Queensland Health
Forensic and Scientific Services

Procedure for Profile Data Analysis using the Forensic Register

1 Purpose

The purpose of this document is to describe the procedure for managing DNA profile results using the Forensic Register (FR).

2 Scope

This procedure shall apply to all Forensic DNA Analysis staff who interpret DNA profile results.

This procedure does not include the guidelines for the scientific interpretation of DNA profiling results. This information can be found in QIS 17117 *Procedure for Case Management*.

Use of the Profiler Plus amplification kit within Forensic DNA Analysis was ceased in January 2018 (Appendix 13 – Profiler Plus). From this date all samples were amplified using the PowerPlex 21 amplification kit.

3 Definitions

To date, the interpretation and management of DNA profile results in Forensic DNA Analysis has been referred to as "Case Management". Within the Forensic Register, the term "Case Management" refers to the management of a case as a whole rather than the individual exhibit results. It is therefore necessary for terminology within Forensic DNA Analysis to be brought in line with the FR. The interpretation and management of DNA profile results will now be referred to as "Profile Data Analysis" and a person who performs Profile Data Analysis will be referred to as a "Profile Analyst".

Forensic Register (FR)	Forensic DNA Analysis LIMS
PDA	Profile Data Analysis
PP21	PowerPlex 21
P+	Profiler Plus
NCIDD	National Criminal Investigation DNA Database
CX	Complex unsuitable
NP	No profile
PU	Partial unsuitable
ST	Sub-threshold peaks
PRT	Profile Record Table
CPT	Case Profiles Table
GM	GeneMapper IDX
WL	Worklist
DNAIntel	Person sample profiles with the descriptor "DNA Person Sample Intel"
AC	Assumed contributor
UK	Unknown (a profile that does not match to a reference or DNAIntel sample)
Epg	Electropherogram

4 Worklists

There are a number of worklists to direct the workflow of samples that require interpretation, review or STRmix analysis. These lists are summarised in Table 1 below. Also refer to Appendix 2 – Profile Data Analysis (PDA) Worklists (Crime Scene).

To access these lists, the profile analyst / reviewer needs to navigate to the sample management pages of the FR. This can be done by entering 'sm' into the global search field of the primary case management page.

If a sample has populated a crime scene PDA list but one or more batches are under investigation then the 'GMIDx' column will display 'INV' and the sample will be greyed-out at the bottom of the list. Once all batches are completed the sample will appear as normal to the appropriate place on the list.

To action exhibits that are no longer required, refer to QIS 34006 – see Appendix 7. Whilst to action samples with no DNA detected or DNA insufficient for further processing results, refer to QIS 34064.

Table 1 – Worklists

Worklist	Sub-list	Purpose	Population triggers	Removal triggers	Default filter	Additional optional filters
Profile Data Analysis	Reference	Reference sample analysis	CE batch passed; QFLAG passed; profile PDF uploaded and a reader comment that doesn't trigger an auto-rework	Profile copied down or rework ordered	Date & time of receipt	ALL OK EVDRW FTP LINK UK INV
	Case Work PP21	PP21 profile data analysis (Priority 1 and 2 samples)	CE batch passed; QFLAG passed; profile PDF uploaded	Rework ordered; 'STRMix' technique (worklist) ordered; 'Profile Review' test ordered	1. User is PDA analyst 2. User is Reporter 3. Priority 1 then 2 4. Date & time of receipt 5. Samples with batch at investigation (INV)	ALL SS MIX COMPLEX UNDEFINED INV ENV
	Case Work PP21 (P3)	PP21 profile data analysis (P3 samples)		Rework ordered; 'STRMix' technique (WL) ordered; 'Profile Review' test ordered		
	Case Work UK CE	Profile data analysis of samples with unknown chemistry (dilutions and cut-over samples)		Rework ordered; 'STRMix' technique (WL) ordered; 'Profile Review' test ordered		
	Case Work + Ref	Profile data analysis of completed samples where new reference samples have been received	Casework sample adds to list if: 1. Ref newly associated to case 2. Ref comment is 'OK' and PDF uploaded 3. PDA results for casework sample are validated	'Profile Review' test ordered	1.User is PDA analyst 2. User is Reporter 3. Priority 4. Date & time of receipt	

			4. Casework sample is 1, 2, 3 or 4 contributors			
Profile Review	Case Work PP21	PP21 profile review (P2 samples)	'Profile Review' test ordered	'Profile Review' test incorrected, validated or 'Click to Rework' selected	1. User is Reviewer 2. Priority 3. Date & time of receipt	ALL SS SSNCIDD MIX MIXNCIDD COMPLEX PATERNITY ENV (except Case Work + Ref list)
	Case Work PP21 (P3)	PP21 profile review (P3 samples)				
	Case Work Unknown	Review of profiles with unknown chemistry (dilutions and cut-over samples)				
	Case Work +Ref	Profile data analysis of completed samples where new reference samples have been received				
STRmix		STRmix analysis request	'STRMix' technique (WL) ordered	'STRMix' test ordered	Date & time of receipt	None
Awaiting Review	STRmix	STRmix analysis allocation and completion	'STRMix' test ordered	'STRMix' test validated	Date & time of receipt	None
Interim DNA Results		Profile data analysis or review of interim results	'-interim' suffix in Profile Record Table	Same profile copied down into Profile Record Table with a suffix other than '-interim'	1.User is PDA analyst 2. Priority 3. Date & time of receipt	None

For additional optional filters, it is possible to request more through the FR provider if a specific workflow requirement is identified. For example, an OQI filter for samples affected by a specific adverse quality event.

5 Basic Functions of the PDA Page

The PDA page is split into five main sections:

- Exhibit Detail – provides relevant information about the sample
- Profile Analysis – provides batch information including volumes. Where GeneMapper IDx information and STRmix import files can be obtained
- Profile Interpretation – used to record basic interpretation information and STRmix deconvolution. Where auto-add result lines can be generated
- Profile Record – used to record single source profiles and contributors resolved from a mixture. Also used to record profiles for upload to NCIDD

- Case Profiles – used to record all associated reference samples, reference sample comparisons and unknowns for a case

Other functions on the page are as follows:

 This icon is found in the top right hand corner of the page. From here STRmix report files (in PDF format) can be added. Clicking this icon will open the 'STRmix File Import' page. The scientist can drag the required files into the box (or browse by clicking 'Add Files') and click 'Start Upload'. Once the upload is complete, click the save icon () and the STRmix files will be filed in the Profile Interpretation section of the PDA page. Also refer to Section 12. The STRmix PDF must have the following naming convention:

- For a deconvolution 'QPxxxxxxxxxx_yyyyyyyyy' where 'xxxxxxxxx' is the QP number and 'yyyyyyyyy' is the crime scene sample barcode
- For a LR 'QPxxxxxxxxxx_yyyyyyyyy_LRPrev_1_zzzzzzzzz' where 'xxxxxxxxxx' is the QP number, 'yyyyyyyyy' is the crime scene sample barcode and 'zzzzzzzzz' is the reference sample barcode

 This icon is found in two places on the page:
In the top right hand corner – clicking this icon **will change between the PDA page and the** Exhibit Testing / Movement page
Above the Case Profiles table – clicking this icon will produce a profile table for all reference samples and unknowns in the case. This table will default to the kit type used for the processing of the sample. This can be changed between P+ and PP21 by clicking on [P+] and [PP21] underneath the table. Clicking [P+ All] or [PP21 All] will display all profiles in the case that have been entered into the Profile Record table

 This icon is found in the top right hand corner of the page. Clicking on this icon will open a new window containing the GeneMapper® record for all CE runs for the sample. The information in this record is the same as that detailed in Section 6.2 however it does not contain the height and size columns. All epgs can be opened from this window either individually by clicking on the relevant PDFs or all at once by clicking on 'Open All'

 This icon is found in the top right hand corner of both the PDA page and Exhibit Testing / Movement page. Clicking on this icon utilises a built in 'PDA Robot' designed to check all results lines entered for a sample against the completed information in the PDA page. A new window opens and any discrepancies are highlighted with a red cross showing anticipated result lines versus entered result lines. These potentially incorrect results should be investigated prior to PDA review (Section 18).

 This icon is found above the Profile Interpretation table. Clicking on this 'Add Results' icon generates the exhibit result lines for a sample (only three lines at a time) based on the completed information in the Profile Interpretation, Profile Record and Case Profiles sections of the PDA page (Section 18).

 This icon is found above the Profile Analysis table. Clicking this icon will allocate the sample to the scientist clicking the icon and their name will populate to the left of the icon. If a second scientist were to subsequently click this icon, then the sample will be allocated to this scientist in place of the first scientist. Once a sample is allocated it cannot be unallocated, it can only be reallocated to another scientist.

 This icon is found above the Profile Analysis table and is used to enable the page to be edited.

This icon replaces the edit icon when enabled and is used to save changes made to the page.

The Sample Notes section can be used to record auditable notes against a sample.

6 Profile Analysis Table

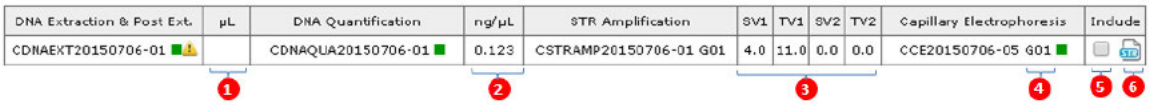


Figure { SEQ Figure * ARABIC } – Profile Analysis Table

1. Volume post extraction – applies to microcon batches only
2. Quantification value (short fragment)
3. Amplification volumes
4. CE batch position – click here to access GeneMapper Record (Section 6.2)
5. Check box to show that this run is to be included in STRmix analysis
6. Click to export STRmix input file for this run

Hovering over the quant value will display a pop-up box with all of the Quant Trio results (Figure { SEQ Figure * ARABIC }).

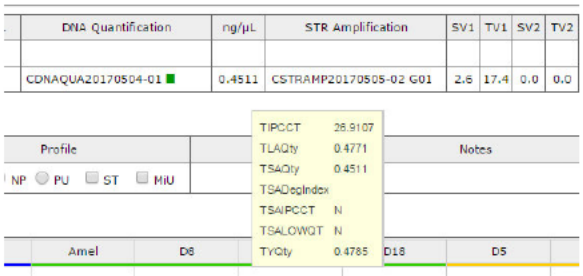


Figure { SEQ Figure * ARABIC } – Quant Trio Values

6.1 Quality Control

When entering into a sample to interpret the results, the first action by the scientist is to check the quality markers of the batches associated with the sample.

The 'Profile Analysis' table (Figure 1) details all of the batches that a sample has been processed on. Each batch will have a quality marker in the form of a coloured square. The colour of the square indicates the status of the batch as follows:

Red = batch failed
Orange = batch in progress or under investigation
Green = batch passed

If there is a ⚠ symbol, this indicates there is a batch comment. Hovering over this symbol or the batch id will show all or part of the comment and the progress of the batch. If the comment is '<3', this means there are less than 3 peaks in a negative control and the comment does not need to be actioned further. If the comment is 'see batch', this means the scientist needs to enter into the batch and read the associated notes to ensure the result for the relevant sample is reportable. The batch notes should be acknowledged as 'noted' in the 'Sample Notes' section of the PDA page.

Quality flags can be acknowledged by the reviewing scientist, provided both entering and reviewing scientists are aware of any critical quality issues.

A batch can be entered into by clicking on the batch id in the Profile Analysis table.

Results should not be reported until all batches have passed and display a green square. However, there are exceptions to this stipulation. For urgent results, the scientist can check all batch notes and any associated control profiles for issues. If no quality issues are identified, the urgent results can be interpreted with notes added to the Sample Notes section accepting all batches. For no DNA detected or DNA insufficient for further processing results, the scientist can interpret these samples once the quantification batches have passed.

6.2 GeneMapper® Record

Clicking on the position number adjacent to the CE batch id will open a new window containing the GeneMapper® record for that CE run (Figure { SEQ Figure * ARABIC }). The 'Alleles (GeneMapper)' column (highlighted in green) displays all of the designations as exported from GeneMapper at the time of plate reading; the information in this column cannot be changed. The 'Alleles' column displays all of the designations as exported from GeneMapper at the time of plate reading and the information in this column can be changed. The 'Height' and 'Size' columns display the peak heights and sizes of the alleles in their respective order.

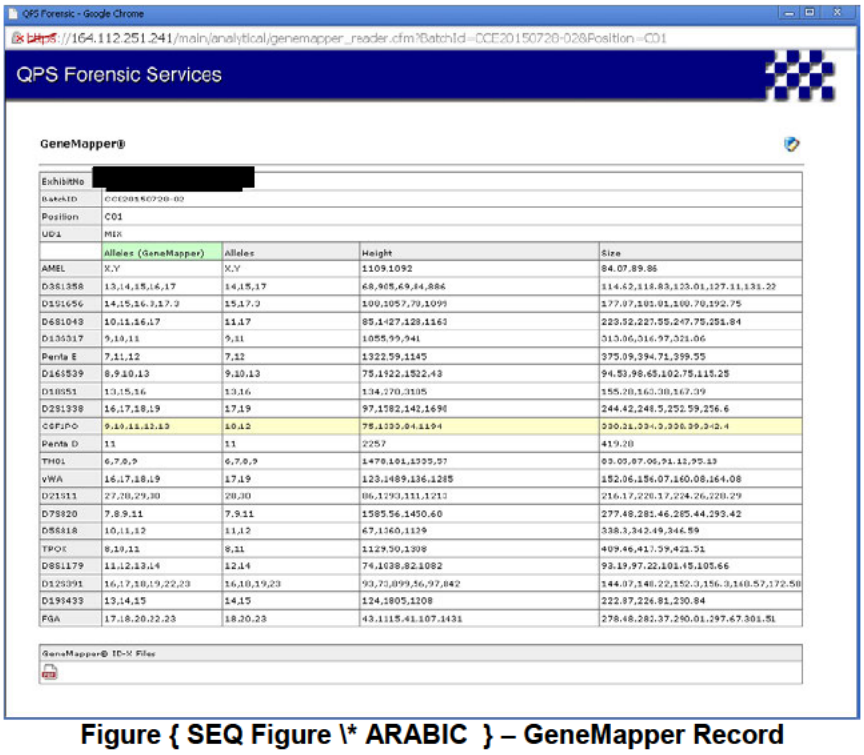


Figure { SEQ Figure * ARABIC } – GeneMapper Record

6.2.1 PowerPlex 21

The following functions apply to this page:

1. In the default view, the 'Alleles' column shows the allele designations only, the stutter peaks are hidden from view. Clicking the edit button ( ) displays the stutters as well

as the alleles. Clicking the save button ( ) reverts to the default view (without stutters). The heights and sizes relating to all peaks (stutters and alleles) are displayed in the 'Height' and 'Size' columns at all times

2. The 'Alleles', 'Height' and 'Size' columns are used to generate the input file for STRmix. These fields can be edited
3. When the record is edited, the line will highlight yellow to show that the record has been changed. The reason for any manual changes should be recorded in the Sample Notes
4. PDFs of the epg can be accessed from the 'GeneMapper ID-X Files' box at the bottom of the window

6.2.1.1 Removing Peaks from PP21 Profiles

On occasion a peak may be left on the profile by the plate reader in error, such as a -2 repeat stutter peak or an artefact peak (QIS 34112). This peak can be removed from the GeneMapper Record by the following process:

a. Click the edit button ( )
b. Delete the allele in question along with the respective height and size
c. Click the save button( )

It is important to ensure that the correct height and size is removed. Following the removal of the peak, only the non-zoomed epg needs to be updated / annotated and uploaded into the FR. This can be done as described in Appendix 3 – Amending PDFs, alternatively the peak can be removed in GeneMapper and the epg re-PDF'd. Add a sample note detailing the amendment.

6.2.1.2 Adding Peaks Back on to PP21 Profiles

On occasion a peak may be removed from the profile by the plate reader in error. In order to add the information back into the GeneMapper Record it is necessary to obtain the correct allele designation and its associated height and size from GeneMapper. The Profile Analyst must add the peak onto the profile using GeneMapper and re-PDF the epg ensuring that the alleles are labelled with the allele designation, the height and the size of the peak. This is required so that the reviewer is able to easily check this information from the epg. This peak can be added to the GeneMapper Record by the following process:

a. Click the edit button ( )
b. Enter the allele into the alleles column ensuring the alleles are in number order and are separated by a comma
c. Enter the height into the height column ensuring that it is in the same position as the allele, e.g. if the allele is the second entry in the 'alleles' column, the height must be the second entry in the 'height' column
d. Enter the size into the size column ensuring that it is in the same position as the allele and height
e. Click the save button( )

The new non-zoomed epg must be uploaded into the FR as described in Appendix 3 – Amending PDFs. Add a sample note detailing the amendment.

7 Profile Interpretation Table

The Profile Interpretation table is where the number of contributors, STRmix deconvolution including resolved alleles and simple interpretations for a DNA profile can be recorded. The notes section within this table is for reminders only since the entries within this section are not recorded in the audit trail. An example of when this notes section might be used is to remind the scientist to look at a particular locus when the rework is completed. Since it is expected that the majority of profile data analysis will be paperless, this section is analogous to using a sticky note in a case file.

7.1 PowerPlex 21

Figure 1 – PP21 Profile Interpretation Table

1. This section is used to record the number of contributors to a profile
2. With the exception of ST, this section is used to record interpretations that don't require any further action:
   a. CX is to record a profile that is a complex mixture and is unsuitable for further interpretation
   b. NP is used to record a no profile result
   c. PU is used to record a profile that is partial and unsuitable for further interpretation
   d. ST can be used in conjunction with the number of contributors or NP to record that there are also sub-threshold peaks within the profile
3. When a STRmix deconvolution PDF file is uploaded (Appendix 6 – STRmix Workflow), a PDF icon will be displayed. Clicking on this icon will download the PDF
4. Notes section (not audited)

When a STRmix deconvolution PDF is uploaded into the FR the individual contributions will be displayed at the bottom of the Profile Interpretation Table (Figure { SEQ Figure * ARABIC }).

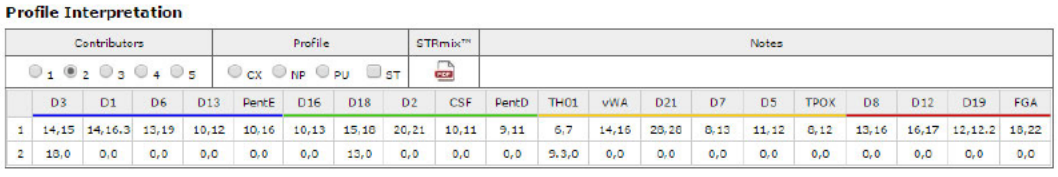


Figure { SEQ Figure * ARABIC } – Profile Interpretation Table with Mixture Contributions

8 Profile Record Table

The FR contains a database of profiles from various sources including casework and reference profiles, staff profiles and elimination database profiles and person sample profiles with the descriptor "DNA Person Sample Intel" (DNAIntel samples). A crime scene profile (single source or resolved component of a mixture) is added to this database when it is entered into the Profile Record table and the record saved. A profile can be added to the table manually as well as by a process called 'copy down' from the GeneMapper Record, a STRmix results file or a combination of 'copy down' followed by manual edit (Section 8.3.2 and Appendix 4 – Profile Data Analysis of a Single Source PP21 Profile for NCIDD).

When entering a profile each locus must have two alleles separated by a comma and missing alleles must be represented as a zero '0'. 'NR' is not recognised in this table and should not be used. Amelogenin must be represented as 'X,X'; 'X,Y'; 'X,0' or by leaving the field blank. 'X' on its own must not be used as this is not recognised by NCIDD.

The Profile Record table can be cleared whilst in edit mode by clicking the icon. This will delete all records in the table that have not been validated. Clicking the 'CLR' button above the Profile Record table will clear the entry that has been made in the same edit.

The '+NCIDD' box (see ❹ in Figure 10) enables the scientist to nominate the profile for upload to NCIDD.

A suffix should be selected for all profiles copied down into the Profile Record table to describe the profile type (see ❸ in Figure { SEQ Figure * ARABIC }). If the profile is nominated for NCIDD, this is the suffix that should be used for NCIDD.

Refer to Section 8.3.1 and Section 9 for a description of the '+CPT' box.

The following profiles MUST be recorded in the Profile Record table:

- All single source profiles with ≥ 12 alleles;
- All resolved components of mixed profiles with ≥ 12 alleles;
- Single source profiles with <12 alleles where the profile is able to be matched / designated (one sample per case);
- Resolved components of mixed profiles with <12 alleles where the component is going to be matched / designated (one sample per case), e.g. PP21 two person conditioned mixture where the remaining consists of 7 alleles and is being designated as UKM1
- All conditioned components of mixed profiles

Unresolved mixed profiles should not be recorded in the profile record table.

The Profile Record table should be completed for a single contribution in one action as once the record is saved it can only be edited by deleting the whole record (by clicking the button whilst in edit mode).

8.1 FR Database Matching

If a profile entered into the Profile Record table consists of ≥12 alleles, clicking the icon (❺Figure 10) will cause it to be searched against the FR database for possible matches in the following order:

1. Staff elimination database (Forensic DNA Analysis staff, QPS staff and FBUNKs)
2. Reference samples within the case
3. DNAIntel (reference) samples external to the case
4. Unknown profiles within the case

If a match is obtained it will be displayed in the match cell below the profile (❺). The matching rules allow one mismatch with the number of matching and mismatching alleles being displayed in brackets in the match cell; the first number is the number of matches, the second number is the number of mismatches.

If a match to the staff elimination database occurs, refer to QIS 34281 for required action.

If the scientist agrees with the match nominated by the database then the designation can remain, if the scientist does not agree with the match the scientist can overwrite the match information.

If a partial profile is copied down and a match to a reference sample is displayed, the scientist may have additional information (such as sub-threshold peaks) that excludes that person as being a match. In this instance the scientist may decide that the profile is unknown and overwrite the match information with an unknown designation in the format described below.

If a partial profile is copied down and no match to existing profiles is displayed, the scientist needs to be aware that if there are less than 11 matching alleles, it is possible for a match to an existing partial profile to be missed by the FR (Figure 6). In this instance the scientist can manually add the match information to the Profile Record table (i.e. remove the FR generated designation and replace with the designation of the matching profile).

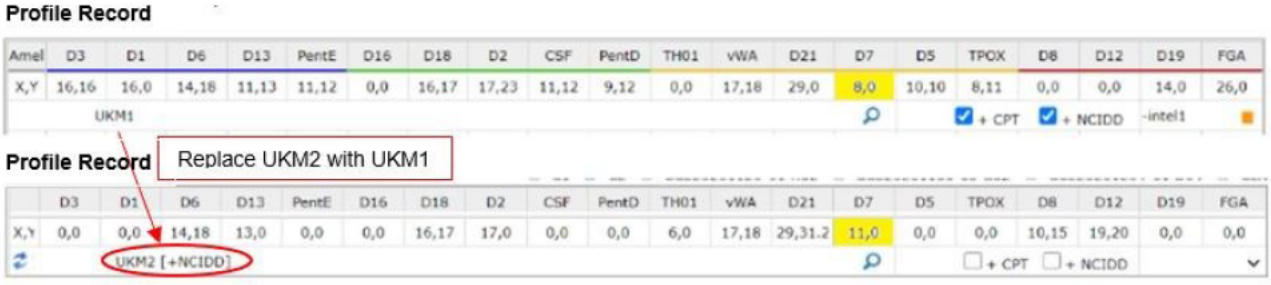


Figure 2 – Partial Profile Matching in the Profile Record Table

If no match is obtained, the FR will suggest the next unknown designation available for use in the case. This means that if a previous profile in the case has been designated as unknown male 1 (UKM1), the FR will suggest the next unknown male profile be designated UKM2.

Although this matching function is of assistance to the scientist, this does not override the requirement for the scientist to check the match through the comparison of epgs.

Profiles consisting of <12 alleles will not be searched and will populate the match cell with its own exhibit barcode. The designation for this profile should be entered manually into the match cell (❺) in the following format:

- If the designation is new the format is xxxxxxxxx UKyz (where 'xxxxxxxxx' is the barcode of the sample being interpreted; 'y' is 'M', 'F' or 'P' representing male, female or person respectively; 'z' is the number of the unknown designation). There should be only one space between the barcode and the designation
- If the designation is pre-existing (either an unknown, a named individual or DNAIntel) then the barcode and name / designation should be copy and pasted from the CPT with a space in between the barcode and the name / designation (Figure 7).

Figure 3 – Pre-existing Designation

8.2 Nomination for Upload to NCIDD

When a search against the FR database has been performed (≥12 alleles), the FR will highlight whether a profile / component should be considered for upload to NCIDD as follows:

1. If the profile / component matches to a reference sample in the case and a representative profile has not been nominated for upload to NCIDD, then '[+NCIDD]' will appear in the match cell (Figure 8);
2. If the profile / component is a new unknown for the case or a representative profile of the unknown has not been nominated for upload to NCIDD, then '[+NCIDD]' will appear in the match cell;
3. If a representative profile has previously been nominated for upload to NCIDD and the current profile / component would be a better upload then '[+NCIDD [Replace xxxxxxxxx-yy]]' will appear in the match cell (Figure { SEQ Figure * ARABIC }) where 'xxxxxxxxx' is the barcode of the sample requiring replacement and 'yy' is it's associated suffix. Refer to Section 9 for guidance on replacing a NCIDD upload with a better profile.

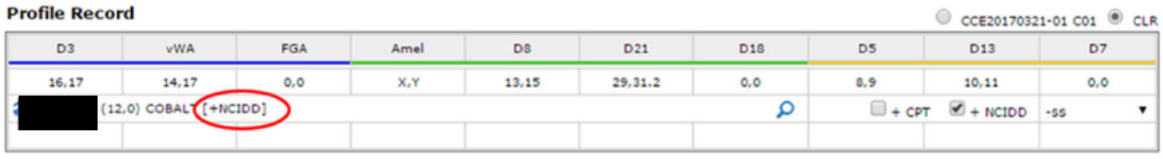


Figure 4 – NCIDD Indicator

Figure { SEQ Figure * ARABIC } – Replace NCIDD Indicator

8.3 PowerPlex 21

When a DNA profile is obtained that is either single source or one or more contributions are able to be resolved then the Profile Record table is to be completed as per Section 8. Upon review these resolved profiles will be added to the FR database as a record of profiles that have been obtained for this sample. For a PP21 profile, an allele or genotype is considered to be resolved if it has a weighting of ≥ 99% from the STRmix deconvolution.

Clicking the edit icon on the PDA page will enable the Profile Record table to be edited. The profile can then either be entered manually or 'copied down' from the resolved contributions in the Profile Interpretation table or the GeneMapper file (❶ Figure { SEQ Figure * ARABIC }) by clicking on the appropriate circle. If required, the CLR button (❷) will clear the profile entered. If there is more than one GeneMapper file for the sample then there will be the option to choose which result to copy down (distinguished by the CE batch id).

The suffix list (❸) records the type of profile for identification of individual contributions in NCIDD (Table 2). A suffix should be selected for every profile / contribution that is copied down into the Profile Record table. If there are multiple resolved contributions from a mixture, the FR will automatically number this suffix.

If a profile requires upload to NCIDD then a NCIDD process is automatically ordered for each nominated upload (Section 11.1.1).

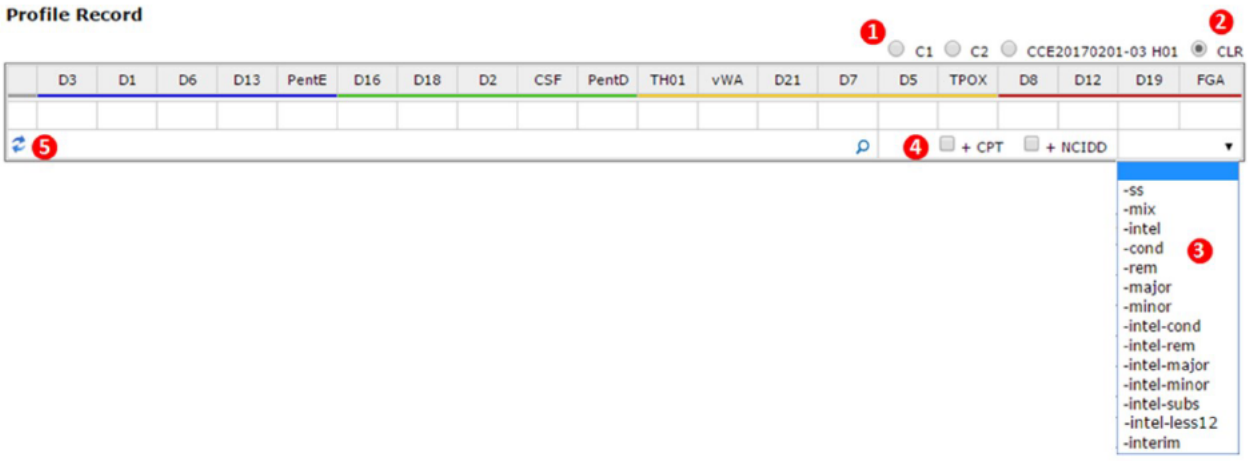


Figure { SEQ Figure * ARABIC } – PP21 Profile Record Table

8.3.1 Single Source Profiles

For important procedural information, refer to Appendix 4 – Profile Data Analysis of a Single Source PP21 Profile for NCIDD.

Single source profiles can be copied down in the following ways:

- By selecting 'C1' (❶ Figure { SEQ Figure * ARABIC }) if a STRmix deconvolution has been uploaded. In this instance the scientist will need to complete the 'Amel' box manually with 'X,X', 'X,Y', 'X,0' or leaving the field blank
- By selecting the appropriate CE batch (❶) if a STRmix deconvolution has not been uploaded. In this instance, any loci that have only one allele will be assigned the values "allele,0" to represent the inability to designate a locus as homozygous without STRmix. Stutter peaks may need to be removed.
- By entering the profile manually

Before saving the record, the scientist will click the icon (❺) to commence searching.

If the profile is ≥ 12 alleles then the FR will suggest a designation / match for the profile (refer to Section 8.1 for further details). If the scientist does not agree with the match / designation proposed by the FR database then the scientist must replace it with the correct match / designation in the format described in Section 8.1.

If the profile is <12 alleles then no designation / match will be suggested by the FR and the match cell (❺) will populate with the barcode of the sample. The scientist must enter a designation / match manually in the format described in Section 8.1.

If the profile is required to be loaded to NCIDD then the '+NCIDD' box (❹) should be checked and the '-ss' suffix selected from the drop-down list (❸). If the profile consists of <12 alleles then the '-intel-less12' suffix is to be used. Profiles consisting of <12 alleles are only to be loaded to NCIDD in exceptional circumstances and this should be discussed with a Supervising Scientist or above before doing so. In the case that a profile with <12 alleles is to be loaded to NCIDD the Intelligence Team should be notified as the profile will need to be searched in NCIDD manually and added to a search list.

If the profile is not being uploaded to NCIDD then the '-ss' suffix should be selected from the drop-down list (❸).

If the profile is unknown and is not listed in the 'Case Profiles' table then the '+CPT' box must be checked to add the profile to the table.

If a reference sample matches the casework profile and they are an assumed known contributor then the appropriate 'AC' box must be checked in the Case Profiles table (Section 9).

Table { SEQ Table * ARABIC } – Suffix Meanings

Suffix	Purpose	Kit
-ss	Single source component	PP21
-mix	Fully deconvoluted mixture component	PP21
-intel	Partially deconvoluted mixture component	PP21
-cond	Conditioned component	PP21
-rem	Remaining component	PP21
-intel-cond	Conditioned component where the profile is conditioned for intelligence purposes only	PP21
-intel-rem	Remaining component where the profile is conditioned for intelligence purposes only	PP21
-intel-subs	Single source component where sub-threshold peaks are used for intelligence purposes only	PP21
-intel-less12	Single source component with less than 12 alleles	PP21
-interim	Any component that is loaded as an interim measure pending rework results	P1 cases only

8.3.2 Resolved (Fully or Partially) Mixed Profiles

When a profile can be resolved (fully or partially) into its individual contributions, and the STRmix PDF has been uploaded, then each contribution should be recorded in the Profile Record table as per Section 8. This is done as follows:

a. Click the edit icon
b. Copy down the profile by selecting the appropriate contribution
c. Complete the 'Amel' box manually with 'X,X', 'X,Y' or 'X,0'
d. Click the icon (❺ Figure { SEQ Figure * ARABIC }) to commence searching
e. Check / enter the match / designation into the match cell (❺) in the format as described in Section 8.1
f. Check the '+NCIDD' box (❹) if this contribution is required to be loaded to NCIDD (ticking this box triggers the ordering of an 'NCIDD' process when the record is saved)
g. Select the appropriate suffix. If appropriate, FR will add numbering (Table { SEQ Table * ARABIC })
h. Check the '+CPT' box (❹) if this contribution is a new designation for the case
i. Save the record by clicking the save icon
j. If appropriate, repeat the process for the other resolved contributions of the profile (≥ 12 alleles)

When accepting a mixed profile with a labelled stutter peak (below the laboratory stutter threshold) that is presenting in the Profile Record table as an allele because it is above the STRmix stutter threshold, add explanatory notes to the 'Notes' field including any amendments necessary due to uploading to NCIDD.

8.3.3 Complex Profiles

If a profile is considered unsuitable for interpretation, it is not necessary to copy down the result. In this instance only the ○ CX or ○ PU box is checked in the Profile Interpretation table.

The PDA analyst may add notes to the Sample Notes section explaining why the profile has been assessed as complex, particularly if the reasons for this determination are not obvious (e.g. unable to determine the number of contributors or some unusual processing / analysis issue).

8.3.4 Tri Alleles

The Profile Record table should only contain two allele designations. If a tri-allele is obtained, drop the locus and add a sample note stating that a tri-allele is present and all three designations. If the profile is required for upload to NCIDD then the details of the tri allele should be added to the 'NCIDD User Comment' field in the NCIDD process (Section 11.1). This will assist with the investigation of any potential mis-matches on NCIDD.

9 Case Profiles Table (CPT)

This table lists all of the reference samples (including their NCIDD category) associated with a case and can be expanded to include unknown profiles and profiles matching to DNAIntel samples.

All evidence reference samples that are associated to the case, including reference samples that are registered by Forensic DNA Analysis, will populate this table by default.

Unknowns populate the table at the request of the scientist by checking the '+CPT' box in the Profile Record table when an unknown is designated. The barcode in the table relating to the unknown is the barcode of the exhibit from which the unknown originated. If a better profile of the unknown is obtained from another exhibit in the case, the table should be updated by checking the '+CPT' box relating to the better profile and replacing the matching barcode in the match cell with the barcode of the exhibit from which the better profile has been obtained. This will ensure that the barcode of the better unknown profile populates the Case Profiles table.

For example, the exhibit in Figure { SEQ Figure * ARABIC } has the barcode 690153578. You can see that it has matched to UKM1 which has come from exhibit 690153595 (displayed in the match cell of the Profile Record table). Exhibit 690153578 has a better profile for UKM1 than its originating exhibit (690153595). In order to update the profile for UKM1, the barcode in the match cell (inside the red circle) needs to be manually edited and replaced with barcode 690153578. This will enable both the profile and originating barcode for UKM1 to be updated.

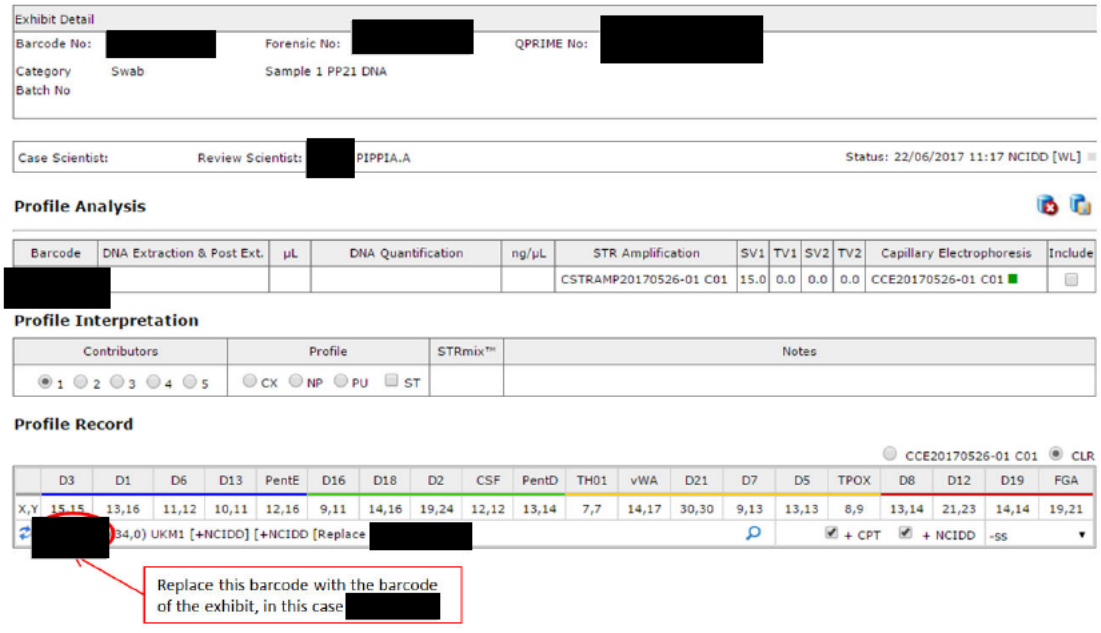


Figure { SEQ Figure * ARABIC } – Updating Unknown Profile in CPT

Any unknown profiles should be added to the Case Profiles table to alert scientists working on other samples in the case that the unknown has been identified.

Profiles matching to DNAIntel samples populate the table at the request of the scientist by checking the '+CPT' box in the Profile Record table when a DNAIntel match is identified.

ALL newly identified unknown profiles and profiles matching to DNAIntel samples should be added to the Case Profiles table.

Clicking on the barcode associated with the reference sample, DNAIntel sample or unknown will open the PDA page for that sample.

Clicking the icon above the Case Profiles table will produce a table in a new window containing the profiles of all of the samples in the Case Profiles table (Figure 12).

Once the table has been produced, the information can be displayed in a number of ways. Clicking [P+] will display the only the Profiler Plus loci, clicking [PP21] will display the PP21 loci. Clicking [P+ All] or [PP21 All] will display all profiles copied down into the Profile Record table for all exhibits in the case in the appropriate format.

A reference sample profile will not populate this table until the reference sample PDA page has been validated. Refer to QIS 34245 for information regarding the profile data analysis of reference samples.

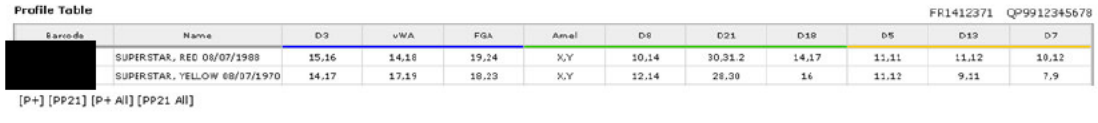


Figure { SEQ Figure * ARABIC } – Profile Table

There are a number of indicators in the category column of the Case Profiles Table (Table 3).

