >>>
A fair idea

Do you want me to discuss with Tom

>>> Amanda Storer Wednesday, 24 October 2007 3:12:31 pm >>>
agree :)

>>> Justin Howes 10/24/07 3:02 pm >>>
Hi Sam
I think the first thing to happen, before having the many questions answered, is for every reporting scientist (+ the three trainees) to read and understand the SOP back-to-front then go into the section for a demo of a real extraction.
The workflow, use of forceps/fire, suction of SlicPrep etc seem to be the main concerns in the YT so far.
JAH

~ 1mth after implementat^

Re: Stats project ideas

Allan McNevin <[redacted]>

Mon 26/11/2007 12:19 PM

To:Amanda Storer <[redacted]>;Cathie Allen <[redacted]>;Emma Caunt <[redacted]>;Justin Howes <[redacted]>;Kylie Weller <[redacted]>;Paula Taylor <[redacted]>;Robyn Smith <[redacted]>;Sharon Johnstone <[redacted]>;Thomas Nurthen <[redacted]>;Vanessa Ientile <[redacted]>

Hi guys,

something I have noted, and the project team would have done if they had the time :) is that the profiles we obtain from DNA IQ seem to be a lot more balanced in pk height from Amel across to D7 compared with chelex, there are a large number of validation samples which were prepared the same way and then extracted with the only variable being the extraction method ... therefore could assess the balance of the profiles (ratio of average pk ht D3:D7 for example) ... or could be rolled into one of the other projects ... also there is of course our AT threshold and pk height thresholds which are basically straight statistical analysis projects of previously obtained data ... I think some of the other would be hard to draw conclusions as samples are chosen to be sent to one extraction type or another and therefore your success rates are skewed based on the initial sampling decisions, whereas I think Josie's idea is probably better as it is looking at the area sampled, providing there are enough items where both areas were sampled on the same item??,

just my rambling thoughts
cheers
Al

Allan McNevin
Senior Scientist - Analytical Section
DNA Analysis (Forensic Biology)
Forensic & Scientific Services
Queensland Health

Phone: [redacted]
Email: [redacted]

>>> Paula Taylor Monday, 26 November 2007 12:01:40 pm >>>

From the management team meeting on Firday, I have asked Megan, Alanna and Josie to email me with what ideas they have come up with.

Can you have a look, and let me know what you think, or if you have any suggestions.

Thanks

Paula

Project ideas

Megan

My idea for a project is to compare Pre-IQ the success rates of initial profiles ordered as cells v nucc and blood v nucb to see if initial nucleospinning would have been a better way to go.

Alanna

Comparing the success rates of normal chelex (no n/spin or microcons) versus DNAIQ – for about the first month of two of running DNAIQ.

Josie

So far I have come up with a couple of ideas for the project. The main one is looking at the success rate of tapelifts taken from shirts and comparing the success of tapelifting from different locations (collars/necks, underarms and cuffs/wrists). I think this would have a few variables and give me a bit of scope for different statistical analyses. I thought that this might be useful for the lab to see if there is any trend with success rates from a particular area that we could then target when sampling in the future

idea for project

Megan Penny <[redacted]>

Mon 26/11/2007 3:43 PM

To:Paula Taylor <[redacted]>

Hi Paula
Al and Tom had the idea to look at the quant values and success rates of dig bulls pre DNA IQ (as we can compare this to DNA IQ later on when we have a bit more information from this). They thought it would be interesting to look at Cells and NUCC from these and the range of results we obtain and likely hood of obtaining a profile.

Thanks

megan

Idea for stats assignment

Alanna Speirs <[redacted]>

Wed 5/12/2007 3:42 PM

To:Paula Taylor <[redacted]>

Hey Paula,

My idea is this...

to compare the first run success rate of chelex with DNAIQ extraction.

I would probably want to focus on a fairly narrow sample type, so perhaps straight blood extractions. Or straight cell extractions. Or NUCC extractions compared to IQ cell.

