CASE MANAGEMENT		
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Case Management

GUIDING PRINCIPLES AND SCOPE

Case management is the process by which an analyst shepherds the evidence through the testing process. It is the responsibility of the analyst to ensure that evidence receives the necessary analysis, analytical results are evaluated promptly, any analytical problems resolved, the results interpreted, and the final report written within the time frame dictated by the target date.

Since the Department has different teams, this procedure discusses the process in general. Refer to the specific procedures within the technical manuals, if necessary.

PROCEDURE

Most case management steps are done using the Laboratory Information Management System (LIMS); however, the "legacy" case management and documentation system in Forensic Biology--which utilizes various hard copy forms—is available for documenting the examination of evidence that was submitted for testing prior to the activation of the LIMS and for exigent circumstances when the LIMS is unavailable for an extended period of time.

A. Production Team System

1. Many of the processes described in the following sections are handled by the Production Team staff and not necessarily the interpreting/reporting analyst (IA/RA). One goal of the Production Team system is to rapidly and efficiently extract, quantify, and amplify samples. Workflow and preparation of test batch samples is coordinated by the Production Teams.

2. Testing results for post-LIMS evidence will be available to the IA/RA through the LIMS interface. Printouts of the functional reports that contain the test results will be needed for the hard copy case file. Printing can be done at any time after a test is complete; most often it will be done by the reporting analyst.

3. It is the *responsibility of the test batch reviewer* to examine the samples and batch set-up information for completeness and accuracy of case numbers, sample identifiers, etc. Any discrepancies, inconsistencies, or omissions must be resolved by the analyst, in

consultation with a supervisor if needed, before obtaining a witness and/or commencing testing.

4. It is the *responsibility of the witness* to examine the samples and batch set-up information for completeness and accuracy of case numbers, sample identifiers, etc. As above, resolve any issues prior to commencing testing.

B. Case assignment

Case management begins as soon as an analyst accepts a case for evidence examination.

1. Cases are self-assigned by the analyst by taking the next case in priority and target date order. An initial priority level is assigned during the Sign-In process, but can be adjusted later.
   a. **High Priority –** All parts of case that were promised (could just be semen Y/N, for example, or it could be a complete DNA report) are done ASAP, using overtime if necessary. Designating a case as **High Priority** requires a phone call from an NYPD high-level manager to a Forensic Biology (FB) manager, or a phone call from a DAO Bureau Chief-level to an FB manager. A "regular" ADA cannot make such a request. The target date should reflect the date that the results were promised – this will show up in LIMS, and if the cases waiting to be examined are *sorted by target date,* a case such as this will pop up at the top ahead of all the rest. If the status goes away later, the priority can be downgraded and the target date adjusted to a normal one.
   b. **Priority** – Started next, but the rest of the case gets processed as usual; this is the same as "expedite". All stranger rapes are in this category. The target date will be a normal one. Remember that "stranger rape" is NOT the same as "no suspect". A "stranger rape" is a "stranger rape" whether there is a named/arrested suspect or not.
   c. **Routine** – Average, everyday, sort of case (excluding stranger rapes).

   An examining analyst (EA) who will also be the IA/RA should enter their identifying information in LIMS or "Access", as appropriate.

2. Review the case information (see evidence exam - general guidelines).

   If this is additional evidence or an exemplar on a previously reported case, evaluate the earlier work.

a. It may be necessary to submit earlier DNA extracts for additional testing.

b. If an exemplar is submitted, type it in all DNA systems necessary for comparison.

3. The RA/IA should enter their initials in the appropriate location within Access or LIMS. This will usually involve modifying an RA record created at sign-in; however, it is possible that a new "RA" record will have to be added to the case.

a. LIMS cases: The RA should verify the accuracy of the "Assignment Start Date" and modify the date as needed. The "Assignment Start Date" is equivalent to the date when a testing request was received and officially accepted for processing. This can vary depending upon the case scenario. Analysts must evaluate the particular circumstances of their case and enter the appropriate date. The following is guidance for determining the correct "Assignment Start Date":

Case scenario	Create New RA Entry Line?	Assignment Start Date Should Equal:
Outside submission, new FBio case	Yes	EU Received Date for first voucher
New outside submission for existing FBio case, new report to be written	Yes	EU Received Date for first additional voucher
New outside submission for existing FBio case, testing to be included with existing assignment	No	N/A
New FBio case with post mortem items	Yes	EU Received Date for PM items
Additional testing without new outside submissions	Yes	Date new testing was accepted or decided upon
DNA testing on Sexual assault kits after a serology report	Yes	Date of RA report review (i.e., draft date for serology report)

Case scenario	Create New RA Entry Line?	Assignment Start Date Should Equal:
Storage cases that are activated; for example a missing persons case	Yes	Date of request or decision to start testing
Report only cases	Yes	Date of decision to write report

4. Obtain the evidence from the evidence storage area and complete the chain of custody.

C. Initial analyses

1. Examine the evidence (see Evidence Exam procedure).

2. Submit samples for PSA testing, amylase testing, and/or DNA extraction as needed. Ensure that "true exemplar" samples and "pseudo-exemplar" samples are submitted on the appropriate exemplar extraction batches and that evidence samples are submitted on the appropriate non-exemplar extraction batches.

