FORENSIC BIOLOGY EVIDENCE AND CASE MANAGEMENT MANUAL

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Highlighted section(s) indicate new revisions to that procedure.

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 DAC 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)
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.

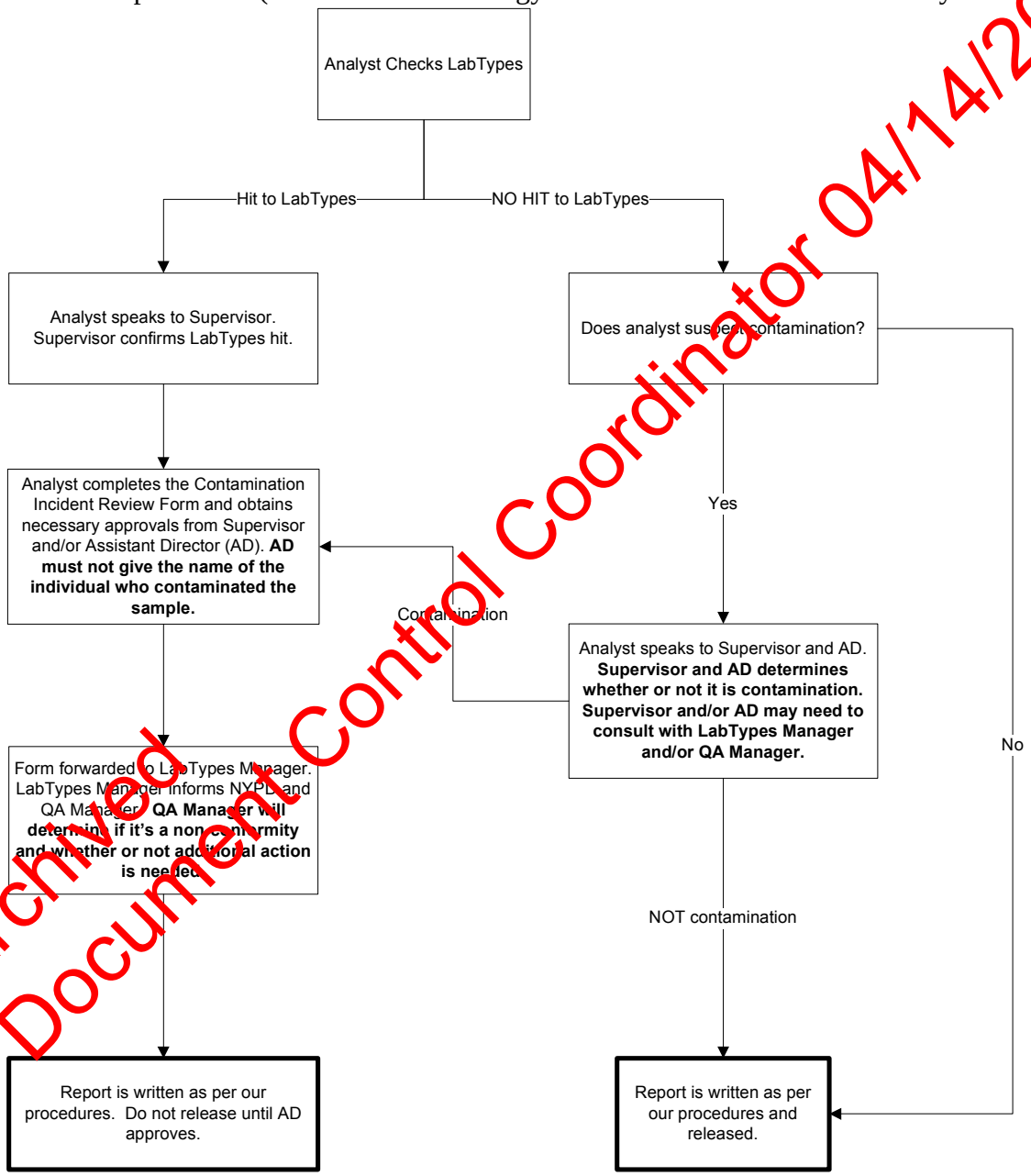
g. Are there other samples that may require duplication? If so, identify those samples and start the appropriate steps (i.e., re-extraction or re-amplification).

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.

Revision History:

February 9, 2010 – Initial version of procedure.

April , 2011 – Revised Section D.3 for the discovery of partial matches.

July 16, 2012 – Revisions for LIMS implementation, mostly to remove references to specific worksheets. Deleted "Finalization of Case File" from Section E

October 1, 2012 – Added explanation of case priority levels in Section B.1. Inserted a new Section D.3 that directs analysts to check Lab Types as part of STR profile evaluation; flowchart inserted for guidance. Existing sections that follow are renumbered.

August 14, 2015 – Removed references to the old Rotation system and replaced it with Production Teams. Updated references to LIMS usage. Changed references of P30 to PSA. Removed out of date practices.

Case Files

GUIDING PRINCIPLES AND SCOPE

Each Forensic Biology case has an associated "case record" that consists of all examination and administrative documentation, whether electronic or hard copy, generated or received for the case. Case record information may be in more than one location. The term "case file" refers to a subset of the case record. It is a hard copy collection of selected examination and administrative records, usually maintained in a letter size tabbed folder ("the file"), which supports the results of analysis found in the case report(s). Each Forensic Biology case record may include more than one case file.

Case files facilitate technical and administrative review and the creation of certified copies to fulfill discovery requests. This is true whether the examinations and reports are generated outside of the Laboratory Information Management System (pre-LIMS) or by using the LIMS (post-LIMS).

This document describes the general process for how **case files** are compiled.

PROCEDURE

A. General Guidelines

Cases/evidence in Forensic Biology can be classified as "pre-LIMS" and "post-LIMS". The classification status of a case and/or its associated evidence will affect how and when case files are generated and used. In pre-LIMS work the case file is the primary location for records related to a particular case. For most evidence received post-LIMS, the LIMS is the primary location for records related to the particular evidence, and any associated case files fill a secondary role.

Because there are many possible scenarios, the following is provided as guidance:

1. Pre-LIMS cases/evidence "in progress" at the date of LIMS "go-live" will continue to be maintained in the hard copy case files that were created for the associated cases.

2. When additional evidence for "in progress" pre-LIMS cases is received post-LIMS, the analyst should use the existing case file if space allows.

3. Case files for post-LIMS evidence/cases need not be created at Sign-In. It will usually be the reporting/interpreting analyst who will label a file folder with the FBio case number so that it may be used as the collection point for the hard copy records described in the "Administrative Records" and "Examination Records" discussions that follow. **To minimize the transfer of case files within the laboratory, it is strongly recommended that a separate case file be created for each case report that will be produced.** This will also keep case files from getting too large. For example:

   a. When additional evidence for pre-LIMS cases with no open assignments is received post-LIMS, the analyst should create a new case file for the additional testing and case report.

   b. When cases have assignments in multiple functional groups, e.g., missing persons and mitoDNA, a case file should be created for the missing person report and supporting documents and a case file will be created for the mito report and supporting documents.

B. Case File Contents

1. The majority of the paperwork in the "post-LIMS" case files will be printouts of attachments and functional reports from the LIMS case record. For "pre-LIMS" testing the paperwork in case files consists of original handwritten examination notes and photocopies of documents such as batch worksheets.

2. Case files created by a contract laboratory will not contain much of the information listed below. The administrative paperwork, analytical paperwork, report format, etc. will differ from case files created by the Department of Forensic Biology.

3. Suspect files are arranged in the same format as evidence files.

4. Paperwork in case files must be maintained in a neat and organized manner. There should be no loose pages, Post-Its, etc.

Administrative records. Administrative records are information not resulting from evidence examination, for example, vouchers and requests for lab testing. All administrative documentation **must** be identified for association to the case file with the appropriate case number. Multipage (stapled together) administrative documents should be marked with a case number on each page. The following are clipped to the left-hand side of each file, as applicable to the specific case:

a. Communication Log Reports

b. Scheduled analysis report

c. Copies of NYPD paperwork: 61 form (NYPD complaint report), request for laboratory examination forms, ECT collection forms (if present), evidence vouchers (documentation of evidence collected), contracts with outside jurisdictions

d. Miscellaneous correspondence, such as, **copies** of sexual assault kit paperwork or memos to and from outside laboratories.

e. Chain of custody reports

f. DNA extract tracking reports

g. Forensic Biology laboratory case report, route sheet, and fax confirmation sheets

h. CODIS paperwork

Examination records. Examination records contain information related to evidence testing. All pages of examination documentation must have the case number, dates the testing was done, the handwritten initials/name or electronic equivalent of the interpreting/reporting analyst for the case, and page numbers (double sided pages must contain page numbering on both sides of the page). The handwritten initials/name or electronic equivalent of the analyst performing a particular test must be present on the pages representing that analyst's work. For functional reports generated within the LIMS, the names of analysts, witnesses, and reviewing supervisors are considered electronic signatures, and are traceable within the LIMS system. The following are clipped to the right-hand side of each case file, as applicable to the specific test request:

a. Autopsy case worksheet

b. Exemplar processing notes

c. Examination notes and photos documenting the evidence examinations

d. PSA testing and/or amylase notes

e. DNA extraction notes

f. Quantitation notes

f. Amplification notes

g. Electropherograms

h. Pre-LIMS testing only: The case productivity worksheet, documenting the total number of examinations and tests for laboratory statistical purposes.

Page numbers are placed at the bottom margin of the pages on the examination documentation (right-hand side) of the case file, starting with the bottom page. Continue the page numbering if additional analyses are done after a report has been issued and/or if there is more than one file folder for a case. It is recommended to not start page numbering over with page one in the second case record.

Supplemental Records. Supplemental records contain summary information derived from testing recorded in the examination records. Supplemental records are used to aid case analysts in their interpretations and report writing. All pages of supplemental records must have the case number, the handwritten initials/name or electronic equivalent of the interpreting/reporting analyst for the case, and page numbers. The following are clipped to the right-hand side of each case file, as applicable to the specific test request:

a. Results table (if applicable)

b. PCR statistics worksheets

c. CODIS match estimation worksheets

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Revision History:

February 9, 2010 – Initial version of procedure.
July 16, 2012 – complete re-write of procedure to limit the scope of the document to a description of the contents of case files and to include information needed for laboratory function in a LIMS environment.
December 30, 2013- Removal of results table/ profile generation sheet and PCR statistics worksheets from the "Examination Records" section and creation of a new section titled "Supplemental Records". Addition of the statement to the Examination Records section recommending to not start page numbering over with page one in a second case record.
September 1, 2014 – Changed "Results table/profile generation sheet" to "Results Table" for consistency between manuals.
May 1, 2015 – Clarified page numbering of double sided pages in Examination Records section.
August 14, 2015 – Updated Administrative Records section and changed references of P30 to PSA.

Evidence Sign-in

GUIDING PRINCIPLES AND SCOPE

The Department of Forensic Biology receives evidence primarily from New York City law enforcement agencies for DNA testing. On occasion the Department will accept cases from other agencies; however, these agencies must have prior authorization to submit evidence. Evidence submitted for DNA analysis, regardless from which agency it is submitted, must be vetted by the Sign-In Team or a supervisor.

The primary responsibility of the Sign-In Team is to triage any evidence submitted for DNA analysis before it can be examined. The two main purposes are to determine the probative value of the evidence and, once that has been established, to assign the evidence to a Forensic Biology case. The procedures below describe the evidence sign-in process.

PROCEDURE

Email Accounts. The DNA Sign-In email account (DNASignIn@ocme.nyc.gov) is used by the Sign-In Team for case-related communications such as requests for exemplars, clarification of discrepancies in submitted paperwork and customer requests for expedited testing, and any other case-related inquiries. The Sign-In Team monitors this account throughout the day and updates the cases and the communication log as necessary.

The High Sensitivity DNA Testing email account (HighSensTesting@ocme.nyc.gov) is used for fee-for-service cases from outside of the City of New York. Members of the High Sensitivity team monitor this account.

A. Evidence Sign-in Process

Evidence is evaluated for acceptance using the following general guidelines. Not all steps are completed for all cases. For example, Step 3 (checking DEMP) is not applicable for cases from jurisdictions outside of New York City. At any point, if additional information is required before accepting the evidence, the appropriate agency is contacted to obtain the information needed.

1. The Forensic Biology Sign-In Team and/or a supervisor evaluate the submitted case information for each item of evidence. During the evaluation process, the communication log and case notations may be created and additional documents may be considered (e-mailed pdf forms from DAOs, NYPD, etc.)

a. Review the case details to determine if enough information is available to accept the case.

b. The criteria to accept an outside jurisdiction case for High Sensitivity Testing also includes completion of a legal contract and submission of the appropriate fees. The High Sensitivity team, with the aid of legal counsel, will track these factors.

c. Outside jurisdiction cases submitted for Missing Persons/Unidentified Human Remains cases must have a blanket legal agreement approved and signed prior to the evidence being submitted. A copy can be obtained from the Legal Department. In addition, a supervisor will have also had communication with the agency regarding cases that will be submitted for anthropological exam and DNA testing.

2. Check the Forensic Biology case databases ("Access" and LIMS) to determine if the evidence is from a new incident or is additional evidence for an existing Forensic Biology case.

   a. If the evidence submitted is additional evidence connected to a sexual assault kit, it should be noted as such and the additional evidence will remain in a pending status until a Criminalist IV supervisor evaluates the evidence for acceptance.

3. Check the DNA Evidence Management Program (DEMP) to determine if there is any related evidence or a case conferral.

4. Make case conferrals, if necessary, and create or update the communication log.

   a. If a request or communication comes into the lab prior to the evidence, a communication log can be started within the LIMS and attached to the applicable case record after the evidence is accepted in Forensic Biology.

   b. If the case will be deferred, proceed with the Deferral Procedures outlined in Section C.

5. New cases are automatically assigned the next available Forensic Biology number by the LIMS. Each incident gets a unique Forensic Biology (FB) number, which usually means one case record per victim. However, some types of cases with multiple victims, e.g., homicide/suicide, double homicide, assaults/sexual assaults with more than one victim, or mass disasters; are counted as one incident, and therefore would be a single case. *Serial or pattern crimes* (more than one homicide, sexual assault, or assault but over a period of time) have individual cases per victim. All evidence associated with each incident will use the same FB number (See the Evidence Sign-In procedure for a description of FB number formats).

   If the evidence is from a case that was started prior to the LIMS, the original FB number can be entered manually in the LIMS.

   a. The format of the case number varies by case type. The case number formats for new Forensic Biology cases are:

Criminal cases:	FBXX-YYYYY
Missing Persons cases:	FBXX-YYYYY
Suspect cases:	FBSXX-YYYYY
Proficiency Tests:	FBPTXX-YYYYY
Random Reanalysis (STRs):	FBRAXX-YYYYY
Training cases:	FBTRXX-YYYYY

      XX = last two digits of the calendar year
      YYYYY = a 5-digit number corresponding to the order in which the case was received during the calendar year

      For example, the 10th case accepted in calendar year 2013 that is categorized as either Criminal or Missing Person would be assigned case number FB13-00010.

   b. Forensic Biology also has "case" designators for the following miscellaneous testing activities: QC Box, Reagent, Research, SRM, WTC-Disaster Manhattan, and WTC-Reported Missing.

6. Complete the Scheduled Analysis and confirm that the appropriate target date was assigned to the evidence.

7. **Important:** Add an "RA" entry for each anticipated case report. This is equivalent to creating an "assignment" for testing. Initial information will be the functional group(s), assignment start date, and target date. The actual RA for the assignment can be selected later.

8. Enter case information into the Forensic Biology case record.

    a. Outside jurisdiction cases submitted for High Sensitivity testing arrive with an assigned "OJ" number that should be entered into a cross reference field of the case record.

    b. For Missing Persons/Unidentified Human Remains cases submitted from jurisdictions outside of New York City, enter "NYS Grant case" into the Notes field in the case record.

9. Once the sign-in process is complete, the case may require a supervisor review. If a review is not required, it is submitted directly for evidence exam. If a review is required, a supervisor shall review the submission and the schedule of analysis, and either accepts it or rejects it back to sign-in for correction. Most property crimes, weapons cases, and suspect files may not require sign-in review.

    Note: Any "high priority" designation must be first approved by a Forensic Biology Manager. Stranger cases (i.e., no suspect cases) must be visibly indicated for proper processing.

10. After the case is accepted by the sign-in supervisor, the EU will be notified through the LIMS that the evidence is ready for examination and should move it up to the 5th floor for analysis.

B. Additional Evidence for Previously Submitted Cases

1. If the case existed prior to the LIMS, request the case file from the analyst if the case is still open or from the Administrative Team if the case has been completed.

2. Determine if the additional evidence requires testing. Proceed with evidence sign-in or evidence deferral.

3. If the additional evidence is for a High Sensitivity or Hybrid case still in progress, send a notification to the High Sensitivity or Hybrid supervisors to alert them to the additional evidence.

C. Evidence Deferral

At any point of the case acceptance evaluation process the following steps must be followed to defer any evidence from testing:

1. Contact the NYPD DNA Liaison Unit (LU) and/or District Attorney's office (DAO) via telephone or e-mail to obtain authorization to defer evidence. All contacts are documented in the communication log for the case.

2. After authorization is granted, deferral notifications are generated and distributed to the LU and DAO.

    a. Notifications are completed by a member of the Sign-In team or a Forensic Biology supervisor or manager.

    b. The LIMS has functionality for generating and distributing the notifications.

Revision History:
February 9, 2010 – Initial version of procedure.
June 14, 2011 – Added information regarding network folders for outside jurisdiction cases; in A.7, added steps "a" and "b" regarding outside jurisdiction cases; in A.9, added info regarding file folder colors; Added step A.10 to describe the procedure when case files are returned by EU to DNA Sign-In.
February 2, 2012 – Procedure change in Step A.1 to modify the sign-in workflow of additional evidence connected to a sexual assault kit.
July 16, 2012 – Content made more generic so that it can apply to both pre-LIMS cases and evidence received after LIMS implementation; added case numbering format information (A5).
October 29, 2013 – Revised Section A.9 to allow signed-in cases to be submitted to evidence examination without a supervisor review.

Case Acceptance

A. Types of cases accepted by the Department of Forensic Biology

Case Type	Associated Samples	Case Designation
Homicide	- Evidence - Elimination exemplars*	FBYY- #####
Sexual Assault	- Evidence - Elimination exemplars*	FBYY- #####
Suspect	- Pseudo-exemplars (such as bottles, cups, cigarettes) - Exemplars (oral swab, blood)	FBYY-S####
Property Crimes	- Evidence - Elimination exemplars*	FBYY- #####
Weapons (CPW, Found Firearm)	- Evidence - Exemplars	FBYY- #####
Assault	- Evidence - Exemplars	FBYY- #####
Forensic Paternity	- Product of conception - Exemplars	FBYY- #####
Unidentified Human Remains ("Missing Persons")	- Post-mortem samples - Kinship exemplars - Pseudoexemplars (razors, toothbrushes, underwear, etc.)	FBYY- #####
Mass Disaster	- Post-mortem samples - Kinship exemplars - Pseudoexemplars (razors, toothbrushes, underwear, etc.)	D@YY-##### (where @ = One-letter borough designation)
Mitochondrial DNA Testing (mtDNA)	- Evidence - Exemplars	FBYY-#####
Outsourced	- Evidence - Exemplars	Assigned by contract lab
Proficiency	- Evidence - Exemplars	Designated by vendor

***** A biological sample from a known individual (commonly a consensual partner, homeowner, or employee of a business), other than the alleged perpetrator or victim, which is analyzed for purposes of identifying those portions of a forensic DNA profile attributable to the alleged perpetrator.

B. PCR DNA tests available for use

Supplier	Kit	Loci	CODIS eligible
ABI	**Identifiler***	**D8S2279, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, Amelogenin, D5S818, FGA**	**Yes**
	MiniFiler	D13S317, D7S820, Amelogenin, D2S1338, D21S11, D16S539, D18S51, CSF1PO, FGA	Yes
	Yfiler*	**DYS456, DYS389I, DYS390, DYS389II, DYS458, DYS19, DYS385 a/b, DYS393, DYS391, DYS439. DYS635, DYS392, Y GATA H4, DYS437, DYS438, DYS448**	**YES** (Missing Persons Cases Only)
OCME	mtDNA	HVI, HVII direct sequencing	Yes

*Systems used for routine casework

C. Scheduled analysis

Depending on the case, it may be necessary for other types of examinations to be done before or after the Department of Forensic Biology examines an item. Fingerprint processing, gunshot residue, hair and fiber examinations, etc., may be equally or more important than the presence of biological fluids.

1. The scheduled analysis can range from determining only the presence of semen, saliva, or blood on an item to DNA analysis of stained or touched items for comparison with victims, elimination samples, and/or suspects. The decision of what analyses are to be performed is made by a member of the evidence sign-in team or Criminalists III, IV or Assistant Director after evaluation of the evidence through review of the NYPD paperwork (vouchers, requests for laboratory examinations, and NYPD reports), discussions with the NYPD, and/or discussions with assistant district attorneys. The scheduled analysis can change if prioritized items are negative and additional evidence must be examined, or if additional evidence is accepted by the laboratory.
2. For post-mortem items submitted by the OCME medical examiners, the decision of what analyses are to be performed is generally made by a Criminalist III or IV after evaluation of the items through review of the OCME paperwork and/or discussions with the medical examiner. For post-mortem sexual assault kits (or

swabs submitted separately), serology testing and DNA testing is not done automatically (with the exception of homicide cases). Instead, the medical examiner responsible for the autopsy is notified and asked to reply if testing is needed. For most such items, the Department of Forensic Biology will assign a case number and store the items without scheduling testing. The Scheduled Analysis can change if the medical examiner, NYPD and/or assistant district attorneys later decide the analysis is needed.

3. For documented instances where a decedent (ME cases) is also the named suspect in another case, a portion of the PM Bloodstain should be transferred into an S-file (analogous to suspect sexual assault kit buccal specimens) for typing, comparison and entry into LDIS as per normal procedures for suspects.

D. Target dates

Target dates are assigned by the evidence sign-in team and/or supervisors based on the available information. Target dates for amended reports are entered by the individual who creates the assignment for the amended report.

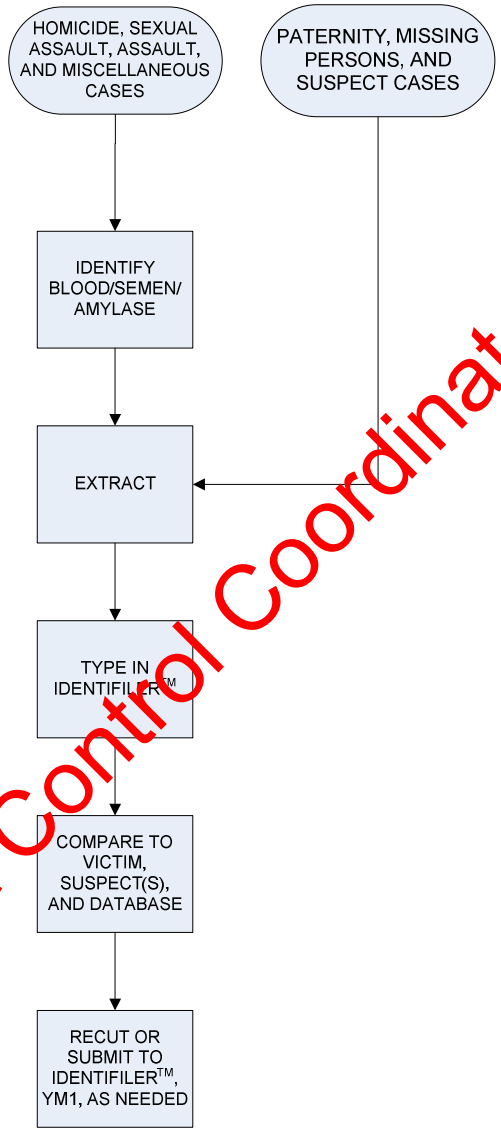
Case Type	Default Target Date
Homicide	60 days
Sexual Assault (Kit DNA Report)	60 days
Sexual Assault (Additional Evidence)	60 days
Forensic Paternity	60 days
Property Crimes	60 days
Weapons	60 days
Assault	60 days
Missing Persons	30 days
Suspect	30 days
Mitochondrial DNA	90 days
Proficiency	Assigned by vendor
Amended Reports (all Case Types)	Same as Assignment Start Date
Miscellaneous	60 days

Target dates can fluctuate in order to accommodate court dates, investigative leads, high priority case, or if additional evidence is signed into the laboratory.