The idea of focussing on the first run success rate is to keep it simple for me and to help estimate the costs of the processes, assuming that most unsuccessful samples will undergo some sort of rework.

I am open to ideas!

Alanna

12

Fwd: DNA IQ docs

Vanessa Ientile <[redacted]>
Wed 24/10/2007 11:42 AM

2 attachments (630 KB)
DNA IQ FSS Factsheet.pdf; 24897R0.doc;

P3

Good morning everyone

A Go Live date for the Extraction automated platforms has been set and we are ramping up to prepare for this.

The Analytical and Automation teams will start using both platforms for casework extractions from Monday the 29th October. Initially as training both in Analytical and other areas is running, the samples will mainly be some of the backlog samples. I would also expect that we will not reach full capacity on these platforms until the new year.

As you would be aware, only Blood and Cell extractions will be run on the new platforms at this stage and this excludes tapelifts.

I understand there are discussions underway about when Major Crime team will commence sampling in the new size format and I would expect this to be in place within the next few weeks.

One of the other areas for us to address is to ensure that all staff have an understanding of the new protocol and the underpinning knowledge of the DNA IQ system. This is especially critical for all reporting scientists.

→ no inclusion of reporting scientist.

Attached is the SOP now active in QLS and a Fact Sheet prepared by Iman. Please read both of these and ensure you are familiar with them.
A training module has also been developed and is currently being put into the new format. Once this is done is will be activated in QLS.

] fact sheet misleading

I expect that at least all reporting scientists will complete the Part B competency and we'll need to set some timeframes about how this will be able to be achieved.

The other action that will be scheduled is a briefing session provided by the Automation team where we will go through in detail the validation report. This will include what was done in the evaluation phase, validation of the manual process, the verification of the automated process and all work done to ensure no cross contamination occurs on the platform.
At this stage, I would like attendance at this workshop to be mandatory for all reporting scientists but of course would like it if as many people as possible attended.

The last thing I wanted to mention was to clarify the use of the 2 platforms designated "A" and "B". At this stage only casework extractions are going live, FTA processing will remain as is for the moment. Both instruments will be utilised for casework.

While casework and reference batches will continue to be extracted separately, I would expect that both platforms at times will be used to do either. This is due to the workload of outstanding casework samples requiring extraction and also in case of any instrument downtime.

The automation team has done an enormous amount of work to get us to this stage and the implementation of these platforms is a major milestone, so I would appreciate everyone getting on board and assisting to make this transition successful. That being said, if anyone has any questions they don't feel are being answered or if there are any suggestions on how to improve the implementation process, I would be more than happy to listen to them and act.

Jo Veth testimony
o about using for ref samples.

Regards

Vanessa

Vanessa Ientile
Managing Scientist

Another record week

Allan McNevin <[redacted]>
Mon 3/12/2007 12:24 PM
To:Emma Caunt <[redacted]>
Hello all,

Just for your interest, Analytical have had another record week last week - 1150 samples through Extractions (that's samples completed in AUSLAB), the previous high was 1104 on the week starting 29/10. This would not have been done without the invaluable help of the Automation team.

Cheers
Al

Allan McNevin
Senior Scientist - Analytical Section
DNA Analysis (Forensic Biology)
Forensic & Scientific Services
Queensland Health

Phone: [redacted]
Email [redacted]

Through put became the measure of success

V.

Another Record Week!

Allan McNevin <[redacted]>
Mon 14/04/2008 12:16 PM

To:Emma Caunt <[redacted]>;Shannon Merrick <[redacted]>

Hi all,

I just want to highlight the amazing work that the Analytical team does :-

we have had another record week - 1178 extraction completed last week - special thanks to all the team members who came in and chugged through over a 100 microcon's on the weekend

cheers
Al

Allan McNevin
Senior Scientist - Analytical Section
DNA Analysis (Forensic Biology)
Forensic & Scientific Services
Queensland Health

Phone: [redacted]
Email: [redacted]