3. If work is performed outside of LIMS, a case tracking worksheet may be started by the analyst. These worksheets allow for tracking of samples, including analytical results, dates of submission for the different tests, etc. For cases performed within LIMS, this tracking worksheet is created by LIMS.

4. PSA or amylase results are reviewed by the analyst for completeness and accuracy. Discrepancies or omissions need to be corrected by the analyst who performed the test. Check especially for correct FB number, swab description or stain description.

5. Extraction and quantitation results reviewed by the analyst (EA or IA/RA) for completeness and accuracy; any discrepancies or omissions need to be corrected by the analyst who performed the test. Check especially for correct FB number, swab description or stain description. The following information should be checked:

   a. Does the extraction negative contain DNA?

b. If neat and dilution results were tested, do the results correlate with each other?

c. Is the DNA concentration too high?

d. Was there a problem with inhibition and/or background fluorescence preventing a determination of the DNA concentration? If so, the sample may need to be cleaned via microcon and re-quantified.

Re-quantitation needed due to any of the aforementioned reasons is generally taken care of in the Production Team System.

Microcon clean-up may be performed either by the analyst, or as part of the Production Team System.

D. DNA typing and case evaluation

1. Once acceptable quantitation results are available, the DNA samples requiring amplification will be processed.

   a. In some instances, the duplication process of amplification is automatically performed by the STR rotation. If this duplication is not performed and is necessary, or if the sample needs reamplification, the sample must be placed into an amplification batch.

2. The analyst reviews amplification and DNA typing results for completeness and accuracy; any discrepancies or omissions need to be corrected by the analyst who performed the test. Check especially for correct FB number, swab description or stain description. In addition, review all the electropherograms for your case.

   a. Review the STR 3130xl Control Review report to ensure that the positive control, amplification negative, and extraction negative (if applicable) gave the expected results. If not, the samples may need to be re-amplified or even re-extracted.

   b. Did your samples amplify? If not, it may be necessary to re-amplify with more DNA extract or less DNA extract (if PCR inhibitors are suspected), or perform a microcon procedure.

In some situations, it may be necessary to start the DNA analysis over at the DNA extraction step or consider organic extraction.

c. Was a partial DNA profile detected in your sample? If so, it may be necessary to perform further testing.

Depending on the system, a complete DNA profile may be obtained by re-running the sample with more amplification product or a longer injection time. If so, add it to the batch of samples to be re-run and specify how much amplification product should be run or increased injection time. Racks to hold samples to be re-run are in the amplified DNA refrigerators.

Alternatively, it may be necessary to re-amplify with more DNA extract or less DNA extract (if PCR inhibitors are suspected), or perform a microcon procedure.

d. Was your sample over-amplified? If so, was the sample added to the list of samples requiring re-run?

Alternatively, submit the sample for amplification again with less DNA extract.

e. Were your samples properly edited? Evaluate any editing that was done on your samples; examine the electropherograms for artifacts, over-amplification, or other problems. If the sample was not edited properly, ask the analyst to re-edit and reprint the electropherograms; make sure the new editing is added and dated on the editing worksheet.

f. Is there a mixture of DNA in your sample? If so, it may require duplication in a DNA system (the same one or a different one). Mixtures may also be amplified with more template DNA for better results.