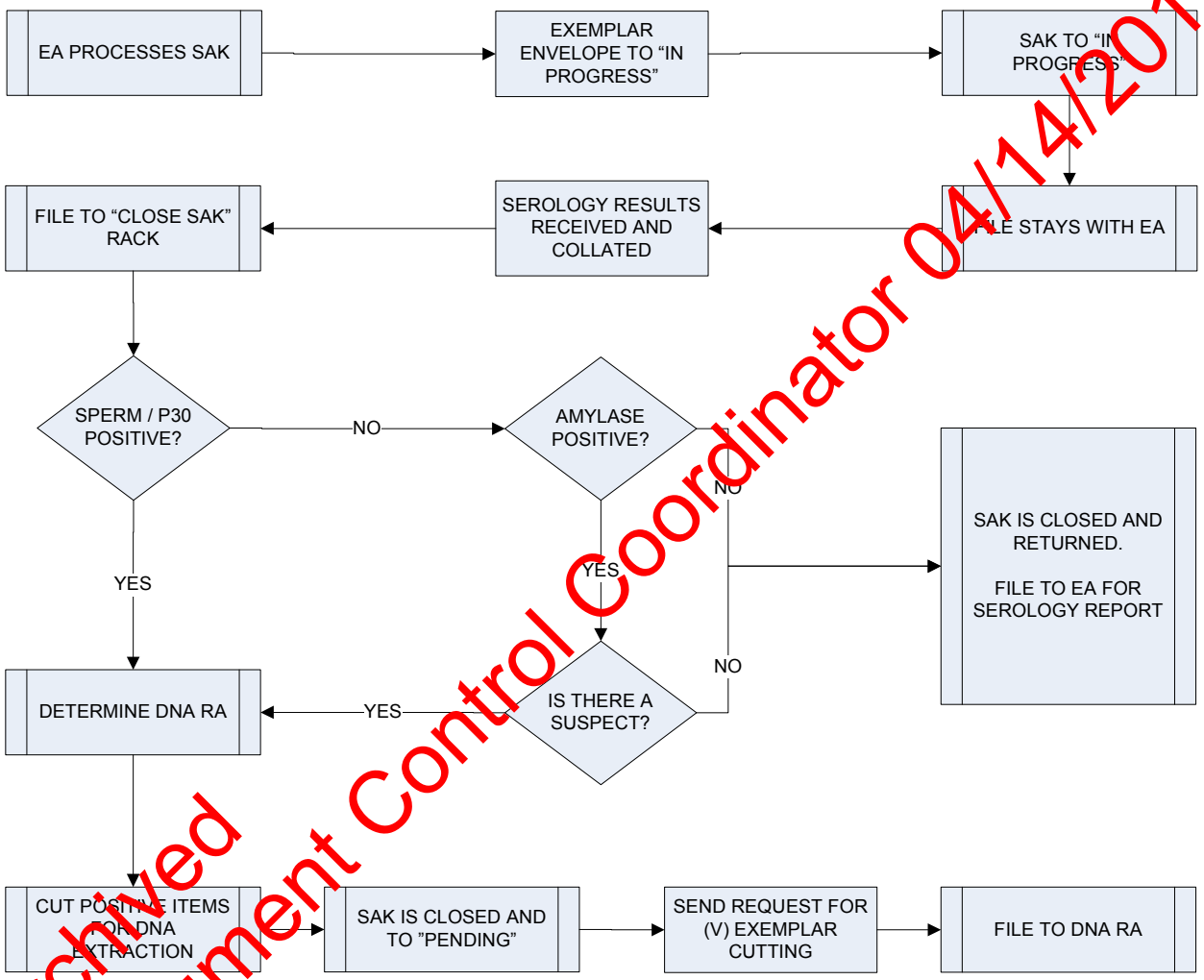
Regardless of the target date, a report should be written and submitted for review no later than seven calendar days after the last analytical results are available.

E. Case flow

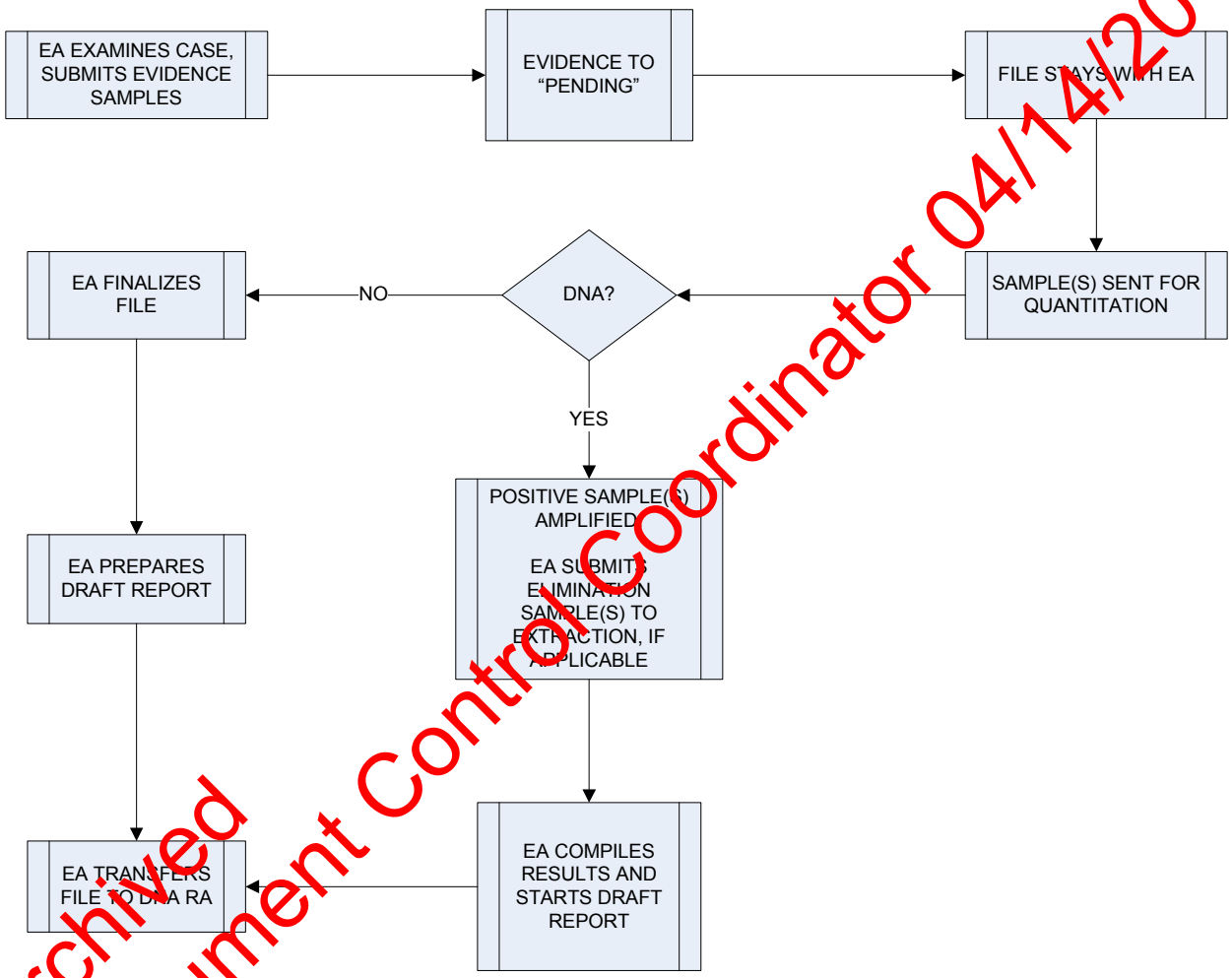
General Processing Flow Chart



Sexual Assault Kit (SAK) Processing Flow Chart



Property Crimes Processing Flow Chart



F. Sample Scheduling and Submission for High Sensitivity Testing and Case Transfer

High Sensitivity testing is an additional type of testing that is available for samples from all case types. Candidate samples for this testing are touched objects which likely consist of only skin or epithelial cells, and samples that were found to contain biological fluid but did not yield results with HCN DNA testing techniques. Samples with low amounts of DNA template are referred to as Low Template DNA (LT-DNA) samples, while those with high amounts of DNA template are called High Template DNA (HT-DNA) samples.

The Laboratory may accept cases with touched clothing for homicide, assault, and sexual assault cases if this is the only evidence in the case or if this is the evidence of last resort after all other testing options have been exhausted.

Touched objects often yield potential LT-DNA samples and as such should be tested with High Sensitivity methods. Cases tested initially for HT-DNA may also contain samples with the potential for High Sensitivity testing. When HT-DNA testing has been completed, the Reporting Analyst and/or supervisor should evaluate the case for potential High Sensitivity testing.

Detecting DNA on a touched object simply indicates the presence of DNA and does not infer the mechanism of deposition of that DNA. If DNA is not detected on a touched object, this does not indicate lack of contact. Therefore, the relevance of generating a DNA profile(s) on an item should be carefully considered prior to testing. For most cases, if informative profiles are produced with HT-DNA testing, additional High Sensitivity testing is not warranted. Even if there are no informative profiles in a case, before initiating High Sensitivity testing, if there is an arrested suspect, the ADA assigned to a case should be consulted. If there is no arrested suspect, and no or insufficient informative profiles, High Sensitivity testing may be attempted.

1. Sample Triage

   A sample may be designated for High Sensitivity testing upon initial acceptance or following testing with HT-DNA testing which does not yield sufficient DNA or a robust profile. A supervisor must approve submission of a previously processed sample for High Sensitivity testing. Since DNA extracts degrade with time, High Sensitivity testing may commence prior to completion of standard testing and its review.

a. Samples that would potentially yield low amounts of DNA are typically objects that have been handled and do not contain biological fluid such as blood, semen, saliva, or even sweat. If an analyst is swabbing such an item, the High Sensitivity swab and swabbing procedure should be utilized. These samples may include but are not limited to:

1) Any touched object
   a) Side of bottles, cans or containers (not mouths)
   b) Business, credit, identification, metro, or phone cards
   c) Keyboards or computer mice etc
   d) Keys
   e) Handles of various items such as brushes, combs etc
   f) Jewelry
   g) Letters or envelopes
   h) Pens or markers
   i) Pouches for cell phones, glasses, PDAs, MP3 players etc
   j) Ropes, strings, tape, zipties, or objects used for binding or strangulation
   k) Wallets, purses, or bags including garbage bags
   l) Wrappers for condoms or candy etc
   m) Weapons
      i) Bat, broom, hand saw, ice pick handles
      ii) Bombs
      iii) Gun handles, triggers, magazines
      iv) Knife handles

2) Finger or palm prints

3) Swabs that were previously taken from touched objects such as:

a) Counters or banisters (these may often yield mixtures and should be accepted as a last resort item)

b) Headboards

c) Portals such as window sills or door handles

d) Switches for lights etc

e) Steering wheels or handles of car doors

4) Swabs taken by the latent print laboratory prior to fingerprint treatment unless it is specified that possible blood, semen, or saliva was recovered with the swab. (If the swab is KM positive upon examination for High Sensitivity testing, the sample should be sent for HT-DNA typing if enough DNA is recovered.)

b. There are some samples that may not easily be categorized as either High Sensitivity or HT-DNA testing appropriate; sample triage will depend upon the specifics of the case. Nevertheless, as a general guideline, consider samples that are handled to be High Sensitivity samples whereas samples that could potentially contain saliva, sweat, blood or semen should be deemed HT-DNA samples. If HT-DNA samples do not yield DNA, they can be subsequently transferred for High Sensitivity testing.

1) Some examples of samples that typically contain low but sufficient amounts of DNA for HT-DNA testing are:

a) Cell phones (particularly the mouth piece)

b) Clothing that will be scraped

c) Food items that have been partially consumed

d) Gloves

2) If an analyst is swabbing such an item, the High Sensitivity swab and swabbing procedure should be utilized.

c. If a case does not produce an informative DNA profile with HT-DNA testing, the following samples should be considered for submission to High Sensitivity Testing pending approval of a supervisor:

1) Those with insufficient DNA for PCR DNA typing, but

a) Amylase, PSA, or KM positive

b) Scrapings or swabs of any handled objects

2) Those that produce a poor STR profile despite a sufficient quantitation value

3) Note that if HT-DNA testing indicates the presence of a mixture, at best LT-DNA testing can only generate the profile of the major component of the mixture. Minor components may be used for comparisons, but cannot be deduced unless the sample is an intimate sample.

d. For cases with touched clothing, specific information is needed on where the individual was touched ("On the arm" or "On the neck" is acceptable; "somewhere on the shirt" is not acceptable). Exemplars from the victim(s) must be submitted prior to any touched clothing is tested.

2. Sample Scheduling

a. When a case is submitted for High Sensitivity DNA testing, all relevant logbooks and databases should be completed as with HT-DNA testing. If the case already has an entry in the database for HT-DNA testing, a second entry should be made for the High Sensitivity DNA testing portion. In this instance, the date received is defined as the date the case was transferred to the High Sensitivity team. However, if the evidence is not stored in the Forensic Biology Department, the date received is defined as the day the evidence returns to the lab.

b. High Sensitivity cases have a 60 day target date.

c. If cases only contain LT-DNA-type items scheduled for examination, the case should be transferred directly to the High Sensitivity team for examination. A rack is situated in the evidence exam room for these files. These items are scheduled with the letter on the Scheduled Analysis designated for "High Sensitivity testing".

d. If HT-DNA type evidence is the only type of evidence scheduled in the case, but LT-DNA-type evidence is also included, the LT-DNA items(s) should be scheduled with the appropriate letter for "Do not schedule for examination until supervisor establishes case status." OR if, in general, 5 or fewer HCN type items are scheduled along with 5 LT-DNA items, the case may be assigned as a "Hybrid" case. See Section F below.

1) After HT-DNA testing has been completed and case circumstances suggest that LT-DNA testing should be done on some items/samples, the Reporting Analyst and/or supervisor may submit the file to the High Sensitivity team for evaluation..

a) If there is an arrested suspect, first contact the ADA assigned to determine whether High Sensitivity DNA testing is warranted.

b) If there is no suspect, consult the relevant agency investigating the incident.

3. Case Files and Transfer

a. If HT-DNA testing has already been started or completed in a case, a second file may be generated when items are tested by the High Sensitivity team. The HT-DNA testing results may be located in file 1 of 2, and the second file may contain High Sensitivity DNA testing results.

b. If HT-DNA testing has concluded and the report has been reviewed, forward the file to the High Sensitivity DNA team for evaluation..

c. High Sensitivity DNA testing may begin prior to completion of HT-DNA technical review, upon supervisory approval. It is advantageous to perform High Sensitivity DNA testing promptly since small amounts of DNA likely degrade with time, and thus, over time, the probability of a good result may decrease. See below for details pertaining to case transfer.

d. Transfer of a sample for High Sensitivity DNA testing for a case also undergoing HT-DNA testing or technical review involves the following:

1) The HT-DNA analyst should submit the case file to a High Sensitivity supervisor so that copies of the contact sheet to date, the 61 report, and relevant laboratory requests and vouchers can be made and included in the High Sensitivity file.

The High Sensitivity supervisor should then evaluate the case to determine which samples need LT-DNA testing. If items need additional examination, the High Sensitivity supervisor will schedule those items for examination, create a new database record, and transfer the relevant chain of custodies to the new High Sensitivity case file. (Following examination, the High Sensitivity analyst should return the original chain of custody to the original case file).

2) If the sample has already been extracted, the extract location, and the name and location of the relevant extraction or microcon negatives will be noted by the High Sensitivity supervisor. When the samples are brought into the LT-DNA laboratory, state "transferred to HiSens" (or a similar statement indicating the transfer) in the DNA tracking sheet. The High Sensitivity team will temporarily transfer the extract tube to the LT-DNA facility, where it will be stored in a cryobox labeled "transferred from HSC testing". A new tracking sheet will specify all aliquots for High Sensitivity testing and will be kept in the High Sensitivity file. Upon completion of High Sensitivity PCR DNA testing, the original extract tube will be returned to its original storage location with a note on the tracking indicating its transfer.

3) When necessary, the High Sensitivity team may re-cut a sample whose chain of custody is in the original case file. The High Sensitivity team member will arrange with the original HT-DNA case analyst, if necessary, for temporary possession of the file in order to gain custody of the sample.

4) The original HT-DNA analyst should notify the High Sensitivity team regarding the victim's profile, if available.

5) The High Sensitivity team should be notified immediately of any relevant suspect profiles.

4. **Report Notations**

In both reports, a reference to the other report should be made according to the following situations:

a. HT-DNA report: If the case file will be submitted to the High Sensitivity team for evaluation, state "This case will be forwarded to the High Sensitivity group for further evaluation."

b. High Sensitivity DNA report:

1) If the HT-DNA report, was already issued state "This is an additional report. For previous results, evidence received, and disposition, see report dated…"

2) If the HT-DNA report was not yet issued, the HSC report will be an additional report to that of the High Sensitivity report.

5. Communication

When a case is processed for High Sensitivity and HT-DNA testing simultaneously, analysts of both teams must communicate and share results. Moreover, when testing occurs subsequently, the High Sensitivity DNA analyst should relay results to the HT-DNA analyst.

Communication between analysts sharing cases facilitates such necessary tasks as the following:

a. Comparison of foreign profiles in either file to mixtures suitable for comparison in the other
b. Assignment of foreign profile monikers (i.e. Male Donor A, B, C…)
c. Establishment of report dates and report order

G. Sample Scheduling and Submission for Hybrid Testing

Hybrid cases are those cases classified as either a homicide or assault and which include informative HT-DNA and LT-DNA type items. In general, the number of each type of sample scheduled is limited to 5 HT-DNA and 5 LT-DNA type items (for a total of ten items per case). In some instances, it may be appropriate to split the case into HT-DNA and High Sensitivity portions and to process the samples separately. However, in these situations, the results of each type of testing will need to be compared with each other as with any other case split between two groups for testing. Refer to the appropriate sections in this manual for scheduling of High Sensitivity and HT-DNA items.

1. Examples of cases appropriate for Hybrid testing are as follows:

   - Assault allegedly committed by a person or persons unknown to the victim

   - Cases including gun swabs, plus 5 or fewer HT-DNA type items

2. Examples of cases that are NOT appropriate for Hybrid testing are as follows:

   a. Assault or homicide cases where the HT-DNA evidence is likely to be more informative to the investigation than the High Sensitivity evidence.

   b. Assault cases with weapons such as knifes, bats, sticks, etc., for which there is an arrest and/or the individuals involved obviously knew each other (i.e., mother- daughter, husband-wife) **should NOT** be scheduled as hybrid cases. The handle of the weapon should NOT be scheduled for High Sensitivity testing

   These cases should be assigned for HT-DNA testing only; if in the future, testing of the handle of the weapon is requested, this can be done by analysts trained in High Sensitivity methods.

3. Homicide cases with arrested suspects SHOULD have weapons scheduled for High Sensitivity testing (if applicable).

4. If knifes, bats, etc., are found in suspect's homes, cars, or on the suspect's person, these should be scheduled for blood and HT-DNA testing only as well.

5. Sample Scheduling

When a case is submitted for Hybrid testing, all relevant logbooks and databases should be completed as with any other testing. If the case already has an entry in the database for testing with the same or another group within the lab, a second entry should be made for the Hybrid testing portion. In this instance, the date received is defined as the date the case was transferred for Hybrid testing. However, if the evidence is not stored in the Forensic Biology Department, the date received is defined as the day the evidence returns to the lab.

Hybrid cases have a 60 day target date.

The Schedule of Analysis for a Hybrid evidence item may indicate that no High Sensitivity samples are to be collected and/or sent for extraction unless a KM+ stain has been identified on that item. The likelihood that a given item of evidence is truly associated with a perpetrator should be considered when making the above determination. For example, in an assault case where the victim was stabbed, no further testing would typically be performed on a knife from which no KM+ stains were found unless it is somehow clear from the available information that the knife was handled by a perpetrator (and there is no other evidence in the case from which the identification of the perpetrator's DNA profile is likely to be more successful and/or significant).

a. Sometimes, in addition to the actual evidence item, swabs collected from that item by the NYPD are also received for testing. In these situations it is often appropriate for the Schedule of Analysis to indicate that KM testing on the item is not necessary if one of the associated NYPD swabs is found to be KM+.

b. If other evidence is included in the case that does not warrant testing, these items should be scheduled: "Do not schedule for examination until supervisor establishes case status."

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Revision History:

February 9, 2010 – Initial version of procedure.

September 27, 2010 – Added MiniFiler and PowerPlex Y to the list of PCR DNA Tests Available for use (Section B). Added information for touched clothing acceptance.

April 30, 2012 – Default target date for Sexual Assault DNA Reports was changed to 60 days; Sexual Assault Serology Report was deleted as a "case type." Sexual Assault Kit Processing Flow Chart was revised since positive serology reports are no longer written routinely.

April 4, 2013 – Footnote in Section A concerning "known individuals" was revised.. Added target date information for Amended Reports to the chart in Section D; language on time period for supervisors to complete technical reviews softened to "should" to infer guidance rather than absolute requirement. Policy for processing of non-homicide post-mortem items (Section C.2) was added.

April 1, 2014 – Procedure revised to include YFiler information.

May 1, 2015 – Section B revised to allow Yfiler kit be available for CODIS eligibility of Missing Persons cases. Information added to Section C concerning instances when a decedent is also the named suspect in a case.

August 14, 2015 – Updated section in general. Removed Power Plex Y and YM1 references as well as references to teams (Rotation System). Changed references of P30 to PSA.

Evidence Control

GUIDING PRINCIPLES AND SCOPE

The appropriate tracking and storage of evidence and work product is critical for ensuring that the value of the Department's testing results is not compromised. Chain-of-custody refers to the documentation that tracks the receipt of evidence (either post-mortem autopsy specimens or physical evidence obtained through investigations), through the analytical process, until it leaves the control of the laboratory. Unique identifiers on evidence items ensure that chain of custody records and examination records can be associated with the correct evidence.

The laboratory receives evidence primarily from the OCME Evidence Unit. "Evidence" is equivalent to a "test item". The Evidence Unit assigns a number (EU number) to the evidence and stores it under lock and key. Only Evidence Unit personnel have access to these locations.

The NYPD and other agencies and jurisdictions may bring evidence directly to the laboratory. Evidence from the OCME is received from all of the OCME locations via the Evidence Unit. At the conclusion of the scientific testing, the NYPD evidence is usually returned to the Evidence Unit and other evidence is returned directly to the submitting agency.

The Department of Forensic Biology defines "work product" as information or samples generated during the course of a scientific examination of evidence, such as graphs, photographs, extracted DNA, amplified DNA, electropherograms, or stained slides prepared from sample extracts.

PROCEDURE

A. Case numbers

Case numbers are discussed in the Evidence Sign-In procedure.

B. Evidence Item and Sample Identifiers

Each evidence item and sample from the evidence **must** be given a unique identifying number, clearly shown in the notes. A standard approach should be taken. The sections below describe the evidence and sample identification system implemented within the Laboratory Information Management System (LIMS). Evidence and sample identifiers used with evidence received pre-LIMS will not necessarily conform to this specific

system; however, the requirement for uniqueness remains.