Table 2 – Indicators in CPT

Profile Type	Indicator	Colour	Meaning
Reference sample	Square	Orange	Reference sample is being processed
		Green	Reference sample has been validated
	Triangle	Orange	Crime scene profile matching to reference sample has been nominated for upload to NCIDD
		Green	Crime scene profile matching to reference sample has been nominated for upload to NCIDD and this nomination has been validated
Unknown	Square	Orange	Unknown crime scene profile has been identified
		Green	Unknown crime scene profile has been identified and validated
	Triangle	Orange	Unknown crime scene profile has been nominated for upload to NCIDD
		Green	Unknown crime scene profile has been nominated for upload to NCIDD and this nomination has been validated

If a profile previously designated as an unknown subsequently matches to an associated reference sample or an identified DNAIntel sample, this is documented in the 'Association' column. Whilst in edit mode, the barcode of the matching reference sample can be entered into the association field that accompanies the unknown. In turn the association field that accompanies the matching reference sample will update with the unknown designation. Only the association fields that accompany an unknown or DNAIntel sample are able to be edited. Also refer to Section 14.2.

9.1 PowerPlex 21

The Case Profiles table is used to record the results of reference sample comparisons to all crime scene profiles and to store STRmix PDFs relating to LR calculations (Figure { SEQ Figure * ARABIC }).

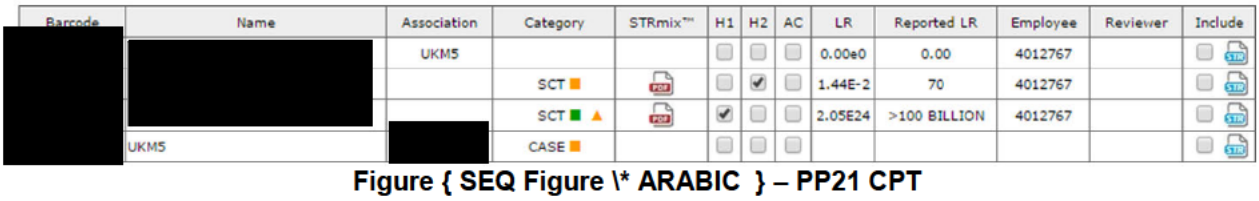


Figure { SEQ Figure * ARABIC } – PP21 CPT

If a STRmix PDF for a LR is loaded into the FR then the LR relating to the comparison of the reference sample will populate the 'LR' box for that reference sample. At the same time the appropriate 'H1' and 'H2' boxes will be checked and the figure will transform into a usable format in the 'Reported LR' box. Alternatively the scientist may enter the LR manually into the 'LR' box in the format described below and the remaining boxes will fill automatically.

A description of the columns used to record the interpretation is as follows:

'H1' – this box is checked if the LR favours contribution
'H2' – this box is checked if the LR favours non-contribution
'AC' – this box is checked if the reference sample is an assumed contributor either for single source profiles or conditioned mixtures (this is a manual function only)
'LR' – the LR in its original form is entered here, this must be in scientific number format to two decimal places, e.g. 1.54e4, 2.63e-7

'Reported LR' – the LR entered into the 'LR' column is transformed by the FR into the format that is required for statement purposes

If the reference sample is an assumed contributor then the scientist should check the 'AC' box. For all other interpretations the analyst is only required to enter the LR in its original form into the 'LR' column. The FR will then check the appropriate 'H1' and / or 'H2' boxes and transform the original number into numbers greater than one as described in the following examples:

LR of 1.10e-4 is entered	→	FR will check 'H2' box to indicate LR favours non-contribution and will populate the 'Reported LR' column with the reciprocal of 1.10e-4
LR of 5.71e17 entered	→	FR will check 'H1' box to indicate LR favours contribution and will populate the 'Reported LR' column with ">100 BILLION"
LR of 1.00e12 entered	→	FR will check 'H1' box to indicate LR favours contribution and will populate the 'Reported LR' column with ">100 BILLION" (single source profile matching to an associated reference sample profile)
LR of 0.00e0 entered	→	FR will not check any boxes but will populate the 'Reported LR' column with "0.00" (exclusion)
LR of 1.00e0 entered	→	FR will check both the 'H1' and 'H2' boxes and populate the 'Reported LR' column with "1.00" (inconclusive)

The LR can be manually edited after a STRmix PDF for an LR has been uploaded. For example, if an LR has been calculated for a reference sample but the analyst subsequently decides the reference sample is intuitively excluded. Entering 0 into the LR column will override the LR and exclude the relevant reference sample.

Unknown profiles are not compared to casework profiles for the purposes of calculating a LR routinely; these calculations are to be performed for P1 samples and at the request of the QPS only. If a LR is calculated for an unknown, the STRmix PDF file is added to a notation and the LR is entered by the analyst.

10 DNAIntel Matching

Person sample profiles with the descriptor "DNA Person Sample Intel" are termed 'DNAIntel samples' and are held in the FR database. When a profile is copied down into the Profile Record table and the search button clicked, this profile will be searched against the FR database as per Section 8.1.

If a profile in the Profile Record table matches to a single DNAIntel sample then this match will be displayed in the match cell (Figure { SEQ Figure * ARABIC }).

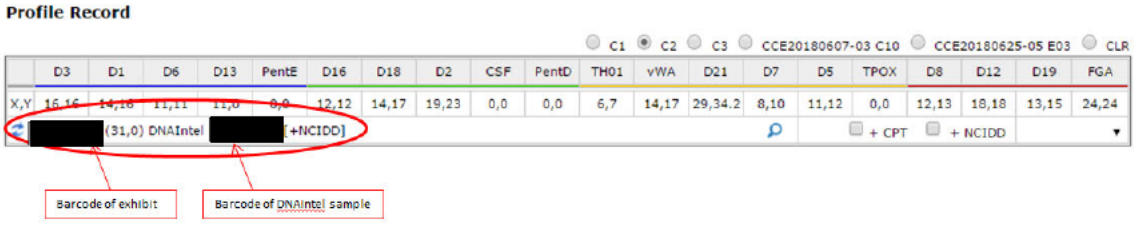


Figure { SEQ Figure * ARABIC } – Match to DNAIntel Sample

If a profile in the Profile Record table matches to multiple DNAIntel samples then the match cell will default to the next unknown designation. Any DNAIntel sample matches can be seen

in a separate table by clicking the button to the right hand side of the match cell (Figure 15).

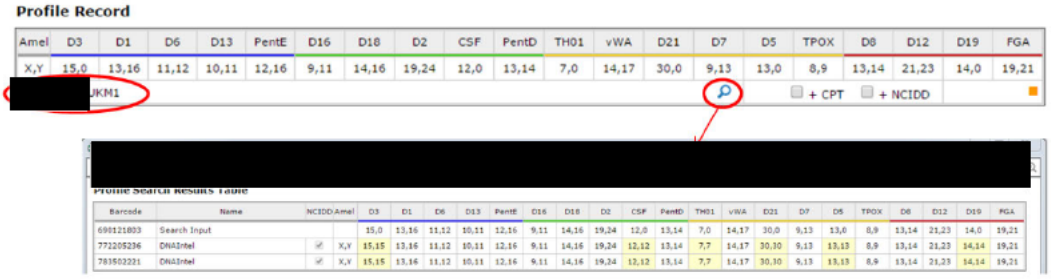


Figure 5 – Match to Multiple DNAIntel Samples

If a profile matches to multiple DNAIntel samples this will not be seen unless the button is clicked as the search will default to the next unknown designation. These DNAIntel matches do not require actioning and the unknown designation can be reported.

If a profile matches to a single DNAIntel sample then this match will be seen in the match cell and the DNAIntel sample profile can be accessed by clicking the button. The profile analyst should compare the DNAIntel sample to the copied down profile of the crime scene sample and the epgs to ensure that there are no exclusions either above or below threshold. It is not necessary to locate the epg of the DNAIntel sample to perform this comparison, it is sufficient to use the allele designations within the table produced by the FR.

If the DNAIntel sample is excluded then the profile analyst should overwrite the information in the match cell with the appropriate match / designation in the format described in Section 8.1.

If the DNAIntel sample is not excluded then the DNAIntel profile should be added to the Case Profiles table (as per Section 9) if it is not there already. This match should then be reported to the QPS via an Exhibit Result line in the same way as an unknown profile, i.e. by using the appropriate line(s) for the interpretation and placing the barcode of the DNAIntel sample in the 'Linked No.' field.

Since DNAIntel samples are reported in the same way as unknown profiles, it is only necessary to report the result to the QPS if the profile is single source or if a component is being uploaded to NCIDD. LR calculations are not required.

In some instances, a DNAIntel match may be obtained part way through the case, i.e. what has previously been reported as UKM1 now matches to a DNAIntel sample. If this occurs, the following process should be followed:

1. Do not update any previously reviewed results
2. For the new sample with the DNAIntel match, in the Profile Record table, tick the '+CPT' box but do not tick the NCIDD box. Click save
3. In the Case Profile table, associate the new sample with the DNAIntel match to the previously reviewed result with UKM1. Add a sample note 'UKM1 = DNAIntel XXX'
4. All samples analysed from this point forward should refer to the DNAIntel match where required

11 Exhibit Testing Table

The Exhibit Testing table is on the Exhibit Testing / Movement page (Figure 16) which can be accessed from the PDA page by clicking the icon in the top right corner of the page.

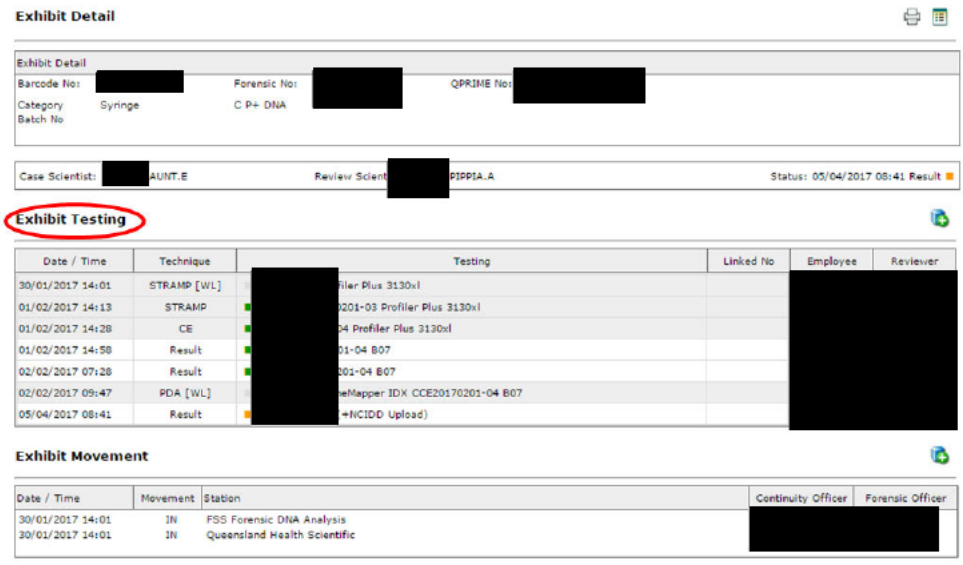


Figure 6 – Exhibit Testing / Movement Page

The Exhibit Testing table records all testing and analyses that have been performed on a sample, all techniques (via worklists) that have been ordered for a sample and all results that have been reported for a sample. The information within the table includes the date and time that the testing was ordered, the type of test and the person that performed / reviewed the test. A test can be added by clicking the add button ( ) which opens the page shown in (Figure 17).

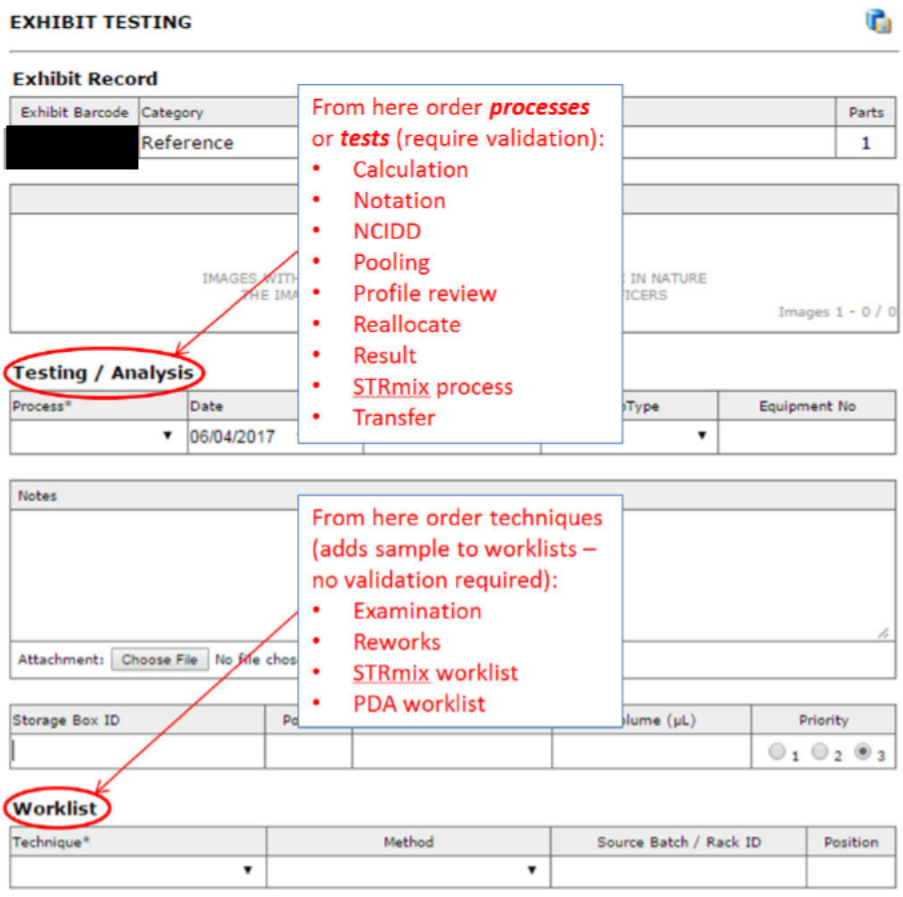


Figure 7 – Page to Order Processes and Techniques

All tests require validation however some tests auto-validate. A test that is awaiting review has an orange box beside it in the exhibit testing table; this box turns green when the review is complete.

Entries in the exhibit testing table that have a grey background represent techniques or worklist / batch list entries. Where applicable the coloured boxes for these entries represent the status of the batch (Section 6.1). Entries in the exhibit testing table that have a white background represent tests that require validation.

If the scientist requires a rework to be performed on a sample, it will be ordered from this page.

11.1 NCIDD

11.1.1 NCIDD Upload

For important procedural information, refer to Appendix 4 – Profile Data Analysis of a Single Source PP21 Profile for NCIDD.

Each crime scene profile / component that is to be loaded to NCIDD must have an NCIDD process ordered. An 'NCIDD' process is ordered automatically when the 'NCIDD' box on the PDA page is ticked and the record is saved (Section 8.3.2 and Figure 4 – NCIDD Indicator).

If necessary, an NCIDD process may be ordered manually as follows:

1. Select 'NCIDD' from the 'Process' drop-down menu (Figure 18)

2. Select 'Upload' from the 'NCIDD Method' drop-down menu
3. Enter the suffix of the profile / component to be uploaded in the exact same format as it is in the profile record table after the barcode number that is already present in this field
4. If required, enter any tri-allele information
5. Click the save icon to save the record
6. Upon validation by the reviewer, this request will automatically populate the NCIDD worklist
7. Repeat this process for all profiles / components to be uploaded for the sample

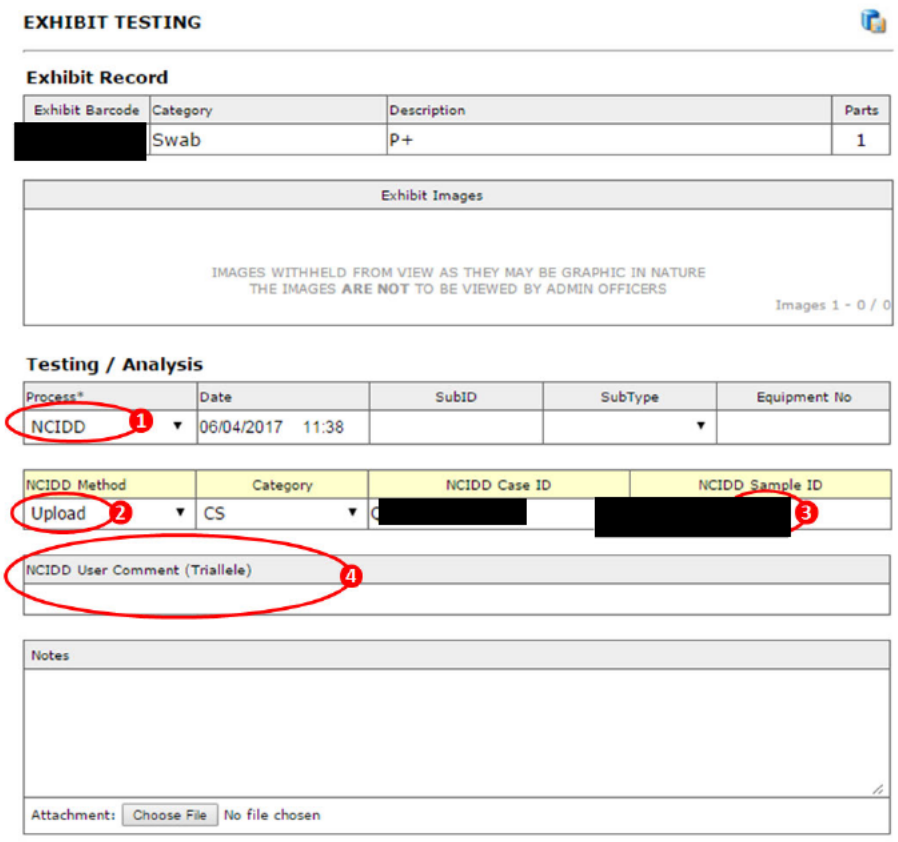


Figure 8 – NCIDD Upload

11.1.2 Modify Profile on NCIDD

If a better profile has been obtained from a different sample within a case and this profile is to be uploaded to NCIDD or if a better profile has been obtained from the same sample but the suffix has changed (e.g. –intel has changed to –mix) then the modify process is not used. In this case, the sample that is being replaced is to be removed from NCIDD and the better profile is to be uploaded to NCIDD as a new upload.

If a better profile has been obtained from the same sample, for example through rework, AND the suffix has not changed then the modify process will be used as follows:

1. On the PDA page, copy down the new profile and select the suffix that is the same as the suffix used for the profile being modified (Figure 19)
2. Select 'NCIDD' from the 'Process' drop-down menu (Figure 8)
3. Select 'Modify' from the 'NCIDD Method' drop-down menu
4. Enter the suffix of the profile / component being modified '-yyyy' after the barcode number that is already present in the NCIDD Sample ID field

5. Enter the reason why the profile / component is being modified in the Notes section
6. Click the save icon to save the record
7. Upon validation by the reviewer, this request will automatically populate the NCIDD worklist

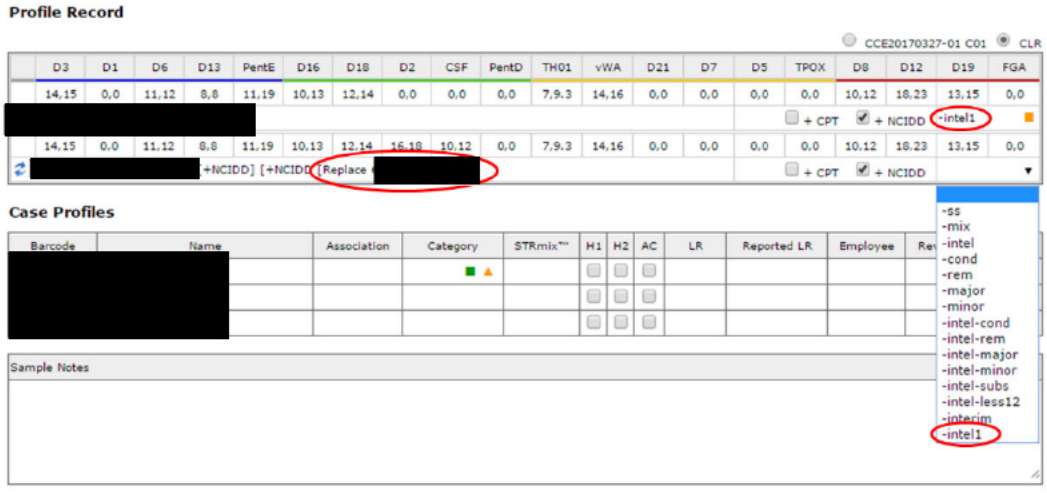


Figure { SEQ Figure * ARABIC } – Modify PDA Page

A profile that has been modified will remain in the Profile Record table but will be greyed out (Figure 20).

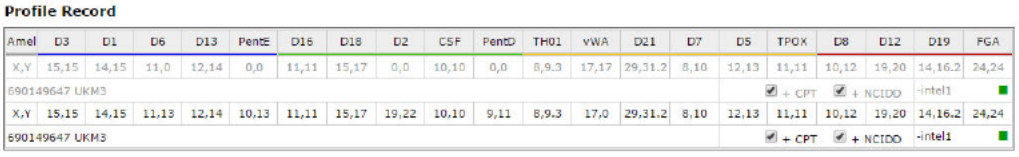


Figure 9 – Modified Profile

11.1.3 Remove Profile from NCIDD

A profile / component can be removed from NCIDD as follows:

1. Select 'NCIDD' from the 'Process' drop-down menu (Figure 18)
2. Select 'Delete' from the 'NCIDD Method' drop-down menu
3. Enter the suffix of the profile / component to be removed in the format '-yyyy' after the barcode number that is already present in the NCIDD Sample ID field
4. Enter the reason why the profile / component is being removed in the Notes section
5. Click the save icon to save the record
6. Upon validation by the reviewer, this request will automatically populate the NCIDD worklist

The Exhibit result line associated with removing a profile from NCIDD should not have anything in the Linked No. field (Section 18).

11.2 Ordering Reworks

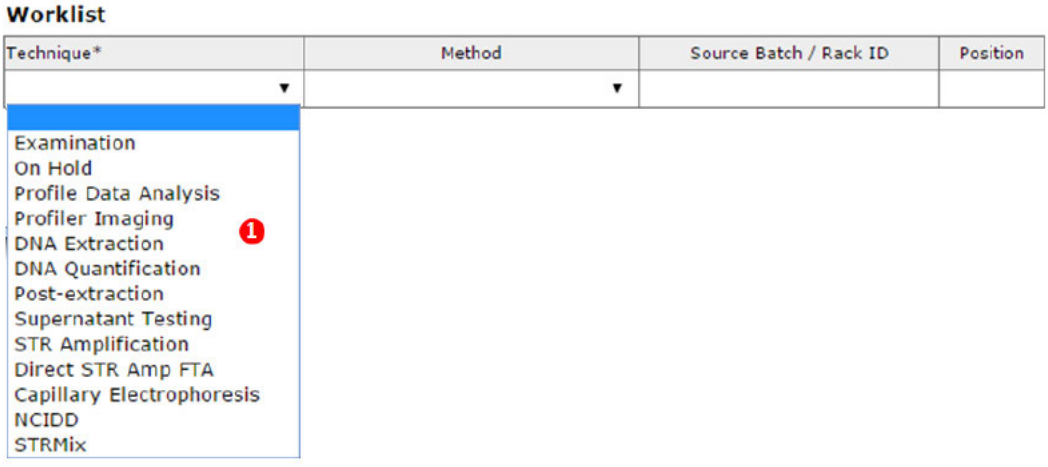


Figure { SEQ Figure * ARABIC } – Technique / Worklist Ordering

11.2.1 Re-amplification

1. If the sample is a dilution with a child / subsample barcode, add the dilution barcode to the 'SubID' field
2. Select 'STR Amplification' from the dropdown list (1Figure 21)
3. An amplification method can be chosen from the drop down menu under 'Method' (Figure { SEQ Figure * ARABIC })

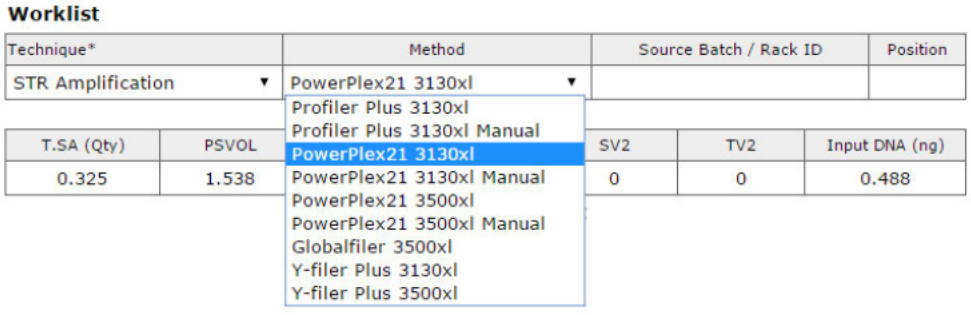


Figure { SEQ Figure * ARABIC } – Amplification Methods

4. An additional box will appear that shows the quant value for the sample and volumes required to amplify at the optimal amount (Figure 23). These volumes can be edited to enable the scientist to change the amount of DNA amplified

T.SA (Qty)	PSVOL	SV1 (µL)	TV1	SV2	TV2	Input DNA (ng)
0.325	1.538	1.5	13.5	0	0	0.488

Figure 10 – Amplification Volumes

5. Click the save icon to save the record (pressing enter will cause the record to save; use the 'tab' key or the mouse to move between fields)
6. This request will automatically populate the appropriate analytical worklist

For PP21, change the default method of 'PowerPlex21 3130xl' in the method box to 'PowerPlex21 3500xl'.

If the sample is likely to have less than 20 µL of extract remaining (if it has previously undergone microcon concentration) then a manual amplification method must be ordered as there will be insufficient volume to be pipetted on the automated platform. Also, if the sample is likely to have less than the requested amplification volume remaining, add an analytical note when the technique is ordered, requesting that all of the remaining extract is amplified.

11.2.2 Microcon / Nucleospin / Dilution

1. Select 'Post-extraction' from the dropdown list (❶Figure 21)
2. The default entry is Microcon PowerPlex 21 however an alternative post-extraction method can be chosen from the drop down menu under 'Method' (Figure { SEQ Figure * ARABIC })

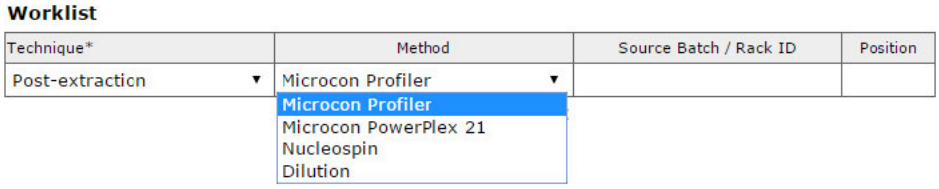


Figure { SEQ Figure * ARABIC } – Post Extraction Methods

3. An analytical note can be added at the same time as requesting the rework to request microcon volumes and dilutions (Section 11.2.6)
4. Click the save icon to save the record (pressing enter will cause the record to save; use the 'tab' key or the mouse to move between fields)
5. This request will automatically populate the appropriate analytical worklist

The default final volume for a PP21 microcon is 35 µL; an analytical note is only required for any exceptions outside of this, e.g. M'con to full.

11.2.3 Re-CE

1. Select 'Capillary Electrophoresis' from the dropdown list (❶Figure { SEQ Figure * ARABIC })
2. For PP21, change the default method of 'PowerPlex21 3130xl' in the method box to 'PowerPlex21 3500xl' (Figure 25)

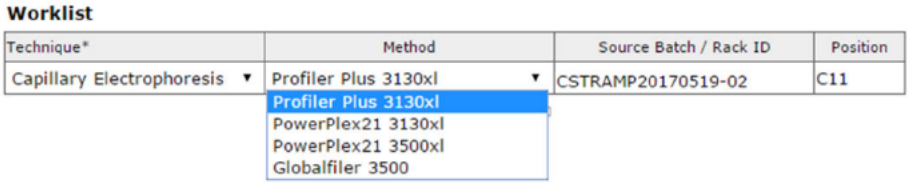


Figure 11 – CE Methods

3. Enter the batch ID and position number of the amplification batch containing the amplification product requiring re-CE by copy and pasting from the PDA page
4. Click the save icon to save the record (pressing enter will cause the record to save; use the 'tab' key or the mouse to move between fields)
5. This request will automatically populate the appropriate analytical worklist

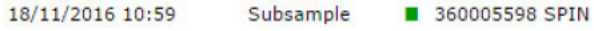
With the implementation of the STARlet in CE, if a DNA profile is obtained from a sample that was previously NAD, the second run can be accepted without further confirmation for both casework and reference samples.

11.2.4 Re-quantification

1. Select 'DNA Quantification' from the dropdown list (❶Figure 21)
2. Quantifiler Trio is the only Method currently available
3. An analytical note can be added at the same time as requesting the rework to request a 'quant and hold' (Section 11.2.6)
4. Click the save icon to save the record (pressing enter will cause the record to save; use the 'tab' key or the mouse to move between fields)
5. This request will automatically populate the appropriate analytical worklist

11.2.5 Re-extraction of Spin Baskets

1. Find the barcode of the spin basket for your sample from the exhibit testing table



2. Register the subsample as an exhibit as described in Appendix 9 – Registering a Subsample as an Exhibit
3. Navigate to the exhibit testing table
4. Open up a test page by clicking the add button ( )
5. Select 'DNA Extraction' as the technique and select the required extraction method (Figure { SEQ Figure * ARABIC })

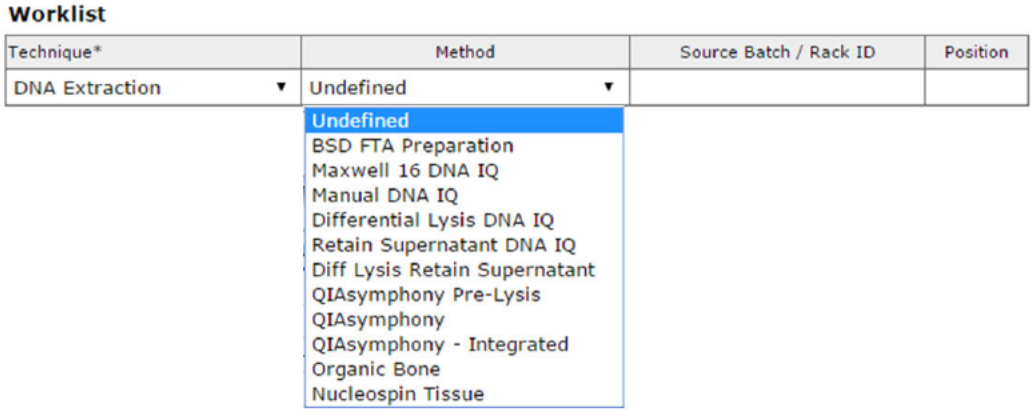


Figure { SEQ Figure * ARABIC } – Re-extraction

6. Click the save icon to save the record (pressing enter will cause the record to save; use the 'tab' key or the mouse to move between fields)
7. This request will automatically populate the appropriate analytical worklist

11.2.6 Analytical Notes

1. To enter an analytical note for a sample (e.g. M'con to full), select 'Analytical Note' from the dropdown list under the 'Testing / Analysis' heading (❶Figure 27).
2. Enter the details of the analytical note into the 'Notes' section (❷)
3. Click the save icon to save the record (pressing enter will cause the record to save; use the 'tab' key or the mouse to move between fields)
4. This request will automatically highlight to analytical scientists that an analytical note exists for that sample
5. An analytical note can be added at the same time any relevant technique is requested

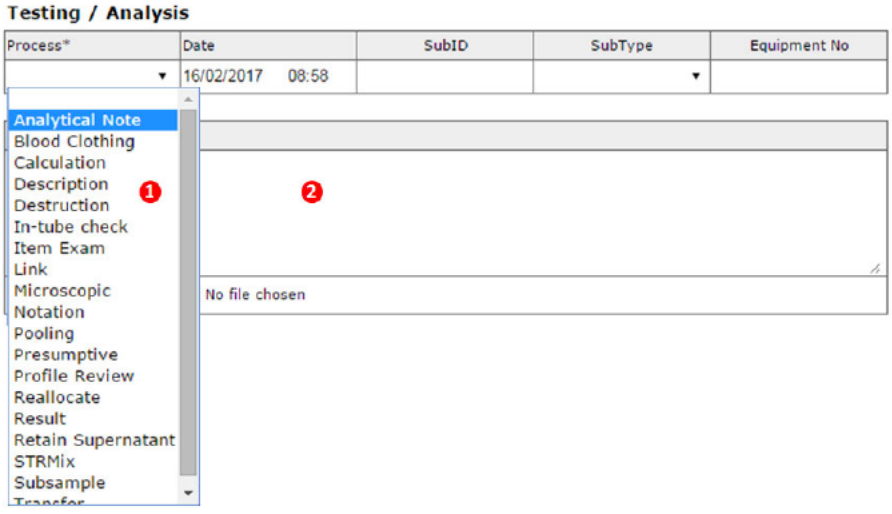


Figure 12 – Analytical Notes

11.2.7 Reviewing

If the PDA Analyst / Reviewer considers further processing / reworking is necessary during the review process, the PDA Analyst will select '[CLICK TO REWORK]' from the profile review page and rework as per Section 11.2 (QIS 34006 – Section 4.4.7).

11.3 Pooling

Before pooling, each sample / subsample to be pooled must be registered as an exhibit (Appendix 9 – Registering a Subsample as an Exhibit). Once registered correctly, refer to Appendix 11 – Process for Pooling Samples.

11.4 Transfer

Samples processed pre-batch functionality were assigned a DNA number. On occasion it is necessary to rework these samples with new technology. Refer to Appendix 10 – Processing of DNA Number Exhibits for the workflow required to register this sample in the FR and order a 'Transfer' process.

11.5 Changing Priority

The priority of samples is set by the QPS, with major crime samples being Priority 1 or 2 and volume crime samples being Priority 3.

It may be necessary for the scientist to change the priority of a sample, for example to meet a court date. This can be done as follows:

1. Select 'Notation' from the 'Process' drop-down menu (Figure { SEQ Figure * ARABIC })
2. Enter appropriate notes in the 'Notes' section
3. Change the priority
4. Click the save icon to save the record
5. This request will automatically update the priority of the sample in all worklists

The priority of a sample can only be changed if there is a process selected.

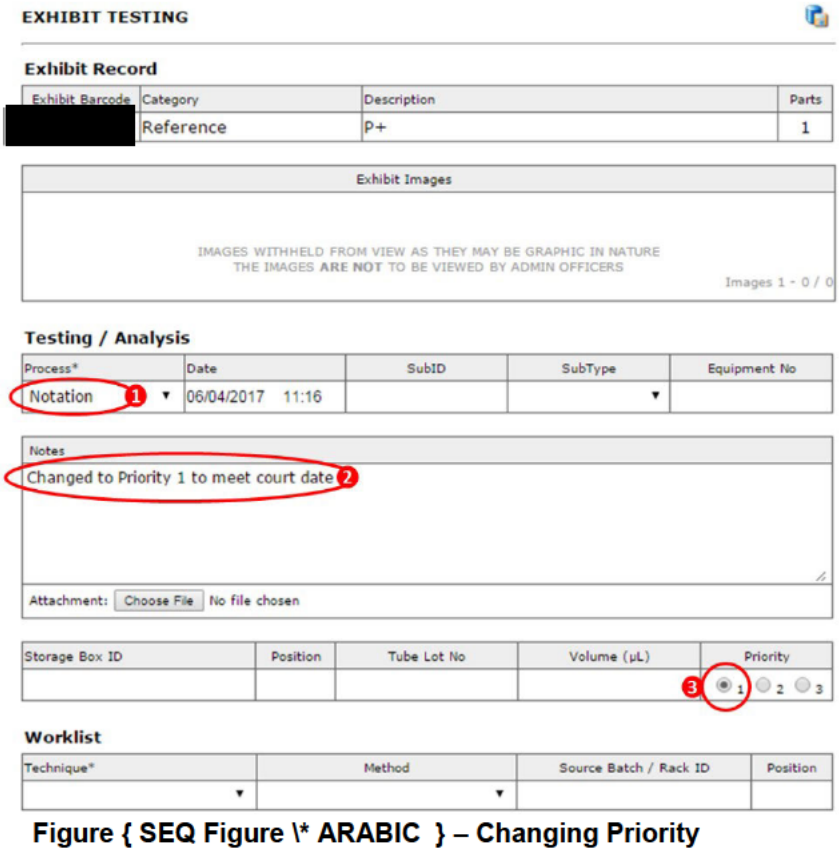


Figure { SEQ Figure * ARABIC } – Changing Priority

11.6 Requesting Additional Examinations

11.6.1 Re-examination

1. Select 'Examination' from the 'Technique' drop-down menu (Figure 29)
2. Select 'Re-examination' from the 'Method' drop-down menu
3. Select 'Notation' from the 'Process' drop-down menu
4. Enter appropriate notes in the 'Notes' section
5. Click the save icon to save the record
6. This request will automatically populate the Examination worklist

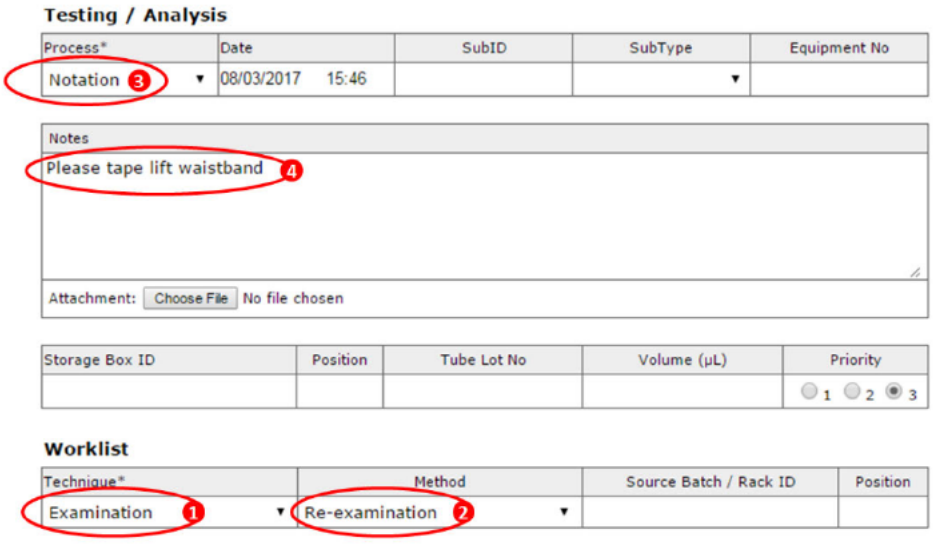


Figure 13 – Re-examination Ordering

11.6.2 Diff Slide Examination

1. Select 'Examination' from the 'Technique' drop-down menu (Figure 30)
2. Select 'Slide microscopy' from the 'Method' drop-down menu
3. Enter the subsample barcode of the diff slide in the 'SubID' box (the SubID of the slide can be found in the exhibit testing table)
4. Click the save icon to save the record
5. This request will automatically populate the Examination worklist

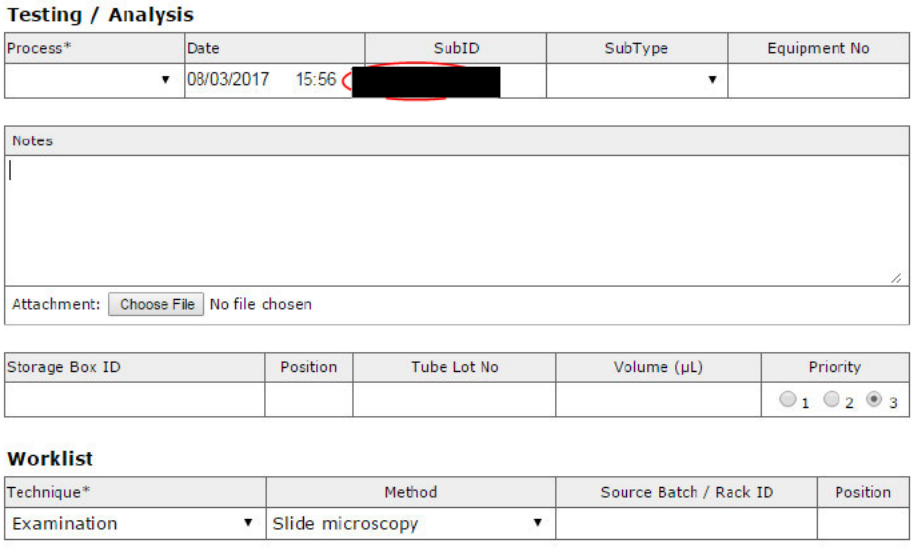


Figure 14 – Diff Slide Examination Request

11.6.3 Examination of Prioritised Exhibits

Select 'Examination' from the 'Technique' drop-down menu (Figure 30)
Select 'Item Exam' from the 'Method' drop-down menu
Click the save icon to save the record
This request will automatically populate the Examination worklist

11.7 Calculations

If a VAR / OLA / ULP / XOVER calculation is required at plate reading the plate reader will order a 'Calculation' process and record the details of the calculation in the 'Notes' section (Figure { SEQ Figure * ARABIC }). The profile analyst will enter into the calculation record and check the calculation. If the calculation is correct then the profile analyst will validate the record by clicking the red 'CLICK TO VALIDATE' bar. If there is an error in the calculation the profile analyst may correct the error however they will be unable to validate the record. In this instance the reviewer will validate the calculation. Alternatively, the plate reader may be contacted to amend the calculation.