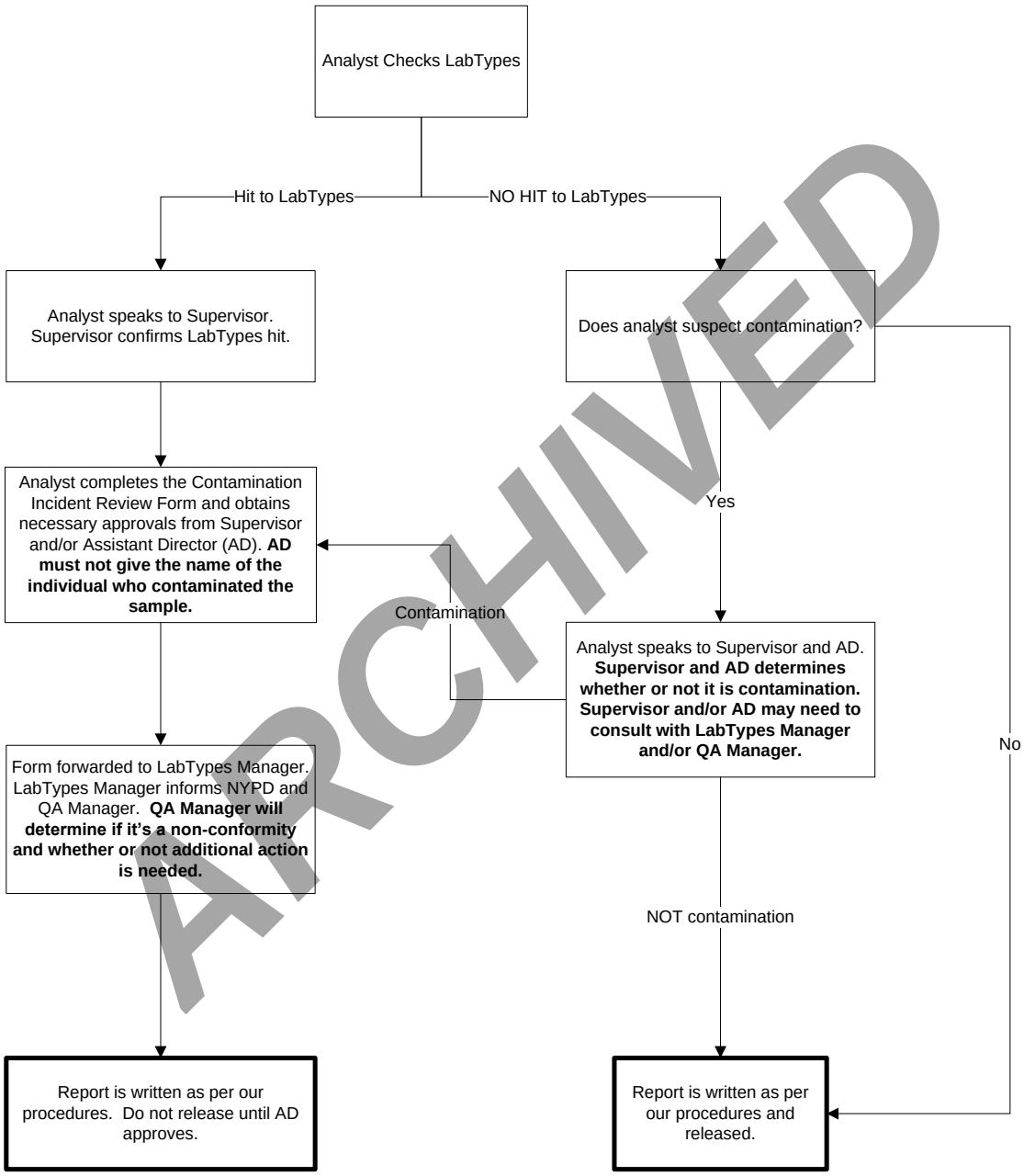
g. Are there other samples that may require duplication? If so, identify those samples and start the appropriate steps (i.e., re-extraction or re-amplification).

h. Do the DNA results make sense in the context of the case and/or sample? If not, there may have been a sample mix-up at the aliquot, amplification, or DNA typing steps. Discuss with your supervisor.

Review the DNA typing results as soon as possible so that ample time remains to deal with any analytical problems.

3. Compare clean or deduced single-source DNA profiles to the Lab Types Database in order to detect possible exogenous DNA. Instructions for how to conduct searches of the database are found in the LAB TYPES DATABASE procedure in the Quality Assurance/Quality Control Manual.

   The following flowchart should provide additional guidance on using the Lab Types Database. If contamination is identified see also the "Exogenous DNA Policy" found in the GENERAL GUIDELINES FOR DNA CASEWORK procedure (in the Forensic Biology Protocols for Forensic STR Analysis manual).



4. Compare DNA results to the LINKAGE database and/or LDIS for potential matches (exact or partial). In addition, it may be necessary to compare DNA profiles within a case to other profiles in the case, and to any suspects submitted for that case, to identify partial matches. This may require you to determine the DNA profile(s) present in a mixture, and may require consultation with a supervisor.

   Only single-source profiles (clean or deduced) with ≥10 CODIS core loci should be compared for the purposes of discovering partial matches. Only such profiles are eligible for evaluation of any partial matches found.

   To compare a profile to LDIS, perform a keyboard search. Only profiles that meet the necessary number of loci and statistical threshold for entry into LDIS should be searched in LDIS.