1. An "item" refers to a single piece of evidence received by the laboratory.

   a. **Vouchered evidence**. Primary evidence items are named as follows:

   (FB#)_(last 3 digits of voucher)_(item#)_(short description ≤ 6 characters)

   For example, FB11-00123_546_1_Hat

   (Note: the short description for the evidence item can be changed by the analyst upon examination)

   b. **Postmortem (non-vouchered) evidence.**

   (FB#)_PM_(item #)_(short description ≤ 6 characters)

   FB12-00009_PM_1_bone

   c. **Subitems**. Occasionally, what is submitted as one item actually consists of more than one item. In these situations a "sub-item" number is incorporated into the item numbering format. For example:

   (FB#)_(last 3 digits of voucher)_(item#).(subitem#)_(short description)

   Two socks listed as item 2 are itemized individually as 2.1 and 2.2. The evidence items will therefore be named as follows:

   FB11-00123_546_2.1_sock and FB11-00123_546_2.2_sock

   d. **Other** (outside jurisdiction, proficiency tests)

   Internal cases, such as proficiency tests, and outside jurisdiction cases do not use a voucher so the OCME ID format is slightly different. The format is:

   (FB#)_(item#)_(short description)

   The OCME ID makes use of the entire FB number and uses only the first 6 characters of the item description. The item number is whatever is listed at the time that the EU number is created.

2. A "sample" is a portion of the evidence item (or sub-item) from which material is obtained that will be subjected to testing. An evidence item may have more than one sample. Evidence samples for vouchered evidence are named as follows:

   (FB#)_(last 3 digits of voucher)_(item#)_(evidence sample#)_(short description ≤ 6 characters)

   The area that is scraped will be considered as evidence sample 1 from the hat and will be named FB11-00123_546_1_1_Hat.

3. A "cutting" is that portion of the sample actually tested, for example the scrapings from an area on an article of clothing or a portion of a bloodstain sent for extraction.

   (FB#)_(last 3 digits of voucher)_(item#)_(evidence sample#).(cutting#)_(short description ≤ 6 characters)

   Therefore, the portion of the scrapings actually being sent for testing would be named FB11-00123_546_1_1.1_Hat.

4. Identifiers for cuttings and samples created for PM, internal, and outside jurisdiction cases will follow the same logic as for the vouchered evidence from external cases.

C. Evidence Seals

A **proper seal** is a seal that prevents loss, cross-transfer, or contamination of evidence while ensuring that attempted entry into the evidence container is detectable. Proper seals could include heat seals, tape seals, or a lock with the initials of the person creating the seal being placed on the seal or across the seal onto the container. **Staples alone are not a proper seal.**

The preferred type of proper seal used internally by the Department is a tape seal that bears the initials of the person who created the seal on the seal or across the seal and onto the container, and the date. **Staples alone are not an acceptable seal**, although they may be used in conjunction with tape to make it easier to apply a tape seal to a container**.**

If evidence that is received by Department does not have a proper seal, an Evidence Deficiency/Discrepancy must be completed and forwarded to a supervisor for approval. The condition of the seal is also recorded during the Evidence Packaging documentation process.

All evidence returned to the Evidence Unit must be properly sealed. Supplement improper original seals with a laboratory seal; however, preserve the original seals (including the initials of the person who created the seal) as much as possible. If this is not possible, consult with a supervisor for the best course of action.

D. Evidence receipt

Most evidence is accepted into the OCME by the Evidence Unit and is assigned an Evidence Unit number. All evidence must be appropriately packaged as suitable for the item type when the laboratory receives it. In general, most evidence should be placed in breathable paper or Tyvek. Sometimes evidence may be received in foil or foil-like containers, cardboard boxes, and plastic containers. All evidence received in the laboratory must be properly sealed.

The paperwork transferred with the evidence is reviewed to ensure that the evidence belongs in the Forensic Biology Department. Generally, the following items are not accepted:

(1) Items requiring fingerprint exams
(2) Items intended for hair/fiber exams
(3) Items intended for gunshot residue exams
(4) Hair, fiber, or other trace evidence
(5) Clothing from the deceased

Autopsy evidence sent from the OCME offices in Manhattan, Brooklyn, Queens, the Bronx, and Staten Island is received in sealed, plastic containers. Inside each container is a Transport Manifest that has a dated Transport Container Number. Pasted to the Transport Manifest are stickers with case numbers and/or bar codes for the specimens inside the container.

E. Chain of Custody

Evidence from user agencies is transferred from the Evidence Unit, where it is stored, to a member of the Forensic Biology Department. The chain-of-custody process records the transfer of evidence between individuals and/or between an individual and a storage location. All dates are recorded contemporaneously.

Transfers of evidence items are subject to full chain of custody requirements. The movement of evidence samples or work product may be tracked to a lesser degree, but these materials are not subject to full chain of custody requirements and do not use the chain of custody mechanisms described in the next paragraph.

Custody transfers for pre-LIMS evidence are recorded on hard copy forms. Custody transfers for evidence received post-LIMS are recorded using the chain of custody function in the LIMS application.

Instances arise that require the Department of Forensic Biology to send evidence to other agencies or laboratories. Under most circumstances this is accomplished using overnight mail services; the shipping paperwork is retained in the case record.

F. Sample witnessing in the laboratory

After samples are removed from the evidence, a witnessing procedure occurs at several points during the analysis to help ensure that testing is being performed on the correct sample. The witnessing step verifies that the sequence of tubes containing DNA or sample matches what is recorded on the applicable batch set-up: bloodstain preparation from whole bloods, DNA extraction, DNA quantitation, amplification set-up, and capillary set-up. The witness documents their witnessing activity.

G. Sample consumption

If possible, the entirety of an item or sample should not be consumed during analysis. It is recommended that at least 25% of the sample be saved for future analysis, if needed. An item or sample may be consumed if the analyst determines that consumption of the sample is necessary to have the best chance to obtain results; the examination notes must clearly state this.

H. Evidence storage and disposition

Evidence is stored in a secure location until it is assigned for analysis. Most evidence is delivered to the Evidence Unit, assigned an EU number, stored in the Evidence Unit and then transferred to the Forensic Biology Department for examination. Most evidence that is not being actively examined, but is still considered to be "in progress" (pending examination, pending review, etc.) is properly sealed and securely stored with the Evidence Unit.

The Department may use secure, locking "cages" within the laboratory for the temporary storage of evidence, such as exemplars, that are being actively examined.

Retained evidence. Evidence items retained for long-term storage, e.g., victim exemplars from sexual assault evidence kits, must be properly sealed and their storage location documented in the Chain of Custody of the case.

I. Retention, return, and disposal guidelines for evidence and work product

1. Post-Mortem Specimens

a. **PM sexual assault evidence** is returned to the Evidence Unit after examination.

b. Other PM specimens

	Blood stain?	Non-Blood?	Retention Schedule
FB cases	Y	Y	Retain all indefinitely.
Non-FB cases	Y	Y	May discard non-blood after 1 year; May discard bloodstain after 4 years.
	N	Y	May discard non-blood after 4 years.
	Y	N	May discard bloodstain after 4 years.
Unlabelled autopsy specimens			May discard
POC/Fetus (criminal activity)	n/a	Y	Retain a small piece and discard the remainder*

*For more detailed information on the retention of products of conception (POC), refer to the Evidence Examination procedure in the Evidence and Case Management Manual.

Bloodstain cards are retained in the laboratory at room temperature.

- Disposal and disposition guidelines for the residual liquid blood are found in the "Bloodstain Preparation from Whole Blood" procedure in the Forensic Biology Serology Procedures Manual.

Non-blood PM items include things such as hairs, fingernails, tissues, bones, etc. Non-blood PM items may be stored at room temperature, refrigerated or frozen.

2. NYPD (Vouchered) Evidence

After the analytical work is completed, reports are written, and technical reviews are complete, the Evidence Unit is notified that the evidence may be returned to the NYPD.

3. Non-NYPD Evidence

All evidence submitted from non-NYPD agencies, with the exception of retained items, is returned directly to the submitting agency.

4. DNA Extracts

a. Retained DNA extracts are stored either refrigerated or frozen.

b. Retention guidelines for DNA extracts:

Extract Source	Suggested Retention
FB evidence, non-exemplar	Retain indefinitely
FB exemplars and pseudoexemplars	May discard after one year
FB missing person cases	May discard after one year*
Labtypes - NYPD personnel	Return extract to NYPD representative
Labtypes - OCME employees, visitors, interns	May discard after one year unless the signed consent form specifies a different retention period

* A due-diligence check on the status of a **missing person case** should be performed prior to discarding extracts. This review will mainly cover post-mortem items and reference samples submitted for Missing Persons, such as razors and toothbrushes, to avoid disposing of DNA

extracts in situations where the actual item may have been consumed and the only samples left for re-testing are the extracts.

c. Extract Tracking. An extract tracking report can be generated by the LIMS and used to note the general location of DNA extracts while in testing or storage status.

d. Extract Disposal

The disposal of DNA extracts is documented either in the LIMS or, for pre-LIMS samples, on the extract tracking sheet, or via a memo or similar document which contains sufficient information to provide traceability to specific extracts, e.g., a list of Cryoboxes from which extracts were discarded. The latter method is suggested for use when large quantities of extracts are being discarded.

Disposal of Labtypes DNA extracts is documented in the LabTypes electronic database.

5. Amplified DNA

Amplified DNA is stored refrigerated. Once final analysis of the amplified DNA is complete, the amplified DNA can be discarded. Documentation of disposal is not required.

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Revision History:

February 9, 2010 – Initial version of procedure.

October 28, 2010 – A definition of proper seal is inserted and more direction is provided regarding what must be done if evidence is received by the laboratory without a proper seal.

April 18, 2011 – Added a section on Retention and Disposal guidelines for evidence, DNA extracts, and amplified DNA; revised retention schedules for post-mortem samples; renamed "signatures" section as "chain of custody"; added updated references to applicable management system documents; combined all chain of custody examples into one section; deleted "OCME transport of specimens from outer boroughs" section and moved the info into the "Evidence Receipt" section; deleted the "Specific guidelines for different evidence types" section, and moved the material into various sections within this revision.

July 16, 2012 – Revisions made for LIMS implementation. Removed large portions of the chain of custody discussion, particularly many examples; added a large section with the description of the system for evidence and sample identifiers.

August 14, 2015 – Updated section by removing out of date procedures.

Evidence Examination

GUIDING PRINCIPLES AND SCOPE

Specific methods to examine evidence varies by case type. Guidelines for the examination of the common types of evidence are presented in this procedure. If an analyst encounters any type of evidence not presented in this procedure, a supervisor shall be consulted for further guidance.

PROCEDURE

A. Note taking – general guidelines

Note taking and evidence documentation is the most important aspect of casework. Done improperly, it can jeopardize any analysis that follows. The notes are used to document the condition of the packaging and evidence, describe stains that may be found, present the results of presumptive and/or visual tests, support the conclusions of the report, and refresh the analyst's memory when required to testify in court. If the use of paper is required for notes, use a permanent medium such as ink—never pencil. Hard copy notes or sketches must be scanned for association to the case record in LIMS (as applicable).

1. Note taking starts with a description of the evidence packaging, including:

   a. Type of package – paper bag, manila envelope, zip-loc bag, etc.
   b. Condition of package – wet, bloody, etc.
   c. Type of seal – stapled, taped, unsealed.
   d. Identifying marks – a brief description of labels, tags, handwritten notations, etc.

   Each package **must** be labeled by the analyst with the evidence item identifier (see Evidence Control procedure for the numbering scheme), date, and his/her handwritten initials. Finding the marks in court is easier if the analyst always chooses the same location to put his or her marks.

2. Next is a description of the contents, the evidence itself. Specific suggestions concerning different types of evidence will be discussed later.

   Discrepancies between the voucher, laboratory request form, and the items in the package must be clearly documented and a deviation must be completed within the LIMS as necessary. This includes, but is not limited to, items that were

submitted, but were not included on the voucher. These items may also need to be examined. Give the item the next item number. If upon opening a package it was discovered that the description on the voucher was incorrect (for example, a tank top was submitted, but the voucher says "T-shirt"), use the correct description in your notes and subsequent analyses. Do not perpetuate the mistake.

Standardized worksheets are available with diagrams of pants, shirts, shoes, etc., to aid in documenting stain patterns. If a diagram must be hand-drawn, make sure it is large enough to allow room to document all of the stains present. It is preferable to have only one diagram per page. When complete, scan this worksheet to a .pdf format and attach to the case record within the LIMS.

The LIMS has specific worksheets for the documentation of different types of items (for example: cigarette butts, fingernails, general items, etc).

Digital photography may be substituted for diagrams. Each photograph **must** have a ruler visible in the frame, either a plain straight ruler or an x, y axis ruler. When the photograph is printed, the analyst must mark the photograph to highlight stains, damage, etc., and add the appropriate item or sample identifier, the analyst's initials and date to the photograph. When complete, scan photographs to a .pdf format and attach to the case record within the LIMS. The original printout may be retained in the case file (if a hard copy exists) or discarded.

Each item of evidence **must** be marked by the analyst with the case number, voucher number, item number, date, and handwritten initials. Marking may be done by affixing a tag with the information or by writing directly on the item.

3. If corrections are made on hard copy examination documentation, a strike-through must be drawn through the error; and initialed and dated by the person making the changes. Additional notations, including interlineations, made on the examination documentation must also be initialed and dated. **Never** obliterate, including using "white-out," any notes or entry in a worksheet.

If an error is found on the data recorded within in the LIMS, the corrections should be made in the LIMS by the appropriate level of user. These changes are tracked within the LIMS, including the date, time, and name of the user making the changes.

4. Each sample/stain that will be tested **must** be given a unique identifying number, clearly shown in the notes. See the "Evidence Control" procedure for the sample identification scheme. Each stain **must** be hand marked by the analyst. Marking may be done by affixing a tag with the information or by writing directly on the item.

   For most tests, the LIMS will generate a functional report documenting the test and the results. It is the responsibility of the IA/RA to ensure that the appropriate reports are printed and inserted into the hard copy the case file.

B. Preparing for evidence examination

Before examining evidence, certain preparations should be made:

1. Review the Schedule of Analysis for analyses to be performed on the item(s) in the case. Review all the information provided in the case record. This includes the Communication Log, vouchers, requests for laboratory examination, any previous laboratory reports, and police reports. If further information or clarification is needed, obtain it before beginning analyses.

2. Plan your approach to the case. Certain items may have greater potential informational value than others, or may need to be analyzed first as an investigative aid.

3. Ensure that you are wearing the proper Personal Protective Equipment.

4. Prepare the work area. The bench must be clean and free of clutter. The LIMS cart should be sufficiently charged if on battery power. Both the bench and the LIMS cart mouse, keyboard, and cart handle should be wiped down with 10% bleach followed by 70% ethanol. The work area should then be covered with paper to prevent the loss of small particles of evidence and to prevent the cross-transfer of materials from one item to another. Change the paper when a new case is begun, between different types of evidence within a case (such as between victim's and suspect's belongings), between different vouchers in a case, or whenever necessary. Gloves should be changed as frequently as bench paper is changed, or whenever necessary.

5. Make sure the necessary tools and reagents for the examination are clean and conveniently located, that there is adequate lighting available, and that note taking materials are at hand to record your observations.

C. Evidence examination – general guidelines

The examination of objects will be described in a general sense, covering a broad range of topics applicable to most items of evidence.

Record the Evidence Packaging as the initial documentation of each item.

NOTE: All cutting utensils, tweezers, etc. must be cleaned before and after each use. The recommended cleaning method is 10% bleach, and/or distilled water, and then 70% ethanol. Gloves should be changed between each item, and as needed. Lab coat should be changed after scraping an item.

1. Individual evidence packages that all relate to one case may be packaged in a mesh bag for convenience. This mesh bag should not be examined or counted as a packaging material. No documents, labels, or notes should be attached or written on the mesh bag. For the individual evidence packages, verify that outer packaging corresponds to lab request/voucher. Open the packaging. Avoid breaking existing seals when possible.

2. Remove items from packaging with care. Remember, materials of evidentiary value may adhere to the item and/or the packaging. Opening the evidence over bench paper will prevent the loss of these materials.

3. Examine one item at a time.

   If it is known that an item still requires trace evidence examinations, place an additional sheet of thin (newspaper weight) paper on top of the regular paper prior to opening an item of evidence. When done examining the item, wrap it up in the thin paper and place the entire bundle back into the original packaging. Any trace evidence that was dislodged from the item must be retained within the thin paper.

4. Be certain that the previous item has been re-packaged before opening another item on the work surface.

5. If an item of evidence is found to be wet when opened, the item should be allowed to air dry. The item should not be heated or exposed to direct sunlight. If the item has become foul smelling, allow it to dry in the fume hood with the fan running. If mold is present, consult a supervisor to determine if further testing is suitable.

6. The initial evaluation of the evidence is a visual inspection. It may be necessary to use a high intensity light source, UV light source, or alternate light source during the inspection, especially if semen or saliva is suspected. Magnification may be necessary. IR light source may be utilized to help find stains on dark colored materials as well.

7. A tactile examination is sometimes helpful for locating some biological stains, notably semen stains. Using gloved fingertips, lightly brush over the surface of the object, feeling for changes in surface texture or stiffness.

8. Remove any easily visible surface debris such as hairs, fibers, wood fragments, etc. and return to the original package within a sealed coin envelope with appropriate markings indicating case number, voucher number, item number, date and initials. The location on the item of all trace evidence removed should be documented by diagram, photography, or described in the notes.

9. Perform the appropriate screening tests, such as Kastle-Meyer or Acid Phosphatase. The lot numbers of all reagents and control testing results must be documented **prior to use** to ensure that the reagent isn't an expired lot within the LIMS.

10. All positive biological stains (KM positive, amylase positive and/or PSA positive) **must** be documented by notes, diagrams, and/or photography. Note the location of the stain, size, heaviness (soaked into fabric, surface smear, etc.). Each photograph **must** have a ruler visible in the frame, either a plain straight ruler or an x, y axis ruler.

    If it is apparent that there is a spatter pattern, consult a supervisor for guidance. Select appropriate stains for further testing based on any spatter analysis.

    Document whether or not the biological stains exhibit directionality, if applicable.

11. Cut, scrape, and/or swab the stain from the evidence item at the time of examination for the purpose of further testing.

    When swabbing an area, the number of swabs collected **must** be recorded. Swabbing should only be done when cutting a stain is not practical or recommended.

12. When the examination of an item or voucher is complete (body fluid identification complete and appropriate samples/cuttings submitted for DNA testing), seal the packaging with a permanent seal. The original packaging must be sealed at all entry points. All seals must be individually initialed and dated across the tape edge. **Barcodes and other agency identifiers on the outer packaging should not be covered or sealed over if possible.**

    If multiple items of evidence are separately packaged for a single case, these items may be collected and stored in a mesh bag. This mesh bag is used only for the sake of convenience in grouping related evidence, and should not be tagged, labeled, or have any documentation attached to the mesh bag itself. Transfer the evidence to the Evidence Unit or secure storage location for storage.

    Since post-mortem items are not vouchered, transfer them to retained storage once they are ready for storage.

    Each time a retained sample is removed for analysis, the chain of custody must reflect this. The retained sample package must be opened and re-sealed according to Departmental guidelines.

13. Unless there is case information to the contrary, all samples will be processed as if DNA typing is to be performed.

    a. For possible bloodstains that have tested positive with a presumptive test for blood, a portion of the stain or swab may be submitted for DNA extraction, depending on the case type.
    b. For possible semen stains that have tested positive with a presumptive test for semen, a portion of the stain or swab is submitted immediately for PSA testing.
    c. For sexual assault kit swabs with accompanying smears, a portion of the swab is submitted directly for DNA extraction if sperm are found on the smears. If no sperm are seen on the smear, perform PSA testing on the swab.
    d. For sexual assault kit swabs without accompanying smears, a portion of the swab is submitted for PSA testing.
    e. For possible saliva samples, a portion of the stain or swab is submitted for amylase testing.

14. If a sample is positive for PSA or amylase, a portion of the stain or swab may be submitted for DNA extraction, as necessary.

15. To prepare samples for DNA extraction, label extraction tubes with the sample identifier and add one of the following:

    a. Blood – portion of bloodstain or swab about 3mm square, enough scrapings to give a light straw colored extract, or 3µL whole blood
    b. Semen – portion of semen stain about 5mm square, one third of a swab, or 3µL of whole semen
    c. Amylase – portion of stain about 5mm square or one third of a swab.
    d. Scrapings (of clothing items)
    e. Swab(s) of touched items

    Be mindful of the amount of scrapings and/or SDS swabs being placed in extraction tubes. Excessive amounts of substrate may hinder the extraction process.

    Create the sample and schedule the appropriate extraction procedure for the sample (exemplars, bloodstains, semen stains, touched items, other evidence, or one-step). Scheduling a sample for an incorrect extraction process may lead to the subsequent results being declared inconclusive; see a supervisor if you have any questions about whether a particular sample is evidence or an exemplar.

    All extraction tubes should be transferred to an extraction refrigerator.

    When handling each sample:

    1) Use a clean cutting surface for each sample, such as a lint-free wipe.
    2) Use clean scissors for cutting each sample.
    3) Use lint-free wipes or clean tube openers to open sample tubes and blood tubes.
    4) If possible, the entirety of an item or sample should not be consumed during analysis. It is recommended that at least 25% of the sample be saved for future analysis, if needed. However, if in the opinion of the analyst (or for touched items), consumption of the sample is necessary to have the best chance to obtain results, the item or sample may be consumed; the notes must clearly state this.

16. During the normal course of examination in a limited access laboratory, evidence need not be sealed when left unattended for a short period of time (such as when the analyst takes a lunch break). However, measures must be taken to prevent the unattended evidence from coming into accidental contact with other items of evidence or personnel. For example, swabs and small clothing items should be returned to its containers, and larger items (such as bed sheets on an examination hanger) should be moved to areas of the laboratory where accidental contact by other personnel will be limited.

    Direct any questions regarding what prevention measures should be taken to a supervisor prior to leaving the evidence unattended.

17. Evidence in the process of examination may not be left unattended overnight without first consulting with a supervisor. Without prior approval from a supervisor, all evidence must be properly sealed and returned to a secure storage location at the end of the day.

    Under certain circumstances, the supervisor may allow evidence in the process of examination to be left unattended overnight. However, this practice is to be limited based on the necessity, and the risk of accidental contact with other items of evidence or personnel must be minimized (see Paragraph 16, above). For example, a supervisor may approve evidence to be left unattended overnight if an item of evidence is found to be wet when opened and must be air dried or dried in a hood with the fan running. However, the supervisor must ensure that all risks of accidental contact with other items of evidence or personnel are minimized.

D. Evidence examination – weapons

Weapons are frequently submitted for bloodstain or tissue examinations or for the recovery of DNA from skin cells. Weapons can consist of knives, guns, bottles, baseball bats, and numerous other items.

Weapons should be thoroughly described and examined. Follow the general guidelines for note taking and evidence examination when examining any weapon.

Beware of sharp objects that have penetrated their packaging and/or are loose inside their package and could inflict injury.

Complete the General Packaging Worksheet as the initial documentation of each item.

Complete the General Item Examination Worksheet for each item.

1. Describe the general condition of the item, such as presence of rust or fingerprint powder. Certain weapons should be tethered within their evidence packaging. If not, a deviation should be logged.

2. Measure the physical dimensions of the item. In the case of a knife, this should include description of knife blade such as thickness, shape, cross-sectional shape, length, width, number of blades, brand names, etc. Trace and/or photograph the knife.

3. If necessary, examine under a magnifier or stereomicroscope for traces of fibers, hairs, blood, or other materials of evidentiary value. All trace evidence removed should be documented in the notes using descriptions, diagrams, and/or photography.

4. Look carefully for directional spatters of blood on weapons. Discuss any directional stains with a supervisor before performing any analyses.

5. Knives, sheaths, or other weapons may be dismantled as necessary for further examination. Always photograph or diagram the intact items before dismantling.

6. All stains **must** be documented by notes, diagrams, and/or photography. Note the location of the stain, size, heaviness (soaked into fabric, surface smear, etc.), and any directionality of the stain pattern. Each photograph **must** have a ruler visible in the frame, either a straight ruler or an x, y axis ruler.

7. Make every effort to avoid positive serology stains when sampling the handle of a weapon. Unless there is an indication that the suspect was bleeding, this technique will assist in isolating the desired DNA profile. In cases where the "handle" of the weapon is unknown (e.g., crowbar), treat each end separately as if it could have been the handle.