For complex profiles not suitable for interpretation, calculations do not need to be checked provided the calculation is not critical to the interpretation. The profile analyst should add 'Calculation not checked' to the top of the 'Notes' section in the calculation record for the reviewer to validate.

Testing / Analysis

Date	Process	SubID	SubType	Equipment No
16/02/2017 10:46	Calculation			

Notes
FCW21GM20160101_01 Ladder 1 D3 (18) 150.89 - (L18) 150.92 = -0.03 (OI) 163.88 - (L21) 163.36 = 0.52 |-0.03-0.52| = 0.55 OL@D3[21.1]
Attachment:

Storage Rack ID	Position	Tube Lot No	Volume (µL)	Priority
				○ 1 ○ 2 ◉ 3

Change Log		
2017-02-16 10:40	INSERT	[redacted]NURTHEN, T
2017-02-16 10:51	CURRENT	[redacted]NURTHEN, T

[CLICK TO VALIDATE]

Figure { SEQ Figure * ARABIC } – Calculations

11.8 Notations

A 'Notation' can be used to record notes against a sample, however it is preferable to use the 'Sample Notes' on the PDA page as this is more easily seen and likely to be included in a case file.

See points 3-6 in Section 11.6.1 for the process for ordering a notation.

Notations self-validate upon saving.

If the sample is on the 'On Hold' worklist, adding a notation will remove it from this list. If this occurs and the sample needs to be on the 'On Hold' list, it will need to be re-added manually.

11.9 Reallocate

The 'Reallocate' process is used to remove a sample from a worklist where the most recent entry in the exhibit testing table displays [WL]. For example, if a re-amp is ordered in error, the sample can be removed from the amplification worklist using the 'Reallocate' process as follows.

Order a 'Reallocate' process from the drop-down menu (Figure { SEQ Figure * ARABIC }) and add a note stating the reason for the reallocate.

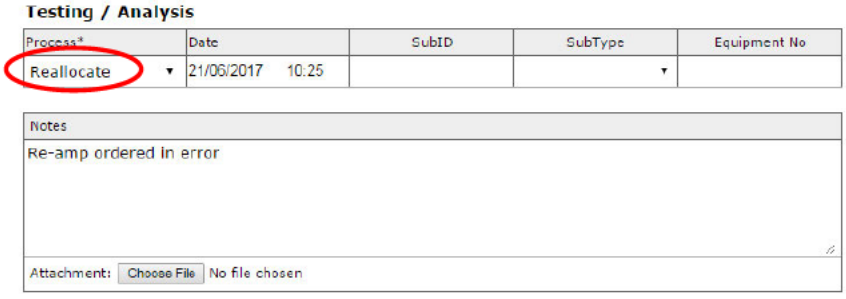


Figure { SEQ Figure * ARABIC } – Reallocate Process

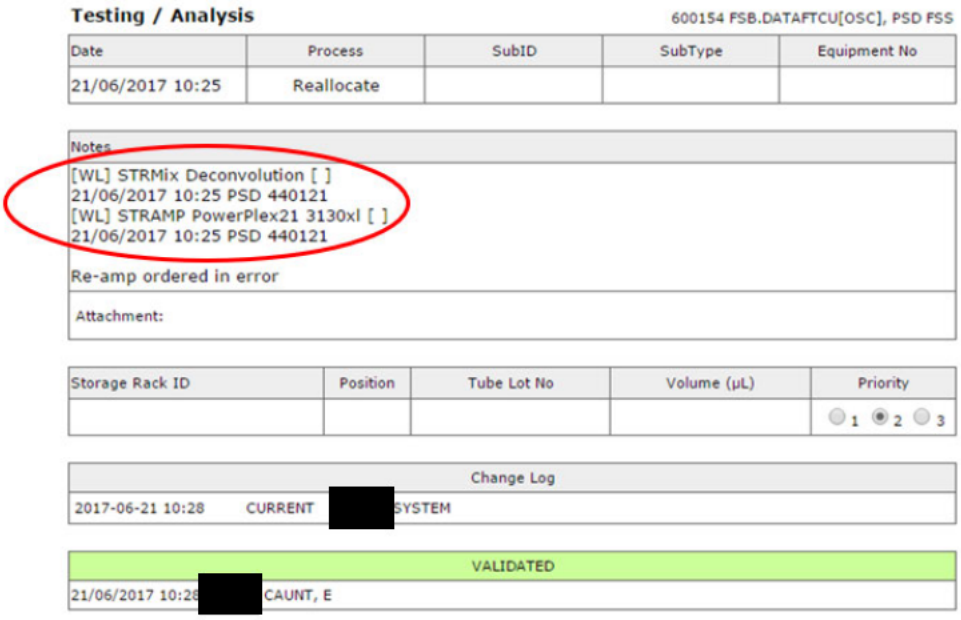
By ordering a 'Reallocate' the sample will be removed from ALL worklists that it is currently sitting on. The scientist will need to add the sample back onto the worklists that it should remain on.

The 'Reallocate' process and the worklist the sample has been removed from will be visible in the Exhibit Testing table (Figure 33).

Figure 15 – Reallocate Display

Clicking on the date and time relating to the reallocate will open the record. This record shows all of the worklists that the sample has been removed from if multiple worklists are involved. From this, the scientist can see what worklists that sample needs to be added to.

The sample below (**Error! Reference source not found.**) has been removed from the STRmix and STRAMP worklists. Since the sample was added to the amplification worklist in error, it only needs to be added back to the STRmix worklist.



Testing / Analysis 600154 FSB.DATAFTCU[OSC], PSD FSS

Date	Process	SubID	SubType	Equipment No
21/06/2017 10:25	Reallocate			

Notes

[WL] STRMix Deconvolution [ ]
21/06/2017 10:25 PSD 440121
[WL] STRAMP PowerPlex21 3130xl [ ]
21/06/2017 10:25 PSD 440121

Re-amp ordered in error

Attachment:

Storage Rack ID	Position	Tube Lot No	Volume (µL)	Priority
				1 2 3

Change Log

2017-06-21 10:28 CURRENT [redacted] SYSTEM

VALIDATED

21/06/2017 10:2[redacted] CAUNT, E

Figure 16 – Reallocate Example

Reallocate processes self-validate upon saving.

If a sample is only added to a worklist when a process is ordered, e.g. 'Profile Review' (no '[WL]' associated with the entry in the exhibit testing table), this sample can be removed from the worklist by selecting '[CLICK TO REWORK]' from the profile review page or by making the process incorrect (Section 13).

11.10 Staff Matches

If a match is obtained to the staff elimination database (Section 8.1) then this needs to be investigated by the Quality team. The sample should be placed on the 'On Hold – Quality Review' worklist as follows:

1. Select 'On Hold' from the 'Technique' drop-down menu (Figure 35)
2. Select 'Quality Review' from the 'Method' drop-down menu
3. Select 'Result' from the 'Process' drop-down menu
4. Enter a note for the Quality team
5. Click the save icon to save the record
6. This request will automatically populate the 'On Hold' worklist

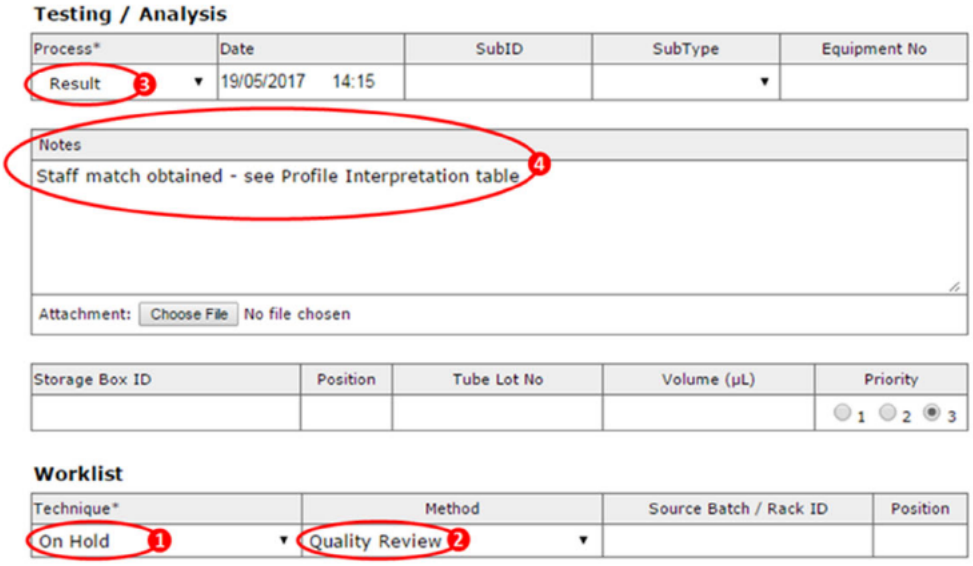


Figure 17 – Staff Match

If the sample is on the 'On Hold' worklist then adding a notation will remove it from this list (this is why a 'Result' is added). If this occurs and the sample needs to be on the 'On Hold' list, it will need to be added manually.

12 STRmix Analysis

STRmix input files for casework samples and reference samples that have been associated to a case are created by the FR. These can be downloaded by clicking the icons located in the Profile Analysis and Case Profiles tables. It is suggested that the downloaded input files be saved in a location convenient for access from STRmix.

Instructions for uploading STRmix PDFs to the PDA page can be found in Section 5 and Appendix 6 – STRmix Workflow.

Scientists may enlist the assistance of HP2 staff to run STRmix analyses. This is managed through the STRmix worklists.

For details on the STRmix workflow, refer to Appendix 6 – STRmix Workflow.

13 Incorrect Results

When a process is ordered it populates the Exhibit Testing table, however if this process is ordered in error it is not possible to remove it from the Exhibit Testing table.

Processes are able to be made incorrect by anybody prior to validation. Once made incorrect, the process will have a strike through in the Exhibit Testing table and will not be able to be accessed.

To incorrect a process, enter into it by clicking on the associated date and time stamp in the Exhibit Testing table (Figure { SEQ Figure * ARABIC }}

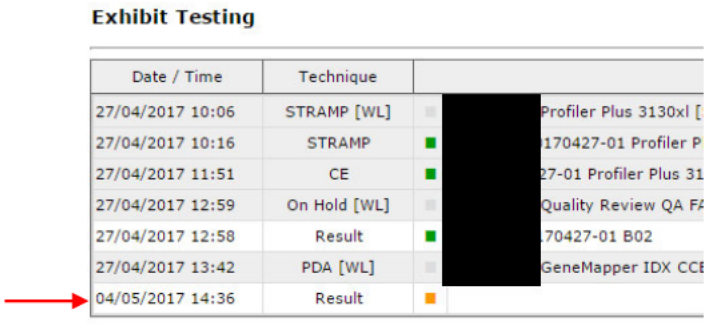
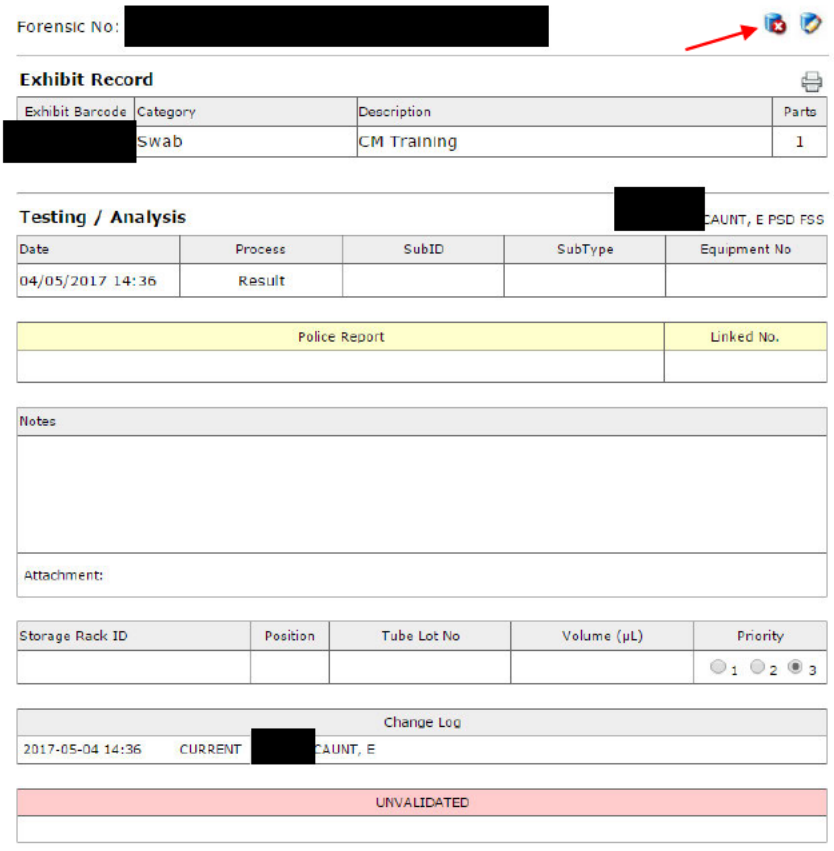


Exhibit Testing

Date / Time	Technique	
27/04/2017 10:06	STRAMP [WL]	[redacted] Profiler Plus 3130xl [
27/04/2017 10:16	STRAMP	[redacted] 170427-01 Profiler P
27/04/2017 11:51	CE	[redacted] 27-01 Profiler Plus 31
27/04/2017 12:59	On Hold [WL]	[redacted] Quality Review QA FA
27/04/2017 12:58	Result	[redacted] 170427-01 B02
27/04/2017 13:42	PDA [WL]	[redacted] GeneMapper IDX CCE
04/05/2017 14:36	Result	

Figure { SEQ Figure * ARABIC } – Incorrect Entry

Click the con in the top right of the page (Figure 37)



Forensic No: [redacted]

Exhibit Record

Exhibit Barcode	Category	Description	Parts
[redacted]	Swab	CM Training	1

Testing / Analysis [redacted] CAUNT, E PSD FSS

Date	Process	SubID	SubType	Equipment No
04/05/2017 14:36	Result			

Police Report	Linked No.

Notes
Attachment:

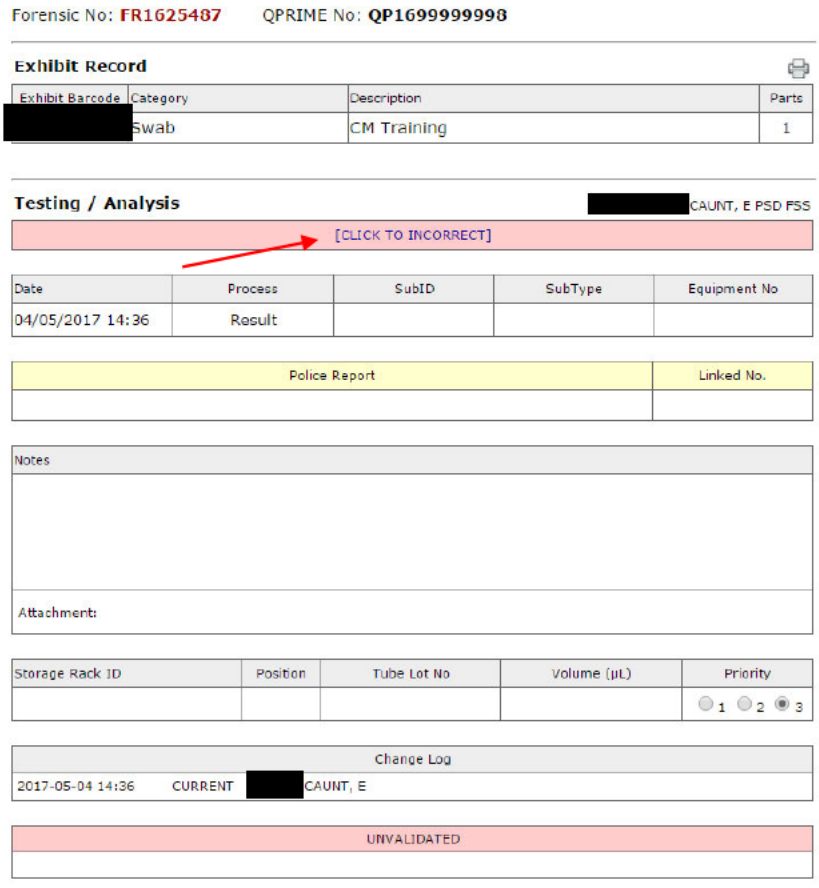
Storage Rack ID	Position	Tube Lot No	Volume (µL)	Priority
				1 2 3

Change Log
2017-05-04 14:36 CURRENT [redacted] CAUNT, E

UNVALIDATED

Figure 18 – Incorrect Icon

Click the [CLICK TO INCORRECT] bar at the top of the page (Figure 38)



Forensic No: **FR1625487** QPRIME No: **QP1699999998**

Exhibit Record

Exhibit Barcode	Category	Description	Parts
[redacted]	Swab	CM Training	1

Testing / Analysis [redacted]CAUNT, E PSD FSS

[CLICK TO INCORRECT]

Date	Process	SubID	SubType	Equipment No
04/05/2017 14:36	Result			

Police Report	Linked No.

Notes

Attachment:

Storage Rack ID	Position	Tube Lot No	Volume (µL)	Priority
				1 2 3

Change Log

2017-05-04 14:36 CURRENT [redacted]CAUNT, E

UNVALIDATED

Figure 19 – Incorrect Bar

The process entry in the Exhibit Testing table will now have a strike through (Figure 39)

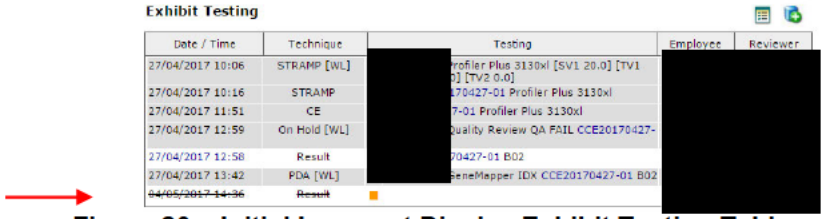
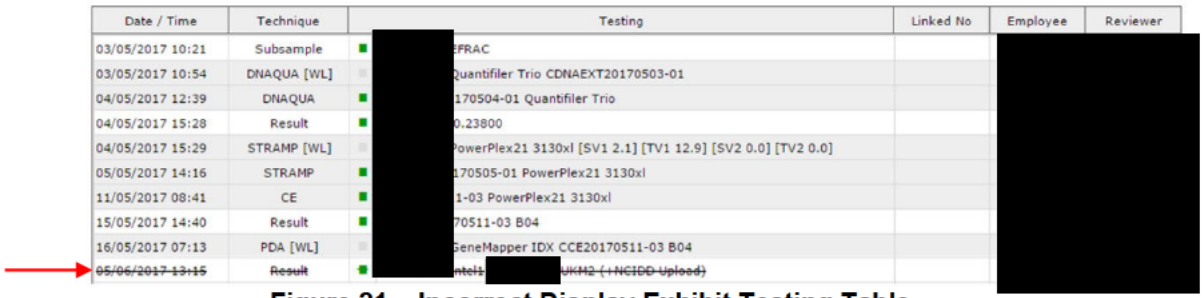


Exhibit Testing

Date / Time	Technique	Testing	Employee	Reviewer
27/04/2017 10:06	STRAMP [WL]	[redacted]	[redacted]	[redacted]
27/04/2017 10:16	STRAMP			
27/04/2017 11:51	CE			
27/04/2017 12:59	On Hold [WL]			
27/04/2017 12:58	Result			
27/04/2017 13:42	PDA [WL]			
~~04/05/2017 14:36~~	~~Result~~			

Figure 20 – Initial Incorrect Display Exhibit Testing Table

Once a copied down profile has been reviewed, this profile cannot be removed from the Profile Record table. If this profile is incorrect then the result in the Exhibit Testing table relating to that copied down profile should be made incorrect (Figure 40)



Date / Time	Technique	Testing	Linked No	Employee	Reviewer
03/05/2017 10:21	Subsample	[redacted]		[redacted]	
03/05/2017 10:54	DNAQUA [WL]				
04/05/2017 12:39	DNAQUA				
04/05/2017 15:28	Result				
04/05/2017 15:29	STRAMP [WL]				
05/05/2017 14:16	STRAMP				
11/05/2017 08:41	CE				
15/05/2017 14:40	Result				
16/05/2017 07:13	PDA [WL]				
~~05/06/2017 13:15~~	~~Result~~				

Figure 21 – Incorrect Display Exhibit Testing Table

In turn, this will strike through the profile in the Profile Record table on the PDA page (Figure 41)

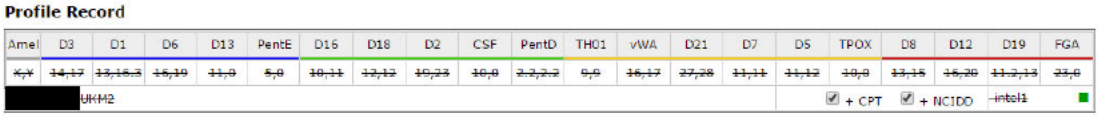


Figure 22 – Incorrect Display PDA Page

Validated results are incorrected in the same way; however these can only be performed by a Supervising Scientist or above.

When a validated result is identified as incorrect, the following should occur:

1. PDA page amended and correct result lines added to the relevant sample by the PDA analyst
2. Note added to the Sample Notes section explaining why the original results are incorrect or Notation added with Intelligence Report (QIS 34308). Requirements for amended results are outlined in Table 4
3. If an Intelligence Report is required, e-mail this report to the QPS DNA Management Unit
4. Ask a Supervising Scientist or above to incorrect the results at the same time the correct results are validated

Table 3 – Requirements for Amended Results

Type of Final Result Change	Intelligence Report Requirement	Managing Scientist Notification
Change in number of contributors only (no LR changes)	No	Yes
Change in LR: Support for contribution to support for contribution (same or different range)	No	No
Change in LR: Support for non-contribution to support for non-contribution	No	No
Change in LR: Support for contribution to support for non-contribution (and vice versa)	Yes	Yes
Change in LR: Support for contribution to exclusion (and vice versa)	Yes	Yes
Change in LR: Support for non-contribution to exclusion (and vice versa)	No	Yes
Any 'suitable for interpretation' to 'unsuitable for interpretation' (and vice versa)	Yes	Yes
Addition or removal of possible sub-threshold information	No	No

14 Additional Workflows

14.1 Suspect Checks

Requests for suspect checks will be received via SSLU or the QPS in a CM request.

Suspect check reference samples are not associated to cases in the FR and therefore these samples will not appear in the CPT.

If the crime scene sample against which the suspect check reference sample is to be compared has been profiled in PP21 then STRmix analysis may be required. As the suspect check reference sample does not populate the CPT, the STRmix input file cannot be obtained from the PDA page of the FR.

If the suspect check reference sample results are located in AUSLAB then the STRmix input file for the suspect check reference sample can be located in I:\STRmix Profiles.

If the suspect check reference sample results are located in the FR then the STRmix input file will need to be generated using the 'Build GMIDX reference' macro located in I:\Macros. Alternatively, this file can be generated from the Reference PDA page of the FR, however it may need to be amended.

The resultant STRmix PDF file should be added to a 'Notation' against the sample.

Exhibit results lines will be used to communicate results back to the QPS for all suspect checks (P+ and PP21) as per Section 18.

Once a suspect check has been completed, where appropriate, it will be necessary to complete the suspect check request.

14.2 Receipt of New Reference Samples

Often reference samples will be received for a case after the profile data analysis has been completed. The reference sample will require comparison to all interpretable DNA profiles in the case. The crime scene profiles with validated results that require comparison will add to the 'Profile Data Analysis – Case Work + Ref' worklist.

If the newly associated reference sample matches to the crime scene profile, the Case Profiles table will need to be updated and new result line(s) added.

In the example below (Figure { SEQ Figure * ARABIC }), consider that the new reference sample matches UKM1. The profile analyst should enter the barcode of the new reference sample into the 'Association' field for UKM1. This will update the association field for the reference sample.

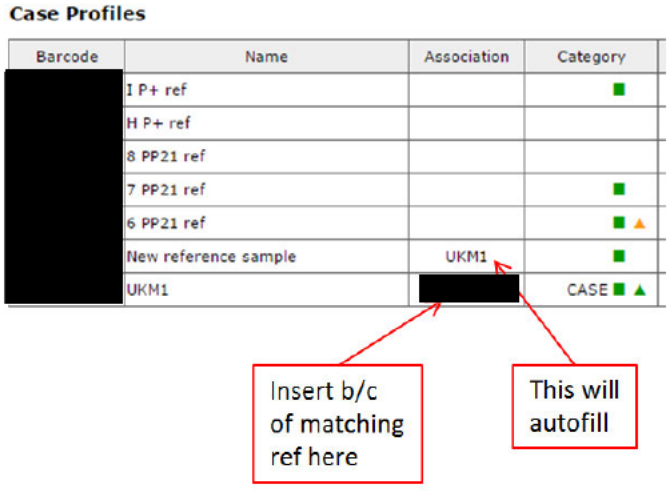


Figure { SEQ Figure * ARABIC } – Association of Unknowns

For new reference samples matching a DNAIntel sample, the profile analyst should update the DNAIntel 'Association' field in the CPT with the new reference sample barcode.

14.2.1 New Reference Comparisons

Newly associated reference samples can be identified by the absence of LR information in the Case Profiles table.

The comparison of the reference sample should be recorded as follows:

1. If required, complete a LR calculation in STRmix and import the PDF
2. If required, manually update the LR information in the Case Profiles table (e.g. intuitive exclusion)
3. If the reference sample matches an unknown or DNAIntel sample for the case, update the 'Association' fields (Figure 42)
4. Re-copy down the profile into the Profile Record table, click the ⇄ icon to perform a search and select the original suffix, provided there is no change to the interpretation. Do not re-tick either the +CPT or +NCIDD boxes
5. Click 'Add Results' from the PDA page to update the result lines for the reference sample comparison. Alternatively, order a 'Result' process for the Exhibit Testing / Examinations table and manually enter the appropriate result lines for the reference sample comparison (Section 18)
6. If no additional results lines are required i.e. the results have not changed, then a Sample Note to this effect should be added (e.g. duplicate reference sample)
7. Order a 'Profile Review' process (a 'Profile Review' process should be ordered regardless of whether a result line is entered)

14.2.2 New Reference Comparisons that Require a Change in Interpretation

If a reference sample is received that requires the original interpretation of the profile to be changed due to the profile now being able to be conditioned, then the following process should be followed (otherwise follow the incorrect process as per Section 13):

1. Upload the new STRmix PDFs to the PDA page (these will overwrite the original PDFs)

2. Click 'Edit' and update the Profile Record table by copying down the appropriate profiles, searching the database, checking the +NCIDD box if necessary and selecting suffixes as per Section 8
3. Incorrect all 'Result' entries in the exhibit testing table that relate to the profiles that were copied down from the original interpretation. Although the original interpretation was correct, this will cross out the profiles originally copied down in the Profile Record table and remove them from the FR database
4. Enter appropriate result lines as per Section 18 (may need 'Sample undergone further work – conditioned' line)
5. Order a 'Profile Review'

14.3 Paternity / Paired Kinship Cases

To enable paperless PDA of paternity / kinship cases, Kinship reports can be printed to PDF and attached to a 'Notation' against the sample. The Kinship report and manual entry audit both have areas for the scientist to sign and date the report. Since NATA require the sign and date fields to be filled, the scientist can edit the PDF and enter 'N/A' in the sign and date fields (Appendix 3 – Amending PDFs for instructions on editing PDFs). Alternatively, these reports can be digitally signed.

14.3.1 Product of Conception (POC) Received

When a paternity / paired kinship analysis is performed on a POC the FR records should be completed as follows:

1. Copy down the profile / resolved component of profile into the Profile Record table and perform a search
2. Check the '+CPT' box and save the record
3. Order a 'Notation' and upload the Kinship report (two 'Notations' will be required if there is an audit report)
4. Order a 'Result', select the appropriate Exhibit Result line and enter the barcode of the alleged parent in the 'Linked No.' field (where subsamples exist for the reference sample of the alleged parent, the parent barcode should be entered into the 'Linked No.' field)
5. Order a 'Profile Review'

14.3.2 Reference Sample for Alleged Child Received

When a paternity / paired kinship analysis is performed on a reference sample then the results are reported to the QPS via an Exhibit Result on the reference sample of the alleged child. The FR records should be completed as follows:

1. Order a 'Notation' on the reference sample of the child and upload the Kinship report (two 'Notations' will be required if there is an audit report)
2. Order a 'Result' on the reference sample of the child, select the appropriate Exhibit Result line and enter the barcode of the alleged parent in the 'Linked No.' field (where subsamples exist for the reference sample of the alleged parent, the parent barcode should be entered into the 'Linked No.' field)
3. Order a 'Profile Review'
4. The reference sample of the child will populate the 'Profile Review' worklist.

14.4 Coronial Cases

If required, Exhibit Results can be reported back to the QPS on a bone sample using the parent barcode in the same way as paternity / paired kinship cases (Section 14.3.2).

14.5 Reactivated Cases

The QPS may request a volume check or 'Quant & Hold' for samples within a particular case type such as 'Cold' Cases.

If a volume check is requested:

1. Send a Request / Task to the Senior Scientist of the Analytical Section
2. Add details to the 'Comments' field
3. Save the record
4. Click the 'Add Exhibits' icon to add samples registered in the FR (refer to Appendix 23.14 for samples not appearing in the FR)

For a Quant and Hold request, refer to QIS 34006 Section 4.4.17 for detailed steps on actioning these samples.

14.6 Covert Samples

The QPS may submit covert samples for DNA analysis. Covert samples may be identified through information entered by the QPS in the 'Exhibit Notes & FSS Advice' field of the Exhibit Record page. Alternatively, the QPS may alert a HP5 or above of these samples. If not clearly identified, a notation should be added to the 'Exhibit Testing / Examinations' table of the relevant samples.

For the PDA page of a covert sample, do not complete the Profile Record or Case Profiles tables. All results for these samples including any reference sample comparisons should be reported back to the QPS in an Intelligence Report for the relevant sample (QIS 34308) and not through the standard exhibit result line process.

15 Sample Status

The status of a sample can be easily seen in the 'Status' field of the PDA page (Figure 43).

Figure 23 – Sample Status

The information displayed in this field is taken from the last entry in the Exhibit Testing table along with the date and time of that entry.

To access the status of all samples for a case, click the sample barcode '690149606' at the top left corner of the Exhibit Detail table. Click the Exhibit Register tab twice, select 'DNA Analysis' then 'All Exhibits' (Figure 44). This can be further filtered by profile type once DNA profiling has been completed:

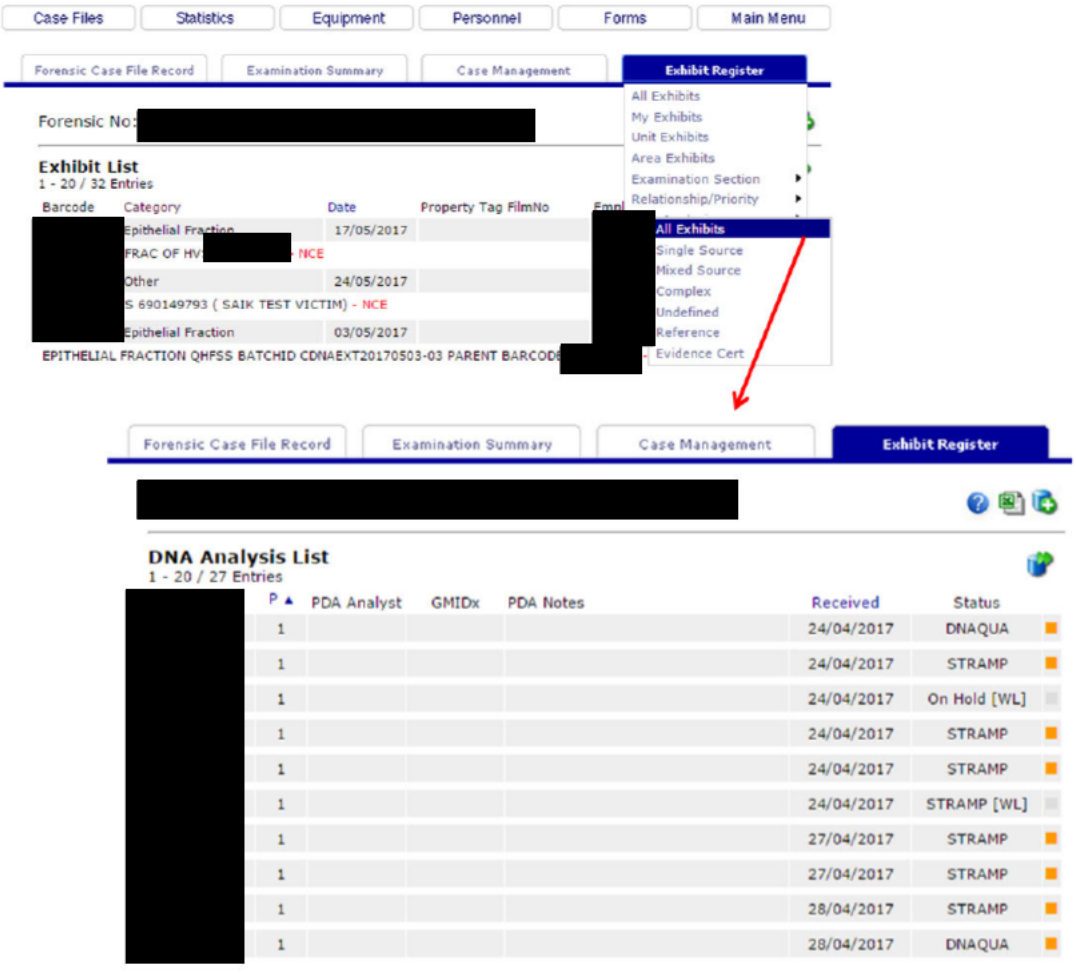


Figure 24 – Status of All Samples in a Case

This sample status summary can also be accessed from the Integrated Case Management System (ICS) page that presents after log-in. Click the 'Case Files' button at the top of the page, enter the case number, click enter and then access the 'Exhibit Register' tab as detailed above.

16 SAIKs and Multiple Items from One Exhibit

Often exhibits are received that contain multiple samples for DNA analysis. For example, SAIKs that contain multiple swabs and exhibits containing multiple cigarette butts.

Once received in Evidence Recovery for examination, these exhibits will be split into their individual components and new barcodes assigned. Consider a SAIK that contains three swabs. Evidence Recovery will register each of the three swabs as individual exhibits; these swabs are 'children' of the 'parent' exhibit (SAIK). As the 'children' are registered as exhibits, they will each have a PDA page and a result for each of these 'children' should be reported back to the QPS.

Since each of the 'child' exhibits from the SAIK will undergo DNA analysis, they will have subsample barcodes associated with them in order to store the individual parts created during the DNA analysis process (Figure 45 and Appendix 12 – Forensic Register Storage Architecture).

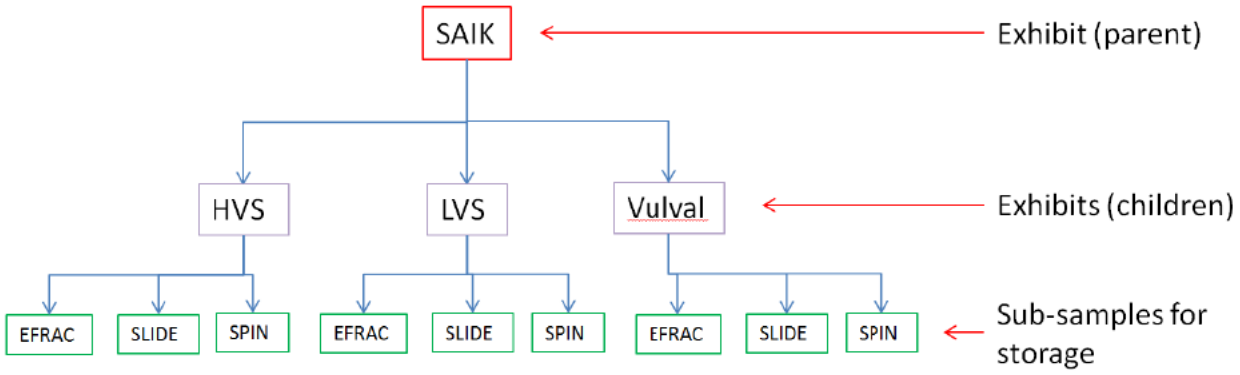


Figure { SEQ Figure * ARABIC } – SAIK Hierarchy

If the spin basket from the HVS requires re-extraction, this will need to be made into an exhibit to enable subsample barcodes to be created for storage of its individual parts (Figure 46).