   See the CODIS Manual for more detailed information regarding DNA matches.

   There are two ways to perform the comparison with LINKAGE; either or both may be used. It is possible for potential matches not to be found using LINKAGE especially when partial profiles are being considered; this is due in part to the inability of LINKAGE to handle more than two alleles per locus.

   Any potential case-to-case matches not identified in LINKAGE will be picked up by LDIS once the profile is entered there.

   If a sample from your case matches a sample from a previous case, consult with your supervisor and follow the current local hit notification guidelines.

   a. Scan LINKAGE visually for your profile.

      This example assumes that LINKAGE is arranged, from left to right, using Cofiler and Profiler Plus loci order. To scan LINKAGE visually for your profile, place the cursor in the D3S1358 field and press Ctrl-Z (zoom), then enter your D3S1358 value (e.g. 15 space 16, or 15) and click on OK. This will take you to the part of LINKAGE where all profiles beginning with that value reside. Move the cursor to the D16S539 column, then page/scroll down to see if your D16S539

value is represented. Repeat for each locus until you discover a potential match or determine there is none.

It is not necessary to scan the partial profiles listed at the beginning of LINKAGE.

b. Perform a query in LINKAGE

This approach may be used for full or partial profiles. Under the File menu, select "NEW", then select "QUERY"; select the LINKAGE database as the database to query. Place a checkmark in **all loci**, FB # and Backlog #. Type in the desired values (e.g., some or all of the alleles in each locus). Enter values for as many or as few loci as desired; understand, however that entering few may yield a large number of potential matches to evaluate and entering many may miss a potential match that is lacking one or more loci. It may be helpful to choose rarer alleles when performing a query. Run the query by pressing F8, clicking on the "blue gears" on the menu bar, or choosing "Run Query" from the Query menu.

When entering values for the DNA alleles, do not use commas or more than one space between alleles. It will cause a potential match to be missed!

5. Not all samples require DNA analysis in all available DNA systems; in fact, the majority of samples require only Identifiler. Submission of samples for Y STR typing is case dependent.

6. The DNA system chosen for additional testing may depend on the nature of the case.

a. Were the only DNA alleles detected in a semen-containing sample those of the victim? If so, amplification using Y STR's may be needed.

b. Does it appear that there are multiple semen donors? If so, amplification in Y-STR's may be needed.

c. Does the case involve a body identification of a male, and are there paternal relatives available for testing? If so, amplification using Y STR's may be needed.

7. Ensure that the laboratory concordance policy is satisfied.

8. Prepare a profile generation report or table of results, if applicable,

9. Prepare a PCR Statistics sheet, if necessary. Enter all alleles that meet the allele calling criteria.

10. Prepare a DNA Profile Evaluation form, if necessary. Follow the guidelines listed for eligible profiles to determine how many (if any) alleles to enter at each locus.

11. Review the case file to ensure that all the necessary paperwork is present and is organized in a logical format.

12. Finalize the draft case report, approve, and submit for the required technical and administrative reviews.

E. Case Completion

A case is considered complete when the analytical work is done, the case report is written and passes technical and administrative reviews, and the case report is distributed to the requesting agency(s).

Evidence Return:

Pre-LIMS evidence: Bring the original voucher(s) to the Evidence Unit.
Post-LIMS evidence: Within the LIMS, mark the individual vouchers of evidence for final return. The Evidence Unit will obtain the item(s) and prepare the item(s) for "pending release to the Property Clerk" using their normal procedures. With the exception of post-mortem items and exemplars, retained samples should no longer be indicated on the chain of custody.

F. Case Report Routing

Pre-LIMS case reports: The IA/RA completes the Forensic Biology Report Route Sheet to indicate which agencies are to receive the case report. LIMS case reports: the intended case report recipients are recorded in the application.

Report distribution is usually done in conjunction with administrative review. For details see the Administrative Review procedure.

Most reports are distributed to the ECMS system of the NYPD. In addition to ECMS reports are distributed as follows:

1. Deaths: Reports are supplied to the OCME Records Department. Optional: The reports may also be supplied to the District Attorney's Office (to the assigned ADA) and/or NYPD units (to the assigned Detective).

2. Sexual Assaults and Suspect files for Sexual Assaults: Reports are supplied to the Bureau Chief of the appropriate Sex Crimes Bureau.

3. Miscellaneous and all other Suspect files: Reports are supplied to the District Attorney's Office (to the assigned ADA) and/or NYPD units (to the assigned Detective).

4. Property Crimes and Weapons case reports are supplied to the District Attorney's offices only if a suspect has been arrested.