8. After examining a knife or other sharp object, package it in a safe manner (fastened and/or wrapped within the original packaging) for return to the Evidence Unit.

E. Evidence examination – clothing

Follow the general guidelines for note taking and evidence examination when examining any item of clothing.

Record the Evidence Packaging Worksheet as the initial documentation of each item.

Complete the Clothing Description or General Item Examination Worksheet for each separate clothing item.

1. Describe the color or pattern of the item of clothing, fabric type (denim, corduroy, etc.), fabric make-up (cotton, polyester, etc., from label, if present), and size (if marked on item). If an item is submitted inside-out, record this information.

2. Spread out the item of clothing, looking carefully at the front, back, and inside for any possible evidentiary material.

3. Describe the general cleanliness of the item of clothing. Note any defined soiled areas (biological and/or non-biological) on the garment, for example, knees, buttocks, or cuffs. Note whether the garment appears freshly washed or not (for example, wet or damp).

4. Describe any damage to clothing, which may have evidentiary value. For example, torn or missing buttons, torn or cut areas, damaged areas, or burned areas should be described.

5. Note the presence of any suspected stab holes or bullet holes. Diagram the location, orientation, size, and shape of any holes. Do not overlook the possibility that more than one hole may be caused by a single stab or shot due to the folding of the fabric. When sampling a stain from the area of a suspected stab hole or bullet hole, **Do not** cut through or otherwise disturb the hole. Take a sample away from the existing hole.

6. Carefully examine any pockets, inside and out. The preferred method is to gently pat the outside of the pocket to determine if there are any contents. Tweezers may be used to turn pockets inside out. **Caution is advised when placing the hand in a pocket. An unexpected sharp object could cause serious injury.**

7. Carefully examine the waistband, lining, cuff area, and collar area. This may require turning an item inside out.

8. Shoes have many crevices, which could retain material of evidentiary value and therefore should be examined carefully. Look carefully in the groove between the sole and upper shoe. Shoes with tongues should be checked for blood, which may have fallen between the shoelaces.

   Shoes may be dismantled as necessary for further examination. Always photograph or diagram the intact items before dismantling.

9. Document stains by diagrams, description, and/or photography. Note the location of the stain, size, heaviness (soaked into fabric, surface smear, etc.), and any directionality of the stain pattern. Each photograph must have a ruler visible in the frame, either a plain straight ruler or an x, y axis ruler.

F. Evidence examination – clothing (for skin cells)

Clothing items that are scheduled to be examined for the DNA of the individual who wore the item should be processed using the scraping method. Follow the general guidelines for note taking and evidence examination when examining any item of clothing.

Complete the General Packaging Worksheet as the initial documentation of each item.

Complete the Clothing Description or General Item Examination Worksheet for each separate clothing item.

After the steps described in E., do the following:

IMPORTANT: Do not perform this procedure near an air conditioning unit. In addition to a new lab coat and new gloves, the analyst should wear a mask/face shield and hair guard. For this technique, you must put on gloves in the following manner; latex gloves, cut-resistant gloves, then latex gloves as the final layer.

1. Make sure bench-top is covered with paper. Take another piece of bench paper and fold the edges on each of the four sides up to form a 1/2 to 3/4 inch high rim. Tape or staple the corners to maintain the raised edges. For small items the bench paper should be folded in half before doing this. This will serve as a collection device for the scrapings.

2. Use a clean unused razorblade to vigorously scrape the inside of the item, paying special attention to friction areas such as the cuffs and the neck line. Do not scrape too hard or you will produce too much lint. Make sure to cover the complete surface, if possible and appropriate. **If the item also contains biological stains, it is important not to include these areas when scraping.**

   The best way of doing this is to fold each item symmetrically, lay it down flat in the collection bin, and scrape the surface. Re-fold and repeat until the complete inside has been scraped. This procedure will produce lint that contains the skin cells; consider this lint as a carrier for the cells.

3. Collect the lint by brushing the fibers into one corner of the bench paper (use razorblade), use tweezers to transfer material into an extraction tube. If no fibers are visible, use the razorblade to scrape the bench paper surface into an extraction tube.

   The scrapings should be divided into two parts; one part goes to extraction. The remaining part is placed into an extraction tube and then packaged within an individual envelope, labeled, and returned to the original packaging.

G. Evidence examination – touched clothing (for skin cells)

Clothing items that are scheduled to be examined for DNA left behind by an assailant after a physical struggle should be processed using either a swabbing or scraping method, as required based on the material being examined Follow the general guidelines for note taking and evidence examination when examining any item of clothing.

Complete the General Packaging Worksheet as the initial documentation of each item.

Complete the Clothing Description or General Item Examination Worksheet for each separate clothing item.

After the steps described in E., do the following:

IMPORTANT: Do not perform this procedure near an air conditioning unit. In addition to a new lab coat and new gloves, the analyst should wear a mask/face shield and hair guard. For this technique, you must put on gloves in the following manner; latex gloves, cut-resistant gloves, then latex gloves as the final layer.

1. Make sure the bench-top is covered with paper. Take another piece of bench paper and fold the edges on each of the four sides up to form a 1/2 to 3/4 inch high rim. Tape the corners to maintain the raised edges. For small items the bench paper should be folded in half before doing this. This will serve as a collection device for the scrapings.

2. Determine the substrate of the item of clothing being examined.

3. Based on the material, choose the best method to examine the item. Refer to the table below:

Recommended method to use for various materials	
Scraping	**Swabbing**
Cotton & Cotton mixture	Spandex
Polyester	Polyester
Wool	Rayon

4. For swabbing, swab the entire area using irradiated SDS swabs prepared by the Quality Assurance team moistened with 0.01% SDS. Combine the swabs inside one extraction tube.

5. For material requiring scraping, scrape the entire area with a sterile blade and place the scrapings inside an extraction tube. Make sure to scrape the entire surface the assailant was purported to have had contact with. **If the item also contains biological stains, it is important not to include these areas when scraping or swabbing.**

6. After scraping the item, you may wipe the blade with an irradiated SDS swab to recover as much skin cell evidence as possible. Place the swab inside the same tube as the scrapings. Both the scrapings and the SDS swab will be extracted together as one sample

H. Evidence examination – sexual assault kits

Follow the general guidelines for note taking and evidence examination when examining any sexual assault kit. Follow the general guidelines for clothing examination when examining any clothing items packaged in a sexual assault kit.

Complete the Evidence Packaging Worksheet as the initial documentation of each item.

Complete the Sexual Offense Evidence Collection Kit Inventory Worksheet and the Clothing Description Worksheet (for testing of underwear or related items) for further documentation of each separate clothing item.

1. Ensure that the name of the victim corresponds to the name listed on the paperwork in the case file.

2. Indicate whether each kit component is sealed, unsealed, not submitted, or present but "not used" (this may require opening of the envelope). Consecutive item numbers are assigned to only those items that are present and used (e.g., 1.1, 1.2, 1.3.1-1.3.2 for swab and smear pairs).

   PM kits (all items packaged together): Inventory kit. Label used envelopes with an item number (see above) and the FB number (label as 1.1, 1.2, etc), analyst's initials, and date of examination. **All the envelopes, whether used or unused** should contain the analyst's initials and the identifying case number. All envelopes and any paperwork associated with the PM kit will be retained in the kit box. For PM SAKs use the Sexual Offense Evidence Collection Kit Inventory Worksheet.

   PM swabs (items packaged separately): Complete the Packaging and Swab Examination Worksheet. These swabs should already have item numbers. Refer to the LIMS Evidence Manual.

   Vouchered kits: Inventory kit. Label used envelopes with an item number (see above) and the FB number, analyst's initials, and date of examination. **All the envelopes, whether used or unused** should contain the analyst's initials and the identifying case number. See following for testing of the vouchered kit.

3. **Underwear or related items contained within kit:**

If **underwear or related items** (e.g., pantiliner) are in the kit, complete the Clothing Description or General Item Examination Worksheet. If stains are observed, underwear can be documented using the diagrams that are available or by a quick sketch. Photography is not generally needed.

Testing of underwear or small clothing items contained within kit:

Visually check underwear for any biological stains. Additionally, observe the underwear using an alternate light source. If any fluorescing areas are observed, circle for further testing.

If a whitish, yellowish, or fluorescing stain is observed on the underwear, test the stain with AP reagent. If the stain is AP positive, make a small cutting and submit the stain for PSA confirmation testing.

If a pink to reddish-brown stain is observed on the underwear, test the stain with KM reagent **and** AP reagent, even if the area does not appear to fluoresce with the aid of the alternate light source. The possible presence of blood can mask fluorescence. Regardless of KM results, the stain needs to be AP tested. KM positive stains should be documented.

If the time since date of occurrence is more than 3 months, the analyst should submit a small portion of the area for PSA testing.

At this point, be sure that any AP positive stains submitted to PSA testing are designated a stain number. A stain number should also be designated for KM positive stains. KM positive only stains do not require further testing.

If oral sodomy is suspected or it is unclear what type of sexual contact occurred in the case, it may be necessary to send stains for amylase testing. Consult with exam supervisor as needed.

If there are no biological stains on the item(s), a diagram is not necessary; write a short description of the item.

Testing of gauze within the kit:

Examination of gauze is similar to underwear, however all AP positive and negative stains should be tested for the presumptive presence of amylase.

Note the location from which the gauze was collected. If the location from which the gauze was taken is known, **this information must be included** on the SAK inventory.

4. The **trace evidence envelope** is used by hospital personnel to collect trace evidence from the victim's body and/or the clothing. The victim disrobes over examination paper, and the examination paper is collected.

   Since trace evidence examinations are not performed in the Department of Forensic Biology, there is generally no need to examine the contents. However, if the envelope appears to contain something other than trace evidence, or markings on the envelope indicate that something other than trace evidence is present, the envelope should be opened to confirm the contents and examination should proceed if needed. If the contents of the envelope are found to be the examination paper, no further examination is needed.

5. The **debris envelope** is used by hospital personnel to collect loose, obvious foreign material from the victim's body and/or the clothing.

   If a debris envelope was used, note the location from which the debris was collected, or note that the location was not given. Since trace evidence examinations are not performed in the Department of Forensic Biology, there is generally no need to examine the contents.

6. The **dried secretions swabs** are used to collect possible biological fluids from areas other than the body cavities.

   If dried secretions were taken, **note the number of swabs and the location from which the secretions were collected, or note that the location was not given**. Each swab must be individually labeled (1.4.1, 1.4.2). See below for further testing procedures.

Testing of dried secretions swabs:

Make a cutting from each of the swabs present for PSA testing. If the location from which the dried secretions swabs were taken is known, and **is not** from the mouth, near the mouth, anal cavity, or near the anal cavity, the swab should also be tested for amylase. Swabs from these locations are not tested for amylase. If the location is unknown, make a cutting from each swab for both PSA and amylase testing. As every case is different, please consult with a supervisor if there is something in the case description that suggests further testing is required.

7. The **fingernail scrapings (or clippings)** are used to collect trace evidence from the fingernails.

   Since trace evidence examinations are not performed in the Department of Forensic Biology, there is generally no need to examine the contents. However, requests are occasionally made to examine the fingernail scrapings; discuss with a supervisor before starting any examinations of fingernail evidence. If fingernail examination has been approved, refer to Section O of this manual.

8. If a **liquid blood exemplar** is present, consult with a supervisor to make a bloodstain card. Fill out a blank stain card (FB number, victim's name, date, and initials), insert into a Kapak envelope and seal it. The FB number should be written on the Kapak and the analyst's initials and date of examination should be written across the seal. This may be used as an exemplar if no buccal specimen is present within the kit.

9. If a **dried blood control** is present, it is only used if there is no buccal specimen present in the kit. If it must be used, fill out a blank stain card (FB number, victim's name, date, and initials), attach the dried blood control to it, insert into a Kapak envelope and seal it. The FB number should be written on the Kapak and the analyst's initials and date of examination should be written across the seal.

10. The **buccal specimen** is used as the victim's exemplar. If present, the buccal specimen would be the first choice in order to avoid potential inhibition of PCR by heme degradation products.

    If no victim's exemplar is present, and there are no serology negative body cavity swabs, it may be necessary at a later time for a supervisor to make a phone call to request one.

11. The **pulled head hair and pulled pubic hair** are collected as exemplars for any future microscopic hair comparisons.

    Since trace evidence examinations are not performed in the Department of Forensic Biology, there is generally no need to examine the contents. However, requests are occasionally made to use the pulled head hair for exemplar DNA testing; generally, hair DNA testing is not performed until hair comparisons have been made by the NYPD forensic laboratory.

12. The **pubic hair combings** are used to collect possible trace evidence from the pubic hair of the victim.

    Since trace evidence examinations are not performed in the Department of Forensic Biology, there is generally no need to examine the contents.

13. The "**body cavity" swabs (oral, perianal, anal, vulvar, vaginal/penile, and cervical)** are used to collect possible biological fluids from those areas; the smears are used for a sperm search.

    Testing of body cavity swabs:

    Visually check the swabs for the presence of biological fluids. If the swabs are pink to reddish-brown in color, test with KM reagent; note the results.

    Refer to the Sexual Assault Kit Processing Flow Charts for guidance.

    Stain one smear accompanying each set of body cavity swabs using the Christmas Tree staining procedure (refer to Christmas Tree Stain for Spermatozoa section in the Forensic Biology Serology Manual) and examined for the presence of sperm; this search need not be exhaustive and should take no longer than five minutes (per smear). It is not necessary to estimate the number of sperm present, but the relative amount (one sperm head, numerous sperm heads, etc.) may be noted.

    If sperm is found on a smear, make a cutting from each positive location on relevant swabs (vulvar, penile, scrotal) for amylase testing.

    If no sperm is found on a smear, make a cutting from each negative location for PSA confirmatory testing. Pertinent swabs (vulvar, penile and scrotal) must also be tested for the presence of amylase.

Body cavity swabs (vaginal, cervical, oral, and anal) should not be tested for the presence of amylase. Swabs labeled "perianal/anal" should not routinely be tested for amylase; however, they may be tested if clearly marked as "perianal".

14. Return all swabs and smears to their respective envelopes.

15. The **questionnaire, body diagram sheets, and instruction sheets** are intended for the use of the medical personnel. If present, make a copy only of the **questionnaire and body diagram sheets** for retention with the case record—as a physical copy in the case file and a .pdf attachment in LIMS (as applicable); leave all originals in the kit. No item number is assigned if present. Label each page with the Forensic Biology case file number, voucher number, analyst's initials, and date of examination.

16. Photographs and/or other paperwork are not supposed to be included in a kit. If present, make a note of it; leave them in the kit. No item number is assigned if present.

17. After kit examination is complete, the kit is now ready to be closed. After the kit is closed, the kit should be placed in a secure location.

Closing of negative kits:

If the kit is negative for semen and amylase, and there is no other evidence to examine, the case is finished and should be submitted to Quality Assurance for reanalysis consideration.

If a buccal specimen is present, the analyst should place the swab(s) in a coin envelope labeled with the FB number, voucher number, item number, victim name, analyst's initials, and date of examination. The coin envelope should be placed in a Kapak envelope and heat sealed. The FB number should be written on the Kapak and the analyst's initials and date of examination should be written across the seal. The buccal should be transferred to a storage location.

If no buccal specimen was present in the kit, retain serology negative body cavity swabs to be used as an exemplar. The oral swab is the preferable choice to be used as an exemplar in the absence of a true exemplar.

Each envelope within the kit should be sealed with evidence tape. The entire vouchered kit or the post mortem items (PM kit) kit can be placed in a secure storage location.

If the kit is negative for semen and amylase, and there is additional evidence, a supervisor will determine whether or not the evidence needs to be signed in and examined.

Closing of positive kits:

If positive swabs/stains/smears were found, see below for guidelines on the cutting of samples for extraction.

If there is additional evidence, a supervisor will determine whether or not the evidence needs to be signed in and examined.

Dried secretions swabs

Whether or not a dried secretions swab continues on for DNA extraction, and if so, which type of DNA extraction, depends on a number of factors: location the sample was taken from, nature of the body fluid present, presence or absence of a suspect, and what other swabs or other evidence has been submitted in the case. Refer to the Sexual Assault Kit Processing Flowcharts for guidance.

If PSA positive, make a second cutting from one swab **from each listed location** that is positive for differential extraction. If the location from which the swabs were taken is unknown, make a cutting of one swab from each separate packaging to go on for differential extraction.

If a swab is PSA negative and amylase positive, the decision on further testing depends on the location the swab was taken from (if known) and whether the case has a suspect.

PSA negative, amylase positive dried secretions from external areas should be sent to extraction. In addition, a supervisor may need to make a phone call to determine the status of the case.

Body cavity swabs (oral, perianal, anal, vulvar, vaginal/penile, cervical)

If sperm is found on a smear, a cutting from the accompanying swab can go for extraction. **If sperm is found on a perianal/anal smear, cuttings from both swabs are combined for extraction**. If multiple smears are sperm positive from similar areas, it is not necessary to cut all swabs for DNA extraction. For the purposes of sending samples

onto extraction, vaginal swabs should be sent first, then cervical swabs, then vulvar swabs. Therefore, if all three swabs are sperm search positive, only send the vaginal swab for extraction. Refer to the Sexual Assault Kit Processing Flowcharts for guidance.

If a swab is PSA positive, a cutting from the swab can go for extraction. If multiple swabs are PSA positive from similar areas, it is not necessary to cut all swabs for DNA extraction. Refer to the Sexual Assault Kit Processing Flowcharts for guidance.

If a vulvar swab is sperm/PSA negative but amylase positive, check to see if the case has a named suspect (listed first and last name). If so, make a cutting from one swab that is amylase positive and submit this cutting to an appropriate DNA extraction. If multiple swabs are amylase positive, it is not necessary to cut all swabs for DNA extraction. Refer to the Sexual Assault Kit Processing Flowcharts for guidance. If the case has no named suspect, consult with a supervisor. It may be necessary for the supervisor to make a phone call to determine the status of the case.

If a penile swab is sperm/PSA negative but amylase positive, make a cutting from the swab and submit to the appropriate DNA extraction.

Underwear or small items

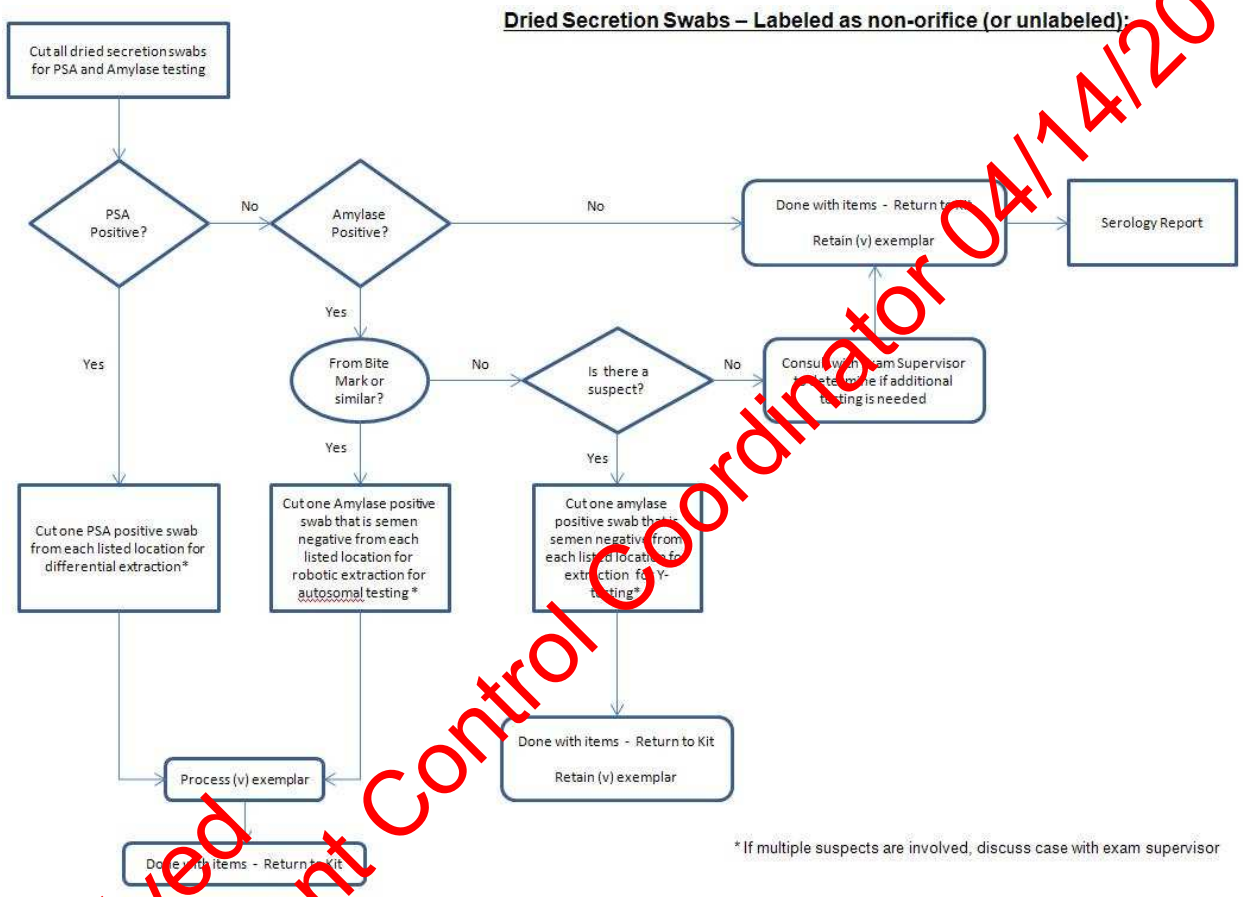
For PSA positive stains, cut positive stain(s) for differential extraction. For multiple suspects, it may be necessary to send multiple stains. Consult a supervisor.

In the event that there are amylase positive stains, the decision for further testing is case dependent. Consult a supervisor.

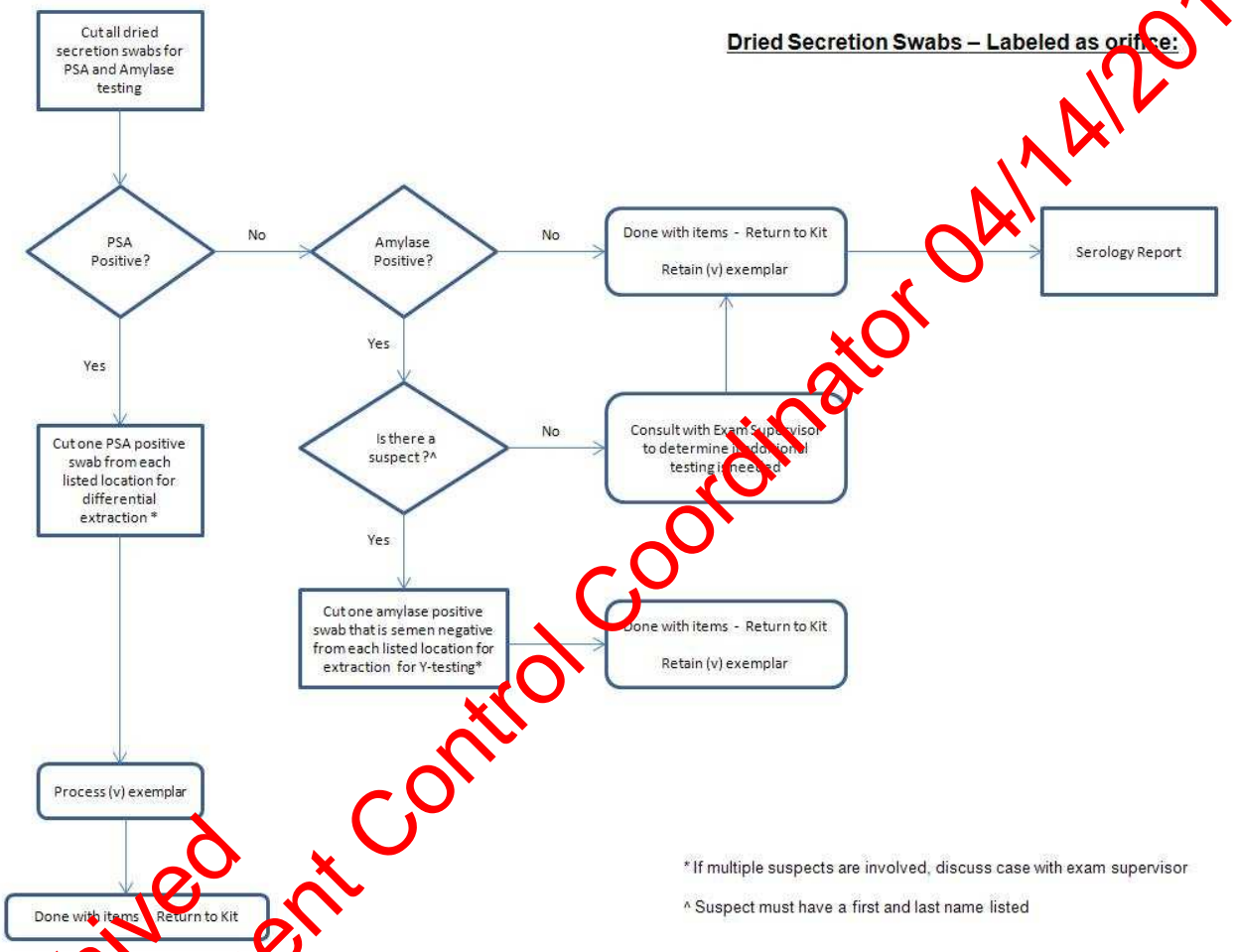
If a buccal specimen is present, make a cutting for extraction. Following this, place the remainder of the swab(s) in a coin envelope labeled with the FB number, voucher number, item number, victim name, analyst's initials, and date of examination. The coin envelope should be placed in a Kapak envelope and heat sealed. The FB number should be written on the Kapak and the analyst's initials and date of examination should be written across the seal.