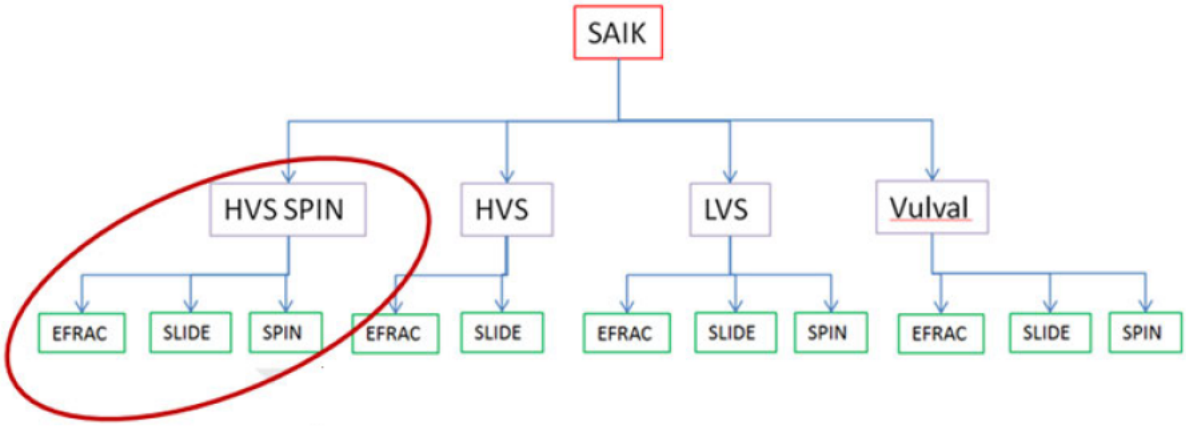
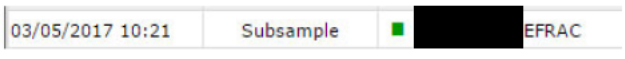


Figure 25 – Re-extract of Spin Basket

The following process should be followed to order the processing of an EFRAC that has been held at extraction:

1. Find the barcode of the EFRAC for your sample from the exhibit testing table



2. Register the EFRAC as an exhibit as described in Appendix 9 – Registering a Subsample as an Exhibit
3. Navigate to the exhibit testing table
4. Open up a test page by clicking the add button ( )
5. Select 'DNA Quantification' as the technique and 'Quantifiler Trio' as the method
6. Click the save icon to save the record

17 Subsamples and Subsample Processing

Subsamples are not exhibits and do not have records in their own right. Any process performed on a subsample is recorded within the parent exhibit from which the subsample originates.

Some exhibits require multiple samples to be processed with only one final result being reported back to the QPS. This is most likely to happen with bone samples when there are multiple aliquots.

In the example below (Figure { SEQ Figure * ARABIC }) the bone exhibit has barcode 695362707; the bone has two aliquots with barcodes 695362647 and 695362638 which are subsamples of the bone. The profile information for both subsamples is displayed in the Profile Analysis table on the PDA page of the bone. This enables the results from both aliquots to be combined into a consensus profile for reporting.

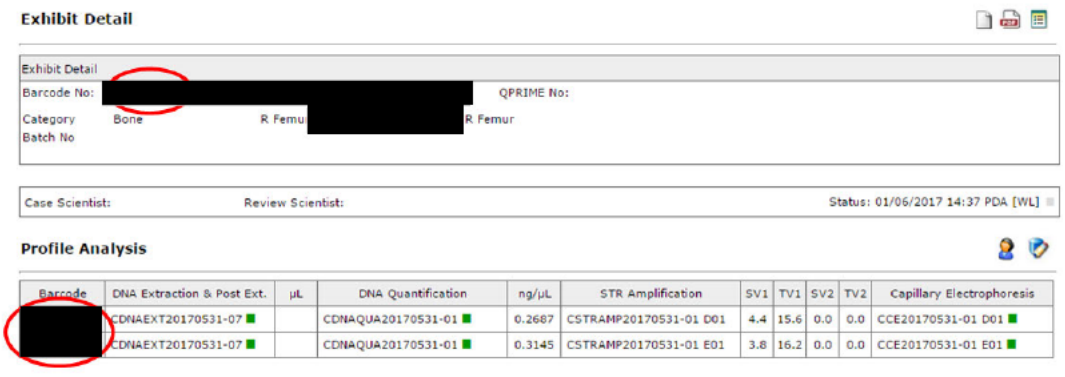


Figure { SEQ Figure * ARABIC } – Bone Exhibit

Another example of when a subsample will be encountered is if a sample has been diluted. Below (Figure 48) exhibit [redacted] has been processed but later needed a dilution which has barcode [redacted] The Profile Analysis table shows the batches that related to the processing of the original extract under the exhibit barcode followed by the processing of the dilution. In this instance the sample has been processed under the dilution barcode but the result will be reported back under the exhibit barcode.

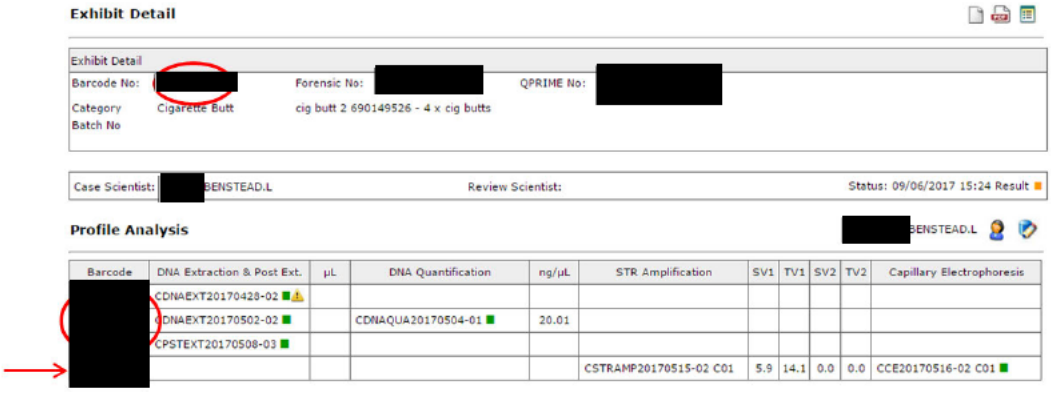


Figure 26 – Dilution

When processing of subsamples is complete they will populate the PDA lists under the subsample barcode; this enables visibility of the progress of each of the individual subsamples. Since the results of the Profile Data Analysis are reported back on the exhibit, it is the exhibit and not the subsamples that will populate the Profile Review lists. Subsamples only remove from the PDA lists when a Profile Review is ordered with the subsample barcode in the 'SubID' field. Alternatively, 'Reallocate' from the parent barcode with the subsample barcode will remove subsamples from the PDA lists.

If a subsample requires a rework, the exhibit test is ordered on the exhibit and the barcode of the subsample should be entered into the SubID field of the exhibit testing page. In the

example below (Figure 49) the subsample with barcode [redacted] is being submitted for re-amplification.

For any action that is required to be performed on the subsample, the barcode of the subsample must be entered into the SubID field.

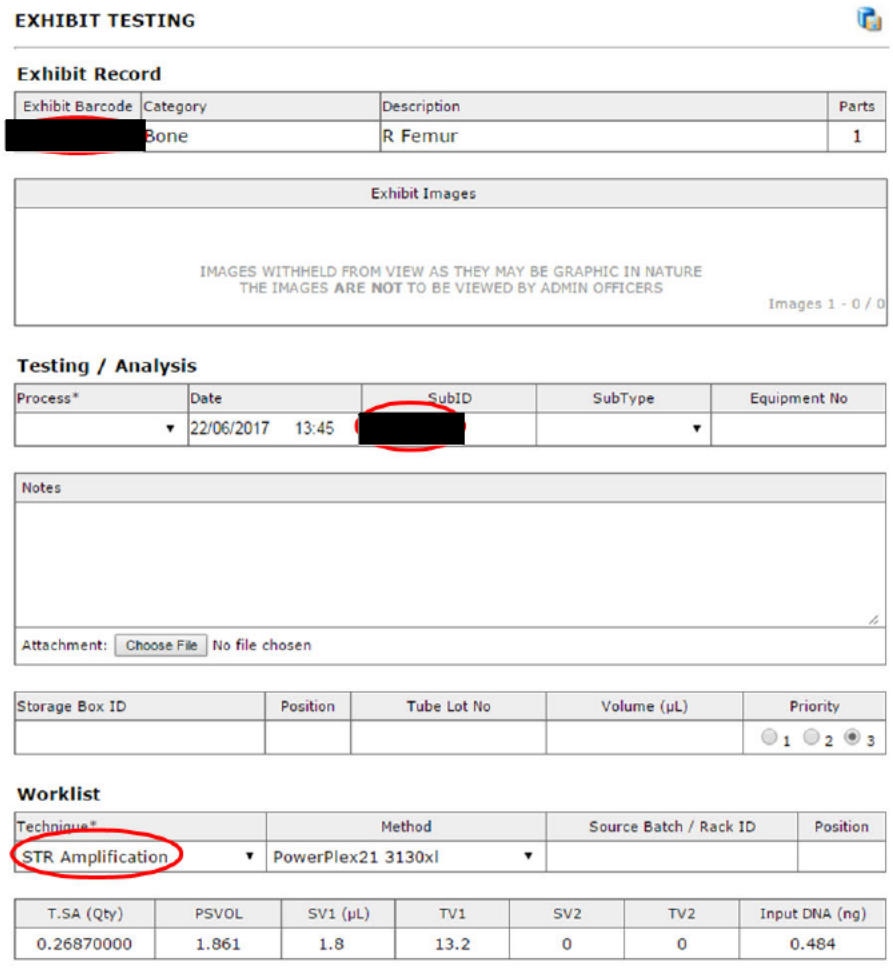


Figure 27 – Processing of SubID

Subsamples may be registered as exhibits if a result needs to be reported back on that subsample in isolation of any other subsamples or if pooling is required (Section 11.3).

In the example of pooling, subsamples are made into exhibits to enable the pooling process to occur however the final result will be reported on the pooled barcode. In this instance the samples that have been pooled require peer review at the same time as the results on the pooled barcode. Each of the exhibits that have been pooled should have a profile review ordered on them to remove them from the PDA list and enable the reviewer to record the review of these samples.

18 Exhibit Results

Exhibit result lines are created to communicate results to the QPS electronically (QIS 34229 for Explanations of Exhibit Results for FR). Exhibit results relating to DNA profile interpretation are entered into the FR by selecting appropriate lines:

1. Select the 'Add Results' icon from the PDA page

2. Check all automated lines
3. Click the save icon to save the record
4. Repeat until all relevant exhibit result lines have been entered ('Add Results' allows for the addition of three lines at a time)

On occasion, it may be necessary to select the appropriate result lines manually:

1. Select the 'Add Results' icon from the Exhibit Testing / Examinations table, followed by 'Result' from the 'Process' drop-down menu (Figure 50)
2. Select the appropriate exhibit result line from the drop-down menu. The mnemonic can be entered into the box for additional filtering
3. Enter the associated reference sample barcode, unknown designation or DNAIntel barcode into the 'Linked No.' field
4. Click the save icon to save the record
5. Repeat until all relevant exhibit result lines have been entered

Provided they are unvalidated, result lines can be edited (e.g. feedback, re-working or finalisation of a critical reference sample). If the selection of result lines from the drop-down menu are limited, edit and save a result line as a blank record and then re-enter this record with the intent to edit. The full complement of result lines should now be available for use.

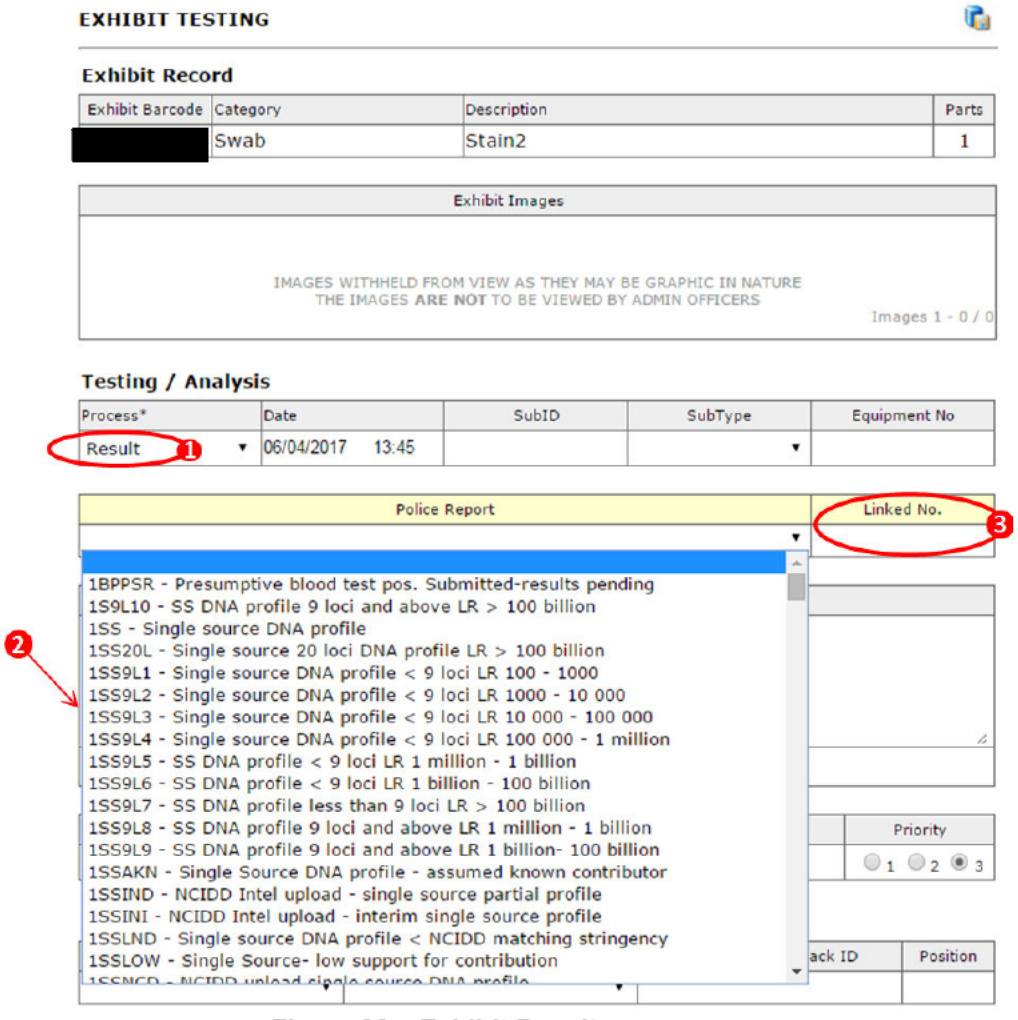


Figure 28 – Exhibit Result

Once all exhibit result lines have been entered a 'Profile Review' process should be ordered (Figure 51) which removes the sample from the PDA list and adds it to the appropriate review list.

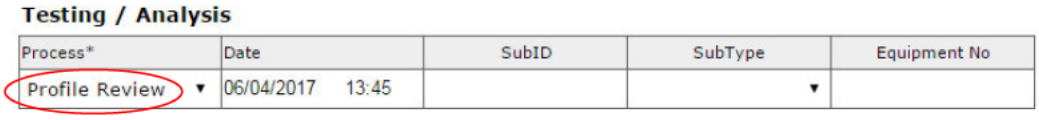


Figure 29 – Profile Review

These result lines can be checked by clicking on the 'PDA Robot' icon . Any discrepancies will be highlighted by a red cross and should be investigated prior to PDA review.

An additional process is required for four person mixtures with an LR in the range 'Mix – Support for contribution 2 to 1 million':

1. Await request from the reviewer for a new task
2. Create a Request / Task from the Case Management tab
3. Allocate this task to the reviewer
4. Select 'CM' as the Request Type
5. In the 'Comments' field add
    a. Sample barcode: XXX
    b. Result reported: Mixed DNA profile
    c. LR reported: Mix – Support for contribution 2 to 1 million; Person barcode XXX
    d. Actual LR: (Value); Person barcode XXX
6. Click the save icon

The exhibit result line associated with removing a profile from NCIDD should not have anything in the Linked No. field (Section 11.1.3).

If a sample undergoes further processing after review, a complete set of new exhibit result lines should be entered (supersedes any previously reported result lines).

19 Case Files

Generally speaking, cases without a statement are managed paperlessly. A paper case file can be created at any stage if it is necessary for efficient case management or if a statement is required (Appendix 8 – Creating and Tracking a Case File).

For cases with paper case files tracked in non-FR LIMS requiring further work or tracking:

1. 'Remove' the case file from the non-FR LIMS storage and add an audit entry 'Removed to track in FR'
2. Create and track this case file in FR as per Appendix 8 – Creating and Tracking a Case File using the existing case file barcode
3. Add a note to the 'Exhibit Notes & FSS Advice' field stating the case file was previously tracked in non-FR LIMS

It is not necessary for epgs within a case file to be labelled; instead a copy of the PDA page can be printed to accompany the epg(s). The PDA page contains all of the sample and interpretation information and can be associated with the epg via its barcode.

Case notes (e.g. GMO notes) are stored in 'Paperless' folders stored in Evidence Recovery, Reporting and Admin areas.

19.1 Case File Storage and Movement

Case files should be tracked at all times. FR storage locations are represented by a nine or ten digit barcode and a description. Each scientist has their own FR storage location, with additional storage locations assigned for general case file storage.

General FR case file storage locations are detailed in Table { **SEQ Table * ARABIC** }.

Table { SEQ Table * ARABIC } – General Case File Storage Locations

Location barcode	Location description	Physical location	Purpose	AUSLAB location
[redacted]	FRIT In-tray - PDA (Paper file)	Block 3	Ongoing case files for PDA	FRITCM
	FRIT In-tray - PDA Review (Paper file)	Block 3	Paper case file requires PDA review	MIXACT
	FRIT In-tray - Case Files for Reporting	Block 3	Case files created by admin for statement	FRITCM
	FRIT In-tray - Statement Review	Block 3	Statements for review	STAREV
	Admin In-tray - No Further Testing Review (Admin)	Block 6	Paper case file, no statement, new pages added, requires admin review	FBPR1
	Admin In-tray - Case File Finish	Block 6	Case file requires filing	FBCFF1
	Admin In-tray – Statements	Block 6	Admin in-tray for statement finalisation	FBSI24
	Admin In-tray – Scanning	Block 6	Scanning in-tray	
	ER In-tray - Incoming Paperwork	Block 6	ER in-tray	CFLIT

20 Records

Nil

21 Associated Documentation

QIS: 17117 – Procedure for Case Management
QIS: 34245 – Reference Sample Result Management
QIS: 34229 – Explanations of Exhibit Results for FR
QIS: 34006 – Forensic Register Procedure for the Release of Results
QIS: 33744 – Forensic Register Training Manual
QIS: 34064 – Miscellaneous Analytical Procedures and Tasks
QIS: 34281 – Procedure for the Use and Maintenance of the Forensic DNA Analysis Elimination Databases

QIS: 34308 – Procedure for Intelligence Reports and Interstate / Interpol Requests in the Forensic Register
QIS: 34112 – STR fragment analysis of PowerPlex® 21 profiles using GeneMapper™ ID-X software

22 Amendment History

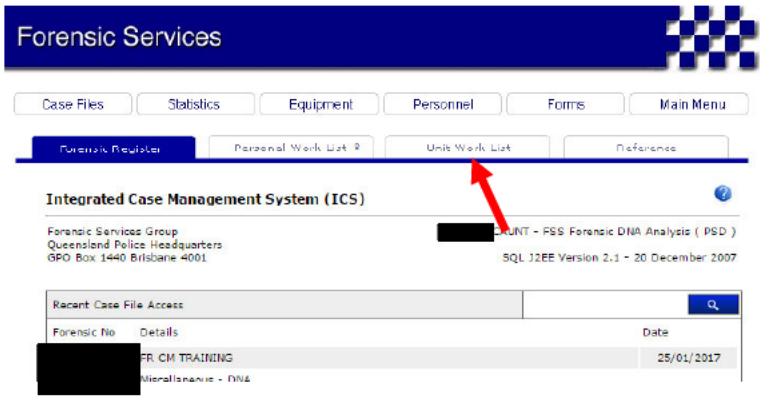
Version	Date	Updated By	Amendments
1	May 2017	E. Caunt	First issue
2	October 2019	A. Keller and J. Entwistle	Incorporated comments including audit recommendations; Incorporated FR enhancements including automatic ordering of NCIDD process; Added appendices; Moved Profiler Plus processes to appendix; General edit of document
3	January 2022	A. Keller and J. Entwistle	Incorporated comments; Upgraded template; Removed Appendix 5; Added Flowchart to Appendix 14

23 Appendices

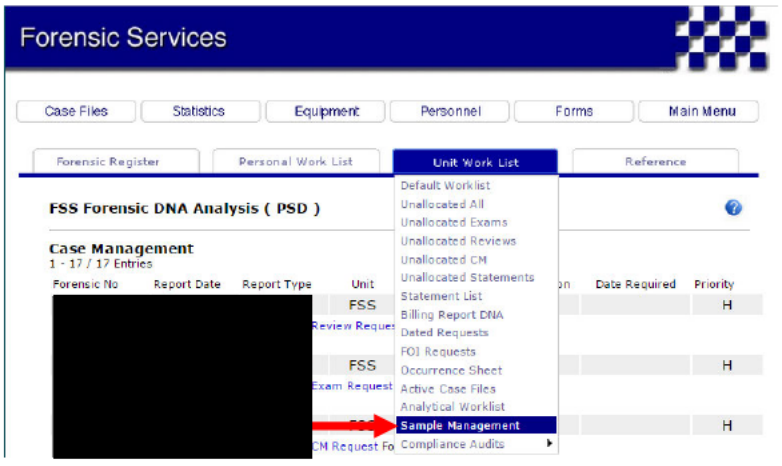
23.1 Appendix 1 – Navigation for Profile Data Analysis

Following log-in, click on 'Forensic Register' button

Click 'Unit Work List' tab

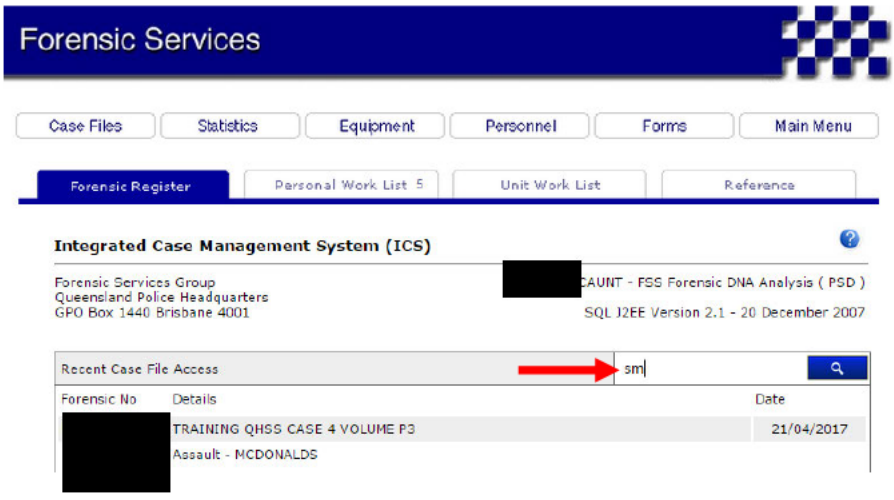


Click 'Sample Management'

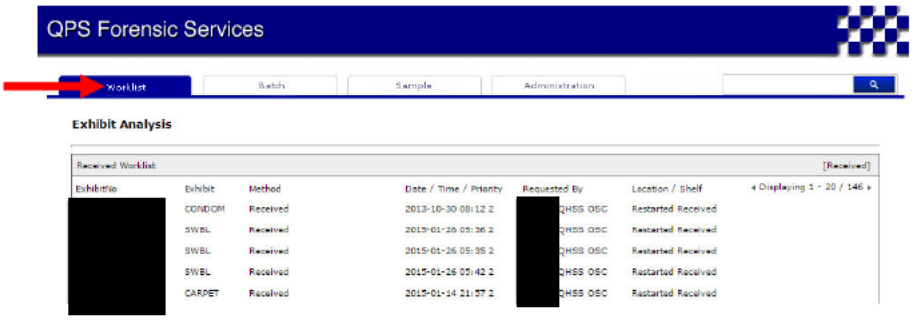


This will open a new tab in Chrome

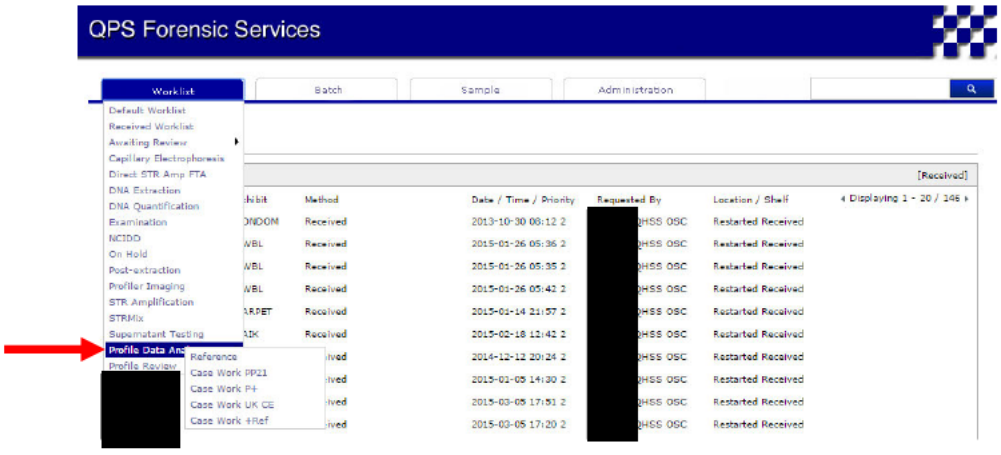
Alternatively, entering ‘sm’ into the search field will take you to the same place



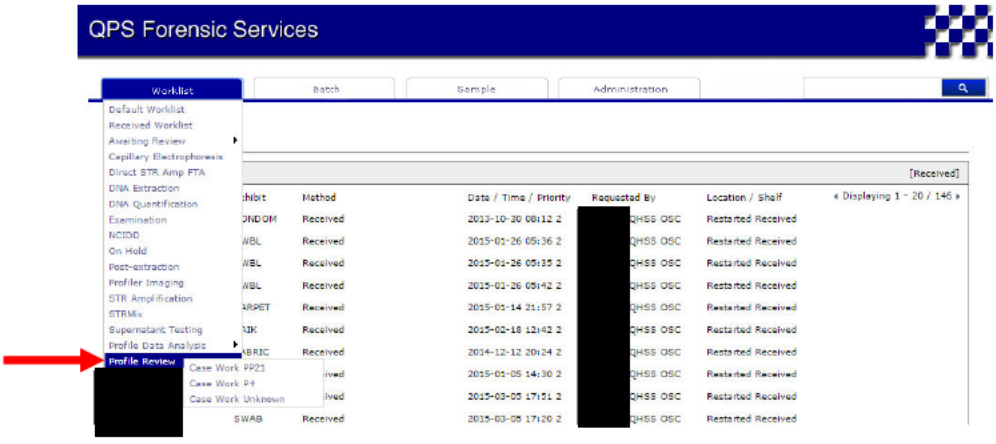
Click the ‘Worklist’ tab



Hover over ‘Profile Data Analysis’ and this will bring up the menu of PDA worklists. Clicking on the appropriate list title will open the list

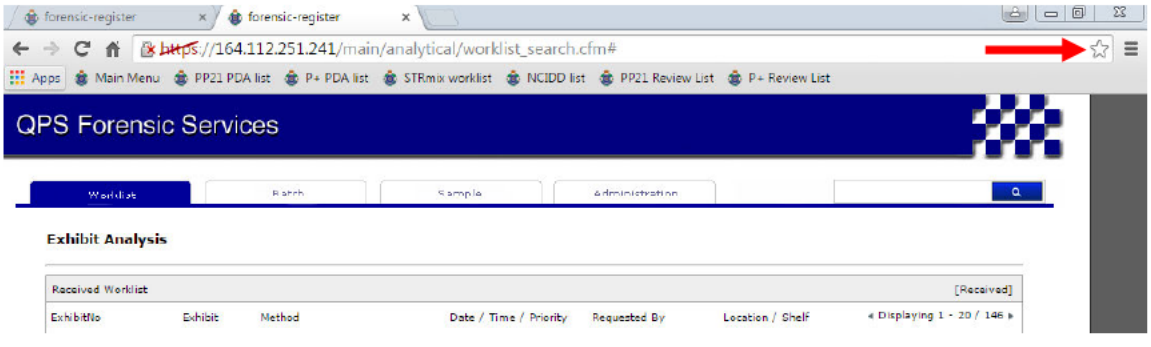


Hover over 'Profile Review' and this will bring up the menu of review worklists. Clicking on the appropriate list title will open the list

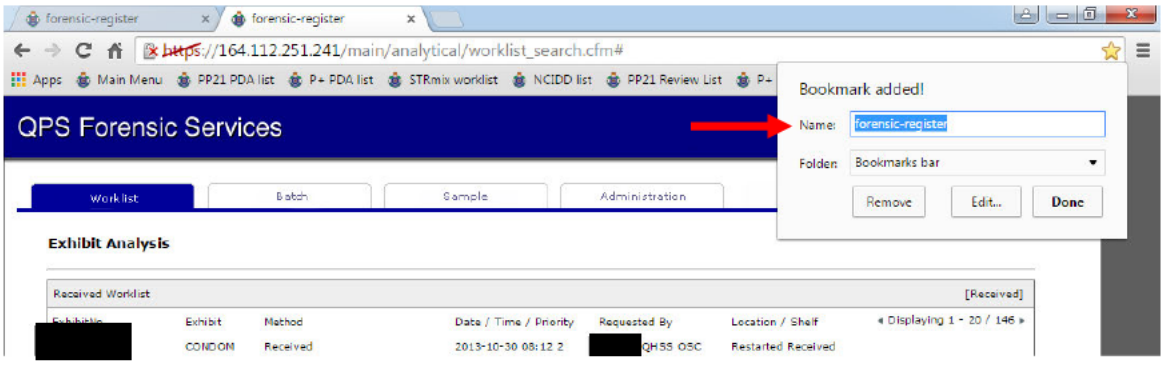


You can bookmark any page in the FR to your tool bar as follows

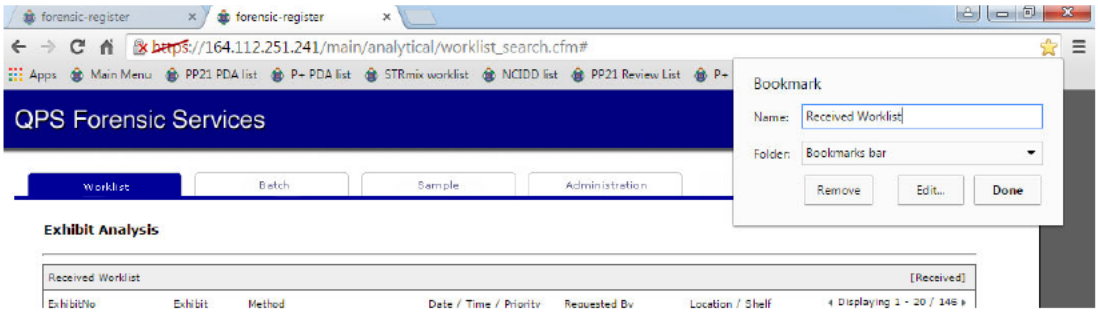
When on the page that you would like to bookmark, click the star in the toolbar



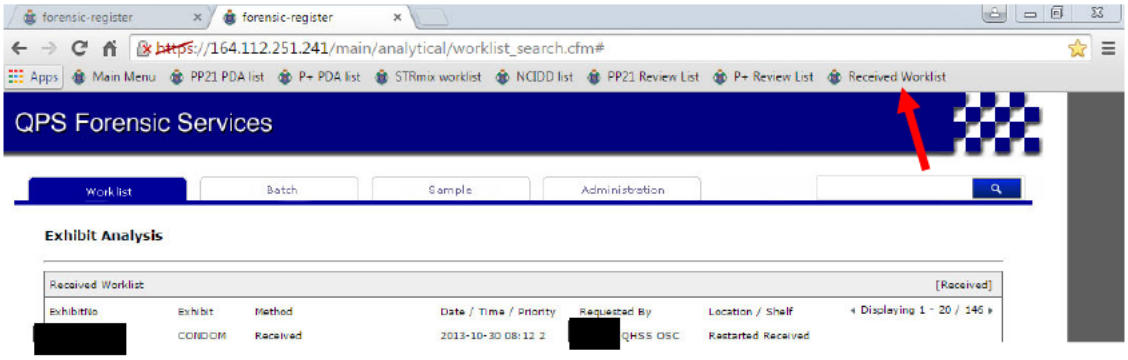
This will bring up a window for you to name your book mark



Type in a name for your book mark and click 'Done'



Your book mark will appear on your tool bar



Also refer to QIS 34006 Section 4.1.1 for Navigation to PDA Worklists

23.2 Appendix 2 – Profile Data Analysis (PDA) Worklists (Crime Scene)

The PDA worklists for casework are detailed in Table 1. These worklists populate and sort in the same way.

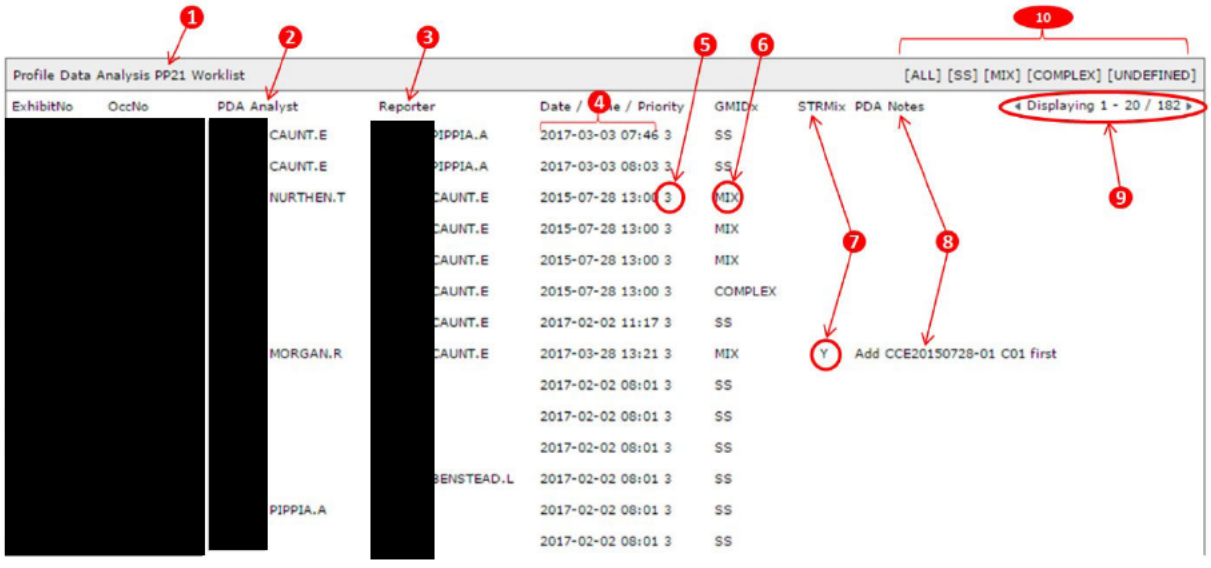
A sample populates the relevant PDA list under the following circumstances:

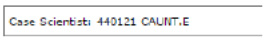
- The GeneMapper file has been uploaded and a profile PDF has been added, unless a QFLAG is raised in which case the sample will populate the 'On Hold' list
- Upon completion of the STRmix process which requires validation of the STRmix page
- The sample is manually inserted onto the PDA list

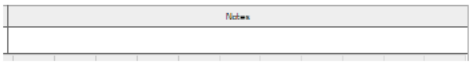
Samples processed through PP21 will populate onto lists based on the amp batch type and priority. If there is no amp batch present, the sample will populate the 'UK CE' worklist.

For the 'PP21 + Ref' worklist, all validated mixture and single source samples for a particular case populate this worklist when any associated reference samples are finalised.

