EXTRACTION BATCH CONTAMINATION

Batch: [redacted]

Contaminated profile:

- Position No: 65
- Lab No: [redacted]
- Case No: [redacted]
- Case details: Sexual Assault
- Profile details: An incomplete mixed DNA profile was obtained with an indication of two contributors. This profile could be separated into major and minor DNA profiles. The major DNA profile which was incomplete matched the reference DNA profile from the complainant, where information was obtained. The minor DNA profile was incomplete and matched the DNA profile from 320126522 (LVS swab:[redacted]) where information was obtained.

Contaminating profile:

- Position No: 50 or 51,52 (mixed) (posn 49 PP, Quant 4.3, diluted)
- Lab No: [redacted])
- Case No: [redacted]
- Case details: Alleged Sexual Assault
- Profile details: Female DNA profile obtained from LVS, Vulval, Labial swabs matching the reference sample from Emma Rose DEVLIN.

Notes:

- These cases appear to be unrelated.
- The mixed DNA profile was unexpected in the former case.
- There does appear to be another instance of obvious/detectable contamination on this extraction batch. This sample also appears to have contaminated positions 53,55,56,57 which have been pooled and reported under lab number [redacted]). This also appears to be an unrelated 'blue' case.
- Spin baskets will be re-extracted and re-sampling of exhibits where possible will be conducted.
- Suggest NSD/PP profiles on this batch be reworked to determine whether further contamination has occurred involving other cases.

Investigation:
This OQI relates to potential contamination of the following samples [redacted],

[redacted] by one of samples [redacted] during the processing of extraction batch [redacted] Samples [redacted] were subsequently pooled after initial extraction and processed under lab-number [redacted] It is this lab-number that was identified as being contaminated. During the investigation, the stored lysate and stored substrate for all ten samples were re-extracted. The results from the original extraction and subsequent re-extractions were analysed using GeneMapper ID-X software with a peak detection threshold of 20RFU to gain the most information.

The re-extraction of the stored lysate (i.e. lysed material retained after removal from the para-magnetic resin during the automated DNA IQ extraction process) for sample [redacted] showed the same profile as that obtained from the profiling of sample [redacted] (the sample containing the pooled extracts). The lysate re-extractions for samples [redacted] showed DNA profiles consistent with the profile obtained from pooled sample [redacted] with the contaminating alleles removed. The re-extraction of the stored substrate (i.e. the material originally submitted for DNA extraction that had passed through the initial off-deck lysis step of the original extraction process) for each of the four samples all gave a mixed DNA profile matching the lysate profiles of [redacted], again consistent with the profile obtained from pooled sample [redacted] with the contaminating alleles removed.

The re-extraction of the stored lysate & stored substrate for samples [redacted] all gave profiles consistent with the original extraction results. This then indicates that contamination of [redacted] has occurred at some step of the process between the manual processing of the substrate during off-deck lysis and prior to or during the removal of the lysed supernatant from the para-magnetic resin during the automated extraction procedure. Contamination of the pooled DNA extract sample [redacted] has occurred by combining the contaminated DNA extract [redacted] with uncontaminated [redacted].

The re-extraction of the stored lysate & stored substrate for sample [redacted] gave differing results. The stored lysate yielded a mixed DNA profile consistent with that obtained from the original extraction. The stored substrate yielded a single source profile consistent with one of the contributors to the mixed profile initially

obtained. The other contributor to the mixture was consistent with profiles obtained from samples [redacted]. This then indicates that contamination of [redacted] has occurred at some step of the process between the manual processing of the substrate during off-deck lysis and prior to or during the removal of the lysed supernatant from the para-magnetic resin during the automated extraction procedure.

The re-extraction of the stored lysate for sample 342281906 gave 6 alleles, these were consistent with the two alleles obtained from the initial extraction. Neither of these alleles were consistent with the contaminating profiles. The re-extraction of the stored substrate gave no DNA. This would indicate that no contamination of sample 342281906 has occurred.

The potential steps at which contamination may have occurred are:

1. During the transfer of the lystate obtained from manual lysis into the deep-well plate via the use of the STORstar. This is unlikely as staff are trained to perform such steps with due diligence and care. This is also unlikely in the case of sample 333846478 as there is a full column separating this sample and the proposed contaminating sample.

Due to character space limitations, the investigation is continued in Action below.

2. Seepage of sample into an adjacent well (e.g. contamination of sample [redacted] by sample [redacted]) during cold storage of the lysed material in the deep-well plate. After the cessation of processing and the carrying out of investigations, it was noted in one instance that a heavily blood-stained lysate had condensed on the underside of the adhesive seal used to seal the stored plate. This had seeped across into an adjacent well. This was possibly due to insufficient application of the adhesive seal to the interstitial barrier. This mechanism is unlikely for sample [redacted] due to the wells not being adjacent.

3. During the removal of the adhesive seal. It was noted during Audit 8227 that condensation on the underside of the adhesive seal was not removed after centrifugation. Given that two contamination events have occurred (most likely contamination of samples [redacted] & [redacted] by sample [redacted] in a left-to-right manner, this scenario seems most likely.

4. Operator error during the manual addition of DNA IQ para-magnetic resin during the start of the automated extraction procedure (i.e. incorrect pipetting procedure), however this is unlikely as staff are trained to perform such pipetting steps with due diligence and care. This mechanism is unlikely for sample [redacted] due to the wells not being adjacent.

5. During the mixing of the deep-well plate (containing 1.5mL of buffers and resin within a 2.2mL well) on the extraction platform DPC shaker. This had not been observed, however has been proposed a possible mechanism for adjacent well contamination during close scrutiny of the automated procedure. This mechanism is unlikely for sample [redacted] due to the wells not being adjacent.

6. During the lysis removal from the para-magentic resin to the storage plate. This procedure occurs twice during the automated extraction protocol (fresh disposable tip for each step). If there was drippage of the lysate containing unbound DNA and this was to drip from one well to another well this may account for the contamination event. The same mechanism may occur where a bubble forms at the end of the pipette tip and bursts whilst still in the vicinity of another well.

Action:
As a result of previous OQI's raised and concerns identified around the automated DNA IQ extraction process, the extraction of samples using the automated DNA IQ procedure was halted on the 28-7-2008.

Prior to this, Audit 8227 had been commissioned and carried out. A number of areas for improvement were identified through the audit, and these have been implemented or are under investigation as outlined in OQI's 20367, 20368 and 20369.

After the cessation of the automated DNA IQ extraction protocol, a review of all batches processed through this protocol was carried out by a specially commissioned team. A number of potential contamination events were identified and each is to be investigated on batch-by-batch basis.

Additionally, careful review of results obtained from samples processed through the automated DNA IQ extraction procedure prior to reporting will be carried out. Every DNA result obtained from these samples will be interpreted with caution.

Modifications have been made to the automated DNA IQ extraction procedure (including the use of an alternative to the adhesive seal and an alternative resin mixing procedure). This modified procedure is undergoing extensive verification and approval from the DNA Analysis management team must be obtained prior to re-introduction.

The contamination events and concerns and improvements etc. that surround the automated DNA IQ extraction procedure have been discussed at various departmental and team meetings.