The exemplar should be placed in a secure storage location.
After cutting all positive items, each envelope within the kit should be sealed with evidence tape and returned to the kit. Seal the kit and return to a secure storage location.

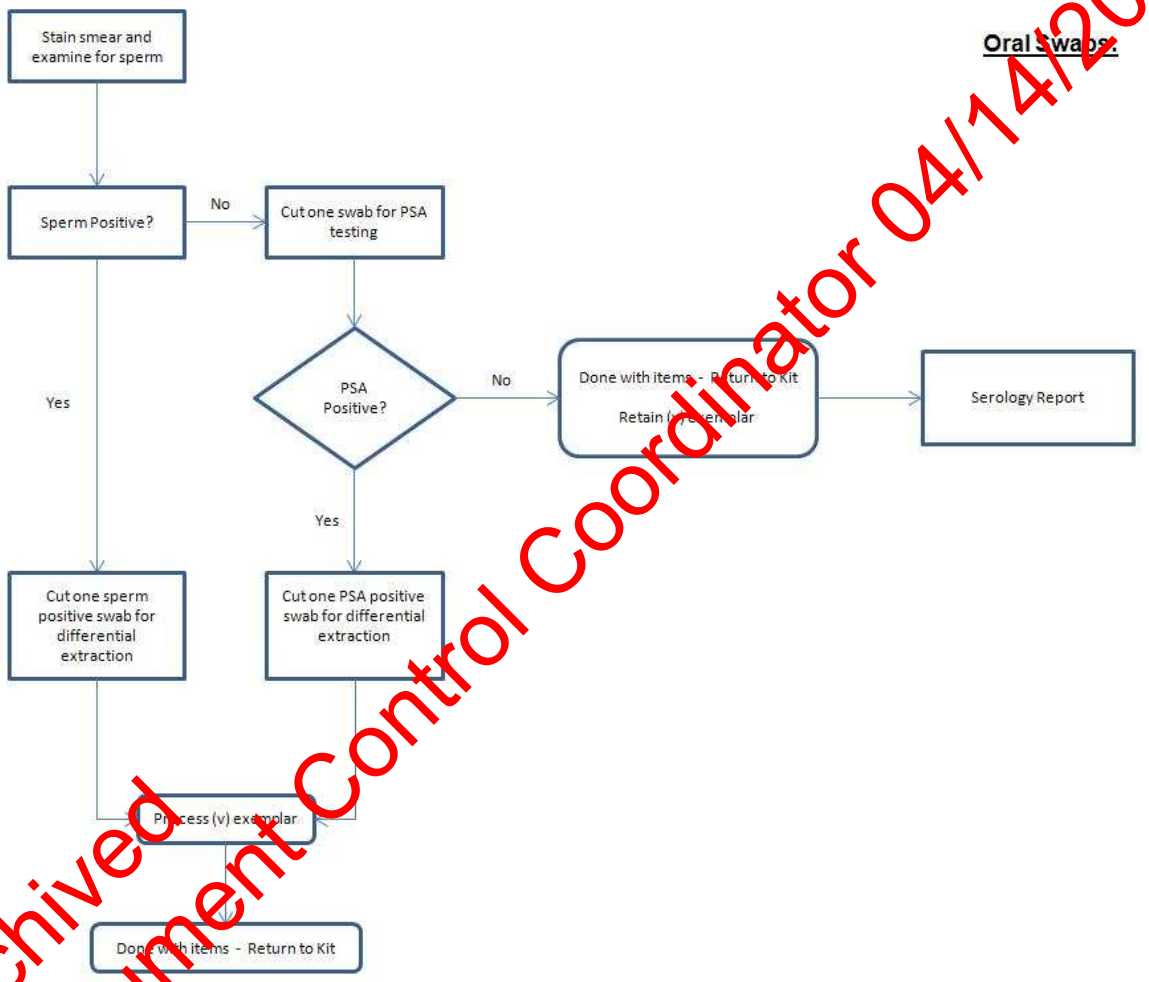
Sexual Assault kit processing flow chart



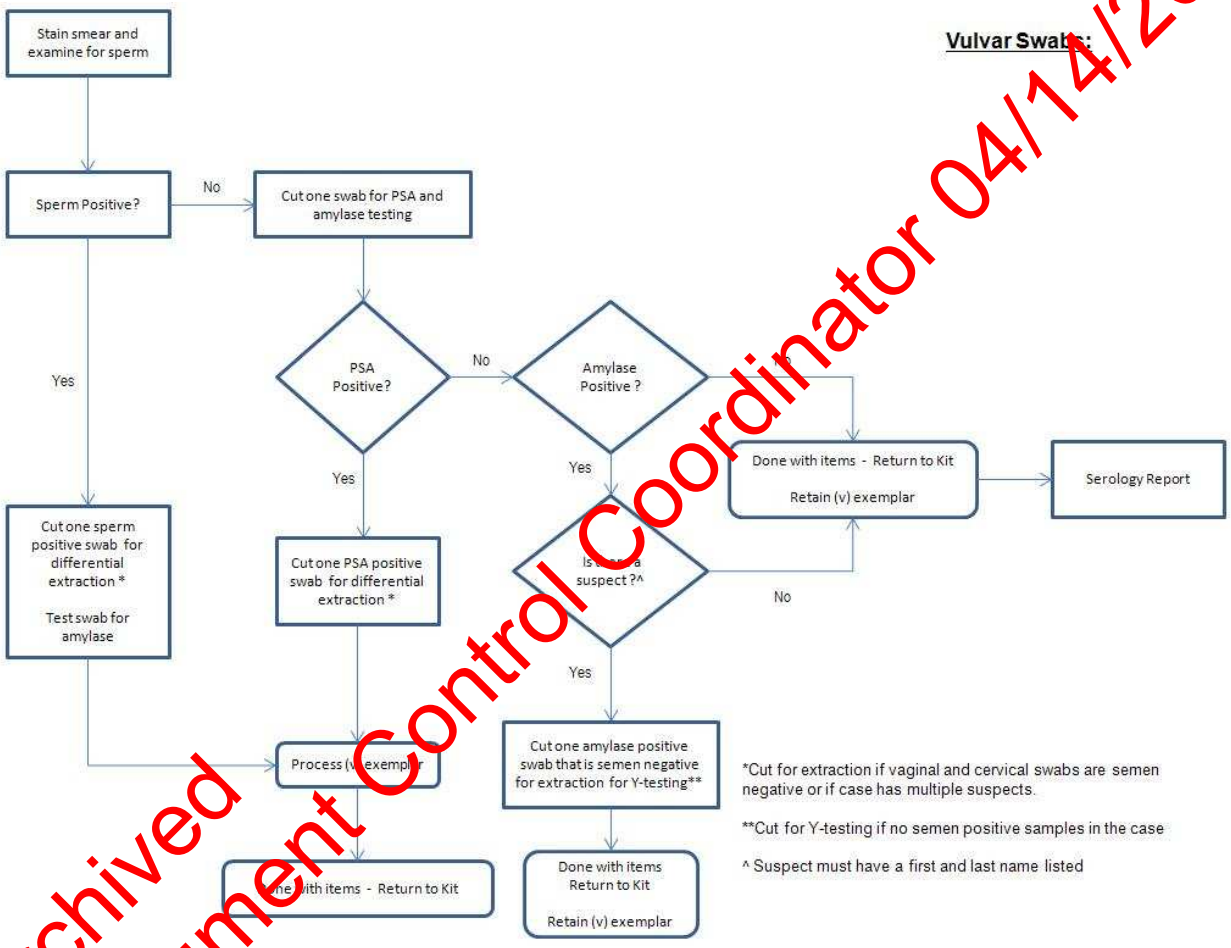
Sexual Assault kit processing flow chart



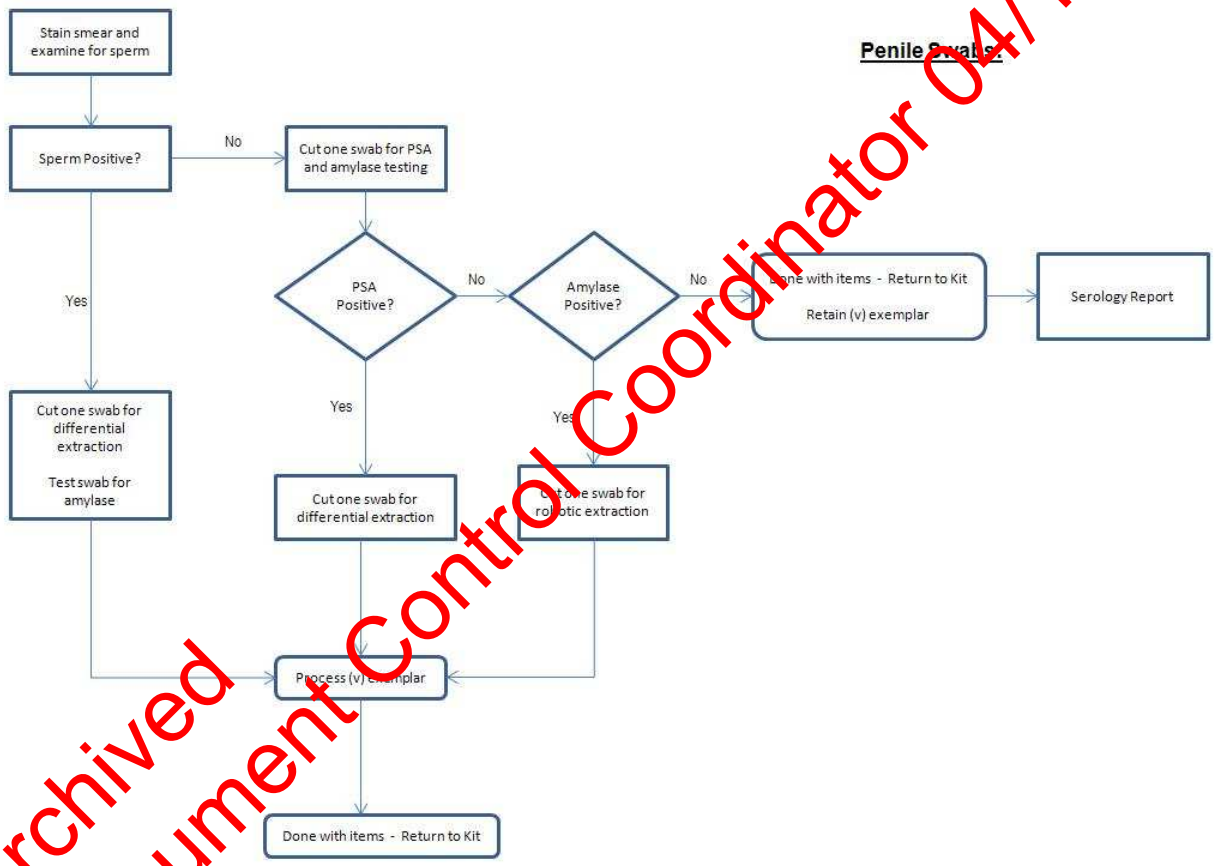
Sexual Assault kit processing flow chart



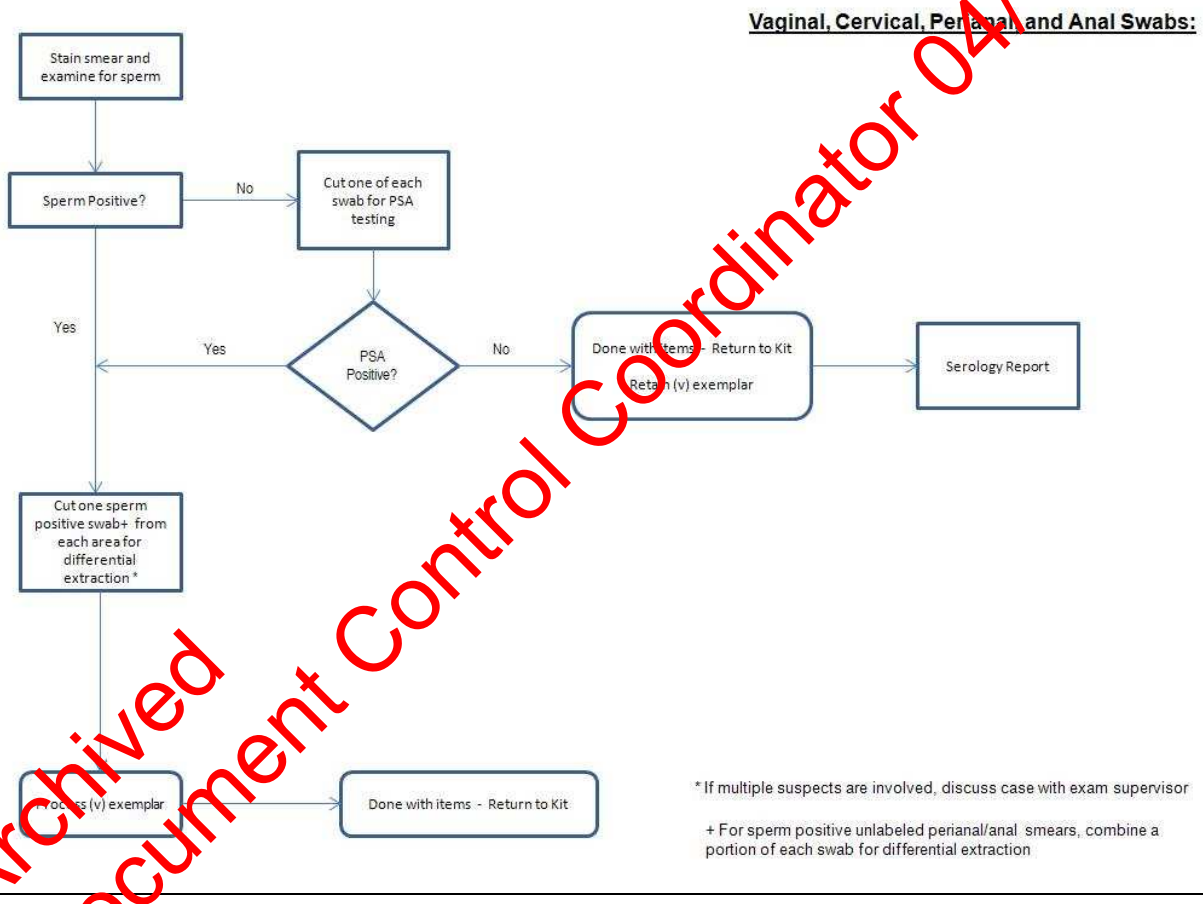
Sexual Assault kit processing flow chart



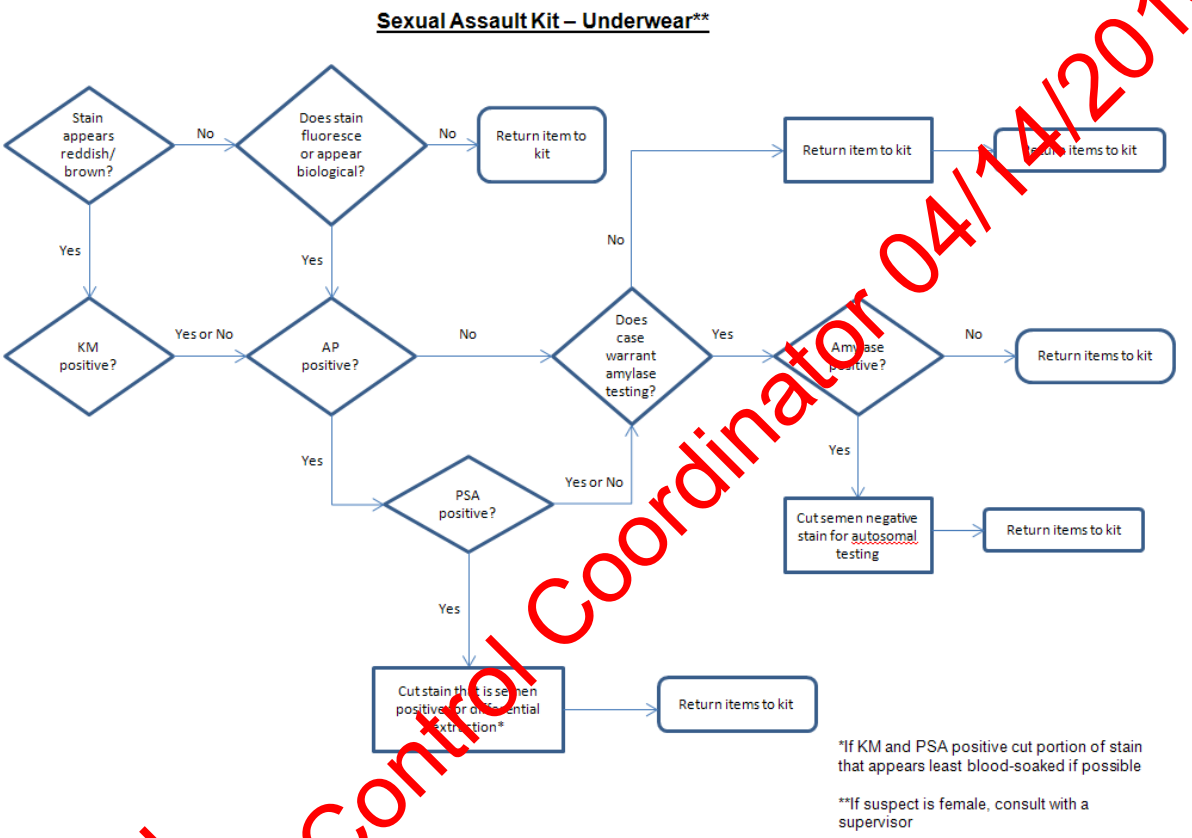
Sexual Assault kit processing flow chart



Sexual Assault kit processing flow chart



Sexual Assault kit processing flow chart



I. Evidence examination – male suspect kits

Although testing procedures are similar to sexual assault kit examination, the goal is to try to find victim DNA when examining any suspect kit. This should be kept in mind during examination of all items within the suspect kit.

In addition to this manual, follow the general guidelines for note taking and evidence examination, and the guidelines for clothing examination when examining any clothing items.

Use an Evidence Packaging Worksheet for initial documentation of each suspect kit.

Use the Suspect Evidence Collection Kit Inventory and Clothing Description Worksheet (for testing of underwear or related items) forms for further documentation.

1. Note the name of the suspect and information about when and where the kit was collected. Ensure that the name of the suspect corresponds to the name listed on the paperwork in the case file.

2. **Inventory kit**: The LIMS will assign an item number to each used envelope. Affix a LIMS packaging label to each envelope. The analyst must mark all envelopes with their initials and date of examination.

   As prompted by the Suspect Evidence Collection Kit Inventory, indicate whether each kit component is sealed, unsealed, not submitted, or present but "not used" (this may require opening of the envelope).

   If a buccal specimen or other exemplar sample is contained within the kit, contact a supervisor immediately to create a suspect file. Suspect file creation is only necessary if an exemplar sample is present.

   Suspect file creation:

   A supervisor is responsible for creating the suspect file. The supervisor must:

   - Create a LIMS record and Schedule of Analysis
   - Include the following paperwork in the file upon completion of kit examination:
     - 61 form (NYPD complaint report)
     - original request for laboratory examination forms

- evidence voucher
- evidence packaging worksheet
- completed kit inventory worksheet

After creation of a suspect file, the buccal swab is cut and duplicate cut for extraction in accordance with laboratory guidelines.

3. **Underwear or related items contained within kit:**

If **underwear or related items** are in the kit, examine them using the Clothing Description Worksheet.

Testing of underwear or small clothing items contained within kit:

Visually check underwear for any biological stains. Then observe the underwear using an alternate light source. If any fluorescing areas are observed, circle for further testing.

If a potentially biological or fluorescing stain is observed on the underwear, test the stain with AP reagent. If the stain is AP positive, make a small cutting for PSA and amylase testing. If the stain is AP negative, make a small cutting for amylase testing.

If a pink to reddish-brown stain is observed on the underwear, test the stain with KM reagent as well as AP reagent, even if the area does not appear to fluoresce with the aid of the alternate light source. Regardless of KM results, the stain needs to be AP tested. If the stain is AP positive, make a small cutting for PSA and amylase testing. If the stain is AP negative, make a small cutting and submit the stain for amylase testing. KM positive stains should be documented but do not require further testing.

In any situation, if the stain is AP negative and the time from the date of occurrence to the date of kit examination is more than 3 months, make a cutting of the stain for PSA testing to confirm negative results (for semen samples older than 3 months, AP can degrade and thus testing may yield a negative AP result).

Remember that the goal is to try to find victim DNA. Therefore, non-fluorescing stains may need to be tested further. Refer to the Suspect Kit Processing Flow Charts for guidance. Stain location and the case scenario will

determine what stains need further testing. As every case is different, consult with a supervisor as needed.

At this point, be sure that any stains submitted to PSA and/or amylase testing and KM positive stains are designated a stain number/letter. Only KM, PSA, or amylase positive stains should be diagrammed.

If there are no biological stains on the item(s), a diagram is not necessary; write a short description of the item using a Clothing Description Worksheet.

4. The **debris envelope** is used by hospital personnel to collect loose, obvious foreign material from the victim's body and/or the clothing.

   If a debris envelope was used, note the location from which the debris was collected, or note that the location was not given. Trace evidence examinations are not performed in the Department of Forensic Biology.

5. The **dried secretions swabs** are used to collect possible biological fluids from areas other than the body cavities. This could include, for example, semen from the skin or saliva from bite marks.

   If dried secretions were taken, note the number of swabs and the location from which the secretions were collected, or note that the location was not given. Each swab must be individually itemized.

   Testing of dried secretions swabs:

   Visually check the swabs for the presence of biological fluids. If the swabs are pinkish to reddish-brown in color, test with KM reagent, and note the results.

   Make a cutting from each of the swabs present for PSA testing. If the location from which the dried secretions swabs were taken is known, and **is not** from the mouth, near the mouth, anal cavity, or near the anal cavity, the swab should also be tested for amylase. Swabs from these locations are not tested for amylase. If the location is unknown, make a cutting from each swab for both PSA and amylase testing. As every case is different, please consult with a supervisor if there is something in the case description that suggests further testing is required.