The PDA lists are structured as shown below:



1. Name of worklist
2. Name of PDA Analyst for sample (assigned by clicking icon on the PDA page)
3. Name of PDA Analyst / Reporter for entire case. Displayed as 

on the PDA page (Appendix 7 – Allocating a Case to a Reporter / Profile Analyst)
4. Date and time that the sample was received
5. Priority of the sample
6. Reflection of plate readers UD1 comment in GeneMapper
    a. If the UD1 comment contains 'SS', 'MIX' or 'COMPLEX' then the sample will appear on the list as 'SS', 'MIX' or 'COMPLEX' respectively;
    b. If the UD1 comment does not contain 'SS', 'MIX' or 'COMPLEX' then the sample will appear on the list as 'UNDEFINED'
7. If the sample has populated the PDA list following STRmix analysis, a 'Y' will populate the STRMix column
8. Notes from the 'Notes' field on the PDA page 

9. Number of samples on the list. You can navigate between pages by clicking on the arrows
10. Filters for filtering the list based on profile type (also refer to QIS 34006 Section for Filtering Samples on Worklists – Section 4.3.1). You can search for a particular barcode by entering it on the Worklist tab page

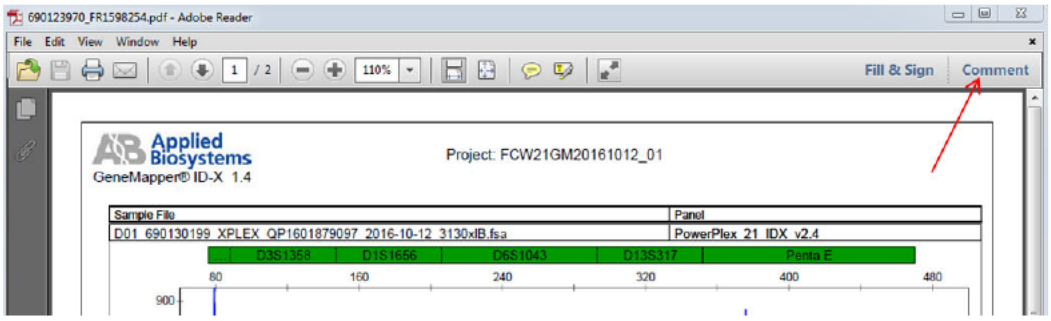
Samples are removed from the list under the following circumstances:

- The sample is added to the STRmix worklist
- A rework is ordered
- A 'Profile Review' process is ordered (with subsample barcode if applicable)
- A 'Reallocate' process is ordered

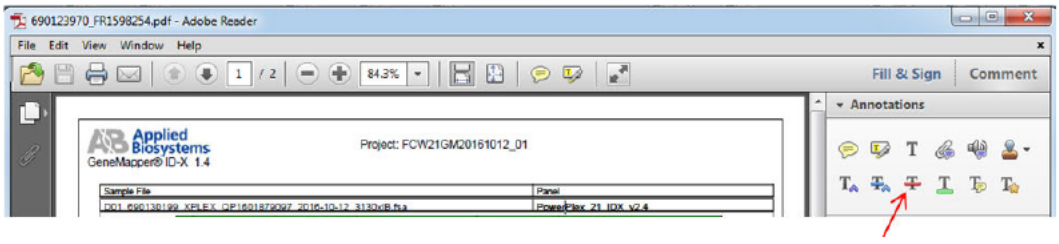
23.3 Appendix 3 – Amending PDFs

Open epg as PDF

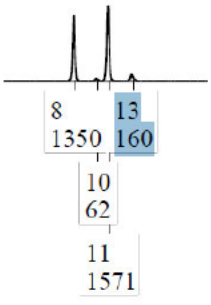
On PDF click 'Comment'



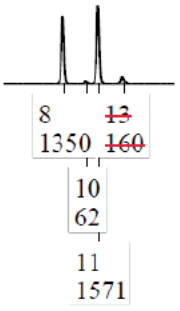
Under 'Annotations' click the strikethrough icon



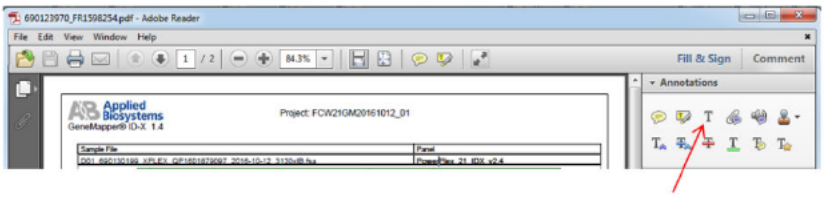
Highlight the text to be crossed out



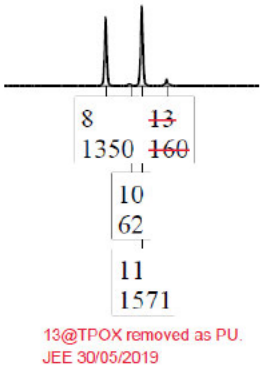
The text will strikethrough



Click the text icon and place the cursor where you need to add text



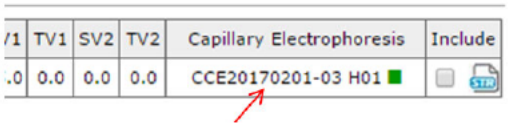
Add a note explaining the reason for the edit and add your initials and date



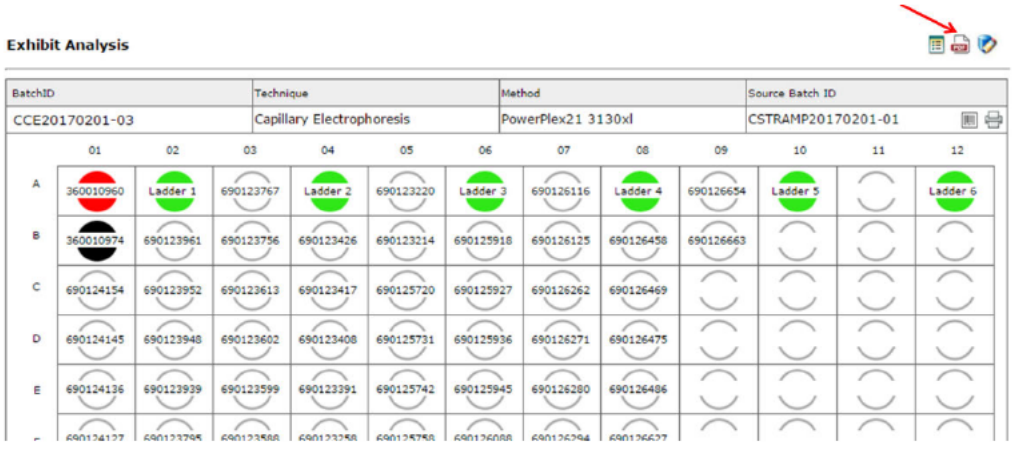
Save the edited PDF to a convenient location with the file name in the format 'CE position number-sample barcode-QP number-suffix' eg H01-690123970-QP1699999978-EJC

The file name requires a suffix to ensure that any previously uploaded PDFs are not overwritten

Open the CE batch for the PDF that has been edited



Click the icon in the top right corner of the batch page



Drag the amended PDF into the box or select the file from its location, click 'Start Upload', click the icon to save. The PDF should now be accessible from the PDA page of the sample

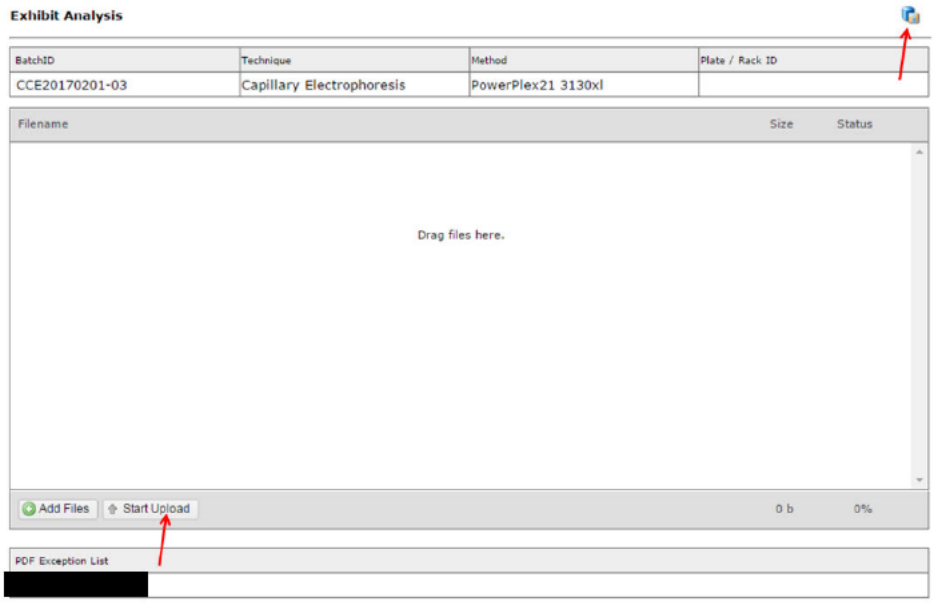
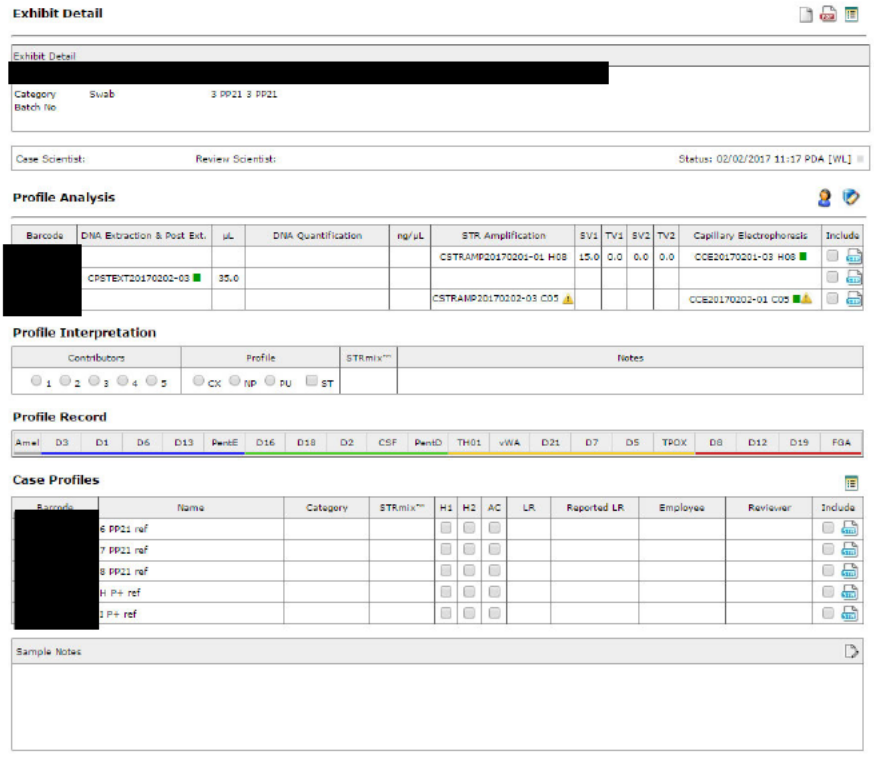


Exhibit Analysis
BatchID
Technique
Method
Plate / Rack ID
CCE20170201-03
Capillary Electrophoresis
PowerPlex21 3130xl
Filename
Size
Status
Drag files here.
Add Files
Start Upload
0 b
0%
PDF Exception List

23.4 Appendix 4 – Profile Data Analysis of a Single Source PP21 Profile for NCIDD

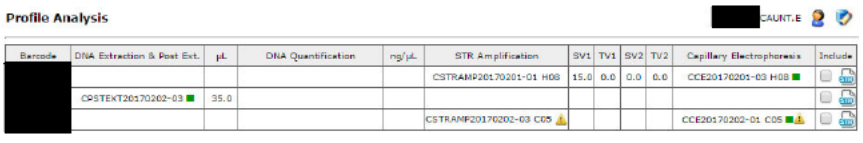
A request for further information may be necessary before proceeding with the PDA of a sample. For example, establishing the ownership of an exhibit taken from a piece of intimate clothing such as underwear, to enable the conditioning of a sample. Refer to QIS 34006 Section 4.4.15 as well as QIS 34006 Sections 4.4.4 and 4.4.5 for detailed steps on accessing further information from cases and associated samples.

The PDA page for a sample yet to be interpreted will look like this



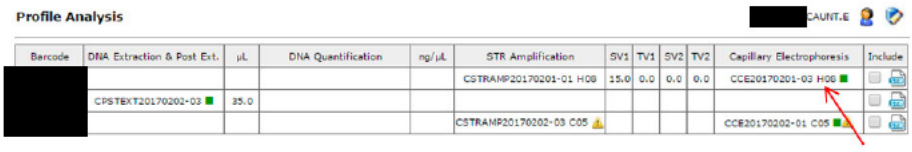
The first action is to allocate the sample to yourself by clicking on the icon

Your name will appear next to the icon



Batch records can be accessed by clicking on the batch id

The GeneMapper record and profile PDFs can be found by clicking on the position next to the appropriate CE batch id

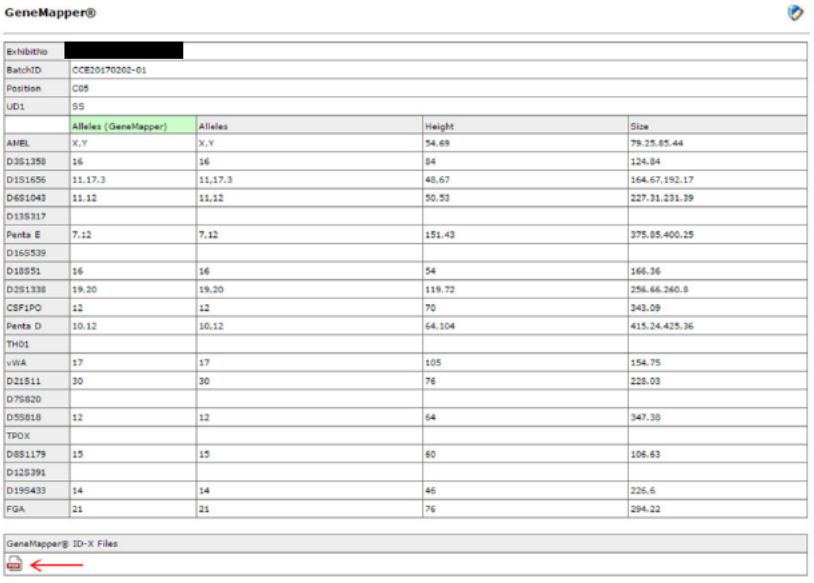


Profile Analysis

[redacted] CAUNT.E

Barcode	DNA Extraction & Post Ext.	µL	DNA Quantification	ng/µL	STR Amplification	5V1	TV1	5V2	TV2	Capillary Electrophoresis	Include
[redacted]					CSTRAMP20170201-01 H08	15.0	0.0	0.0	0.0	CCE20170201-03 H08	
	CPSTEXT20170202-03	85.0									
					CSTRAMP20170202-03 C05					CCE20170202-01 C05	

This will open a new window. The profile PDFs can be opened by clicking on the icon.



GeneMapper®

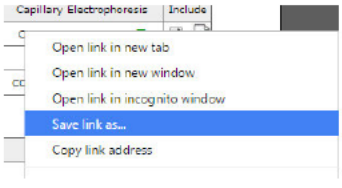
ExhibitNo	[redacted]
BatchID	CCE20170202-01
Position	C05
UD1	SS

	Alleles (GeneMapper)	Alleles	Height	Size
AMEL	X,Y	X,Y	54.69	79.25.85.44
D3S1358	16	16	84	124.84
D1S1656	11,17.3	11,17.3	48.67	164.67.192.17
D6S1043	11.12	11,12	50.53	227.31.231.39
D13S317				
Penta E	7,12	7,12	151.43	375.85.400.25
D16S539				
D18S51	16	16	54	166.36
D2S1338	19,20	19,20	119.72	256.66.260.8
CSF1PO	12	12	70	343.09
Penta D	10,12	10,12	64.104	415.24.425.36
TH01				
vWA	17	17	105	154.75
D21S11	30	30	76	228.03
D7S820				
D5S818	12	12	64	347.38
TPOX				
D8S1179	15	15	60	106.63
D12S391				
D19S433	14	14	46	226.6
FGA	21	21	76	294.22

GeneMapper® ID-X Files

All available profile PDFs can be accessed from the PDA page by clicking on the icon, followed by 'Open All' or individual icons.

The STRmix input files are accessed directly from the FR. Clicking the icon will download the STRmix input file for the associated casework run. This input file can be saved to the desktop or other convenient location for access from STRmix. Alternatively, right clicking on the icon will allow the file to be saved directly.



When setting up the STRmix analysis **only the QP number is to be entered into the 'Case Number' field and only the barcode of the casework sample is to be entered into the 'Sample ID' field**. This is also the case when running LRs. If additional information is to be added, such as the barcode of the reference sample, then this can be added to the 'Case Notes' field.

Once the STRmix analysis is complete, the STRmix macro should be run and the PDFs uploaded into the FR as follows:

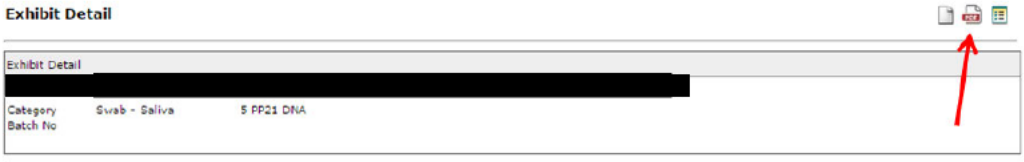
- Run the STRmix macro QIS: 35009 – MoveSTRmixPDF Macro

- The STRmix files and PDF will be stored to I:\STRmix Results and a copy of the PDF will be stored in the FR upload folder (shortcut on desktop)
- The FR upload folder should be emptied at regular intervals as this is only a transient storage location. A copy of the PDF will always be stored in I:\STRmix Results

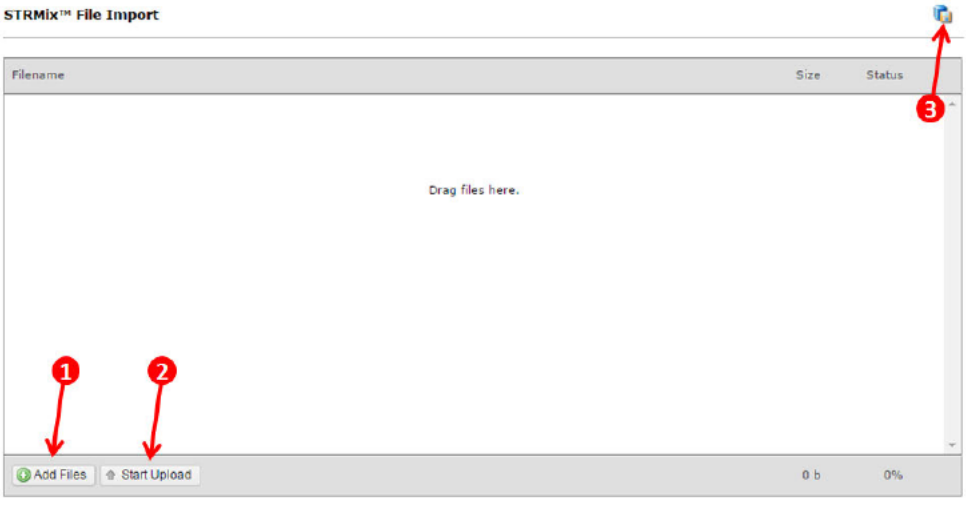
The macro will name the PDF such that the FR will file the PDF in the correct place. This naming convention is based on the 'Case Number' and 'Sample ID' fields in STRmix, therefore if additional information is added into these fields the FR cannot file the PDFs appropriately.

Upload STRmix PDF into the FR as follows:

1. From the PDA page of the crime scene sample, click the icon in the top right corner



2. Drag and drop all of the STRmix PDFs pertaining to that sample into the window or click on 'Add Files' (1) and browse. Once all files are listed in the window, click 'Start Upload' (2) and then click the save icon (3)

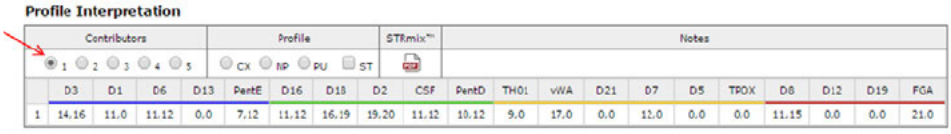


All of the STRmix PDFs will file in the appropriate places. If you have STRmix PDF files for multiple samples they can all be dragged into the window at the same time regardless of which sample the window was opened from and they will all file appropriately.

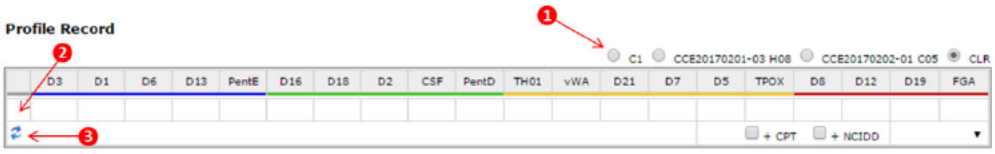
Now you can complete the PDA page

Click the edit icon

Check the '1' circle in the Profile Interpretation table

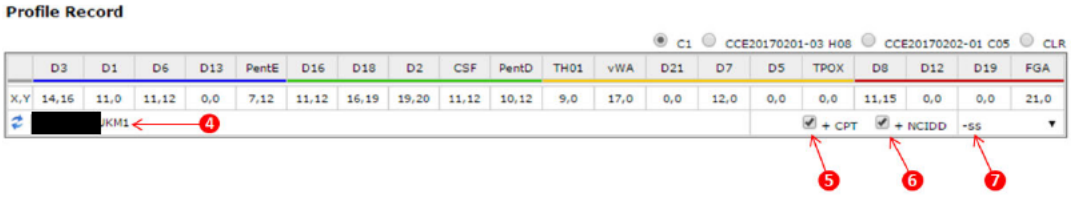


Copy down the profile into the profile record table by checking the 'C1' circle (1); enter AMEL (2) and click the search button (3)

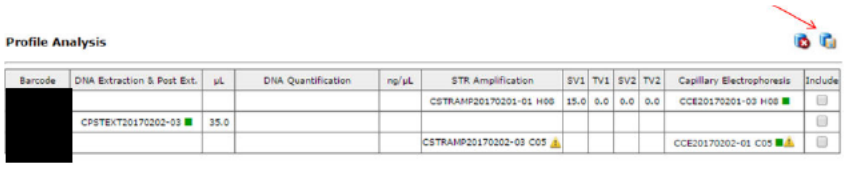


New Unknown

Check that you agree with the FR designation of UKM1 (4) for this sample. If UKM1 does not match any reference samples and is a new unknown for the case, check the '+CPT' box (5); check the '+NCIDD' box (6) and select the '–ss' suffix from the drop-down menu (7)



Click 



Option 1

Whilst still on the PDA page, click the  icon above the Profile Interpretation table. This will open a 'Result' page with automatically populated result lines generated from the completed fields of the PDA page (up to three result lines at a time, repeat this process if more are required). Check that you agree with these result lines. Click

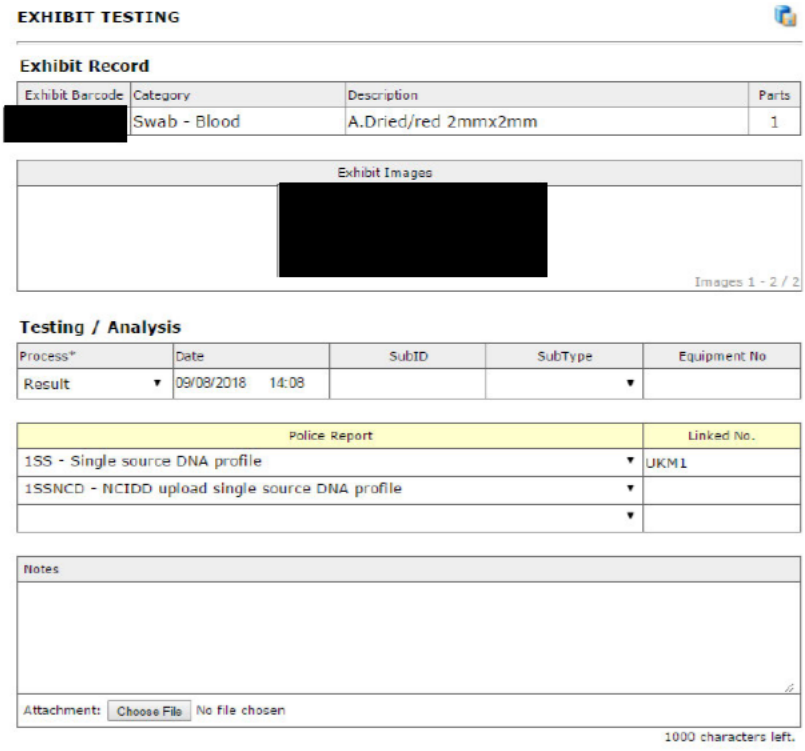


EXHIBIT TESTING

Exhibit Record

Exhibit Barcode	Category	Description	Parts
[redacted]	Swab - Blood	A.Dried/red 2mmx2mm	1

Exhibit Images

[redacted]

Images 1 - 2 / 2

Testing / Analysis

Process*	Date	SubID	SubType	Equipment No
Result	09/08/2018 14:08			

Police Report	Linked No.
1SS - Single source DNA profile	UKM1
1SSNCD - NCIDD upload single source DNA profile	

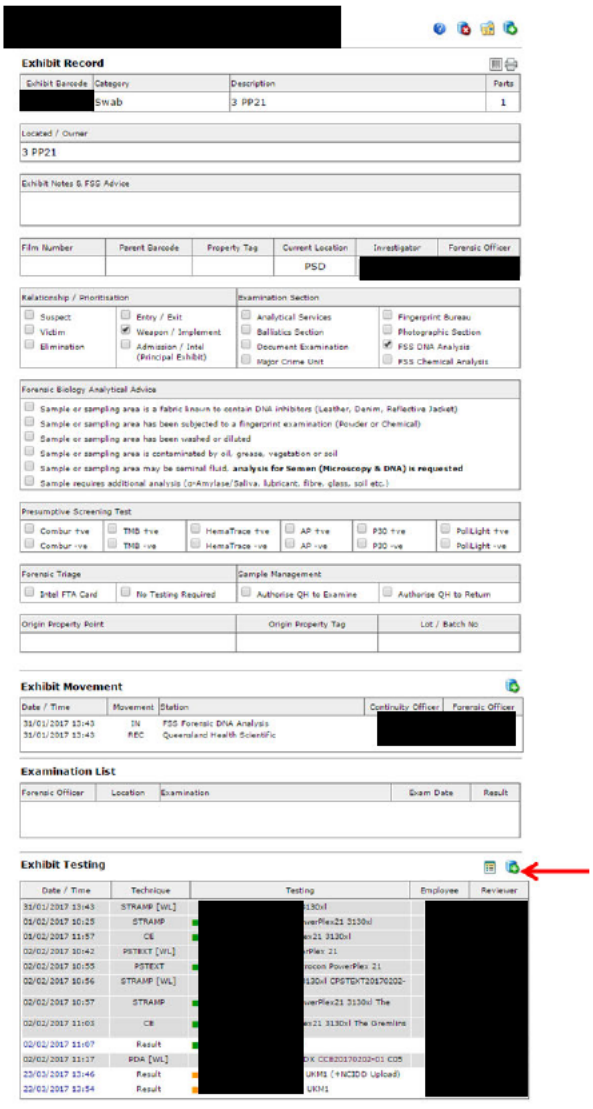
Notes

Attachment: Choose File No file chosen

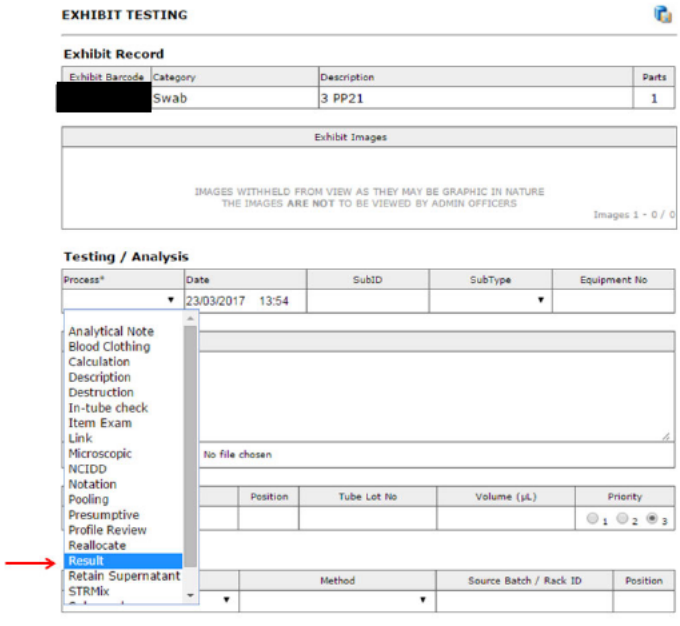
1000 characters left.

Option 2

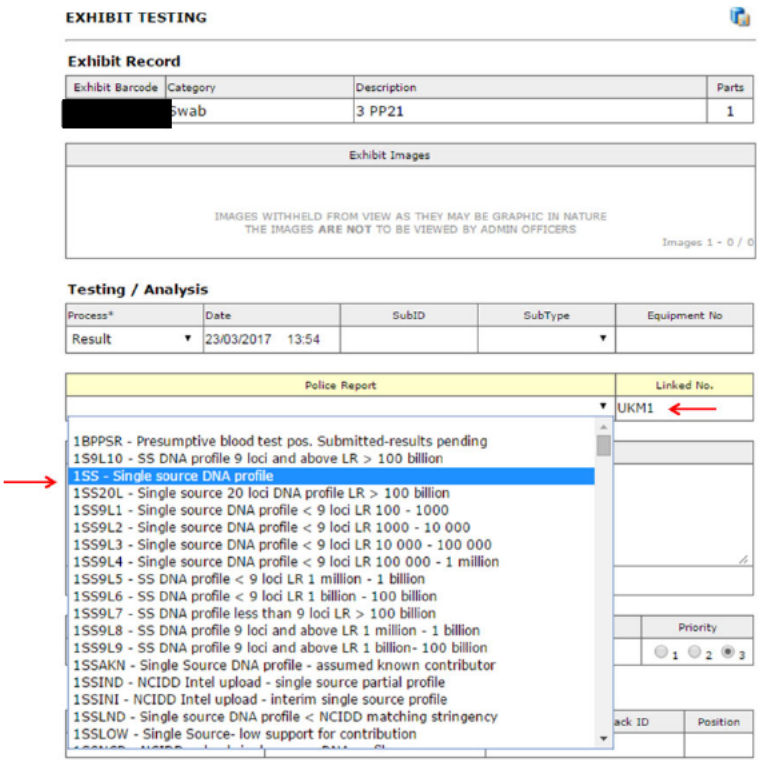
From the PDA page, either click to access the Exhibit Testing / Examinations table on the Exhibit Testing / Movement page OR click the sample barcode to access the Exhibit Testing table as shown below. In both cases, then click the icon



Select the process of 'Result' from the drop-down list

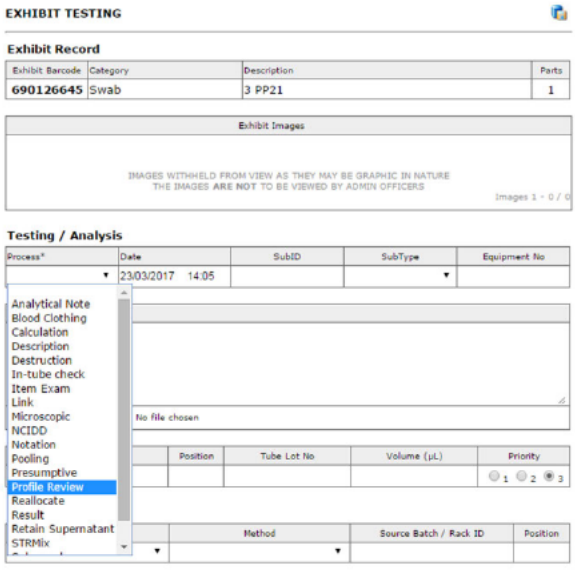


Select the result lines from the drop-down menu and enter the designation in the 'Linked No.' field



Click 

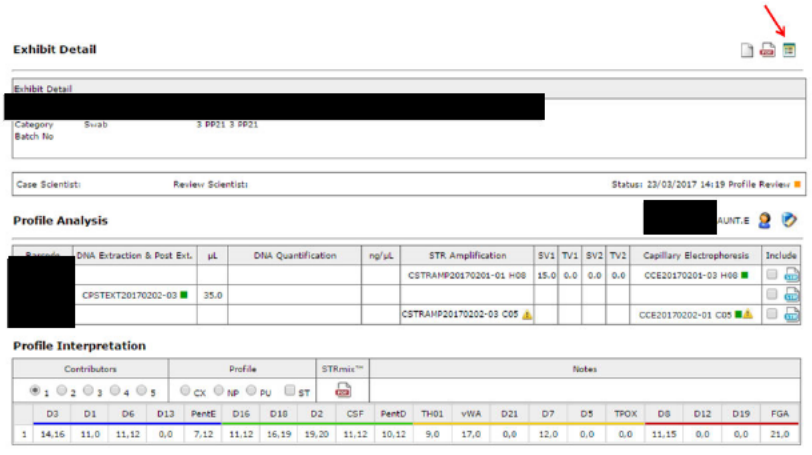
Once all exhibit report lines have been entered, order a process of 'Profile Review'. Click 



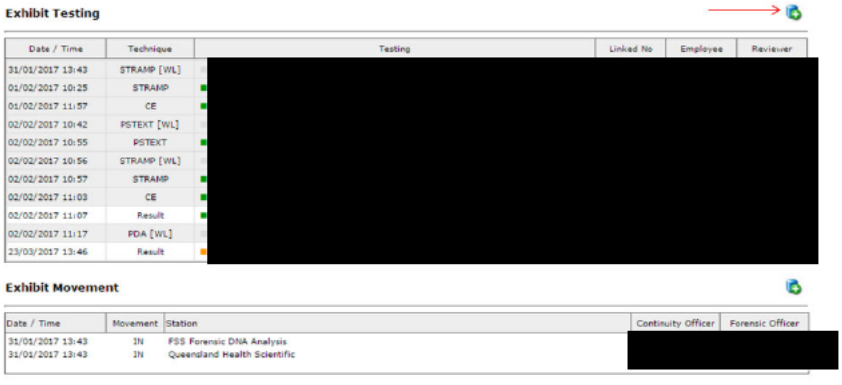
This will remove the sample from the PDA list and add it to the Profile Review list

The Exhibit Testing table should look something like this

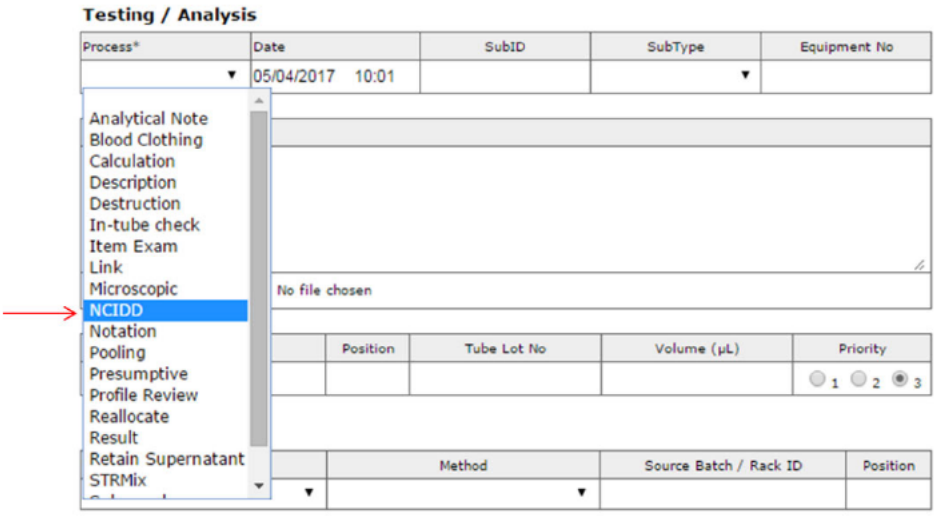
Check an NCIDD process has been added to send the profile to the NCIDD worklist (this process should be ordered automatically when the 'NCIDD' box on the PDA page is ticked and the record is saved). If not, click on the icon in the top right corner of the PDA page



This will take you to the exhibit testing table. Click the icon



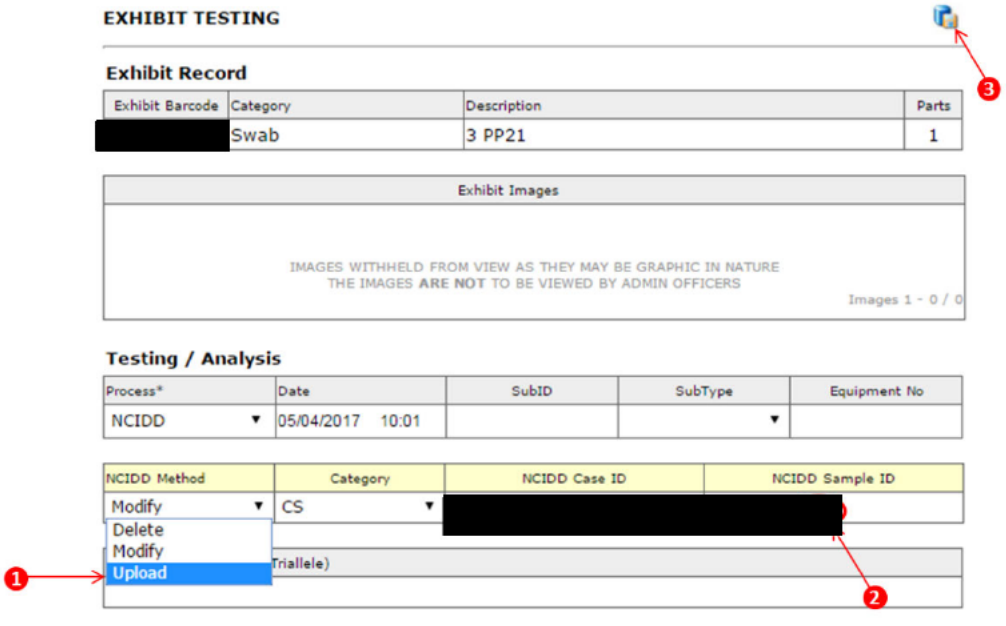
Select the process of 'NCIDD' from the drop-down list



Select the NCIDD Method of 'Upload' from the drop-down box (1)

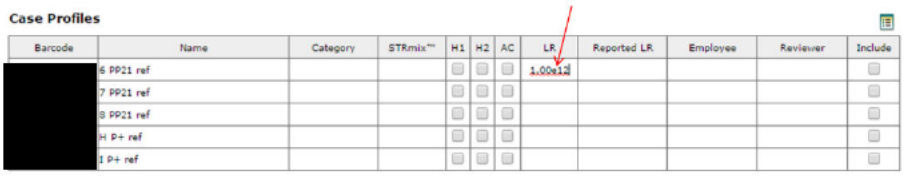
Enter the suffix of '-ss' into the NCIDD Sample ID (2)

Click save (3)



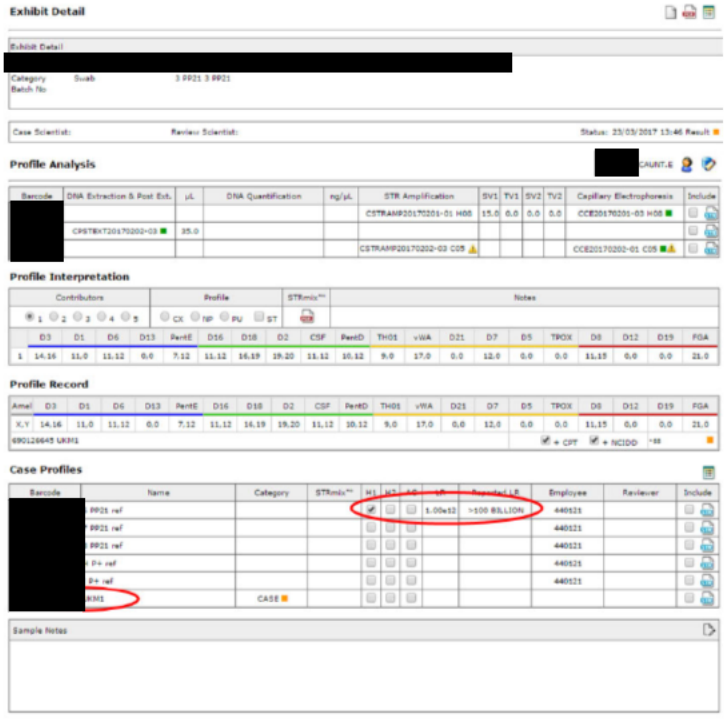
New Reference Comparison

If a previously designed unknown from a crime scene sample now matches a new reference sample for the case, then the Case Profiles table on the PDA page needs updating. Click and type "1.00e12" into the 'LR' box associated to the matching reference sample

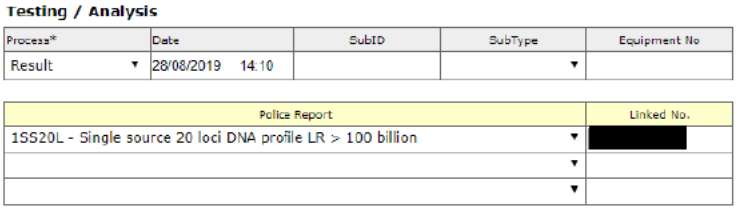


Click

The PDA page will now look like this



Associate the matching reference sample to the unknown by adding the reference sample barcode to the 'Association' column of the unknown. Click the icon above the Profile Interpretation table to update the associated result line



Click

Once the result line has been updated, order a process of 'Profile Review'. Click

23.5 Appendix 5 – PowerPlex 21 Priority 3 Workflow

Profiles assessed as complex:

- Check 'CX' box on PDA page
- Enter result 'CMPU' (complex unsuitable)
- Order 'Profile review'

Single source profiles:

If sub-threshold peaks are present but they do not affect the interpretation, report as per below with the extra result line 'PSTI' (possible sub-threshold information). If at any point the number of contributors is ambiguous, an assessment of suitability needs to be made (is the profile complex). Also, consider the possibility that the profile is a two contributor mixture.