6. The **fingernail scrapings (or clippings)** are used to collect trace evidence from the fingernails.

Trace evidence examinations are not performed in the Department of Forensic Biology. However, requests are occasionally made to examine the fingernail scrapings; discuss with a supervisor before starting any examinations of fingernail evidence. If fingernail examination has been approved, refer to Section O of this manual.

7. The **chest hair combings** are used to collect possible trace evidence from the chest hair of the suspect.

   Trace evidence examinations are not performed in the Department of Forensic Biology.

8. The **oral swabs** are used to collect possible biological fluids from that area; the smears are used for a sperm search in cases with a male victim.

   Refer to the Suspect Kit Processing Flow Charts for guidance.

   For male victims:

   Visually check the swabs for the presence of biological fluids. If the swabs are pink to reddish-brown in color, test with KM reagent; note the results.

   Stain one smear accompanying each set of body cavity swabs using the Christmas Tree staining procedure (refer to Christmas Tree Stain for Spermatozoa section in the Forensic Biology Serology Manual) and examine for the presence of sperm; this search need not be exhaustive and should take no longer than five minutes (per smear). It is not necessary to estimate the number of sperm present, but the relative amount (one sperm head, numerous sperm heads, etc.) may be noted.

   If no sperm is found on a smear, make a cutting for PSA testing.

   For female victims:

   In most cases, oral swabs and smears should not be tested. As every case is different, please consult with a supervisor if there is something in the case description that suggests further testing is required.

9. The **pulled head hair and pulled pubic hair** are collected as exemplars for any future microscopic hair comparisons.

Trace evidence examinations are not performed in the Department of Forensic Biology. However, requests are occasionally made to use the pulled head hair for exemplar DNA testing.

10. The **facial hair combings and pubic hair combings** are used to collect possible trace evidence from the facial hair and pubic hair of the suspect.

    Trace evidence examinations are not performed in the Department of Forensic Biology.

11. The **penile and scrotal swabs** are used to collect possible biological fluids from those areas; the smears are used for a sperm search.

    Testing of penile and scrotal swabs:

    Visually check the swabs for the presence of biological fluids. If the swabs are pink to reddish-brown in color, test with KM reagent; note the results.

    Refer to the Suspect Kit Processing Flow Charts for guidance.

    For male or female victims:

    Stain one smear accompanying each set of body cavity swabs using the Christmas Tree staining procedure (refer to Christmas Tree Stain for Spermatozoa section in the Forensic Biology Serology Manual) and examine for the presence of sperm; this search need not be exhaustive and should take no longer than five minutes (per smear). It is not necessary to estimate the number of sperm present, but the relative amount (one sperm head, numerous sperm heads, etc.) may be noted.

    If sperm is found on a smear, make a cutting from each positive location for amylase testing.

    If no sperm is found on a smear, make a cutting from each negative location for PSA and amylase testing.

12. The **anal swabs** are used to collect possible biological fluids from that area; the smears are used for a sperm search.

Refer to the Suspect Kit Processing Flow Charts for guidance.

For male victims:

Visually check the swabs for the presence of biological fluids. If the swabs are pink to reddish-brown in color, test with KM reagent; note the results.

Stain one smear accompanying each set of body cavity swabs using the Christmas Tree staining procedure (refer to Christmas Tree Stain for Spermatozoa section in the Forensic Biology Serology Manual) and examine for the presence of sperm; this search need not be exhaustive and should take no longer than five minutes (per smear). It is not necessary to estimate the number of sperm present, but the relative amount (one sperm head, numerous sperm heads, etc.) may be noted.

If no sperm is found on a smear, make a cutting for PSA testing.

For female victims:

In most cases, anal swabs and smears should not be tested. As every case is different, please consult with a supervisor if there is something in the case description that suggests further testing is required.

13. The **buccal specimen** is used as the suspect's exemplar. If present, the buccal specimen would be the first choice in order to avoid potential inhibition of PCR by heme-degradation products.

14. The **questionnaire, body diagram sheets, and instruction sheets** are intended for the use of the medical personnel. If present, make a copy only of the **questionnaire and body diagram sheets** for retention with the case record—as a physical copy in the case file and a .pdf attachment in LIMS (as applicable); leave all originals in the kit. No item number is assigned if present. Label each page with the suspect file number, voucher number, analyst's initials, and date of examination.

15. Photographs are not supposed to be included in a kit. If present, make a note of it, alert a supervisor, and leave them in the kit. Label with FB number, date of examination, and analyst's initials. No item number is assigned if present.

16. If no positive swabs/stains/smears were found, make cuttings of appropriate swabs or stains as necessary. Refer to the Suspect Kit Processing Flow Charts for guidance.

17. If positive swabs/stains/smears were found, see below for guidelines on the cutting of samples for extraction. Refer to the Suspect Kit Processing Flow Charts for guidance.

The following kit closing information is for both female and male victims. Use the pertinent information for each case.

Underwear

PSA positive stains should be sent for differential extraction.

PSA negative stains that are KM and/or amylase positive should be sent for robotic extraction.

Dried secretion swabs

If PSA positive, make a cutting from one swab **from each listed location** that is positive for differential extraction. If the location from which the swabs were taken is unknown, make a cutting from one swab to go on for a differential extraction.

If a swab is KM positive and PSA negative, make a cutting from one swab **from each listed location** that is KM positive for robotic extraction.

If a swab is amylase positive, and PSA and KM negative, refer to the Suspect Kit Processing Flow Charts for guidance.

If a swab is PSA and amylase negative, refer to the Suspect Kit Processing Flow Charts for guidance.

Penile and scrotal swabs

If a swab is sperm/PSA positive, make a cutting from each positive location for differential extraction.

sperm/PSA negative stains that are KM and/or amylase positive should be sent for robotic extraction.

If a swab is sperm/PSA and amylase negative, the decision on further testing depends on the sex of the victim. Refer to the Suspect Kit Processing Flow Charts for guidance.

Oral and anal swabs

If a swab is sperm/PSA positive, make a cutting from each positive location for differential extraction

If a swab is sperm/PSA negative, consult with a supervisor.

18. After cutting all pertinent items, return all swabs and smears to their respective envelopes. Seal all kit envelopes with evidence tape and return to the kit. Seal the kit and return to a secure storage location.

J. Evidence examination – female suspect kits

Although testing procedures are similar to sexual assault kit examination, the goal is to try to find victim DNA when examining any suspect kit. This should be kept in mind during examination of all items within the suspect kit.

In addition to this manual, follow the general guidelines for note taking and evidence examination, and the guidelines for clothing examination when examining any clothing items.

Use an Evidence Packaging Worksheet for initial documentation of each suspect kit.

Use the Suspect Evidence Collection Kit Inventory and Clothing Description Worksheet (for testing of underwear or related items) forms for further documentation.

1. Note the name of the suspect and information about when and where the kit was collected. Ensure that the name of the suspect corresponds to the name listed on the paperwork in the case file.

2. **Inventory kit**: The LIMS will assign an item number to each used envelope. Affix a LIMS packaging label to each envelope. The analyst must mark all envelopes with their initials and date of examination.

   As prompted by the Suspect Evidence Collection Kit Inventory, indicate whether each kit component is sealed, unsealed, not submitted, or present but "not used" (this may require opening of the envelope).

   If a buccal specimen or other exemplar sample is contained within the kit, contact a supervisor immediately to create a suspect file. Suspect file creation is only necessary if an exemplar sample is present.

   Suspect file creation:

   A supervisor is responsible for creating the suspect file. The supervisor must:

   - Create a LIMS record and Schedule of Analysis
   - Include the following paperwork in the file upon completion of kit examination:
     - 61 form (NYPD complaint report)
     - original request for laboratory examination forms
     - evidence voucher
     - evidence packaging worksheet
     - completed kit inventory worksheet

   After creation of a suspect file, the buccal swab is cut and duplicate cut for extraction in accordance with laboratory guidelines.

3. **Underwear or related items contained within kit:**

   If **underwear or related items** are in the kit, examine them using the Clothing Description Worksheet. If stains are observed, underwear can be documented using the diagrams that are available or by a quick sketch. Photography is not generally needed.

Testing of underwear or small clothing items contained within kit:

For male victims:

Visually check underwear for any biological stains. Additionally, observe the underwear using an alternate light source. If any fluorescing areas are observed, circle for further testing.

If a potentially biological or fluorescing stain is observed on the underwear, test the stain with AP reagent. If the stain is AP positive, make a small cutting for PSA and amylase testing. If the stain is AP negative, make a small cutting for amylase testing.

If a pink to reddish-brown stain is observed on the underwear, test the stain with KM reagent **and** AP reagent, even if the area does not appear to fluoresce with the aid of the alternate light source. Regardless of KM results, the stain needs to be AP tested. If the stain is AP positive, make a small cutting for PSA and amylase testing. If the stain is AP negative, make a small cutting for amylase testing. KM positive stains should be documented.

In any situation, if the stain is AP negative and the time from the date of occurrence to the date of kit examination is more than 3 months, the analyst should make a cutting of the area for PSA testing to confirm negative results (for semen samples older than 3 months, AP can degrade and thus testing may yield a negative AP result).

At this point, be sure that any stains submitted to PSA and/or amylase testing and KM positive stains are designated a stain number/letter.

If there are no biological stains on the item(s), a diagram is not necessary; write a short description of the item using a Clothing Description Worksheet.

For female victims:

Visually check underwear for any biological stains. Additionally, observe the underwear using an alternate light source. If any fluorescing areas are observed, circle for further testing.

If a fluorescing stain is observed on the underwear, make a small cutting for amylase testing. Designate a stain number/letter to each fluorescing area.

If a pink to reddish-brown stain is observed on the underwear, test the stain with KM reagent. Consult with a supervisor.

Remember that the goal is to try to find victim DNA. Therefore, non-fluorescing stains may need to be tested further. Refer to the Suspect Kit Processing Flow Charts for guidance. Stain location and the case scenario will determine what stains need further testing. Consult with a supervisor as needed.

At this point, be sure that any KM, PSA, or amylase positive stains are designated a stain number/letter.

If there are no biological stains on the item(s), a diagram is not necessary; write a short description of the item using a Clothing Description Worksheet.

4. The **debris envelope** is used by hospital personnel to collect loose, obvious foreign material from the victim's body and/or the clothing.

   If a debris envelope was used, note the location from which the debris was collected, or note that the location was not given. Trace evidence examinations are not performed in the Department of Forensic Biology.

5. The **dried secretions swabs** are used to collect possible biological fluids from areas other than the body cavities. This could include semen from the skin or saliva from bite marks, for example.

   If dried secretions were taken, note the number of swabs and the location from which the secretions were collected, or note that the location was not given. Each swab must be individually itemized.

   Refer to the Suspect Kit Processing Flow Charts for guidance.

   For male victims:

   Visually check the swabs for the presence of biological fluids. If the swabs are pinkish to reddish-brown in color, test with KM reagent, and note the results. Make a cutting from each of the swabs present for PSA testing. If the location from which the dried secretions swabs were taken is known, and **is not** from the mouth, near the mouth, anal cavity, or near the anal cavity, the swab should also be tested for amylase. Swabs from these locations are not typically tested for

amylase. If the location is unknown, make a cutting from each swab for both PSA and amylase testing. As every case is different, please consult with a supervisor if there is something in the case description that suggests further testing is required.

For female victims:

Visually check the swabs for the presence of biological fluids. If the swabs are pinkish to reddish-brown in color, test with KM reagent, and note the results. Make a cutting from each of the swabs present for amylase testing. Swabs with locations from the mouth, near the mouth, anal cavity, or near the anal cavity **should not automatically go on for amylase testing.** As every case is different, please consult with a supervisor if there is something in the case description that suggests further testing is required.

6. The **fingernail scrapings (or clippings)** are used to collect trace evidence from the fingernails.

   Trace evidence examinations are not performed in the Department of Forensic Biology. However, requests are occasionally made to examine the fingernail scrapings; discuss with a supervisor before starting any examinations of fingernail evidence. If fingernail examination has been approved, refer to Section O of this manual.

7. The **chest hair combings** are used to collect possible trace evidence from the chest hair of the suspect.

   Trace evidence examinations are not performed in the Department of Forensic Biology.

8. The **oral swabs** are used to collect possible biological fluids from that area; the smears are used for a sperm search.

   Refer to the Suspect Kit Processing Flow Charts for guidance.

For male victims:

Visually check the swabs for the presence of biological fluids. If the swabs are pinkish to reddish-brown in color, test with KM reagent; note the results.

Stain one smear accompanying each set of body cavity swabs using the Christmas Tree staining procedure (refer to Christmas Tree Stain for Spermatozoa section in the Forensic Biology Serology Manual) and examine for the presence of sperm; this search need not be exhaustive and should take no longer than five minutes (per smear). It is not necessary to estimate the number of sperm present, but the relative amount (one sperm head, numerous sperm heads, etc.) may be noted.

If no sperm is found on a smear, make a cutting for PSA testing.

For female victims:

In most cases, oral swabs and smears should not be tested. As every case is different, please consult with a supervisor if there is something in the case description that suggests further testing is required.

9. The **pulled head hair and pulled pubic hair** are collected as exemplars for any future microscopic hair comparisons.

   Trace evidence examinations are not performed in the Department of Forensic Biology. However, requests are occasionally made to use the pulled head hair for exemplar DNA testing; generally, hair DNA testing is not performed until hair comparisons have been made by the NYPD forensic laboratory.

10. The **facial hair combings and pubic hair combings** are used to collect possible trace evidence from the facial hair and pubic hair of the suspect.

    Trace evidence examinations are not performed in the Department of Forensic Biology.

11. The **vaginal and cervical swabs** are used to collect possible biological fluids from those areas; the smears are used for a sperm search.

Testing of vaginal and cervical swabs:

Visually check the swabs for the presence of biological fluids. If the swabs are pinkish to reddish-brown in color, test with KM reagent; note the results.

Refer to the Suspect Kit Processing Flow Charts for guidance.

For male victims:

Stain one smear accompanying each set of body cavity swabs using the Christmas Tree staining procedure (refer to Christmas Tree Stain for Spermatozoa section in the Forensic Biology Serology Manual) and examine for the presence of sperm; this search need not be exhaustive and should take no longer than five minutes (per smear). It is not necessary to estimate the number of sperm present, but the relative amount (one sperm head, numerous sperm heads, etc.) may be noted.

If no sperm is found on a smear, make a cutting from each negative location for PSA testing.

For female victims:

In most cases, vaginal and cervical swabs and smears should not be tested. As every case is different, please consult with a supervisor if there is something in the case description that suggests further testing is required.

12. The **anal swabs** are used to collect possible biological fluids from those areas; the smears are used for a sperm search.

For male victims:

Visually check the swabs for the presence of biological fluids. If the swabs are pinkish to reddish-brown in color, test with KM reagent; note the results.

Stain one smear accompanying each set of body cavity swabs using the Christmas Tree staining procedure (refer to Christmas Tree Stain for Spermatozoa section in the Forensic Biology Serology Manual) and examine for the presence of sperm; this search need not be exhaustive and should take no longer than five minutes (per smear). It is not necessary to estimate the number of sperm present, but the relative amount (one sperm head, numerous sperm heads, etc.) may be noted. If no sperm is found on a smear, make a cutting for PSA testing.

For female victims:

In most cases, anal swabs and smears should not be tested. As every case is different, please consult with a supervisor if there is something in the case description that suggests further testing is required.

13. The **buccal specimen** is used as the suspect's exemplar. If present, the buccal specimen would be the first choice in order to avoid potential inhibition of PCR by heme-degradation products.

14. The **questionnaire, body diagram sheets, and instruction sheets** are intended for the use of the medical personnel. If present, make a copy only of the **questionnaire and body diagram sheets** for retention with the case record—as a physical copy in the case file and a .pdf attachment in LIMS (as applicable); leave all originals in the kit. No item number is assigned if present. Label each page with the suspect file number, voucher number, analyst's initials, and date of examination.

15. Photographs are not supposed to be included in a kit. If present, make a note of it, alert a supervisor, and leave them in the kit. Label with FB number, date of examination, and analyst's initials. No item number is assigned if present.

16. If no positive swabs/stains/smears were found, make cuttings of appropriate swabs or stains as necessary. Refer to the Suspect Kit Processing Flow Charts for guidance.

17. If positive swabs/stains/smears were found, see below for guidelines on the cutting of samples for extraction.

    Refer to the Suspect Kit Processing Flow Charts for guidance.

    Underwear

    PSA positive stains should be sent for differential extraction.
    Amylase positive, semen negative stains should be sent for other extraction.

    If a stain is KM positive, consult with a supervisor.

    If a stain is PSA and amylase negative, consult with a supervisor.

    Dried secretion swabs

    If PSA positive, make a second cutting from one swab **from each listed location** that is positive for differential extraction. If the location from which the swabs were taken is unknown, make a cutting from one swab to go on for a differential extraction.

If a swab is KM positive and PSA negative, make a cutting from one swab **from each listed location** that is KM positive for blood extraction.

If a swab is amylase positive, and PSA and KM negative, the decision on further testing depends on the location that the swab originated from (orifice versus non-orifice) and the sex of the victim. Refer to the Suspect Kit Processing Flow Charts for guidance.

If a swab is PSA and amylase negative, the decision on further testing depends on the location that the swab originated from (orifice versus non-orifice) and the sex of the victim. Refer to the Suspect Kit Processing Flow Charts for guidance.

Be sure to check for dried secretions with locations from the mouth, near the mouth, anal cavity, or near the anal cavity. Consult a supervisor to determine if a dried secretion from these locations should go on for extraction prior to kit closing.

Vaginal and cervical swabs

If a swab is sperm/PSA positive, make a second cutting from each positive swab for differential extraction.

If a swab is KM positive, consult with a supervisor

If a swab is sperm/PSA negative, consult with a supervisor.

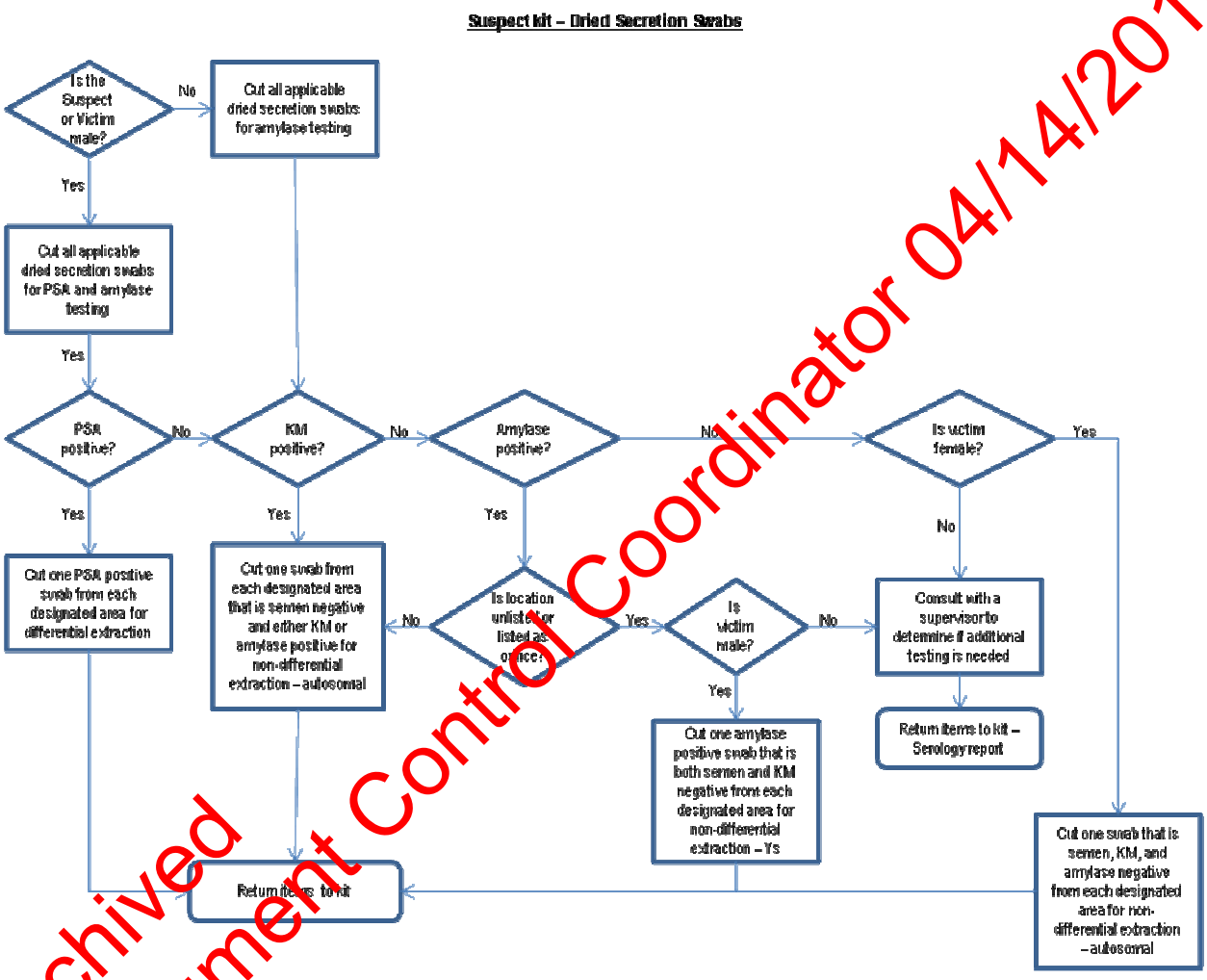
Oral and anal swabs

If a swab is sperm/PSA positive, make a cutting from positive location for differential extraction.

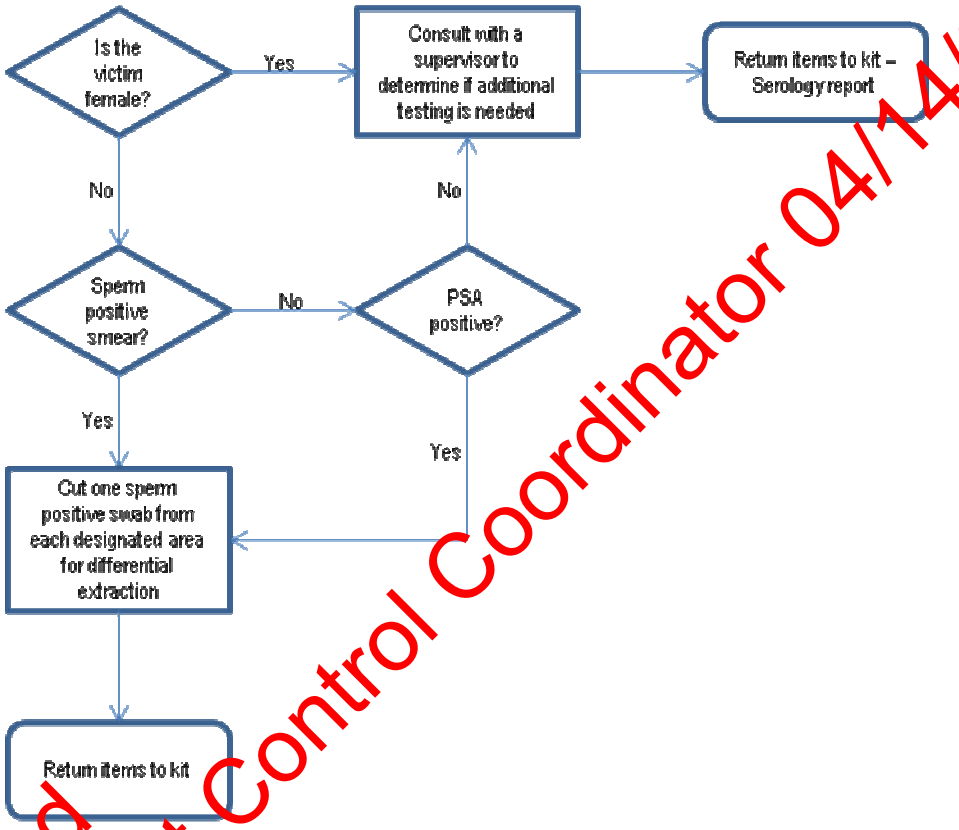
If a swab is sperm/PSA negative, consult with a supervisor

18. After cutting all pertinent items, return all swabs and smears to their respective envelopes. Seal all kit envelopes with evidence tape and return to the kit. Seal the kit and return to a secure storage location.

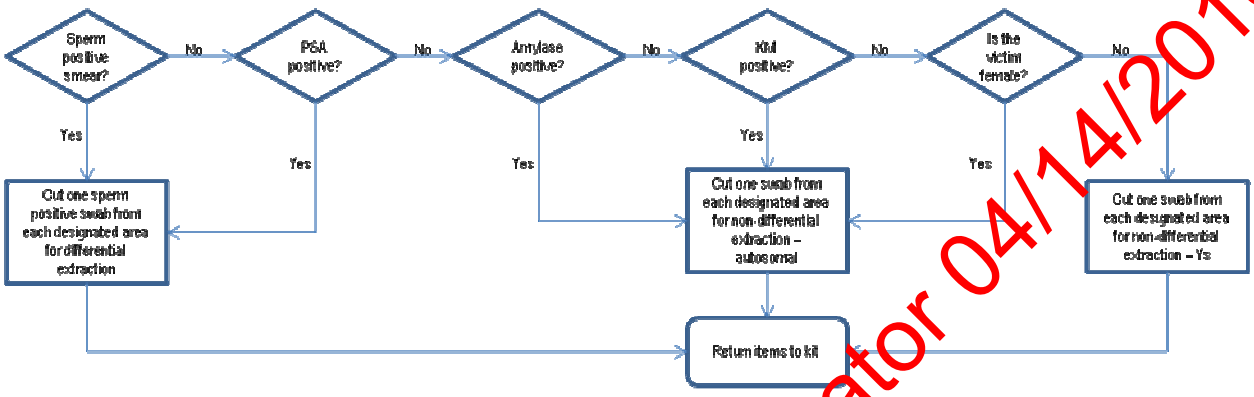
Suspect kit processing flow charts



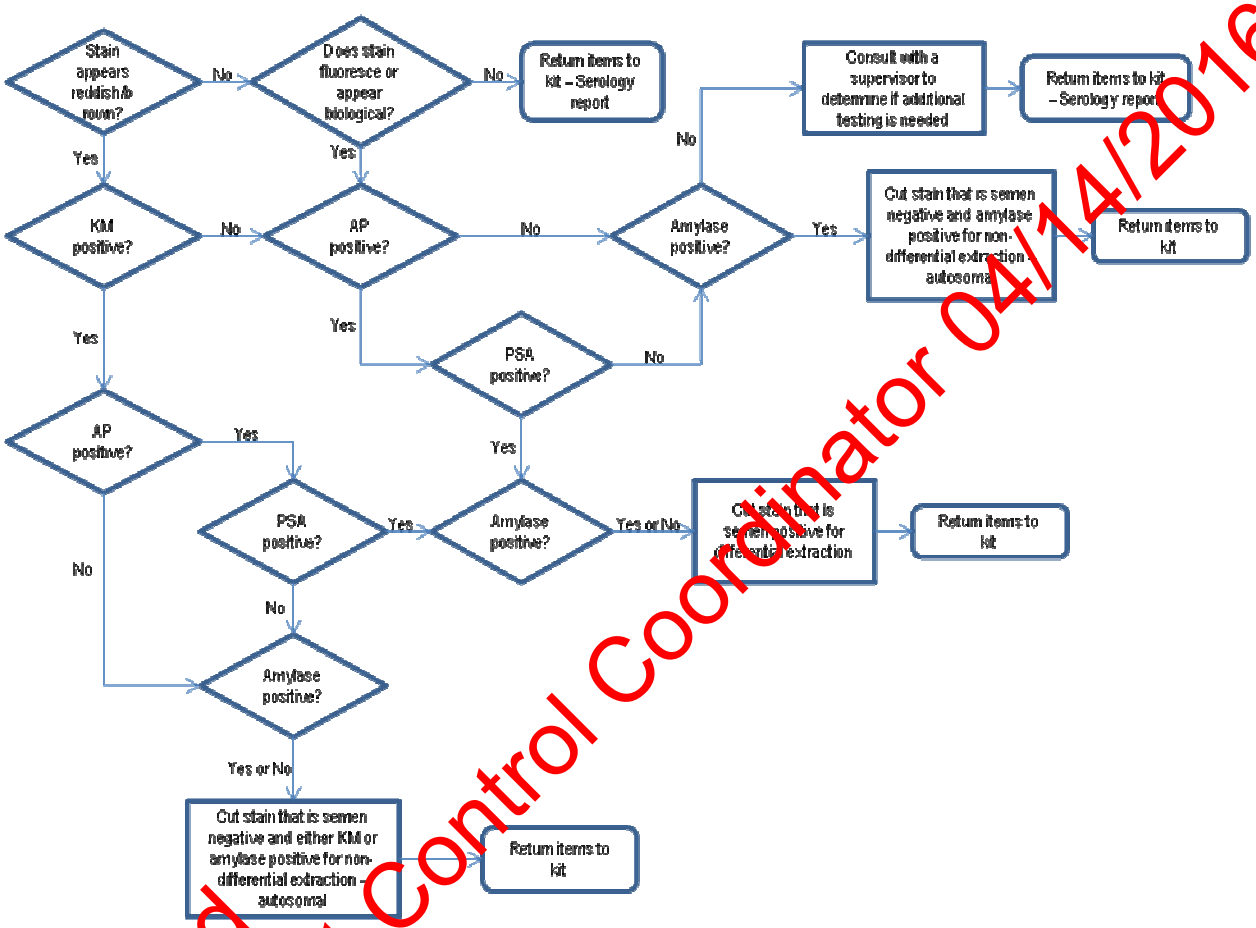
Suspect Kit – Oral, Anal, Vaginal, and Cervical Swabs



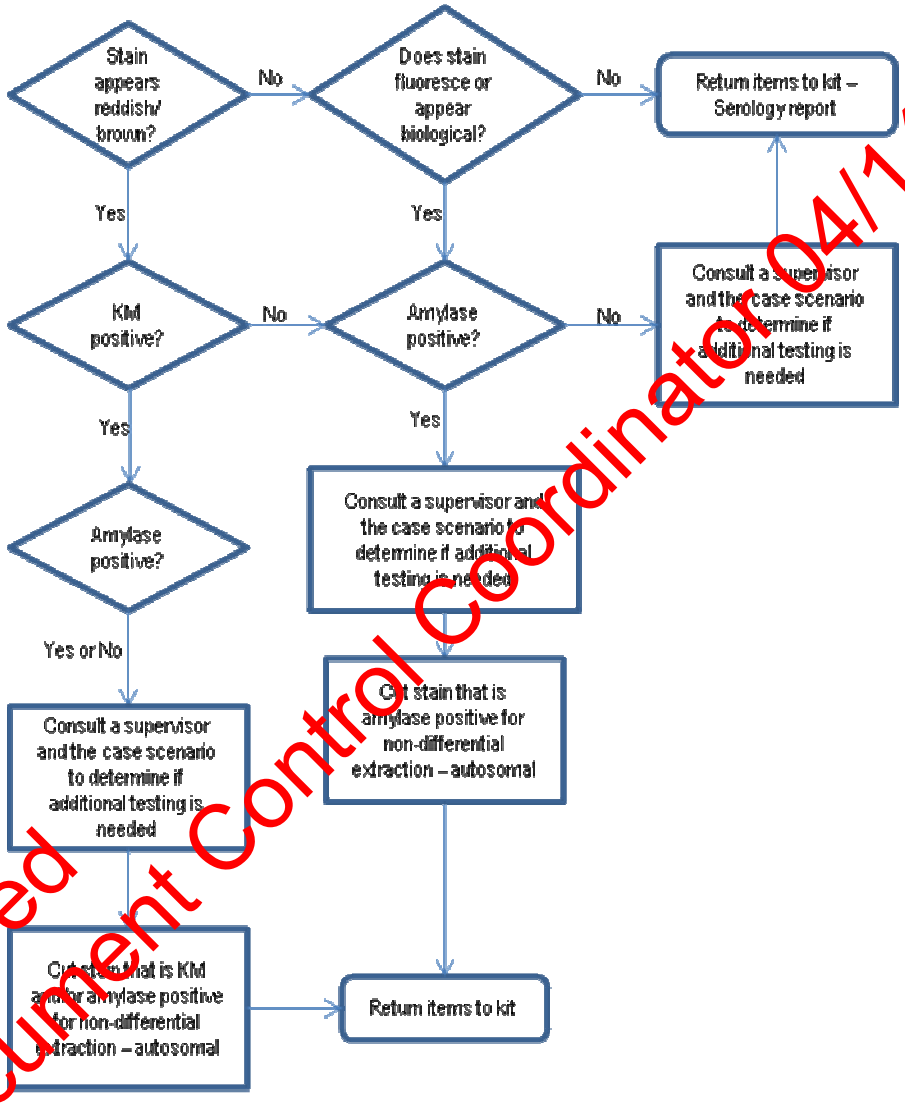
Suspect Kit – Penile and Scrotal Swabs



Suspect Kit – Underwear (Suspect and/or Victim is Male)



Suspect Kit – Underwear (Suspect and Victim are Female)



K. Evidence examination – non post-mortem exemplars

Follow the general guidelines for note taking and evidence examination when examining any exemplar item.

True exemplars:

An exemplar must have documentation stating that it is in fact from the person named. A "true exemplar," such as a blood sample or an oral swab, will include paperwork from the MLI who obtained the sample, paperwork from the NYPD (including a voucher and sometimes a signed consent form), or paperwork from the DAO.

Use the General Packaging Worksheet for initial documentation of each item.

1. For a blood sample, follow the bloodstain preparation section of the Serology Manual. Cut a portion of the dried bloodstain card for exemplar extraction, using the initials of the individual in the short sample name.

2. For an oral swab, document the sample using the General Packaging and Swab Exam Worksheets. Cut approximately ¼ of the swab for exemplar extraction, using the initials of the individual in the short sample name.

3. Retain the victim exemplars from sexual assaults. Place the swab(s) in a coin envelope labeled with the FB number, voucher number, item number, victim name, analyst's initials, and date of examination. The coin envelope should be placed in a Kapak envelope and heat sealed. The FB number should be written on the Kapak and the analyst's initials and date of examination should be written across the seal. Place the exemplar in a secure storage location and return the empty packaging to the EU. For blood samples, retain the stain card and clean the empty tubes with 10% bleach and return them along with the packaging to the Evidence Unit

Pseudo-exemplars:

It is the policy of the Department of Forensic Biology to accept and test "pseudo-exemplars". It is our expectation that NYPD investigators will submit items with a reasonable probability of finding a single-source DNA profile from the suspect. The item must have been abandoned; common examples include a cigarette butt tossed in the street, a coffee cup left behind after questioning, or a bottle the suspect was seen

handling. It is not acceptable to test items taken directly from a suspect (e.g. handcuffs for the DNA of the person that these were last used on) or items of evidence collected from an unrelated incident (e.g., bloody clothes from a suspect who was a victim of an assault).

1. Use the General Packaging Worksheet for initial documentation of each item.

2. For a cigarette butt "pseudo-exemplar," document the sample using a Cigarette Butt Examination Worksheet. Cut a piece of the filter and paper portion for **pseudo-exemplar extraction**.

3. If an item (such as cup or bottle) is submitted, use the General Item Examination Worksheet for documentation. Use a cotton-tipped swab moistened with distilled water to swab the surface of contact. Briefly allow the swab to dry and then cut a portion of the swab for **pseudo-exemplar extraction**. Amylase testing is not necessary for pseudo-exemplars.

4. For other items submitted as pseudo-exemplars, cut or swab the item as appropriate. It may be necessary to consult with a supervisor to determine the best approach.

5. Remember to designate samples taken from pseudo-exemplars using an appropriate LIMS suffix to indicate that it is not a true exemplar. For example: "_AM" for bottles and cups or "_CB" for cigarette butts. For short sample description, include the item type and initials of the person providing the pseudo exemplar. For example: "btlRB" for a bottle or "cigRB" for a cigarette butt.

L. Evidence examination – condom

Condoms are often submitted to the Forensic Biology laboratory for examination. Follow the general guidelines for note taking and evidence examination when examining a condom.

Use an Evidence Packaging Worksheet for initial documentation of each item.

1. Describe the general condition of the condom (laid out flat, wadded up), color, and any trace evidence if present. If the condom was submitted "tied off," document it as received then cut open for sampling.

2. If applicable, any stains **must** be documented by diagrams and/or photography. Note the location of the stain, size, heaviness (surface smear, etc.), and any directionality of the stain pattern. Each photograph must have a ruler visible in the frame, either a plain straight ruler or an x, y axis ruler.

3. Note whether fluids are present (liquid or dried). If the condom is found to be wet when opened, the item should be allowed to air dry after samples are taken. The item should not be heated or exposed to direct sunlight. If the item has become foul smelling, allow it to dry in the hood with the fan running.

4. Separately swab both the "inside" and "outside" of the condom, using no more than two swabs for each surface. Since it usually can't be conclusively determined which surface is which, use quotes to describe the "inside" and "outside."

5. Test both sets of swabs for the presence of blood, semen, and/or amylase as needed. Since the presence of a victim's DNA on a condom can often be important, it may be necessary to perform DNA testing on a sample from a condom even if no blood, semen, or amylase is detected. Consult a supervisor if needed.

6. **Do not sample a condom by cutting a portion of the condom.**

M. Evidence Examination – Products of Conception

The term *product of conception (POC)* refers to either an **embryo** (up to the formation of organs in the first 8 weeks of gestation) or a **fetus** (up to approximately 30 millimeters and weighs approximately 4 grams).

The *placenta* is a temporary organ of pregnancy. Anatomically, the placenta has two parts: **decidua (D),** genetically identical to the mother, and **chorionic villi (CV)**, genetically identical to the **POC**. Decidua appears as a compact tissue, while chorionic villi look more incoherent and loose. Morphological differentiation between D and CV can be made by observation:

- By naked eye (Figure 1a and 1b)
- Using stereo-microscopy (Figure 2a and 2b),
- Using light microscopy of formalin fixed, paraffin embedded, and stained tissue (Figure 3a and 3b).

It is possible for tissues of POCs to lack uniformity, be of different gestational ages, or be differently preserved. Therefore, besides general guidelines for evidence examination, examination of POCs requires that some specific scenarios be taken into consideration.

Follow the general guidelines for note taking and evidence examination when examining POC. Use a Product of Conception (POC) Packaging and Exam Worksheet for initial documentation of each POC item.

1. Describe the general condition of the item (full embryo/fetus, fragments, unrecognizable tissue parts, etc.).

2. Take one overview photograph of each item. Each photograph **must** have a ruler visible in the frame, either a plain straight ruler or an x, y axis ruler.

3. Weigh each item and document the tissue weight.

4. Determine if the POC is more or less than 24 weeks of gestational age (weight of $\geq$ 500g is considered > 24 weeks of gestational age).

5. Sampling of the item depends on the general condition of the item.

   a. If the POC is **morphologically well defined**, take a sample from it for DNA typing; the sample should be approximately 3x3x3 mm in size.

   b. If the POC is <24 weeks of gestational age and/or it is **not morphologically well defined,** rinse it several times in dH_2O using Petri dish and observe it wet under MIDEO stereo microscope (following Protocol for Forensic Mitochondrial DNA Analysis, Section 4: MIDEO Macro/Microscopic Digital Imaging System, page 1-3).

   Referring to Figure 2a and 2b for guidance, take a chorionic villi sample for DNA typing; the sample should be approximately 3x3x3 mm in size. If an exemplar from the mother/victim is not available, take a decidua sample as well.

   c. If the POC is <24 weeks of gestational age, and/or it is **not morphologically well defined,** and/or morphological differences between maternal and fetal part of placental tissue could not be established using MIDEO as in step b above, take several samples from morphologically

different regions and put them in **separate** embedding cassettes (Figure 4) for histological examination.

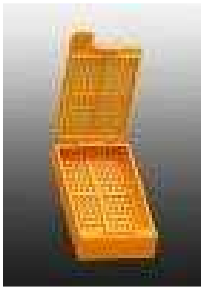


Figure 4
Tissue Embedding Cassette

Each sample should be approximately 10x10x5 mm in size. Close each cassette and label with a pencil. Submerge the cassettes in a prepared jar of formaldehyde. Cassettes, formaldehyde, and jars will be pre-provided by Histology Department.

After collection of all pieces is done, submit them to Department of Histology for further paraffin embedding, cutting, slide mounting and staining procedure. If needed, ask for consultation with a pathologist. Once the samples have been evaluated, follow the section of the Laser Microdissection procedure from Forensic Biology Protocol for STR Analysis (In Section 2: DNA Extraction). Make sure that the chain of custody is maintained.

d. If the POC is >24 weeks of gestational age, retain a sample for further testing. Inform OCME Identification Unit and keep the POC in a freezer, properly packed, until a permit for city burial is obtained by OCME Identification Unit. Return the empty packaging to the OCME Evidence Unit.

6. Submit samples for DNA extraction on an **Exemplar** test batch, using the notation “D” for decidual tissue and “CV” for chorionic villi as appropriate.

7. Depending on the outcome of the DNA testing, the disposition of the POC varies:

Testing outcome	Procedure
No mother/victim exemplar, and DNA profile of the POC is **female**	- Retain the entire POC; - Return the empty packaging to the OCME EU
No mother/victim exemplar, and DNA profile of the POC is **male**	- Retain a sample of POC for further testing; - Dispose the remainder of POC in the red waste trash **(If the POC is >24 weeks old, follow step 5d);** - Return the empty packaging to the OCME EU
No mother/victim exemplar and DNA profile of the POC is a **mixture**	- Repeat testing (See Step 5 above)
There is a mother/victim exemplar and DNA profile of the POC is foreign to the victim (mother), having expected allele sharing	- Retain a sample of POC for further testing; - Dispose the remainder of POC in the red waste trash **(If the POC is >24 weeks old, follow step 5d);** - Return the empty packaging to the OCME EU
There is a mother/victim exemplar and DNA profile of the POC is a deducible mixture	- Retain a sample of POC for further testing; - Dispose the remainder of POC in the red waste trash **(If the POC is >24 weeks old, follow step 5d);** - Return the empty packaging to the OCME EU
There is a mother/victim exemplar and DNA profile of the POC is an undeducible mixture	- Repeat testing, following Step 5a or 5b

8. For the return of empty packaging, bleach each container in which POC have been submitted using 10% bleach prior to return to the Evidence Unit.

Figure 1a: CV by naked eye

Figure 1b: CV by naked eye - detail

Figure 2a:
Stereo-microscopic (MIDEO) image of chorionic villi.

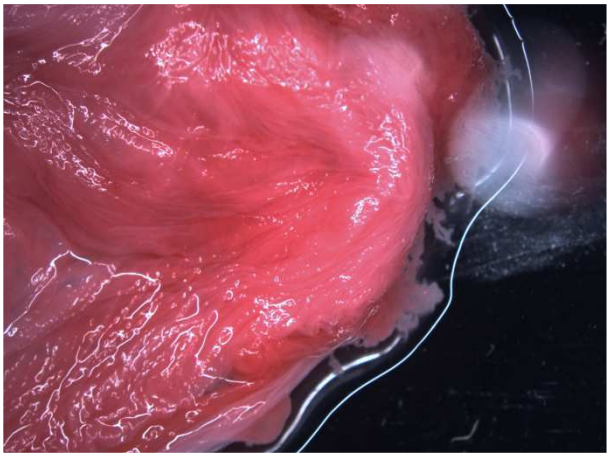


Figure 2b:
Stereo-microscopic (MIDEO) image of Decidua.

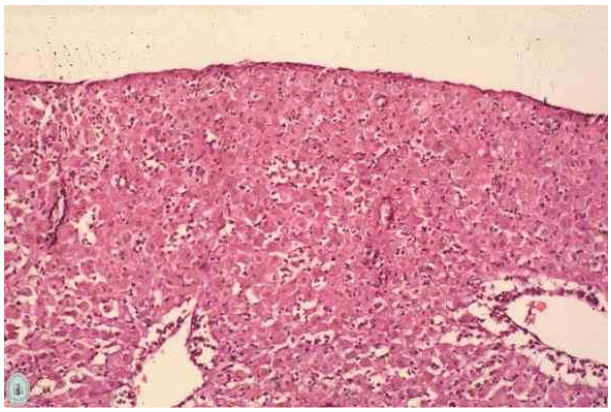


Figure 3a:
Microscopic image of formalin fixed, paraffin embedded and routinely stained decidua

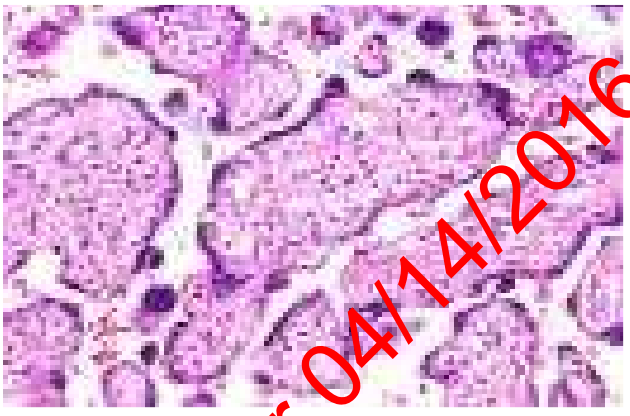


Figure 3b:
Microscopic image of formalin fixed, paraffin embedded and routinely stained chorionic villi

N. Evidence Examination – Touched Items

Held or touched items may be expected to yield low amounts of DNA. These items should be swabbed or scraped according to the protocols described below.

1. Documentation

Record the Evidence Packaging as the initial documentation of each item.

a. Follow the evidence exam guidelines for proper documentation of all items and samples taken. For further clarification see below.

i. Note the general appearance of the item. For example, note the color, the dimensions, and whether the item appeared to be dirty or possibly treated with latent print developers such as fingerprint powders or cyano-acrylate (fuming) etc.
ii. Note the specific area being swabbed and/or any stains observed. Include the dimensions of the stain or area.
   a) If an area is reddish brown, KM test the area if appropriate. For a very small area, consult a supervisor.

b. Determine the areas of the item to be swabbed separately if necessary. Describe the sample assignment in detail in the notes. Examples follow:

i. For duct tape used to bind a victim, multiple samples may be taken depending upon the circumstances of the case and the item. These samples may include the ends of the non- sticky side of the tape, the ends of the sticky side of the tape as well as the middle of the non-sticky side of the tape.
ii. Similarly, a bat may be divided into the following three sections: the top or where the bat came into contact with the victim, the middle or barrel of the bat which may have the victim's and/or the handler's DNA, and the handle of the bat.
iii. Each of the sections will be initially treated as separate samples.

2. Swabbing a touched item using SDS swabs

a. Obtain as many irradiated SDS swabs and aliquots of the 0.01% SDS swabbing solution as may be necessary for the item currently being examined. As a general rule, approximately 6 square inches may be

effectively swabbed with one SDS swab. This is dependent on the condition and type of evidence being examined.

b. Do not open the swab tube until you are ready to swab the item.

c. Clean a set of tweezers with 10% bleach, and 70% ETOH.

d. With a tube opener or lint-free wipe, open the tube and remove the swab with tweezers.

e. Dip a portion of the swab into the swabbing solution (0.01% SDS). Do not saturate, rather moisten, the swab. If too much SDS solution is used, DNA may be left behind on the item.

f. Swab the target area by folding or balling the swab up with the tweezers.

g. Thoroughly swab the target area with gentle pressure making sure to leave as little of the swabbing solution behind as possible.

NOTE: Multiple swabs may be used for a single area, as necessary. Document the use of multiple swabs and note the area which was swabbed. Only submit as many swabs in a single tube as may be effectively covered by digestion buffer (approximately 200µl) at the extraction stage. (The samples divided into separate extraction tubes may then be recombined into one extract in a microcon step.)

h. Should residual SDS be left on an item, use a dry SDS swab to collect it and include it in the extraction tube to be extracted along with the original swab(s).

i. Place the swab(s) into the extraction tube(s).

j. When swabbing more than one item from a case use a fresh tube of swabbing solution for each item.

k. Change gloves between items when swabbing different pieces of evidence.