Single source profile, <6 alleles

- Check '1' box on PDA page
- No STRmix required
- Enter result '1SSUND' (Single source DNA profile- unsuitable for NCIDD searching)
- Order 'Profile review'

Single source profile, ≥ 6 & <12 PP21 alleles

- Check '1' box on PDA page
- No STRmix required
- Enter result '1SSLND' (Single source DNA profile < NCIDD matching stringency)
- Order 'Profile review'

Single source profile, ≥ 12 PP21 alleles

- Check '1' box on PDA page
- Deconvolution in STRmix either by PDA analyst or HP2
- STRmix file imported
- Unknown person assigned
- Uploaded to NCIDD if appropriate
- Enter result
- Order 'Profile review'

For detailed steps, refer to Appendix 4 – Profile Data Analysis of a Single Source PP21 Profile for NCIDD.

2 to 4 contributor mixtures:

Even 2 to 3 contributor mixtures, no reference sample

- Check '2' or '3' box on PDA page
- Deconvolution in STRmix not required
- Enter result '2MX' or '3MX' and NSIP (no statistical interpretation performed)
- Order 'Profile review'

Major / minor mixed profile, expected to resolve, no reference sample

2 contributor mixture

- Check '2' box on PDA page
- Deconvolution in STRmix as 2p either by PDA analyst or HP2
- STRmix file imported

- Unknown persons assigned
- Major uploaded to NCIDD if appropriate
- Enter result of '2MX'
- Check NCIDD upload line entered if appropriate (intel or mix)
- Order 'Profile review'

3 contributor mixture with 2 contributors in the minor / 4 contributor mixture with 3 contributors in the minor (rework recommended)

- Check '3' or '4' box on PDA page
- Deconvolution in STRmix as 3 or 4p either by PDA analyst or HP2
- STRmix file imported
- Unknown person assigned
- Major uploaded to NCIDD if appropriate
- Enter result '3MX' or '4MX'
- Check NCIDD upload line entered if appropriate (intel or mix)
- Order 'Profile review'

Major / minor mixed profile, expected to resolve, reference samples

2 contributor mixture, reference sample matches major (check for the possiblity of conditioning through ownership – QIS 34006; Section 4.4.15)

- Check '2' box on PDA page
- Deconvolution and LR in STRmix as 2p either by PDA analyst or HP2
- STRmix file imported
- Unknown person assigned if any
- Major uploaded to NCIDD if appropriate
- Enter result '2MX'
- Enter reference comparison result
- Check NCIDD upload line entered if appropriate (intel or mix)
- Order 'Profile review'

3 contributor mixture with 2 contributors in the minor, reference sample matches major (check ownership – QIS 34006; Section 4.4.15) / 4 contributor mixture with 3 contributors in the minor, reference sample matches major (rework recommended, check ownership – QIS 34006; Section 4.4.15)

- Check '3' or '4' box on PDA page
- Deconvolution and LR in STRmix as 3 or 4p either by PDA analyst or HP2
- STRmix file imported
- Unknown person assigned if any
- Major uploaded to NCIDD if appropriate
- Enter result '3MX' or '4MX'
- Enter reference comparison result
- Check NCIDD upload line entered if appropriate (intel or mix)
- Order 'Profile review'

Reference samples received after initial PDA finalised (CW+Ref list):

See as per above where there is an associated reference sample. Reworks must be considered at this stage if there is any doubt as to the number of contributors.

23.6 Appendix 6 – STRmix Workflow

For STRmix troubleshooting, refer to QIS 17117.

The Profile Analyst will use the 'Contributors' section in the 'Profile Interpretation' table to inform the HP2 of the number of contributors for the STRmix analysis.

The Profile Analyst will use the 'Include' check boxes on the PDA page to inform the HP2 of the parameters for the STRmix analysis.

The 'Include' boxes in the 'Profile Analysis' table show which runs are to be used in the deconvolution; the 'Include' boxes in the 'Case Profiles' table show which reference samples are to be used in the LR. The 'AC' box in the 'Case Profiles' table is used to show that the associated reference sample is to be conditioned.

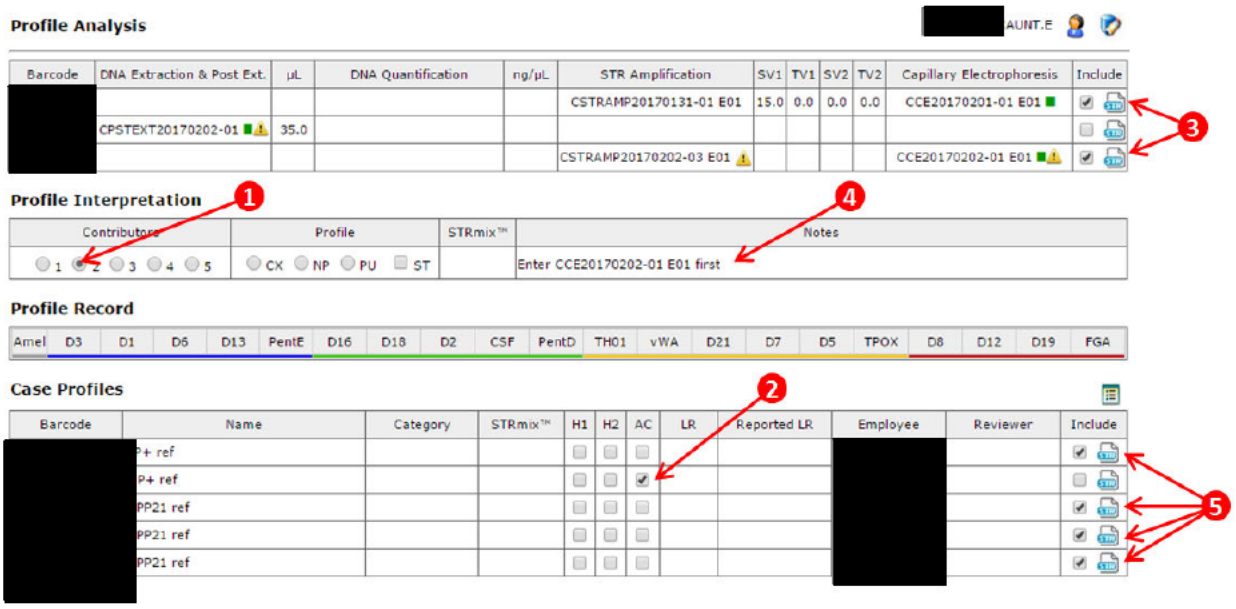
Any further instructions will be entered into the 'Notes' box such as:

- STRmix version
- Extra processing (e.g. re-deconvolution or increased iterations)
- CE instrument
- Dropped loci (e.g. vWA)

In instances where a profile has more than 12 alleles at a locus, the STRmix file may need to be modified prior to analysis.

The example below shows that the STRmix analysis needs to be performed as follows:

1. Two contributors
2. Condition on "H P+ ref"
3. Include two CE runs
4. Any further instructions
5. Calculate LRs for the remaining four reference samples



If a deconvolution already exists and to request that LRs only are performed, add a note 'LRs only' and check the include boxes for the reference samples that require LRs.

The sample now needs to be added to the 'STRMix' worklist by requesting a STRmix deconvolution from the Exhibit Testing / Examinations table. This is done by adding the 'Technique' of 'STRMix'. The method of 'Deconvolution' adds by default and does not preclude the addition of LRs to the list. For samples with dilutions, the Profile Analyst should add the dilution barcode to the SubID field on the STRmix request page. To highlight that the STRmix process needs to be ordered on the dilution barcode, add 'STRmix: DILN' to the 'Notes' box on the PDA page.

Worklist

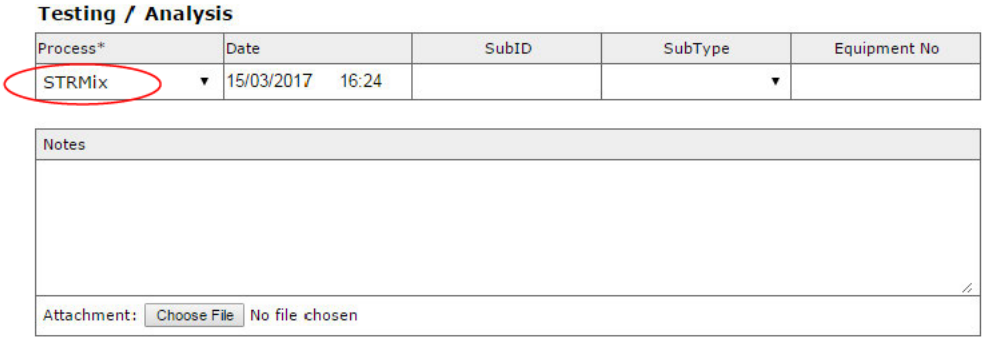
Technique*	Method	Source Batch / Rack / NCIDD ID	Position
STRMix ▾	Deconvolution ▾		

The sample will now be on the STRMix worklist.

STRMix Worklist

ExhibitNo	Exhibit	Method	Date / Time / Priority	Requested By
[redacted]	SWAB	Deconvolution	2017-03-01 15:16 2	[redacted]PSD
	SWAB	Deconvolution	2017-03-15 16:18 3	PSD

When the HP2 takes a sample to run the STRmix analysis the first action is to order a STRmix process. If the sample has the PDA note 'STRmix: DILN', check the sample has a dilution and then order the STRmix process using the dilution barcode in the SubID field.



Testing / Analysis

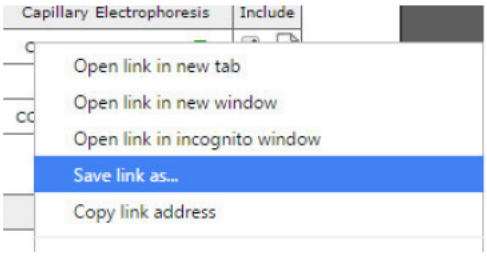
Process*	Date	SubID	SubType	Equipment No
STRMix ▾	15/03/2017 16:24		▾	

Notes

Attachment: Choose File No file chosen

This will remove the sample from the STRmix worklist, thereby preventing anybody else from running the same analysis, and simultaneously add the sample to the STRmix Review worklist. The HP2 will then run the STRmix analyses. If a sample with a dilution needs to be removed from the STRmix worklist, order a reallocate with the dilution barcode in the SubID field. Check the sample has only been removed from the STRmix worklist.

The HP2 will access the STRmix input files directly from the FR. Clicking the  icon will download the STRmix input file for the associated casework run or reference sample. This input file can be saved to the desktop or other convenient location for access from STRmix. Alternatively, right clicking on the  icon will allow the file to be saved directly.



When setting up the STRmix analysis only the QP number (or FR number if there is no QP number) is to be entered into the 'Case Number' field and only the barcode of the casework sample is to be entered into the 'Sample ID' field. This is also the case when running LRs. If additional information is to be added then this can be added to the 'Notes' field.

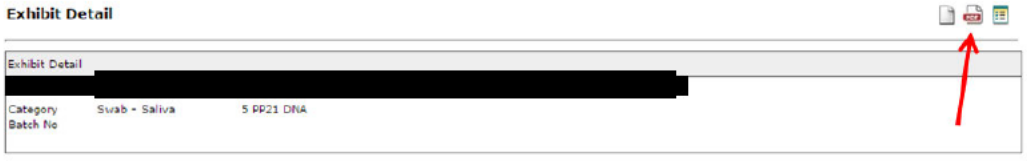
Once the STRmix analysis is complete, close the PDF generated by STRmix. The STRmix macro may be run and the PDFs uploaded into the FR as follows:

1. Run the STRmix macro
2. If not already present, the macro will create a folder called 'FR upload' and add a shortcut to your desktop
3. The STRmix files and PDF will be stored to I:\STRmix Results and a copy of the PDF will be stored in the FR upload folder
4. The FR upload folder should be emptied at regular intervals as this is only a transient storage location. A copy of the PDF will always be stored in I:\STRmix Results

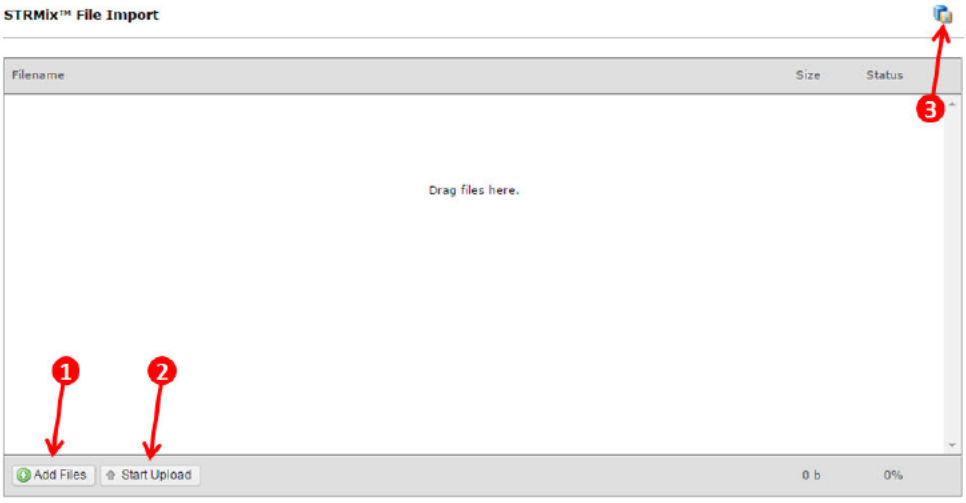
The PDF is named such that the FR will file the PDF in the correct place. This naming convention is based on the 'Case Number' and 'Sample ID' fields in STRmix, therefore if additional information is added into these fields the FR cannot file the PDFs appropriately.

The STRmix PDFs are uploaded into the FR as follows:

1. From the PDA page of the crime scene sample, click the icon in the top right corner



2. Drag and drop all of the STRmix PDFs pertaining to that sample into the window or click on 'Add Files' (1) and browse. Once all files are listed in the window, click 'Start Upload' (2) and then click the save icon (3)



All of the STRmix PDFs will file in the appropriate places. If you have STRmix PDF files for multiple samples they can all be dragged into the window at the same time regardless of which sample the window was opened from and they will all file appropriately.

If an LR has been performed against an unknown profile the STRmix PDF should not be uploaded to the FR using this process, instead the PDF should be attached to a 'Notation' against the sample.

Once the STRmix PDFs have been uploaded, the STRmix process should be closed. Enter into the STRmix process record from the Exhibit Testing table by clicking on the associated date and time.

Click the red '[CLICK TO VALIDATE]' button.

This will remove the sample from the STRmix Review worklist and simultaneously add it to the PDA worklist.

Once a STRmix PDF has been uploaded, it cannot be removed by Forensic DNA Analysis. A second STRmix PDF can be uploaded and it will overwrite the first PDF if the file names are the same.

If a STRmix PDF needs to be completely removed, a Forensic Register Change Request will need to be submitted as follows:

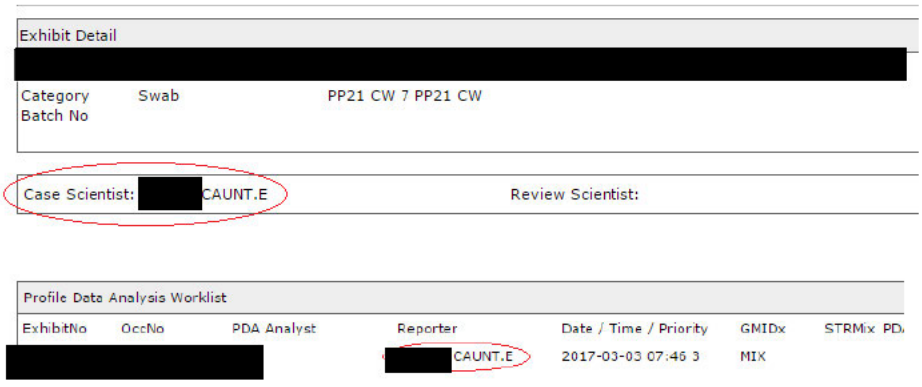
1. Enter into the Exhibit Record for the sample on the Case Management side of the FR
2. Click the  icon in the top right of the screen
3. Complete the change request with the appropriate information

Any STRmix analysis no longer required should not be deleted but moved into a 'Do not use' folder within the relevant case number folder containing all of the STRmix results.

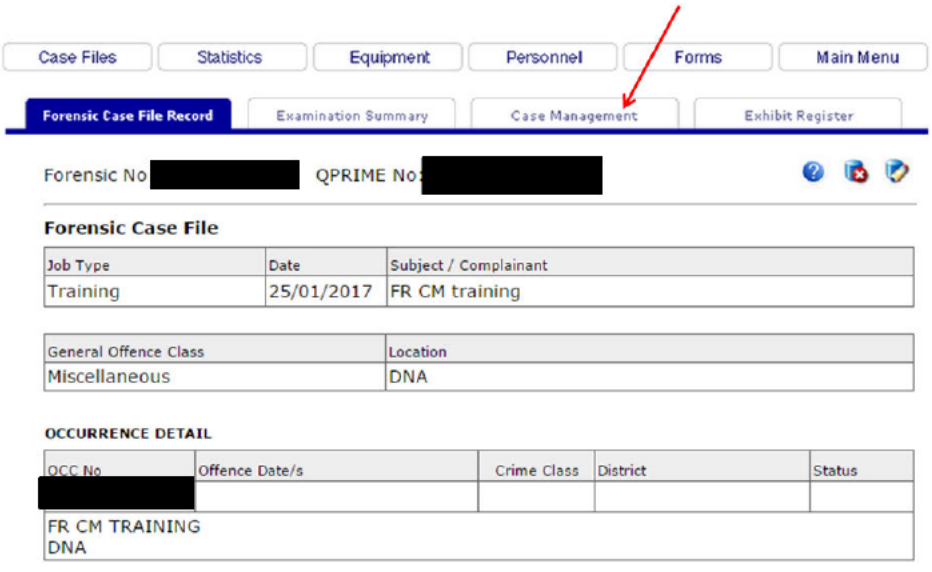
23.7 Appendix 7 – Allocating a Case to a Reporter / Profile Analyst

A whole case may be allocated to a scientist for the purposes of reporting but also during the early stages of a cases progression through the system to assist with consistency and efficiency (e.g. P1, operation, anticipated to be large or unique aspects).

Allocating a case to a scientist for PDA entry adds the name of the nominated scientist to the PDA page for every crime scene sample in the case, including new samples that are received at a later date. The name of the allocated scientist will appear against samples on the PDA and profile review lists.

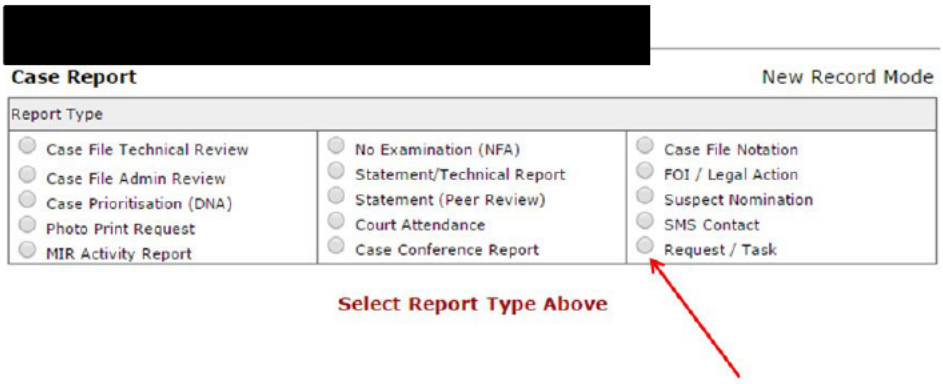


To allocate a case to a scientist enter into the Forensic Case File Record for the case



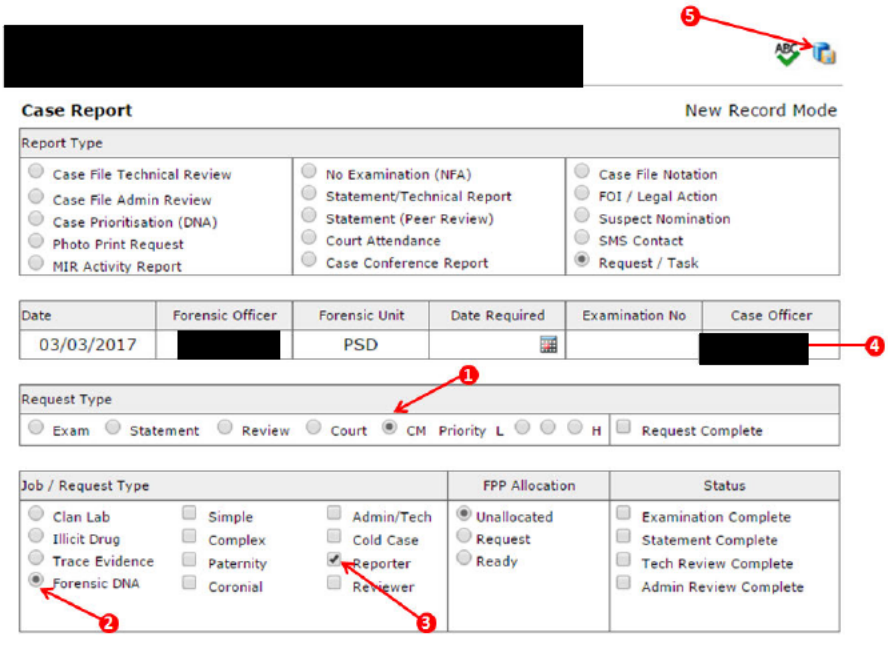
Click the Case Management tab and click the add button

Click Request / Task



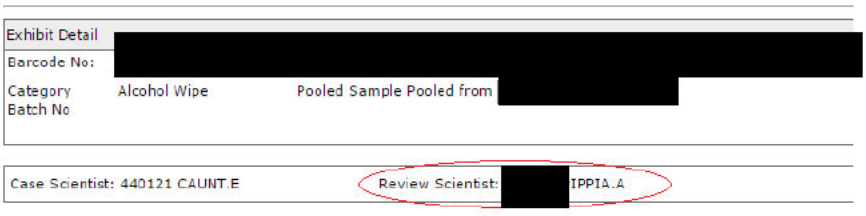
Select the following:

1. CM
2. Forensic DNA
3. Reporter
4. Enter the scientist (QPS user ID) that the case is being allocated to
5. Click save

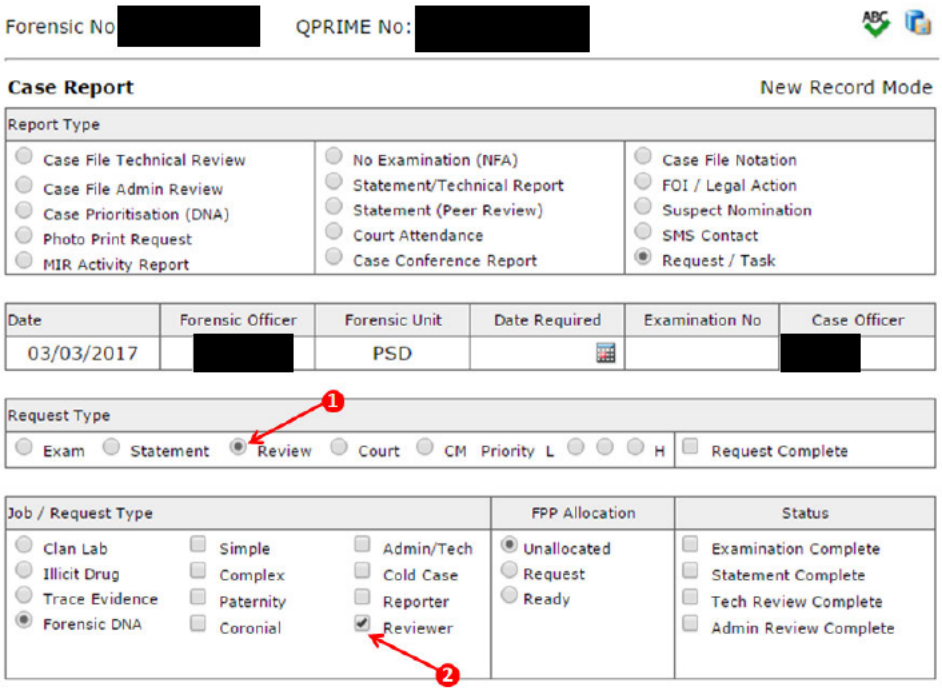


Allocating a Case to a Reviewer

A whole case may be allocated to a scientist for review to assist with reporting, consistency and efficiency. Allocating a case to a scientist for review adds the name of the nominated scientist to the Review Scientist field of the PDA page for every crime scene sample in the case. The name of the allocated review scientist will appear against samples on the profile review lists.

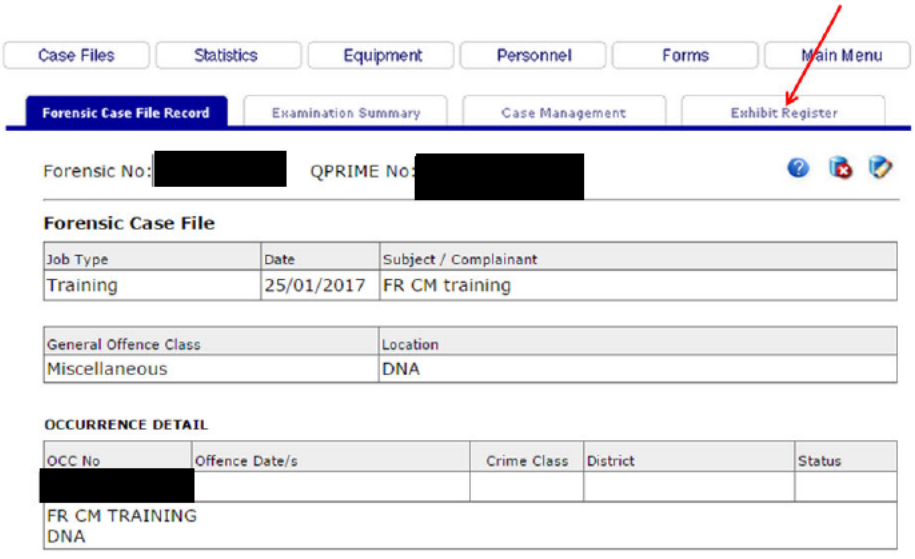


A case is allocated to a reviewer in the same way as allocating the case scientist; however 'Review' and 'Reviewer' are selected in place of 'CM' and 'Reporter' (see 1 and 2 below).



23.8 Appendix 8 – Creating and Tracking a Case File

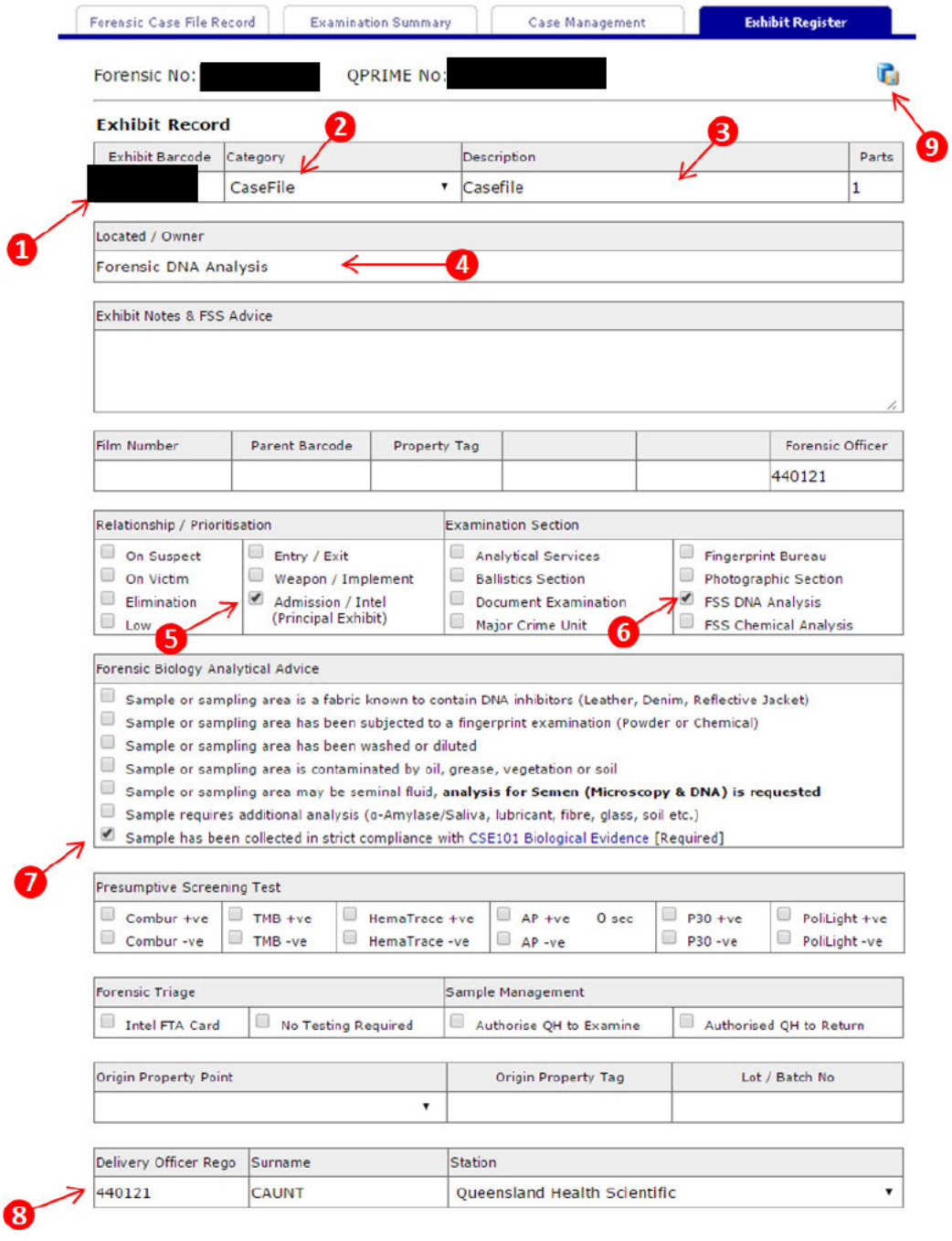
Enter into Forensic Case File Record. Click 'Exhibit Register' tab



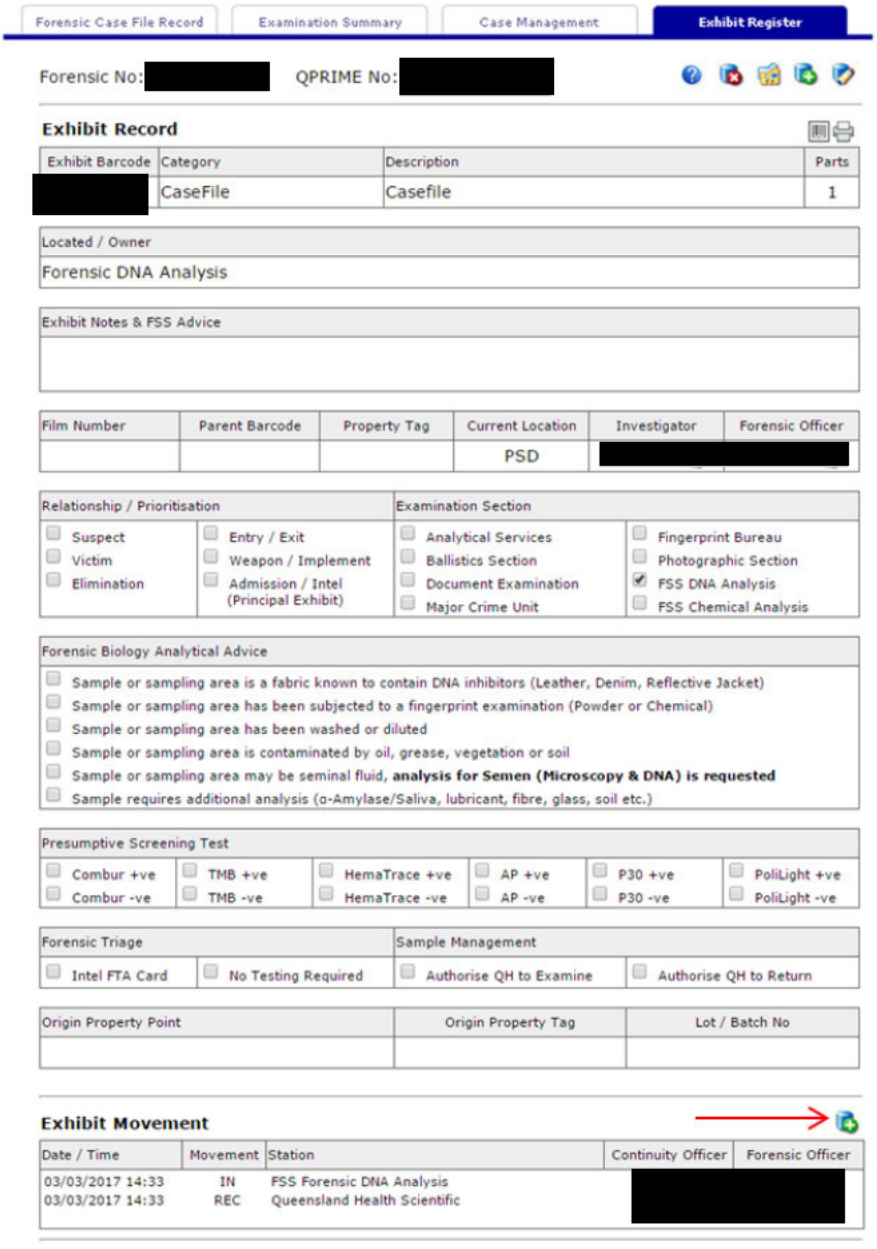
Click the add button

Enter the following information:

1. Barcode of case file (new nine or ten digit number or from existing case file previously tracked in AUSLAB)
2. Select 'CaseFile' from the drop-down list
3. Enter 'Case file' into the description
4. Enter 'Forensic DNA Analysis' into the 'Located / Owner' box
5. Check 'Admission / Intel'
6. Check 'Sample has been collected in strict compliance……'
7. Enter your QPS user ID, check that your surname is correct and select 'Queensland Health Scientific' from the drop-down Station menu
8. Click save



To track the case file, click the add button above the ‘Exhibit Movement’ table



Forensic Case File Record | Examination Summary | Case Management | **Exhibit Register**

Forensic No: [redacted] QPRIME No: [redacted]

Exhibit Record

Exhibit Barcode	Category	Description	Parts
[redacted]	CaseFile	Casefile	1

Located / Owner
Forensic DNA Analysis

Exhibit Notes & FSS Advice

Film Number	Parent Barcode	Property Tag	Current Location	Investigator	Forensic Officer
			PSD	[redacted]	

Relationship / Prioritisation		Examination Section	
☐ Suspect	☐ Entry / Exit	☐ Analytical Services	☐ Fingerprint Bureau
☐ Victim	☐ Weapon / Implement	☐ Ballistics Section	☐ Photographic Section
☐ Elimination	☐ Admission / Intel (Principal Exhibit)	☐ Document Examination	☑ FSS DNA Analysis
		☐ Major Crime Unit	☐ FSS Chemical Analysis

Forensic Biology Analytical Advice
☐ Sample or sampling area is a fabric known to contain DNA inhibitors (Leather, Denim, Reflective Jacket)
☐ Sample or sampling area has been subjected to a fingerprint examination (Powder or Chemical)
☐ Sample or sampling area has been washed or diluted
☐ Sample or sampling area is contaminated by oil, grease, vegetation or soil
☐ Sample or sampling area may be seminal fluid, **analysis for Semen (Microscopy & DNA) is requested**
☐ Sample requires additional analysis (α-Amylase/Saliva, lubricant, fibre, glass, soil etc.)

Presumptive Screening Test					
☐ Combur +ve ☐ Combur -ve	☐ TMB +ve ☐ TMB -ve	☐ HemaTrace +ve ☐ HemaTrace -ve	☐ AP +ve ☐ AP -ve	☐ P30 +ve ☐ P30 -ve	☐ PoliLight +ve ☐ PoliLight -ve

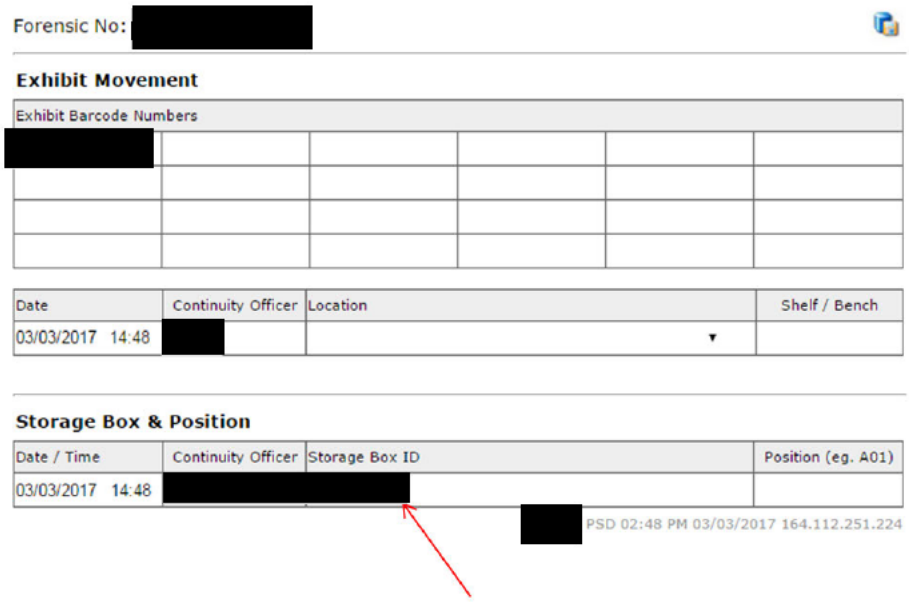
Forensic Triage		Sample Management	
☐ Intel FTA Card	☐ No Testing Required	☐ Authorise QH to Examine	☐ Authorise QH to Return

Origin Property Point	Origin Property Tag	Lot / Batch No

Exhibit Movement

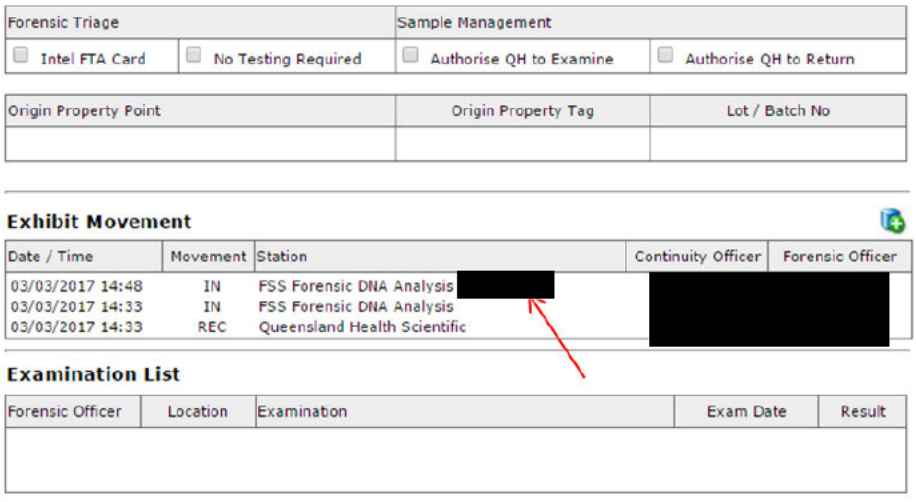
Date / Time	Movement	Station	Continuity Officer	Forensic Officer
03/03/2017 14:33	IN	FSS Forensic DNA Analysis	[redacted]	
03/03/2017 14:33	REC	Queensland Health Scientific		

Enter the number of the storage box where the case file is to be stored in the 'Storage Box ID' field or start typing the name of the storage location and the relevant option will appear for selection (Section 19 and Appendix 12 – Forensic Register Storage Architecture)

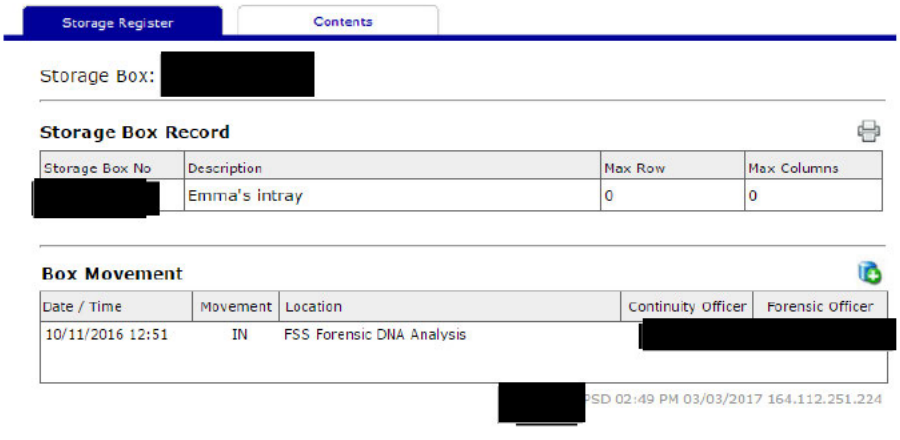


Click save

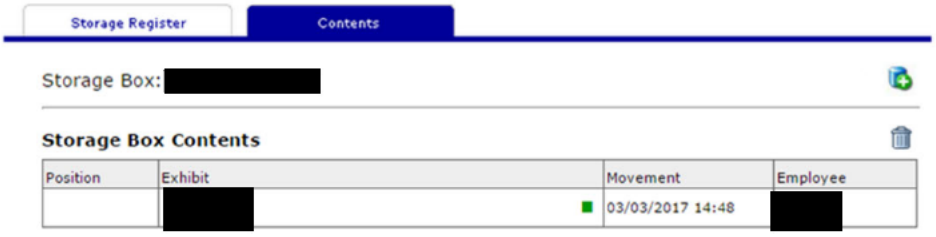
The location of the file will be displayed in the Exhibit Movement table



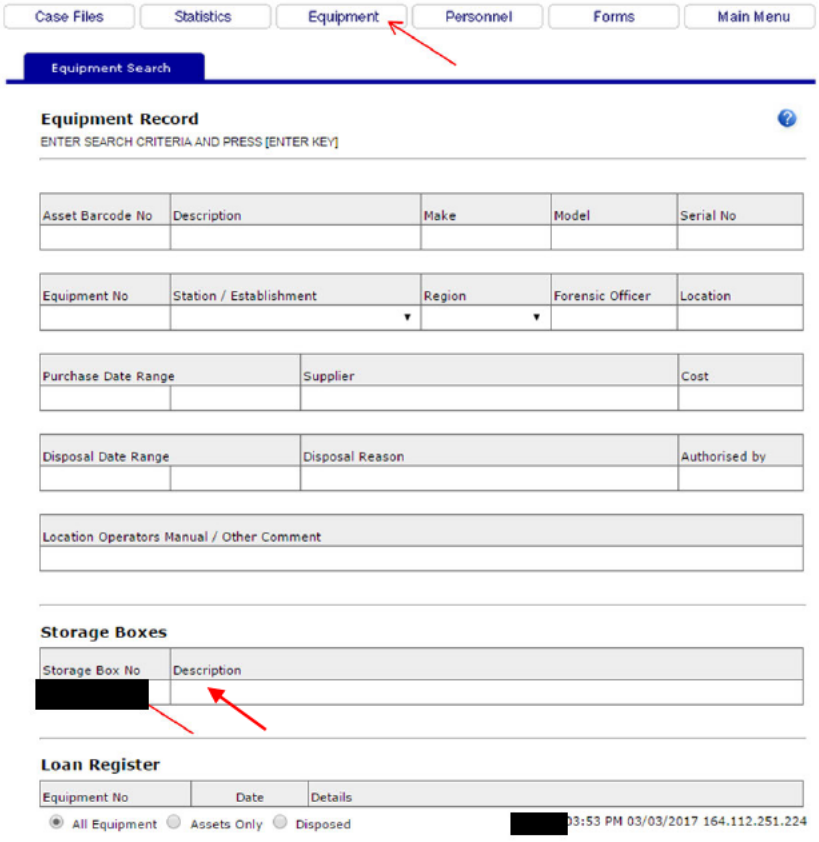
Clicking on the storage location will open the storage box record



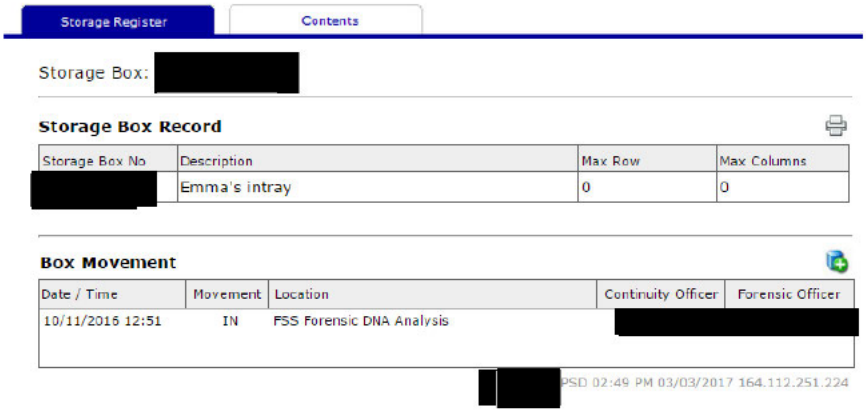
Clicking on the 'Contents' tab will display the contents of the storage box



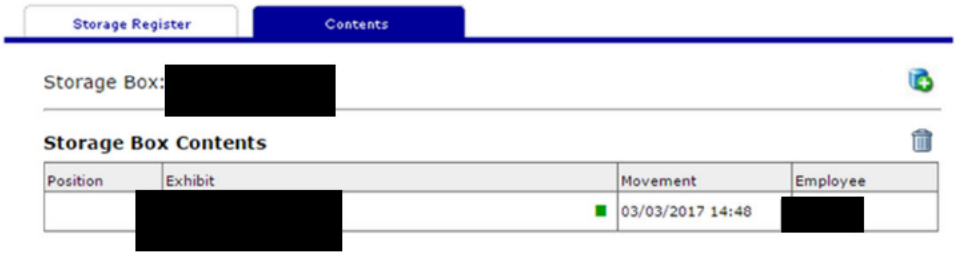
Storage boxes can also be found by clicking on the 'Equipment' tab and searching on the storage box number or the storage box description



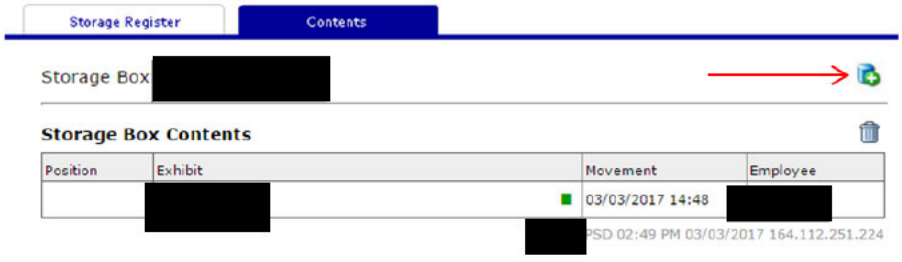
Press 'Enter'



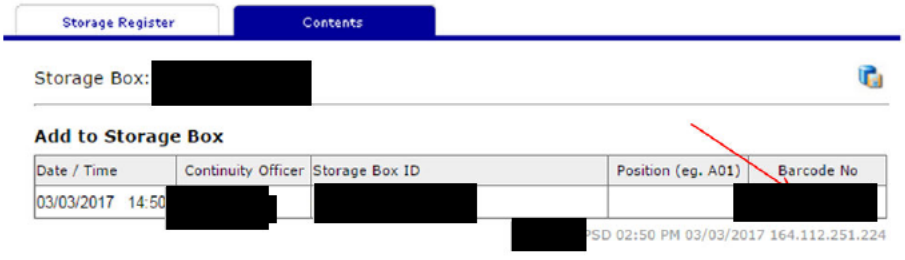
Clicking on the 'Contents' tab will display the contents of the storage box

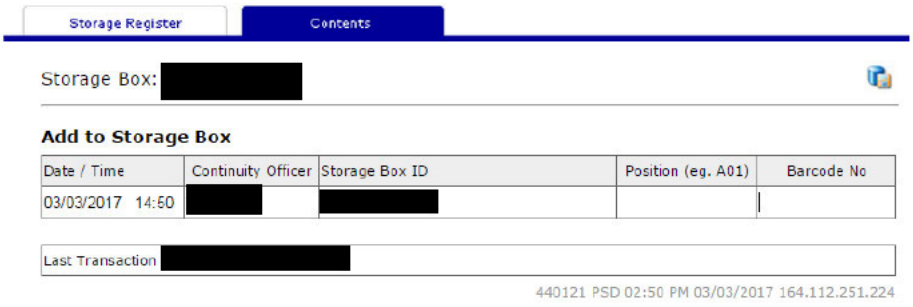


To add an item to a storage box (e.g. case file to intray), click the add button

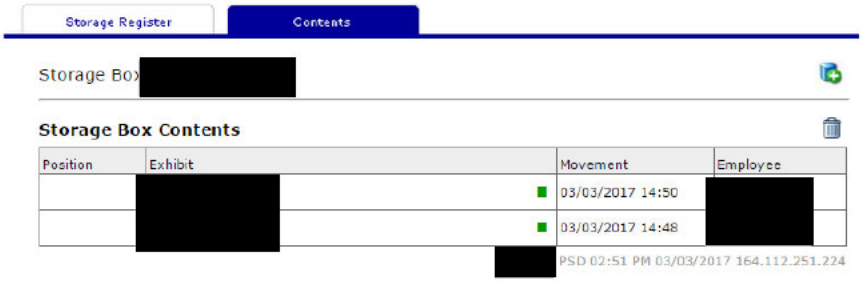


Enter the barcode of the item requiring storage in the 'Barcode No' field and click save

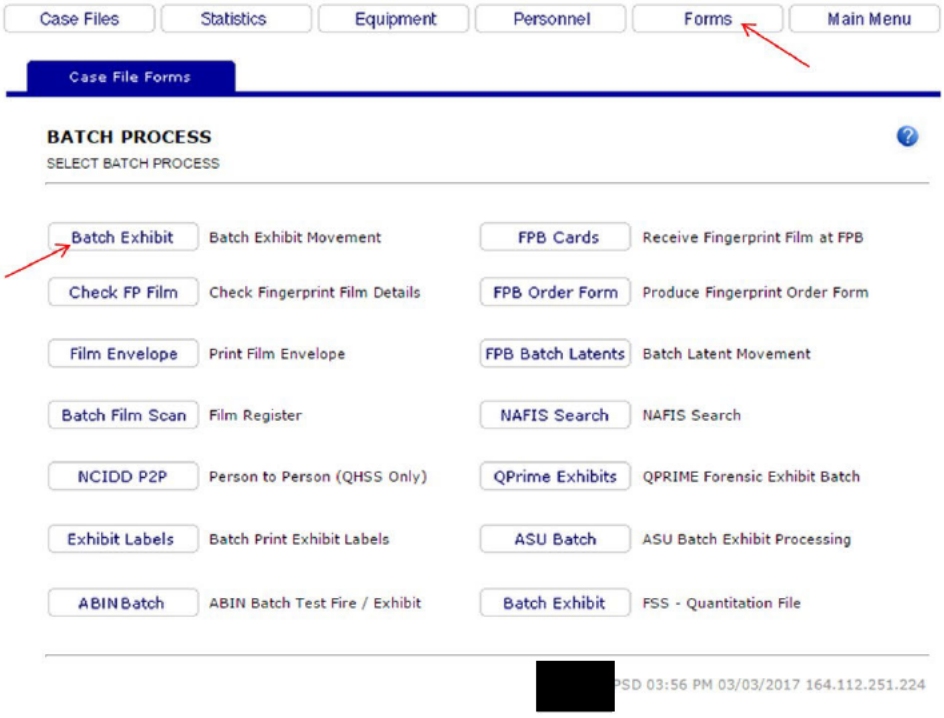




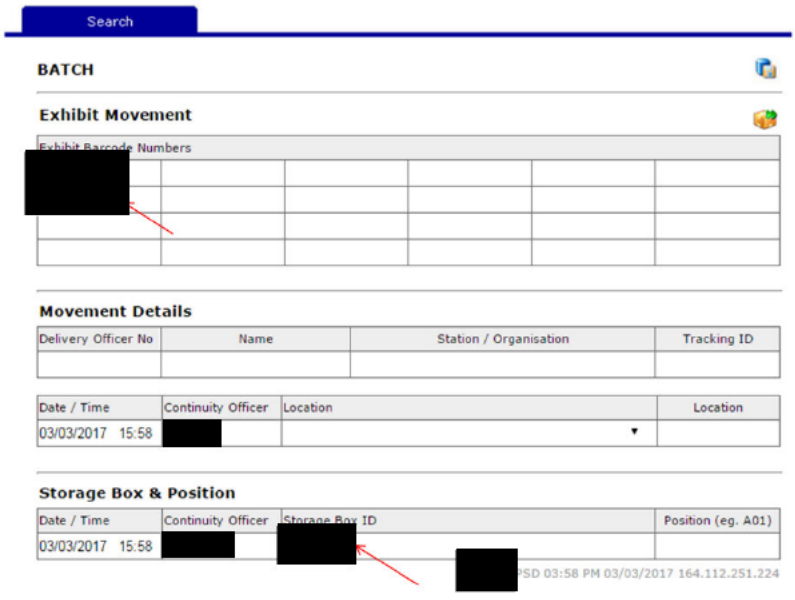
Clicking on the 'Contents' tab again will show the contents of the storage box



Multiple items can be transferred at once by clicking on the 'Forms' tab followed by the 'Batch Exhibit' button



Enter the items to be stored and the storage box ID and click save



Search

BATCH

Exhibit Movement

Exhibit Barcode Numbers					
[redacted]					

Movement Details

Delivery Officer No	Name	Station / Organisation	Tracking ID

Date / Time	Continuity Officer	Location	Location
03/03/2017 15:58	[redacted]		

Storage Box & Position

Date / Time	Continuity Officer	Storage Box ID	Position (eg. A01)
03/03/2017 15:58	[redacted]	[redacted]	

[redacted] SD 03:58 PM 03/03/2017 164.112.251.224

23.9 Appendix 9 – Registering a Subsample as an Exhibit

Registering a subsample as an exhibit may be required for samples such as epithelial fractions from high vaginal swabs, re-extracts of spin baskets (Section 11.2.5) and dilutions.

Consider a high vaginal swab that is submitted for DNA analysis. At the extraction stage a number of subsamples will be created to enable different parts of the high vaginal swab to be stored. These will include a spin basket, slide and EFRAC.

In the first instance the EFRAC from the HVS will not usually be processed, however the profile analyst may require the EFRAC to be profiled. In this instance it will be necessary to register the subsample as an exhibit to enable further processing.

The exhibit testing table for the HVS will show the subsamples that have been created and their barcodes.

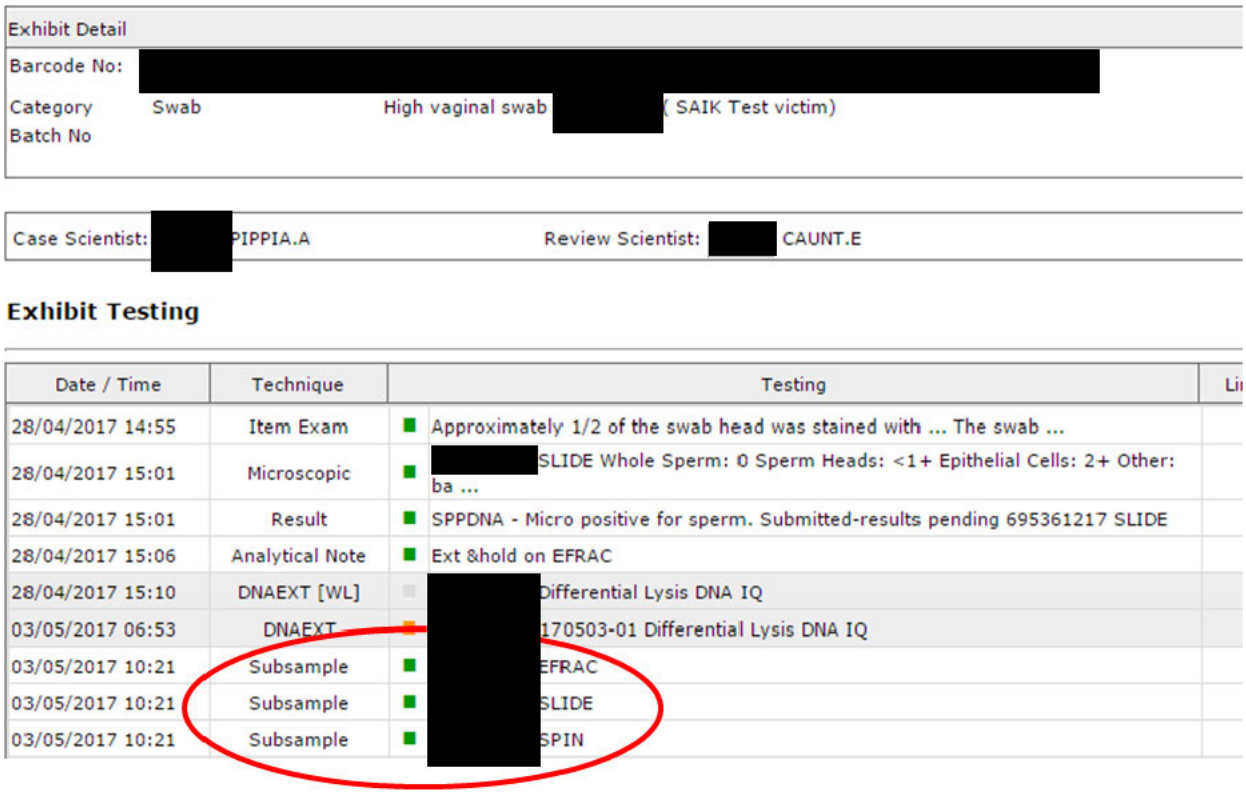


Exhibit Detail

Barcode No: [redacted]

Category Swab High vaginal swab [redacted] (SAIK Test victim)

Batch No

Case Scientist: [redacted]PIPPIA.A Review Scientist: [redacted] CAUNT.E

Exhibit Testing

Date / Time	Technique	Testing	Li
28/04/2017 14:55	Item Exam	Approximately 1/2 of the swab head was stained with ... The swab ...	
28/04/2017 15:01	Microscopic	[redacted]SLIDE Whole Sperm: 0 Sperm Heads: <1+ Epithelial Cells: 2+ Other: ba ...	
28/04/2017 15:01	Result	SPPDNA - Micro positive for sperm. Submitted-results pending 695361217 SLIDE	
28/04/2017 15:06	Analytical Note	Ext &hold on EFRAC	
28/04/2017 15:10	DNAEXT [WL]	[redacted]Differential Lysis DNA IQ	
03/05/2017 06:53	DNAEXT	[redacted]170503-01 Differential Lysis DNA IQ	
03/05/2017 10:21	Subsample	[redacted]EFRAC	
03/05/2017 10:21	Subsample	[redacted]SLIDE	
03/05/2017 10:21	Subsample	[redacted]SPIN	

To register the EFRAC as an exhibit, click on the barcode of the HVS

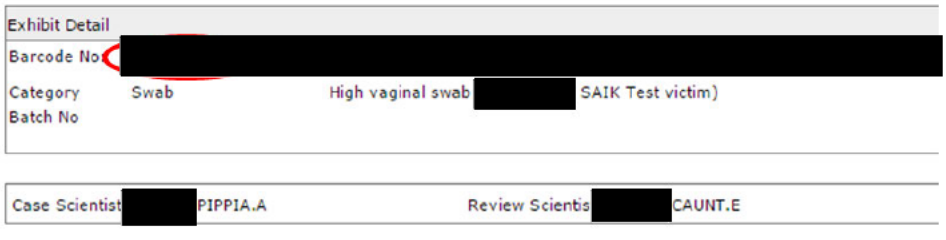


Exhibit Detail

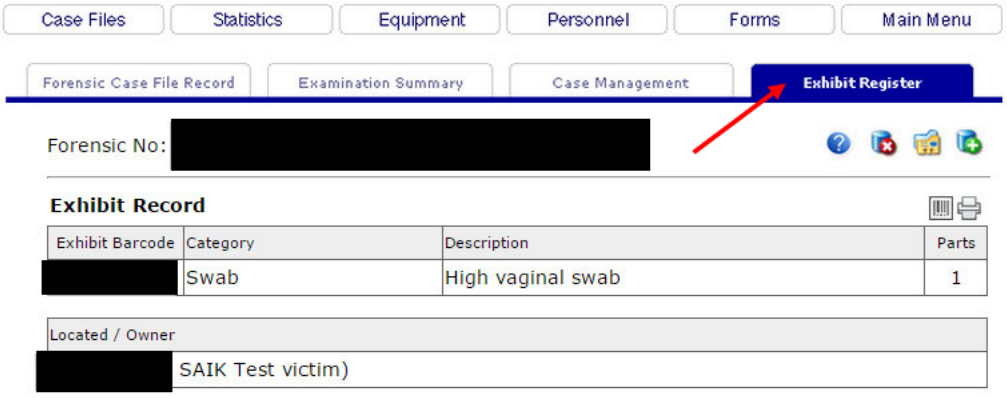
Barcode No: [redacted]

Category Swab High vaginal swab [redacted] SAIK Test victim)

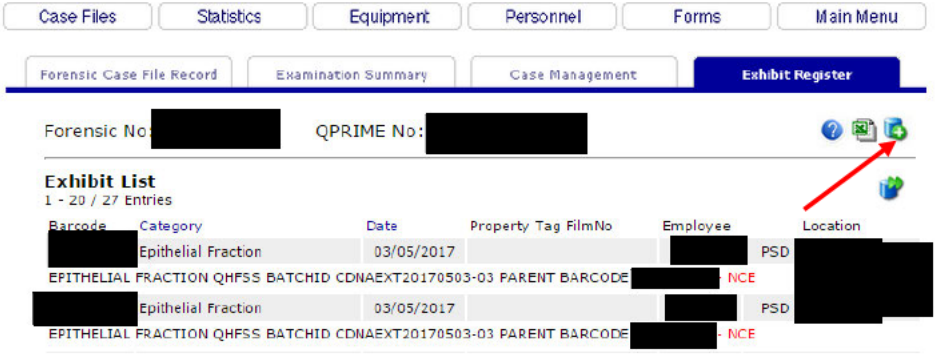
Batch No

Case Scientist [redacted]PIPPIA.A Review Scientis [redacted]CAUNT.E

Click the 'Exhibit Register' tab

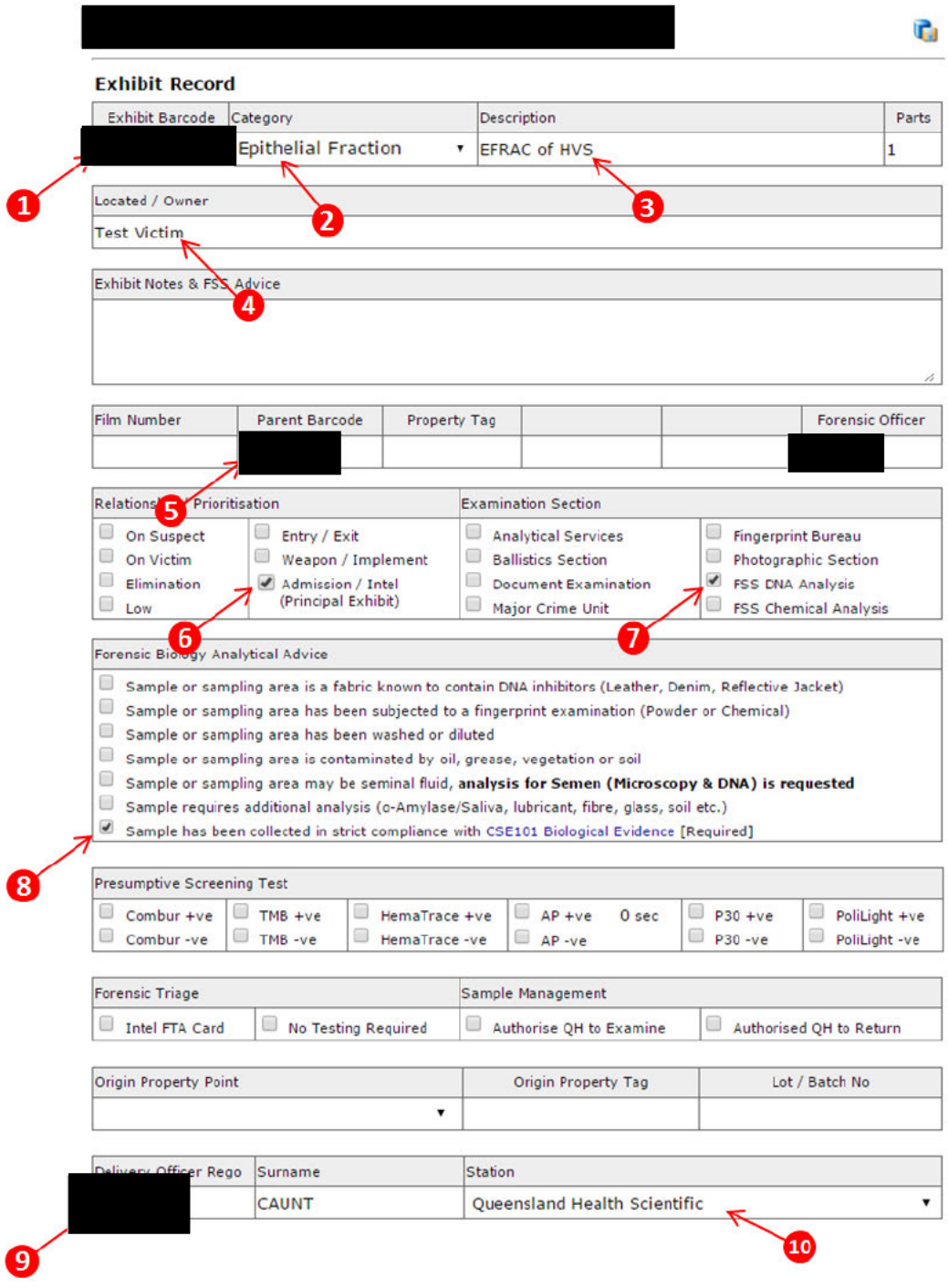


Click the button



Enter the following information:

1. Barcode of EFRAC subsample
2. Select 'Epithelial Fraction' from the drop-down list (or other appropriate category)
3. Enter a description (for re-extraction of spin baskets also add the parent barcode and description 'Spin basket – Parent barcode; Description')
4. Enter information into the 'Located / Owner' box
5. Enter the barcode of the HVS into the 'Parent Barcode' box
6. Check 'Admission / Intel'
7. Check 'FSS DNA Analysis' has been ticked
8. Check 'Sample has been collected in strict compliance……'
9. Enter your QPS user ID
10. Select 'Queensland Health Scientific' from the drop-down list
11. Click save



[redacted]

Exhibit Record

Exhibit Barcode	Category	Description	Parts
[redacted]	Epithelial Fraction	EFRAC of HVS	1

Located / Owner
Test Victim

Exhibit Notes & FSS Advice

Film Number	Parent Barcode	Property Tag			Forensic Officer
	[redacted]				[redacted]

Relationship Prioritisation		Examination Section	
☐ On Suspect	☐ Entry / Exit	☐ Analytical Services	☐ Fingerprint Bureau
☐ On Victim	☐ Weapon / Implement	☐ Ballistics Section	☐ Photographic Section
☐ Elimination	☑ Admission / Intel (Principal Exhibit)	☐ Document Examination	☑ FSS DNA Analysis
☐ Low		☐ Major Crime Unit	☐ FSS Chemical Analysis

Forensic Biology Analytical Advice
☐ Sample or sampling area is a fabric known to contain DNA inhibitors (Leather, Denim, Reflective Jacket)
☐ Sample or sampling area has been subjected to a fingerprint examination (Powder or Chemical)
☐ Sample or sampling area has been washed or diluted
☐ Sample or sampling area is contaminated by oil, grease, vegetation or soil
☐ Sample or sampling area may be seminal fluid, **analysis for Semen (Microscopy & DNA) is requested**
☐ Sample requires additional analysis (α-Amylase/Saliva, lubricant, fibre, glass, soil etc.)
☑ Sample has been collected in strict compliance with CSE101 Biological Evidence [Required]

Presumptive Screening Test					
☐ Combur +ve ☐ Combur -ve	☐ TMB +ve ☐ TMB -ve	☐ HemaTrace +ve ☐ HemaTrace -ve	☐ AP +ve 0 sec ☐ AP -ve	☐ P30 +ve ☐ P30 -ve	☐ PoliLight +ve ☐ PoliLight -ve

Forensic Triage		Sample Management	
☐ Intel FTA Card	☐ No Testing Required	☐ Authorise QH to Examine	☐ Authorised QH to Return

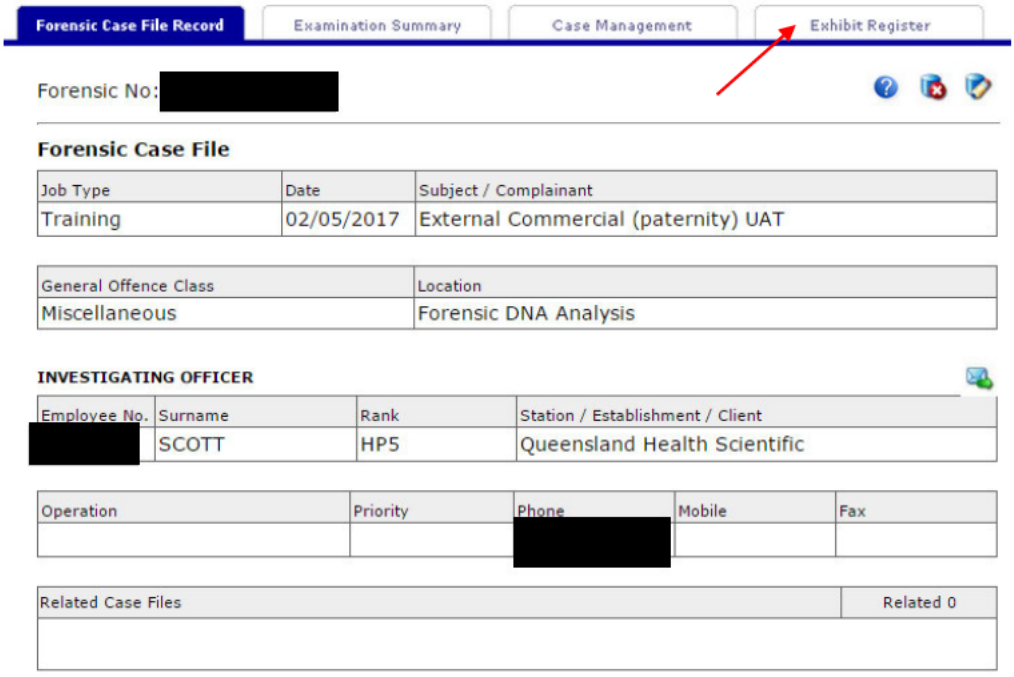
Origin Property Point	Origin Property Tag	Lot / Batch No

Delivery Officer Rego	Surname	Station
[redacted]	CAUNT	Queensland Health Scientific

23.10 Appendix 10 – Processing of DNA Number Exhibits

Register a new barcode for the sample to be transferred as follows (e.g. DNA# / Transfer samples):

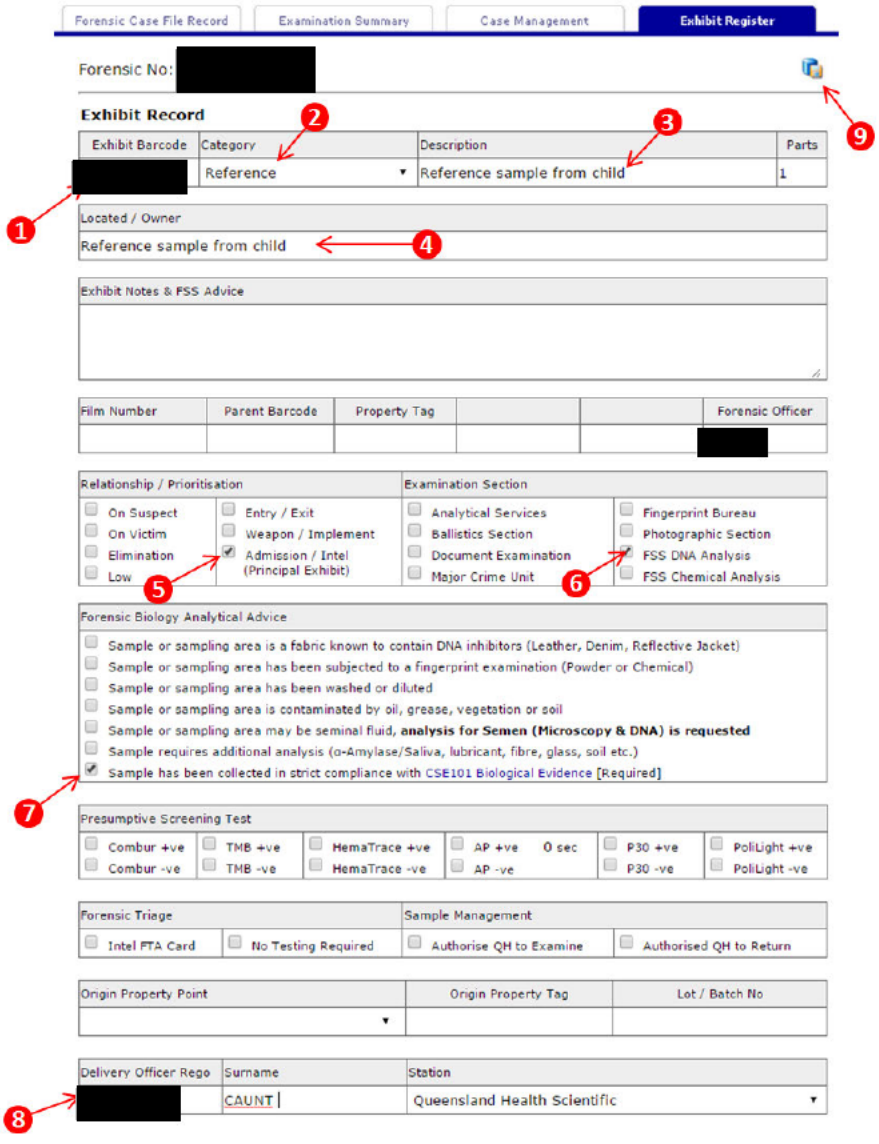
From the 'Forensic Case File Record' for the case, click the 'Exhibit Register' tab



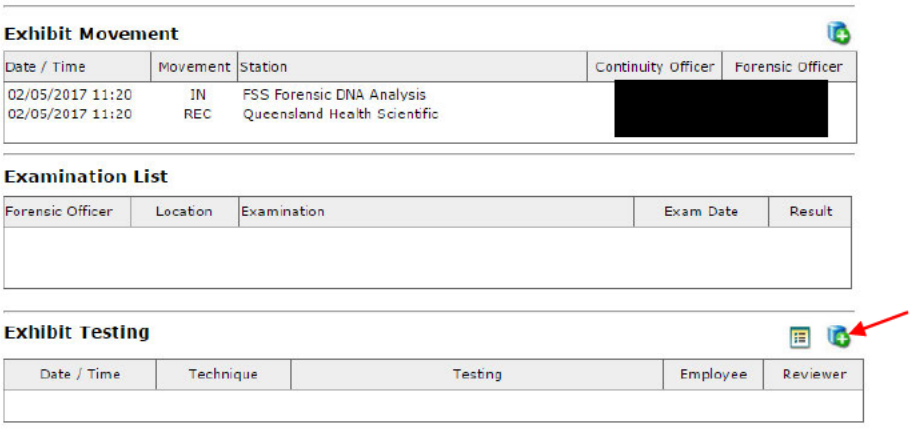
Click the icon to add a new exhibit to the case

Complete the appropriate fields as below:

1. Enter new barcode for the exhibit
2. Select appropriate category from the drop-down list
3. Enter description
4. Enter owner / location (including DNA#)
5. Check the 'Admission / Intel' box
6. Check 'FSS DNA Analysis' has been ticked
7. Check the 'Sample has been collected in strict compliance with CSE101…' box
8. Enter your QPS user ID and press the tab key to fill your name
9. Click save

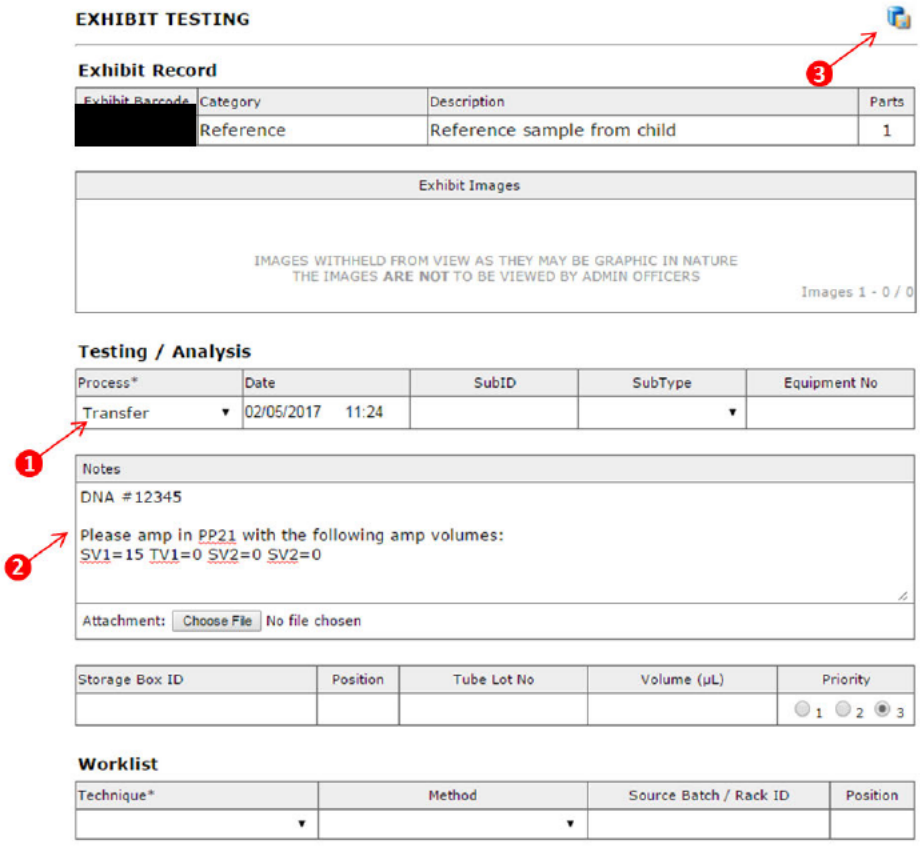


Once the record has been saved, a 'Transfer' process needs to be ordered. Click the icon above the 'Exhibit Testing' table:



Complete the Exhibit Testing page as follows:

1. Select the process of 'Transfer' from the drop-down list
2. In the notes section, enter the DNA number and the details of the processing required
3. Click save

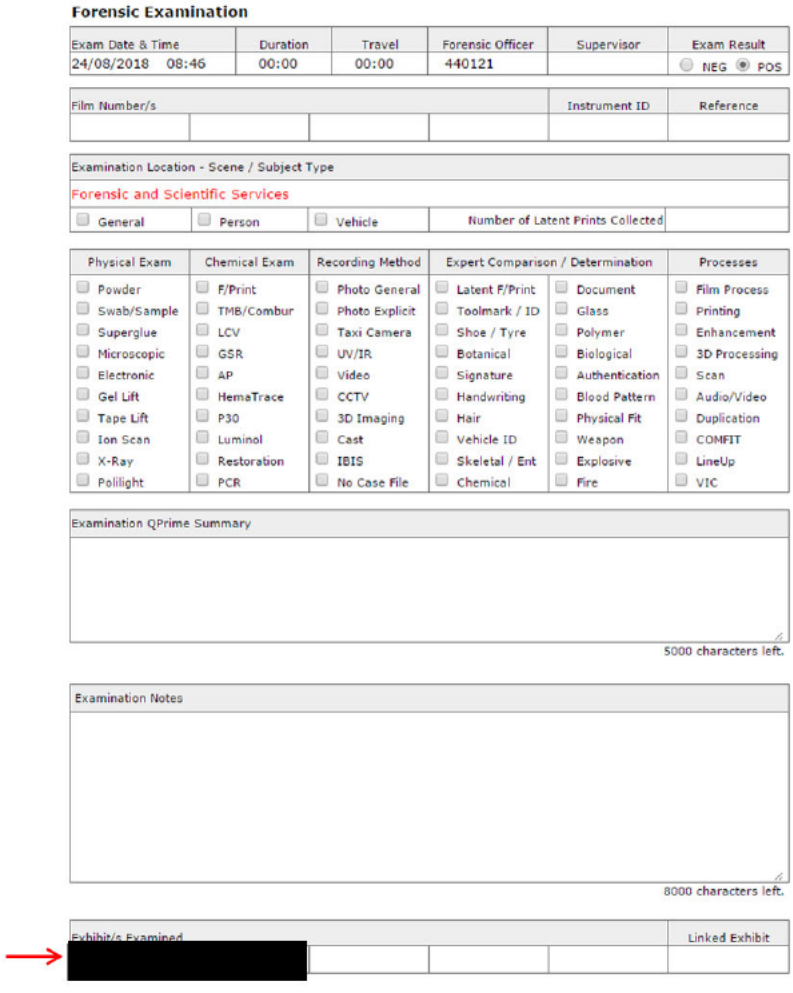


23.11 Appendix 11 – Process for Pooling Samples

1. On the Case Management side of the FR enter into a sample in the case where the pooling is to occur
2. Click the 'Examination Summary' tab

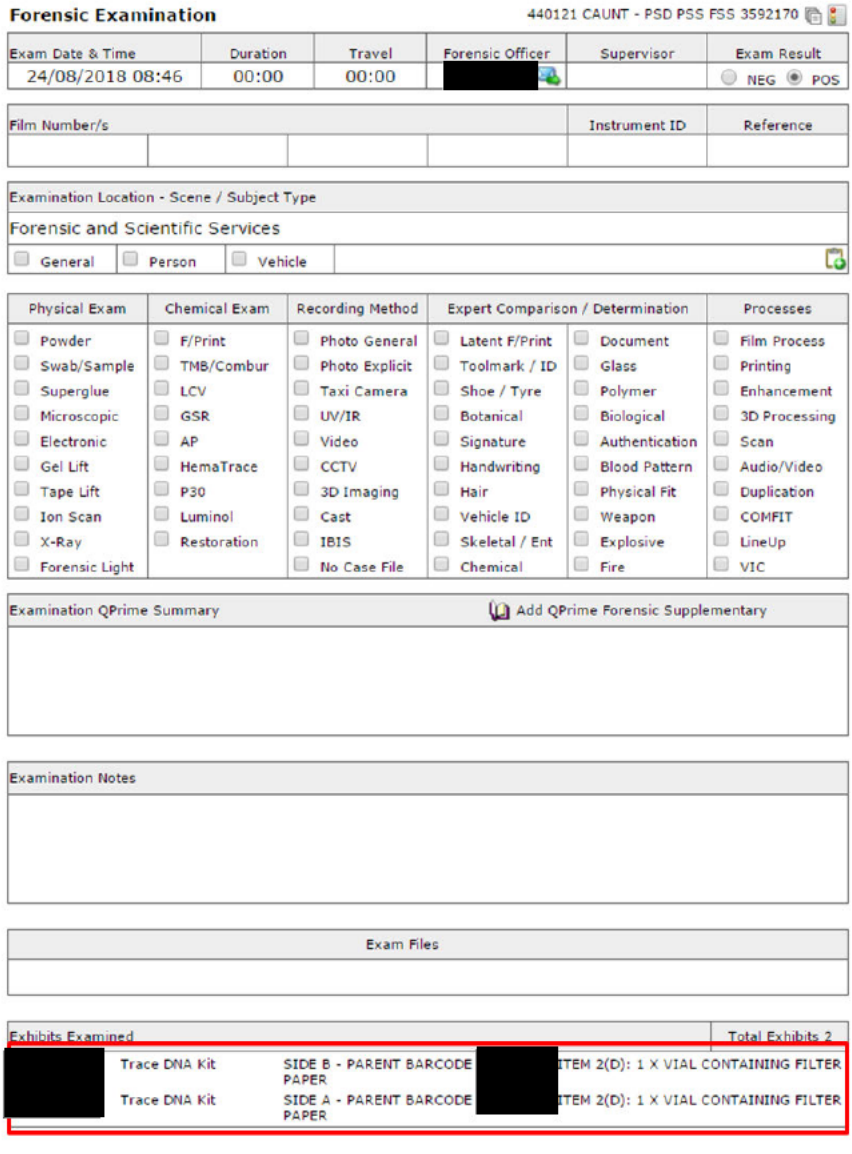
3. Click add

4. Enter the barcodes of the samples that require pooling in the 'Exhibit/s Examined' section. **Ensure that these samples are registered as exhibits before pooling**



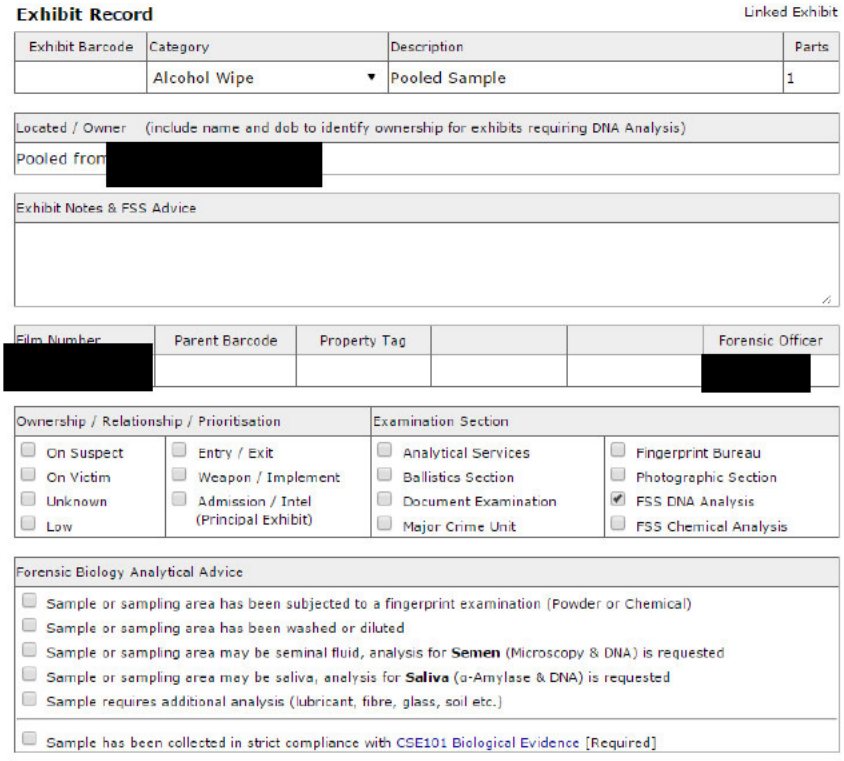
5. Click save

The samples to be pooled will appear on the page as below



6. Add a related exhibit to the examination summary by clicking add

7. The following page will appear which will allow you to register a new barcode for the final pooled sample



8. Enter a new barcode into the 'Exhibit Barcode' field
    a. Change the 'Category' to the same as that for the parent item
    b. Tick the 'Admission / Intel' box
    c. Tick the 'Sample has been collected…..' box
    d. Click save

[redacted]

Exhibit Record Linked Exhibit

Exhibit Barcode	Category	Description	Parts
[redacted]	Trace DNA Kit	Pooled Sample	1

Located / Owner (include name and dob to identify ownership for exhibits requiring DNA Analysis)

Pooled from [redacted]

Exhibit Notes & FSS Advice

Film Number	Parent Barcode	Property Tag			Forensic Officer
D3592170					440121

Ownership / Relationship / Prioritisation		Examination Section	
☐ On Suspect	☐ Entry / Exit	☐ Analytical Services	☐ Fingerprint Bureau
☐ On Victim	☐ Weapon / Implement	☐ Ballistics Section	☐ Photographic Section
☐ Unknown	☑ Admission / Intel (Principal Exhibit)	☐ Document Examination	☑ FSS DNA Analysis
☐ Low		☐ Major Crime Unit	☐ FSS Chemical Analysis

Forensic Biology Analytical Advice

- ☐ Sample or sampling area has been subjected to a fingerprint examination (Powder or Chemical)
- ☐ Sample or sampling area has been washed or diluted
- ☐ Sample or sampling area may be seminal fluid, analysis for **Semen** (Microscopy & DNA) is requested
- ☐ Sample or sampling area may be saliva, analysis for **Saliva** (α-Amylase & DNA) is requested
- ☐ Sample requires additional analysis (lubricant, fibre, glass, soil etc.)
- ☑ Sample has been collected in strict compliance with CSE101 Biological Evidence [Required]

9. The sample will now appear on the 'Pooling' review list for the Analytical section to action
10. Add an 'Analytical Note' to advise what testing is required, eg 'Pool; Quant and hold'
11. The pooled samples will have the 'Sample pooled and processed under' line automatically added and validated. They will also have an examination record. This examination record should be validated as per QIS 34298

Exhibit Testing / Examinations

Date / Time	Technique	Testing	Linked No	Employee	Reviewer
22/08/2018 08:51	DNAQUA [WL]	[redacted] Quantifiler Trio	[redacted]		
22/08/2018 08:51	Analytical Note	Quant and hold			
23/08/2018 07:29	DNAQUA	CDNAQUA20180823-01 Quantifiler Trio			
23/08/2018 10:56	Result	T.SA (Qty): 0.00026			
24/08/2018 08:57	Examination				
24/08/2018 09:05	Result	SPP - Sample pooled and processed under			

23.12 Appendix 12 – Forensic Register Storage Architecture

Exhibit movement in the FR works by updating the location of the exhibit. The most recent location of an exhibit is displayed at the top of the list in the Exhibit Movement table.

Exhibit Movement

Date / Time	Movement	Station	Continuity Officer	Forensic Officer
05/05/2017 14:15	IN	FSS Forensic DNA Analysis	[redacted]	
03/05/2017 11:01	IN	FSS Forensic DNA Analysis		
03/05/2017 07:18	IN	FSS Forensic DNA Analysis		
28/04/2017 15:10	IN	FSS Forensic DNA Analysis		
28/04/2017 13:43	IN	FSS Forensic DNA Analysis		
28/04/2017 13:43	REC	Queensland Health Scientif		
28/04/2017 12:57	IN	FSS Forensic DNA Analysis		

By adding an exhibit to a location, it is automatically removed from its previous location. This means that an exhibit can only be in one location at any one time. An exhibit often comprises of multiple parts that require individual storage. The storage of these multiple parts is managed using subsample barcodes.

When a sample undergoes DNA analysis, it splits into multiple parts. In its most simple form a sample will branch into an extract and a spin basket. The extract will retain the exhibit barcode for storage purposes and a new barcode will be created for the spin basket storage. If the sample requires testing of the supernatant then a new barcode will also be created for the supernatant storage.

In the example below we can see that exhibit 690149615 has a spin basket with barcode 360000490 and a supernatant with barcode 360000501 (additional sample information becomes available by hovering over the individual barcodes on the 'Link Chart').

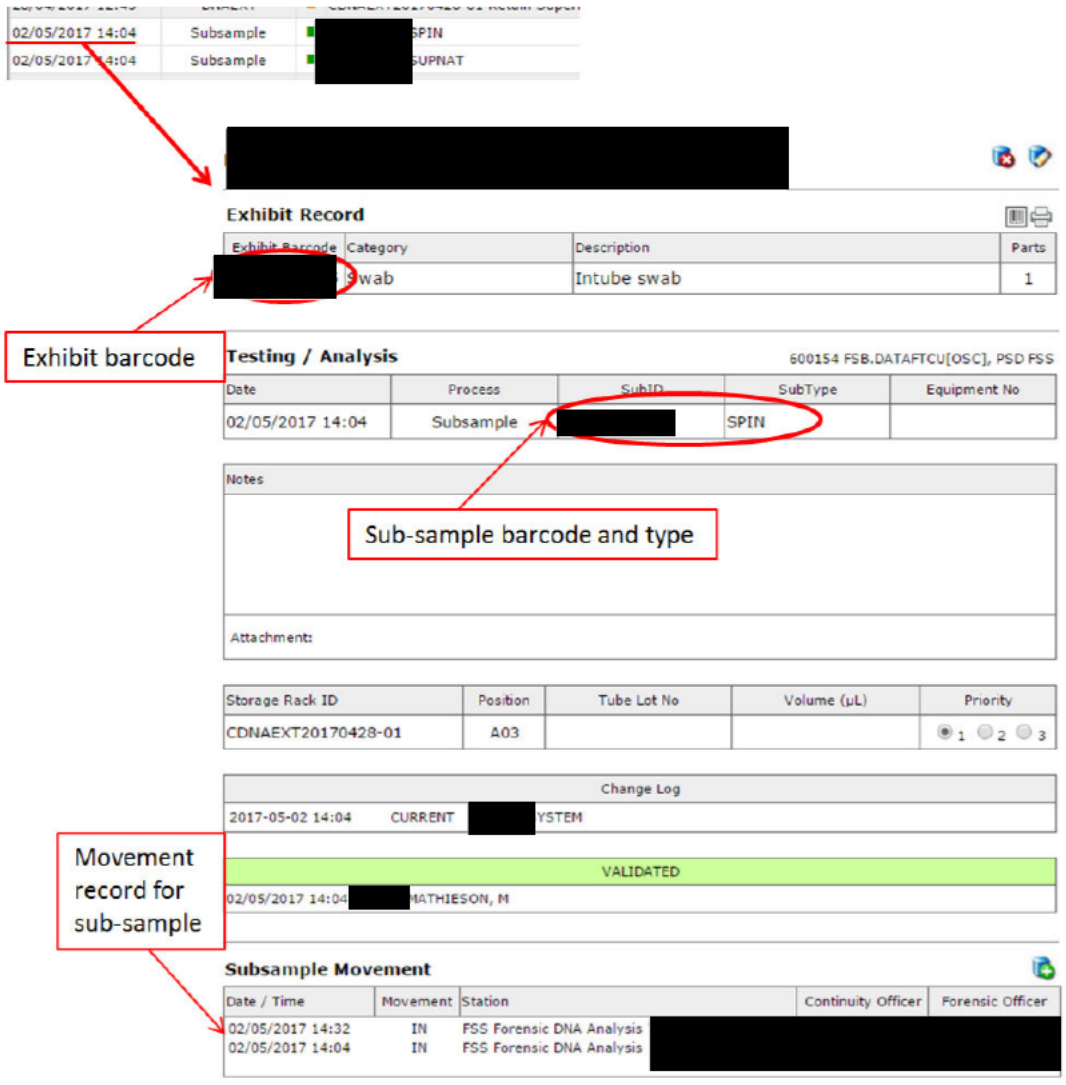
Link Chart

[redacted]

Exhibit Testing

Date / Time	Technique	Testing	Employee	Reviewer
26/04/2017 06:38	In-tube check	The packaging matches the QPS ...	[redacted]	
26/04/2017 06:38	Result	Submitted-results pending		
26/04/2017 10:41	DNAEXT [WL]	[redacted] Retain Supernatant DNA IQ		
28/04/2017 12:45	DNAEXT	Retain Supernatant DNA IQ		
02/05/2017 14:04	Subsample			
02/05/2017 14:04	Subsample			

The storage record for a subsample can be accessed by clicking on the Date / Time associated with that subsample.



For analytical processes, most subsample barcodes that may be required are generated automatically at the extraction stage. The subsample types are:

- Spin baskets (SPIN)
- Microscope slides (SLIDE)
- EFRACs (EFRAC)
- Supernatants (SUPNAT)
- Miscellaneous (MISC)

If a spin basket or EFRAC requires further analytical processing then it will be necessary to change the subsample into an exhibit to allow the parts created from these additional processes to be stored and a PDA page to be created.

Storage boxes are identified by a nine or ten digit barcode and a description. The barcode is displayed in the Exhibit Movement table and is hyperlinked to the storage box record. Hovering over the storage box barcode will show the fixed location where the box is stored.

Exhibit Movement

Date / Time	Movement	Station	Continuity Officer	Forensic Officer
05/05/2017 14:16	IN	FSS Forensic DNA Analysis	[redacted]	[redacted]
02/05/2017 14:29	IN	FSS Forensic DNA Analysis		
28/04/2017 13:06	IN	FSS Forensic DNA Analysis		
26/04/2017 06:39	IN	FSS Forensic DNA Analysis		

Fixed storage locations are identified by a 12 character code e.g. FDNA-EXFZ-0001. The first four letters represent the department e.g. FDNA = Forensic DNA Analysis. The second four characters represent the type of storage e.g. shelf, freezer, fridge. The last four characters represent the shelf number.

The codes for the second four characters for storage locations within Forensic DNA Analysis are as follows:

CMP	Compactus
RT	Returns
FZ	Freezer
FR	Fridge
SH	Shelf
CG	Cage
DR	Drawer
EX	Exhibit room
ER	Evidence recovery
ES	Extraction sorting
ADMN	Admin
INTL	Intel
EVRT	Evidence recovery
LDNA	Low DNA room
AE	Analytical extraction
QA	Pre-PCR
CE	CE
BONE	Bone room
FRXX	Walk in fridge
FZXX	Walk in freezer
AD	Admin
SHLF	Walk in fridge/freezer direct shelf storage
CHST	Chest freezer
QUAL	Quality
ANLT	Analytical
FRIT	FRIT
FILE	File store

Storage Locations

Fixed locations:

- Exhibit room shelves, Fridge shelves, Freezer shelves, Rooms

Storage box (open):

- FTA boxes, Freezer storage tubs, Staff in-trays
- Storage boxes can “move” e.g. Kirsten's in-tray can be stored to the Admin fixed location
- Locally configured, with unlimited storage positions

Storage box (grid format):

- Perm DNA, Temp DNA, ERT-AS boxes
- Storage boxes can “move” e.g. from ERT lab to Freezer in extraction sorting
- Locally configured, with defined and limited positions in the format A01, A02, A03, B01, B02 etc.

General Storage Functionality

Five basic methods / functionalities are available for storage. Use of method is determined in part by storage type e.g. if the storage box is “open” or “grid” format.

1. **Batch exhibit movement (Main Menu – Forms – Batch Exhibit):**
    a. Used to move up to 24 barcodes to a fixed location or open storage box
    b. Not suitable for movements to grid-format boxes
    c. Likely used by property point, storage of FTA cards, storage of case files

2. **Fill box function (Main Menu – Equipment – Search storage box ID):**
    a. Add samples one at a time to a storage box (grid or open format)
    b. Not applicable for fixed locations
    c. Likely used in extraction sorting/Pre-PCR where large number of items stored to grid boxes

3. **Exhibit/Sub-ID movement (Exhibit Movement Table):**
    a. Standard movement to any location
    b. All storage formats: fixed, open box and grid box
    c. Used for single movements of item. Subsamples will have their own movement history

4. **Movement while adding a test:**
    a. Add samples one at a time to a storage box (grid or open format)

5. **Storage box movement:**
    a. Movement of a box (open or grid) to a fixed location. Available from the storage box screen

23.13 Appendix 13 – Profiler Plus Amplification Kit

GeneMapper® Record Page:

When the GeneMapper file is uploaded to the FR, loci with only one allele will be transformed into the format "allele,allele" or "allele,0" in the 'Alleles' column according to the homozygous threshold. Loci with no alleles will be transformed into the format "0,0". The row will highlight yellow to reflect the change.

The 'Alleles' column contains the allele designations to be used on the PDA page.

If a peak requires removing, refer to Section 6.2.1.1.

Profile Interpretation Table:

Figure 30 – P+ Profile Interpretation Table

1 This section is used to record the number of contributors to a profile. If the interpretation is 'at least two' contributors then the '2' is to be checked; likewise 'at least three' will see the '3' checked

2 This section is used to record interpretations or parts of interpretations that don't require any further action:

a. CX is to record a profile that is a complex mixture and is unsuitable for further interpretation
b. NP is used to record a no profile result
c. PU is used to record a profile that is partial and unsuitable for further interpretation
d. can be used in conjunction with the number of contributors or NP to record that there are also sub-threshold peaks within the profile
e. MiU is not used at this stage (for automated Exhibit Results)

3 Notes section (not audited)

Profile Record Table:

When a DNA profile is obtained that is either single source or one or more contributions are able to be resolved the Profile Record table is to be completed for each resolved contribution.

Clicking the edit icon on the PDA page will enable the Profile Record table to be edited. The profile can then either be entered manually or 'copied down' from the GeneMapper file (1 Figure 52) by clicking on the appropriate button. If required, the CLR button (2) will clear the profile entered. If there is more than one GeneMapper file for the sample then there will be the option to choose which result to copy down (distinguished by the CE batch id); this should be the 'Reported profile' result or the profile with the most informative information (statistics for P+ use the 'Reported profile' only).

The suffix list (3) records the type of profile that has been entered. A suffix must be selected for every profile entered into the table.

If a profile requires upload to NCIDD then a NCIDD process is automatically ordered for each nominated upload (Section 11.1.1).

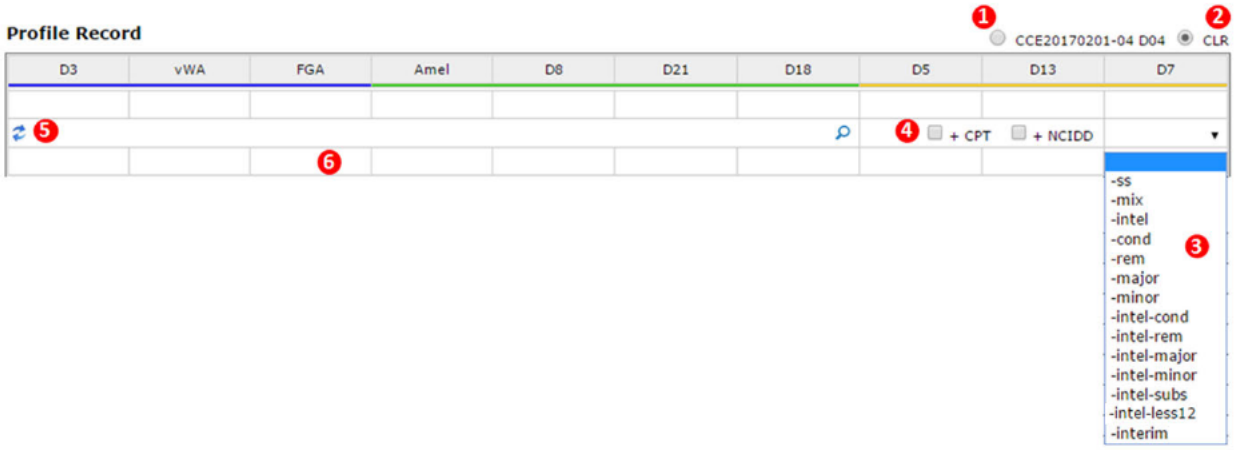


Figure { SEQ Figure * ARABIC } – P+ Profile Record Table

1. Single Source Profiles
   When a single source profile is obtained the scientist will copy down the profile by selecting the appropriate CE batch or entering manually. The scientist will then click the ⇄ icon (❺Figure 53) to commence searching.

   If the profile is ≥ 12 alleles then the FR will suggest a designation / match for the profile (refer to Section 8.1 for further details). If the scientist does not agree with the match / designation proposed by the FR database then it must be replaced with the appropriate match / designation in the format described in Section 8.1.

   If the profile is <12 alleles then no designation / match will be suggested by the FR and the match cell (❺) will populate with the barcode of the sample. The designation for this profile should be entered manually into the match cell (❺) in the format described in Section 8.1.

   If the profile is required to be loaded to NCIDD then the '+NCIDD' box (❹) should be checked. The '-ss' suffix should be selected from the drop-down list (❸) (Table 6).

   If the profile is unknown and is not listed in the 'Case Profiles' table then the '+CPT' box (❹) must be checked to add the profile to the Case Profiles table.

Table 4 – Suffix Meanings

Suffix	Purpose	Kit
-ss	Single source component	P+
-cond	Conditioned component	P+
-rem	Remaining component	P+
-major	Major component	P+
-minor	Minor component	P+
-intel-cond	Conditioned component where the profile is conditioned for intelligence purposes only	P+
-intel-rem	Remaining component where the profile is conditioned for intelligence purposes only	P+
-intel-major	Major component where the term 'major' has been assigned for intelligence purposes only	P+
-intel-minor	Minor component where the term 'minor' has been assigned for intelligence purposes only	P+
-intel-subs	Single source component where sub-threshold peaks are used for intelligence purposes only	P+

-intel-less12	Single source component with less than 12 alleles	P+
-interim	Any component that is loaded as an interim measure pending rework results	P1 cases only

2. Fully Resolved Mixed Profiles
   When a profile can be fully resolved into its individual contributions then each contribution should be recorded in the Profile Record table as follows:

   a. Click the edit icon
   b. Copy down the profile by selecting the appropriate CE batch and delete the alleles that do not apply to the contribution being entered, or enter the profile manually
   c. Click the icon to commence searching
   d. Check the match / designation in the match cell (❺Figure 53) and replace as necessary as per Section 8.1
   e. Check the '+NCIDD' box (❹) if this contribution is required to be loaded to NCIDD (ticking this box triggers the ordering of an 'NCIDD' process when the record is saved)
   f. Select the appropriate suffix for this contribution from the list (❸)
   g. Check the '+CPT' box if this contribution is a new designation for the case
   h. Save the record by clicking the save icon
   i. Repeat the process for the other resolved contributions of the profile entering the mixture ratios into the boxes below each locus (❻).

3. Partially Resolved Mixed Profiles
   When a profile can only be partially resolved, for example a major profile with a complex minor profile, then only the resolved contribution is recorded in the Profile Record table by following steps a.-i. as per above paragraph.

4. Unresolved Mixed Profiles
   When a profile is unable to be resolved then no information will be recorded in the Profile Record table. In this instance only the ○2 or ○3 box is checked in the Profile Interpretation table.

5. Complex Profiles
   If the profile is not suitable for interpretation because it is partial or consists of an unknown number of contributors or ≥ 4 contributors, it is not necessary to copy down a profile. In this instance only the ○CX or ○PU box is checked in the Profile Interpretation table.

6. Tri Alleles
   The Profile Record table should only contain two allele designations. If a tri-allele is obtained, drop the locus and add a sample note stating that a tri-allele is present and all three designations. If the profile is required for upload to NCIDD then the details of the tri allele should be added to the 'NCIDD User Comment' field in the NCIDD process (Section 11.1).

Case Profiles Table:

The Case Profiles table is used to identify reference and unknown profiles that are available for comparison in the case and to associate them with one another (Figure { SEQ Figure * ARABIC }). It is also used to show when a reference comparison has been completed.

Barcode	Name	Association	Category	CE	NM	II	Employee	Reviewer
[redacted]	6 PP21 ref			☐	☐	☐		
	7 PP21 ref			☐	☐	☐		
	8 PP21 ref			☐	☐	☐		

Figure { SEQ Figure * ARABIC } – P+ CPT

When a reference sample has been compared with the crime scene profile then the associated 'CE' box should be checked. This enables any new reference samples to be easily identified.

The 'NM' and 'II' boxes are not used currently.

New Reference Comparisons:

Newly associated reference samples can be identified by an unchecked box in the 'CE' field of the Case Profiles table.

The comparison of the reference sample should be recorded as follows:

a. Once the comparison has been performed, check the associated 'CE' box
b. If the reference sample matches an unknown in the case, update the 'Association' fields (Figure 42)
c. If required, order a 'Result' process and enter the appropriate Exhibit Result line for the reference sample (Section 18)
d. If no additional Exhibit Results lines are required i.e. the results have not changed, then a Sample Note to this effect should be added
e. Order a 'Profile Review' process (Note: a 'Profile Review' process should be ordered regardless of whether an Exhibit Result line is entered)

23.14 Appendix 14 – Managing Cases Across Different LIMS (Pre-AUSLAB, AUSLAB and FR)

Cases from 2017 or earlier, can have samples across a number of different LIMS systems. Flowchart 1 provides a number of different pathways and the SOPs required to manage such cases / samples.

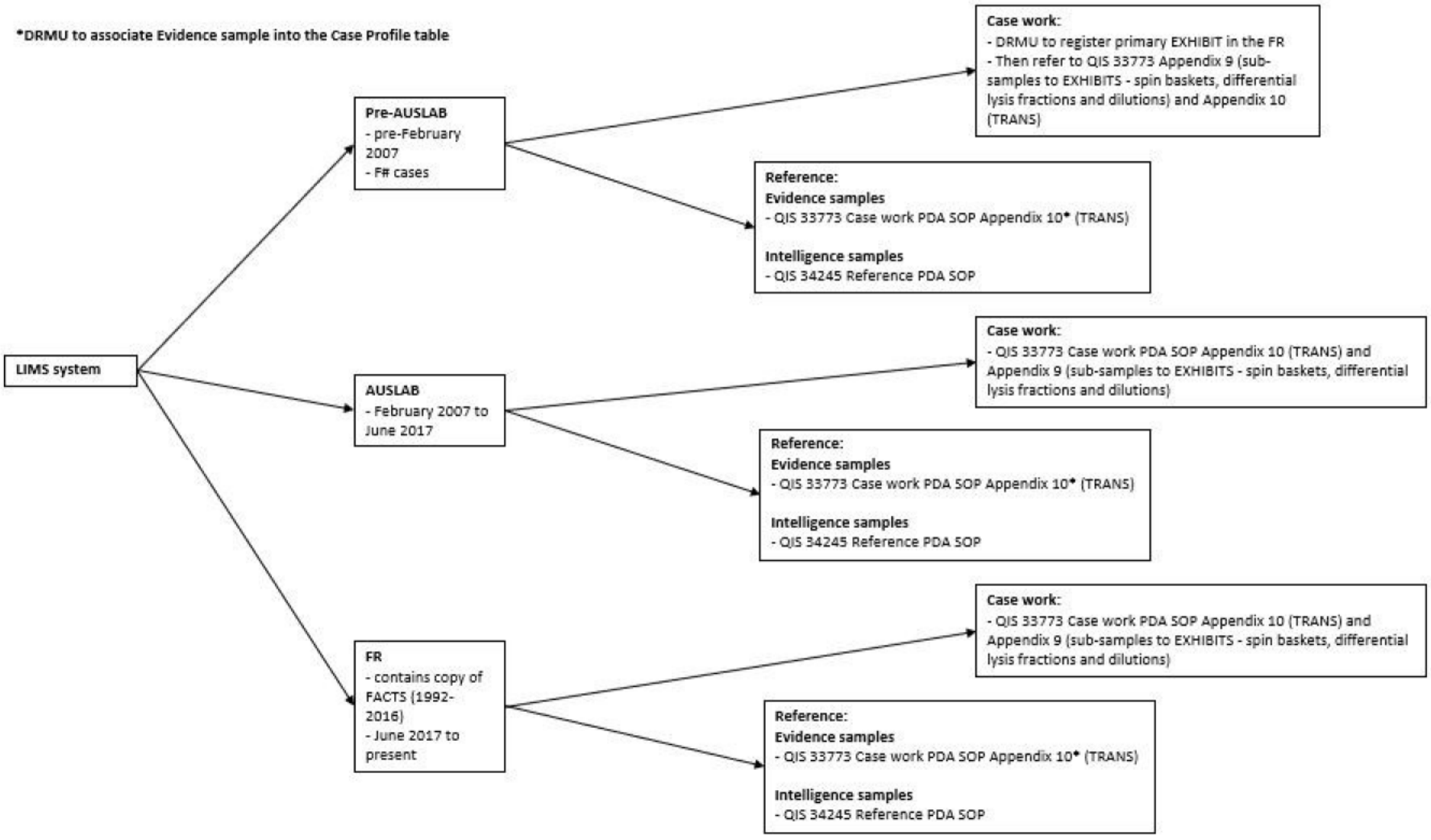
Tracking AUSLAB Case in FR

For cases with paper case files tracked in AUSLAB requiring tracking (e.g. court):

1. 'Remove' the case file from the AUSLAB storage and add an audit entry 'Removed to track in FR'
2. Create and track this case file in FR as per Appendix 8 – Creating and Tracking a Case File using the existing case file barcode
3. Add a note to the 'Exhibit Notes & FSS Advice' field stating the case file was previously tracked in AUSLAB
4. Proceed as normal

Cases with AUSLAB and FR Unknowns

If a case has an unknown in AUSLAB followed by unknowns in the FR, the subsequent FR unknowns will appear in the CP table without accounting for the previously designated AUSLAB unknowns (i.e. they do not appear correctly in the CP table on the PDA page). To resolve this situation, register the sample in the FR, manually enter the DNA profile and designation, and then tick the +CPT box so it appears in the CP table of the FR. Alternatively, contact QPS DNA Management (DRMU) to request registration of the AUSLAB unknown(s).


*DRMU to associate Evidence sample into the Case Profile table
LIMS system
Pre-AUSLAB
- pre-February 2007
- F# cases
AUSLAB
- February 2007 to June 2017
FR
- contains copy of FACTS (1992-2016)
- June 2017 to present
Case work:
- DRMU to register primary EXHIBIT in the FR
- Then refer to QIS 33773 Appendix 9 (sub-samples to EXHIBITS - spin baskets, differential lysis fractions and dilutions) and Appendix 10 (TRANS)
Reference:
Evidence samples
- QIS 33773 Case work PDA SOP Appendix 10* (TRANS)
Intelligence samples
- QIS 34245 Reference PDA SOP
Case work:
- QIS 33773 Case work PDA SOP Appendix 10 (TRANS) and Appendix 9 (sub-samples to EXHIBITS - spin baskets, differential lysis fractions and dilutions)
Reference:
Evidence samples
- QIS 33773 Case work PDA SOP Appendix 10* (TRANS)
Intelligence samples
- QIS 34245 Reference PDA SOP
Case work:
- QIS 33773 Case work PDA SOP Appendix 10 (TRANS) and Appendix 9 (sub-samples to EXHIBITS - spin baskets, differential lysis fractions and dilutions)
Reference:
Evidence samples
- QIS 33773 Case work PDA SOP Appendix 10* (TRANS)
Intelligence samples
- QIS 34245 Reference PDA SOP