3. Cutting swabs submitted by another party

a. If evidence is a swab previously taken, cut the entire swab and place in an irradiated extraction tube.

b. Cut the exterior layer of cotton or surface of the swab that appears to have come in contact with the evidence. Make a cutting of one third of the swab as normal. Then, starting from the area of the initial cut, peel the outer layer of the swab. Cut in circular pattern, essentially lifting that top layer off the stick with the scissors. Take care not to cut the wooden stick.

Repackage the evidence and return to a secure storage location.

O. Evidence examination – Fingernail Scrapings (or Clippings)

Fingernail scrapings or clippings would be examined upon the request of the NYPD or law office and approval by a supervisor. Generally, information that indicates a struggle between the victim and the suspect must be provided in order to approve this testing.

Use the Evidence Packaging Worksheet for initial documentation, where applicable. In many cases, this may have been completed during the original examination of the sexual assault kit or post-mortem kit.

Note: Fingernail scrapings and clippings are to be sub-itemized by how they were received. Most often, they are initially separated by the right hand (containing scrapings or clippings or both) and the left hand (containing scrapings or clippings or both). For example, if the fingernails are item 1.4, they should be sub-itemized as items 1.4.1 (right hand) and 1.4.2 (left hand). Individual scraping dowels and fingernails must then be sub-itemized again before examination.

For example, if the fingernail packaging from a sexual assault kit contains all possible scrapings and clippings, the items should be listed as:

1.4 fingernail scrapings/clippings (itemized below)
- 1.4.1 right hand fingernail scrapings/clippings (itemized below)
  - 1.4.1.1 right hand fingernail scrapings
  - 1.4.1.2 right hand fingernail clipping
  - 1.4.1.3 right hand fingernail clipping
  - 1.4.1.4 right hand fingernail clipping
  - 1.4.1.5 right hand fingernail clipping
  - 1.4.1.6 right hand fingernail clipping
- 1.4.2 left hand fingernail scrapings/clippings (itemized below)

1.4.1.1 left hand fingernail scrapings
1.4.1.2 left hand fingernail clipping
1.4.1.3 left hand fingernail clipping
1.4.1.4 left hand fingernail clipping
1.4.1.5 left hand fingernail clipping
1.4.1.6 left hand fingernail clipping

In cases where the right and left hands are packaged separately, one level of sub-itemization will suffice. For example:

2 right hand fingernail scrapings/clippings (itemized below)
- 2.1 right hand fingernail scrapings
- 2.2 right hand fingernail clipping
- 2.3 right hand fingernail clipping
- 2.4 right hand fingernail clipping
- 2.5 right hand fingernail clipping
- 2.6 right hand fingernail clipping

3 right hand fingernail scrapings/clippings (itemized below)
- 3.1 right hand fingernail scrapings
- 3.2 right hand fingernail clipping
- 3.3 right hand fingernail clipping
- 3.4 right hand fingernail clipping
- 3.5 right hand fingernail clipping
- 3.6 right hand fingernail clipping

1. Fingernail scrapings

a. Complete a General Items Worksheet for the submitted fingernail scrapings. If packaged together, multiple scraping dowels can be examined at the same time (but sampled separately). If fingernail scrapings were received and previously documented in a sexual assault kit, you may need to edit the quantity and itemize the scraping dowels individually.

b. Cut a ~¼ inch piece from both ends of the individual dowel and place into one extraction tube (per dowel). Collect any debris that may have fallen off the dowel and place in an extraction tube.

c. Add the appropriate "_FN" suffix to all collected samples and submit for robotic extraction.

2. Fingernail clippings

a. Complete a Nail Examination Worksheet for each item. If packaged together, multiple fingernails can be examined at the same time (but sampled separately). If broken, pieces of fingernails should be treated as separate samples (there may be more than 10 samples).

b. Fingernails **must** be photographed since they will not be returned to their packaging. Fingernails can be grouped by hand for a photograph; photograph as described in the general guidelines of this manual.

c. Examine the fingernails under the stereoscope. Itemize any discovered skin or debris that can be separated from the fingernail as an additional sample.

d. KM test as needed. If a blood stain is suspected, collect the entire stain with a sterile swab moistened with water. Use a small piece of that swab for presumptive testing. If KM positive, consume the remainder of the collected sample for robotic extraction.
Note: With the exception of homicides, a KM positive sample is sufficient for the first round of testing. (For post-mortem samples, it is more likely that a KM positive is a result of the presence of victim, rather than foreign, blood.)

e. Cut longer fingernails in half; large samples may hinder the extraction process. Add the appropriate "_FN" suffix to all collected samples and submit for manual fingernail extraction.

Note: When submitting fingernails for extraction, the Evidence Item (fingernail) is "consumed". For sexual assault kits, the empty packaging can be returned to the kit. For retained post-mortem samples, create a package in the LIMS and note it as "created in lab". Add any remaining items to this package, print and affix the additional label. Post-mortem samples are to be retained in the appropriate post-mortem storage unit.

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Revision History:

February 9, 2010 – Initial version of procedure.
May 21, 2010 – Added Section C.16 and C.17 to clarify the policy for unattended evidence.
September 27, 2010 – Revised procedures on negative kits with additional evidence to be examined (Page 21).
January 6, 2011 – 1) Sperm searches of the slides in sexual assault kits (SAK) will not be regularly performed. Instead, samples associated with these slides will be cut and sent for further testing; exemplars will remain in the SAK until it is ready to be closed. All flow charts have been updated. 2) Page 21: Clarified process on additional evidence associated with SAK's – supervisors will determine if there is a need to be signed in and examined.
January 30, 2012 – "Positive" serology reports will no longer be written for sexual assault kits. All SAK processing flow charts are updated to reflect this. Additionally, suspect kit processing workflow is modified (pgs 36-37, 47-48).
June 9, 2012 – Sperm searches of the slides in sexual assault kits (SAK) will be a normal part of the workflow. All applicable flow charts have been updated.
June 15, 2012 – Additional clarifications, in conjunction to the changes made on June 9, 2012, were made to Pages 19, 27, and 35.
July 16, 2012 – Reference to LIMS is added. This includes how to take notes and how to document evidence received.
September 17, 2012 – Revisions made to Sections H13, H20, I5, J5, J11, and J17 to remove the requirement to perform amylase testing on true body cavity swabs from sexual assault kits.
April 4, 2013 – Sentence removed from procedure from Page 18 to be consistent with subsequent sections and flowcharts. This sentence should have been removed in conjunction with the 9/17/2012 revision.
October 7, 2013 – Sexual assault kit processing flow chart for Vaginal, Cervical, Perianal/Anal, Anal Swabs revised (Page 20 of 63) to reflect the practice of combining unlabeled perianal/anal swabs for differential extraction.
December 30, 2013- Elaboration on the procedure concerning the examination of the contents of the trace evidence envelope.
April 1, 2014 – Section H16 was modified to clarify that only the questionnaire and body diagram sheets need to be copied for the case record.
May 21, 2014 –Section C12 was modified to clarify the proper procedure for sealing evidence.
September 1, 2014 – changed High Sensitivity DNA Extraction to High Yield DNA Extraction.
October 1, 2014 - Entire Evidence Examination section updated to correspond to new workflow and procedures.
August 14, 2015 – Added use of IR ALS, added a statement about not covering prior marks when sealing evidence. Indicated when a file should be sent to QA for reanalysis consideration and changed references of semen to PSA.

Reports

GUIDING PRINCIPLES AND SCOPE

Case reports bring together all of the analytical results and conclusions found in the case notes. Reports must be clear and accurate, and avoid overly technical terminology and misleading statements.

If it becomes necessary for an additional report to be authored by a criminalist who did not author the previous case report, nor were they the prior Technical Reviewer of the case, the CASE RECORDS REVIEW-PREVIOUSLY REPORTED RESULTS form must be completed and placed in the case file by the author of the additional report.

A. General guidelines

1. Overly technical terminology or misleading statements must be avoided. The conclusions in each report must be supported by the analytical data.

2. A report should be written and submitted to a supervisor for review no later than seven days after the last analytical results are available. Each supervisory level should strive to complete their technical review within seven days; if additional analytical work is needed, the case returns to the analyst.

3. Each reviewer must document the completion of the technical and administrative reviews.

4. DNA reports must include the following:

   a. Case identifiers
   b. List of evidence received
   c. Description of the methodology
   d. Loci tested and/or Amplification Test Kit used
   e. Results and conclusions
   f. An interpretive statement, either quantitative (statistics) or qualitative
   g. Report date
   h. Disposition of evidence
   i. Signature and title of person accepting responsibility for the content of the report
   j. Appendix containing explanatory statements and definitions of terms.

These requirements are met in the sections of the report: top block, RESULTS AND CONCLUSIONS, EVIDENCE RECEIVED, DISPOSITION, signature block, and APPENDIX.

Serology or additional reports may not require all of the above.

5. Report templates are available and should be used. These report templates have many pre-written statements which are applicable to most cases and save valuable time by eliminating the need to write the same sentences repeatedly. There are different template reports depending on case type and testing performed (Serology, DNA, suspect, missing persons, etc.); make sure the correct template is used for the type of case analyzed. Pre-written statements cannot cover every possible case scenario and should be modified as necessary for accuracy.

B. Evidence reports versus suspect (exemplar) reports

1. The DNA typing of evidence is often completed long before a suspect is identified or an exemplar is provided from an identified suspect. Sometimes, more than one suspect is developed on a case, such as when the initial suspect has been eliminated (especially with pattern cases). It is also possible for a suspect whose blood was collected for one investigation to end up linked to a totally different case. *For these reasons, an evidence report stands alone, without inclusion of any suspect DNA typing results.*

   The evidence report describes the examination of any evidence that was submitted, DNA typing results from the evidence and victim(s), and the statistical statements of the DNA typing results of the evidence.

   The evidence report may have the name, arrest number and/or NYSID (New York State Identification) number of an identified suspect in the top block of the report.

2. If an evidence case is linked to another evidence case or pattern, *the link between the cases is described in the evidence report(s)*. When making comparisons to other cases in the pattern, list the linked cases (case number, victim, complainant, and/or entity names, and all report dates or LIMS Report IDs) in the summary and include the pattern designation if known.

3. If a suspect is linked to a case or pattern, *the link between the suspect and the evidence is described in the suspect report.* If the suspect is linked to only one case, the precinct and complaint number information can be included; if linked to a pattern, the information may be left out.

   a. Where a suspect sample is being compared to DNA profiles in multiple cases, each suspect report (suspect to case 1, suspect to case 2 etc.) should be able to stand on its own if the cases are of vastly different types (e.g., a burglary and a sexual assault) or reporting comparisons from different test types (e.g., Identifiler 28 cycles vs. Identifiler 31 cycles or autosomal vs. mitochondrial).

   b. If the multiple cases are part of a "normal" pattern, a single suspect report will address the matching cases simultaneously. List all cases where comparisons are being made (case number, victim, complainant, and/or entity names, and all report dates or LIMS Report IDs) and include the pattern designation if known.

4. A table of DNA results may be included in the suspect case record as needed. This table includes the DNA profile of the suspect along with the relevant DNA typing results from the linked previous cases. Generally, the table will include deconvoluted mixtures (mixture and the deconvoluted profile) and single-source samples matching the suspect. A non-deconvoluted profile that the suspect is positively associated with does not need to be in the table, as the data will be displayed on the table in the FST report. If the evidence results are clean types, the DNA profile of the victim(s) may not be necessary.

5. Evidence reports and conclusions should be completed by the analyst before a suspect comparison report is completed. **Careful case management is required to ensure that the suspect report contains an accurate report identifier (LIMS REPORT ID, if applicable, or report date) for the evidentiary case report to which comparisons were made.**

6. If a suspect is excluded from a particular case or case(s) the suspect report is issued as described in Step 5, above. For high priority suspect cases, a suspect exclusion should be conveyed by a Criminalist IV or above to the NYPD or District Attorney's Office.

7. If a suspect is subsequently found to match a case, an additional report is issued using the format described in 3 above.

8. For pseudo exemplars, in most cases, only one or two items are submitted for an individual. However, testing will generally be done on all items. Independent of the detection of a match, the ensuing single-source result scenarios are resolved as follows:

SINGLE-SOURCE RESULTS			
Scenario		**Comparison and Reporting**	**LDIS Y/N**
1	Items generate one DNA profile	Compare the DNA profile to LINKAGE and directly to any case(s) specifically indicated. Issue report clearly stating that DNA profile was obtained from a pseudo-exemplar. Request oral swab in report.	Yes
2	Items generate two or more different DNA profiles	Compare all DNA profiles to LINKAGE and directly to any case(s) specifically indicated. Issue report clearly stating that the DNA profiles were obtained from pseudo-exemplars and the types were not consistent with each other. Request oral swab in report.	No
3	Not all tested samples yielded a result; one or more of the samples are negative.	Depending on the results of the samples yielding a result, follow Scenario 1 or 2 above. Request oral swab in report.	Follow Scenario 1 or 2 above.
4	None of the samples yielded a result; all samples are negative.	Issue a negative report. Request oral swab in report	N/A

The detection of a mixed DNA profile in a pseudo-exemplar clearly raises concerns about the validity of the association of the individual to the item submitted as the pseudo-exemplar. It is possible that the individual is a source of some component of the mixture or perhaps is not the source of any part of the mixture. Because of these possibilities, such results will not be the basis of any comparisons. **Therefore, if a mixture was detected on a pseudo-exemplar, report the mixtures as "not suitable for comparison." Additionally, request an oral swab in report.**

When reporting results on pseudo-exemplars it should be clear from the report that the result was not from a buccal- or blood-sample. Depending on the results obtained, there may need to be additional statements about mixtures. In all pseudo-exemplar reports, a request for a true exemplar (oral swab) must be made. See the template report for the wording to address these situations.

9. For a kinship (paternity, maternity, etc.) case, a single report is generated using the paternity report template. Both FB numbers are used on the report and a copy of the report is kept with each case record.

C. Additional and Amended Reports

1. If an additional report is generated, this will be noted immediately prior to the RESULTS AND CONCLUSIONS section using the following standard statement:

ADDITIONAL REPORT

This is an additional report. For previous examinations, evidence submitted, and disposition, see report(s) dated (insert date or dates of all prior reports).

In instances where additional reports are generated, the analyst who worked on that portion of the case will sign the most recent report. The RESULTS AND CONCLUSIONS section generally discusses only the new analyses. If the new data includes additional genetic testing, the report may be cumulative, including the new genetic testing results plus the genetic testing results from past reports.

2. If an amended (corrected) report is generated, this will be noted immediately prior to the RESULTS AND CONCLUSIONS section using the following standard statement:

AMENDED REPORT

This is an amended version of the report dated (insert date of original report). *An additional sentence describing the nature of the correction must be included.*

In instances where amended reports are generated, the original reporting analyst will sign the most recent report. The entire report, including the amendment, is generated.

D. Top block

Each report will be on the most current version of the department letterhead and will have specific identifying information in the top block. Not all of the following are available for each case. The information may vary depending on the case type and/or whether the case is an NYPD submitted case.

a. Report date indicating the date the final report was generated
b. Name of deceased, victim, complainant, or entity
c. FBio case number
d. ME (Medical Examiner) number
e. Physician that conducted the autopsy and autopsy date
f. Name of suspect
g. Arrest number and/or NYSID number of suspect
i. NYPD complaint number

E. Results and Conclusions

The Results and Conclusions section contains a summary of results and/or conclusions and the interpretive statement (quantitative or qualitative) that provides weight to any associations made.

Before writing results and conclusions, ask yourself **"WHAT DOES THE READER OF THE REPORT NEED TO KNOW?"** Then write short, clear statements answering those questions.

The template reports contain many pre-written sentences to guide the explanations and interpretation of results.

The first part of Results and Conclusions should be a brief synopsis of the analytical results; it should **answer the questions** that were posed by the submission of the physical evidence, such as: Is there blood? Could it be the victim's? Are there samples foreign to the victim? Is there semen? Was the DNA profile of the semen donor determined? Are there any other body fluids?

The synopsis should also contain information, where applicable, regarding database comparisons or suitability of entry of profiles into DNA databases.

1. Positive associations of evidentiary or suspect DNA profiles to DNA profiles in local databases are reported in the applicable case report.

2. Negative results on database searches of evidentiary or suspect profiles should be reported in a case report only in the following circumstances:
   a. The search is a one-time event and the evidentiary or suspect DNA profile will not be entered into the local databases, and/or
   b. A suspect sample was submitted specifically for comparison to local DNA databases.

3. Case reports must identify the DNA profiles that are suitable for entry into DNA databases, and which level of database/CODIS the profile will ultimately reside.

Other things to consider:

1. For the majority of the DNA cases, the following manner of reporting serological results is sufficient:

   a. Testing indicates the presence of human blood on the knife.

   b. Spermatozoa were found on the vaginal swab.

d. Amylase was found on all three cigarette butts found in the "living room."

e. No blood was detected on the pants or shoes taken from the "suspect."

f. The standard forensic paternity conclusions.

2. DNA results are dealt with in the RESULTS AND CONCLUSIONS section as well, for example:

a. List samples that do not yield enough DNA for typing.

No human DNA suitable for STR DNA typing was detected on the following samples:

b. List samples where typing was attempted with no alleles detected.

DNA typing using the AmpF*l*STR® Identifiler® PCR Amplification Kit was performed on the samples listed below; however, these samples are not suitable for comparison due to no alleles detected.

c. List samples that were extracted but not typed (such as multiple samples from a single item).

The following samples were extracted, but STR DNA typing was not performed:

d. List samples with no foreign DNA (intimate samples such as body swabs, underwear, etc.).

DNA typing using the AmpF*l*STR® Identifiler® PCR Amplification Kit was performed on the samples listed below. A DNA profile was determined and matches the DNA profile of *Jane Doe*.

3. Complicated or unusual cases involving mixtures of body fluids, multiple contributors, etc. can be difficult to write. The template reports are a place to start, and many valuable insights can be gained by reading previous reports covering similar cases. It is a good idea for each analyst to maintain a file of copies of his or her complicated reports for future reference.

4. Clearly differentiate between similar items so that there is no confusion regarding which test results and conclusions apply to which items. For example, for items that can be differentiated by color or other descriptions:

   a. Human blood was found on the blue shirt. No blood was found on the green shirt.

   b. Human blood was found on the samples from the "doorway" and "hall."

5. Avoid the exclusive use of item numbers, since that forces the reader to look elsewhere to find out what is being described. However, item numbers may be used in conjunction with the item descriptions. Notations used by the collecting officer to identify samples may be useful to differentiate between many items.

6. If items were removed from an object, location or person, it is useful to put that information in the summary. Quotation marks may be used to indicate wording that has been copied EXACTLY as it is written elsewhere, including any misspellings or abbreviations:

   a. sample taken from the "bedroom door."

   b. shirt taken from "the defendant."

   If there is conflicting information in the voucher, request for laboratory examination, and/or crime scene report, it may be impossible to determine which is correct; in that case, do not include any information.

7. Trace evidence (hairs, fibers, etc.) collected while examining evidence should be mentioned in the summary:

   a. Trace evidence included with the following items was not examined and will be returned with the evidence:

8. All items submitted must be mentioned in the report. If nothing of evidentiary interest was found on an item:

   a. Spermatozoa were not identified on the following items:

   b. No semen was detected on the following items:

9. Quantitative (statistical) statements are often part of the summary. They are calculated for probative samples when:

   a. The sample is apparently unmixed.

   4. The sample appears to be a mixture of two components and the source of one component is known (i.e. when epithelial cells are present in the sperm cell fraction).

   c. If there is a large difference in peak heights between the major and minor components and the genotype of the major component is easily inferred.

   d. Statistics are not calculated for expected inclusions such as epithelial cells from a swab giving a profile consistent with the donor of the swab.

10. After a summary is written, review it carefully. Does it answer all of the questions? Is it clear? Are all submitted items accounted for?

F. Examinations

The examinations section contains a description of the methodology and the loci tested. **This section does not appear in case reports with an "Appendix" section that contains equivalent information.**

Standard explanatory statements are in the template reports; use the correct explanatory statement for the type of genetic markers you used. The explanatory statements consist of several paragraphs; choose those that apply to the results in the case, deleting any paragraphs or loci that don't apply.

The explanatory statement can be further modified to reflect the analyses performed in a specific case, if necessary.

G. Evidence received

This section lists all evidence received, whether from a submitting agency or from an autopsy. The post-mortem items from autopsy are given PM numbers to differentiate them from other evidence.

All items signed into the case, whether or not they were examined, are listed in the EVIDENCE RECEIVED section.

The Evidence Received section should list the item number, voucher number, date received, and description of each item. If items were removed from an object, location or person, it is useful to put that information in the description. Use quotation marks to indicate an exact copy of information written elsewhere.

1.

ITEM	VOUCHER	DATE REC'D	DESCRIPTION
1	E111111	4/15/99	sample from "bedroom door"
1	E222222	4/21/99	shirt from "suspect"
PM 1	—	4/10/99	blood sample from victim

2. If several items are submitted as one, give all items individual identifiers.

ITEM	VOUCHER	DATE REC'D	DESCRIPTION
1.	E111111	4/15/99	cigarette butt 1
1.2			cigarette butt 2
1.3			cigarette butt 3

On the voucher, the cigarette butts were identified as "item 1". Upon opening the package, there were three; they were given the identifiers 1.1, 1.2, and 1.3.

3. List submitted items that weren't included on the voucher:

ITEM	VOUCHER	DATE REC'D	DESCRIPTION
1.1	E111111	4/15/99	shoe
2.1			sock (not listed on voucher)

4. If upon opening the items it was discovered that the description on the voucher was incorrect (for example, a tank top was submitted, but the voucher says "T-shirt"), put the correct description in the EVIDENCE RECEIVED section.

5. List missing items (listed on the voucher, but not present upon opening the packaging for examination):

ITEM	VOUCHER	DATE REC'D	DESCRIPTION
1.1	E111111	4/15/99	shoe
2.1			sock (not received)

6. List items submitted to the laboratory, but not examined. These items should be marked as (not examined)

ITEM	VOUCHER	DATE REC'D	DESCRIPTION
1.1-1.2	E111111	4/15/99	shoes (not examined)

H. Disposition

1. This section describes what has happened to the exemplars, vouchered evidence, post-mortem evidence, and samples removed from the evidence.

2. Always keep victim exemplar from a sexual assault kit. If no buccal sample was submitted in a sexual assault kit, keep the saliva sample or other suitable item, such as an orifice swab negative for PSA. (Exemplars from vouchered sexual assault kits are retained; all other contents are returned to the Evidence Unit.)

3. All sexual assault kit items from post-mortem samples are returned to the Evidence Unit. Any post-mortem samples that are not a part of a sexual assault kit will be retained.

4. Neither vouchered evidence nor samples from vouchered evidence are retained. DNA extracts are retained.

   a. Example of how to list retained items

      i. The following items will be retained in the laboratory:
      ii. DNA sample from Jane Doe
      iii. Item PM3, fingernails from victim
      iv. DNA extracts from samples and controls tested

5. If an item has left the lab, but NOT through the Evidence Unit:

   The gun was returned to Det. Smith, shield # 2345 on 5-7-90.

6. List any items/samples consumed during the analysis. The following statement may be added and referenced in the evidence list using a symbol such as "*":

   Sample(s) collected from this item and/or the submitted swab was consumed.

7. State when items have been transferred to the Evidence Unit:

   The remainder of the evidence will be released to the Evidence Unit.

I. Signature block

Each report has two signatures

1. The reporting analyst for the case, and
2. The administrative reviewer

Reports generated within the LIMS are electronically "signed" after validating the user's credentials.

J. Comparison only reports

A "comparison only" report provides the results of a comparison in the absence of any additional DNA typing. For example, this could include the comparison of a previously typed exemplar from a suspect file to a second case or to a newly discovered "unknown" donor to previously issued case results. Because no additional testing was performed, a disposition section is not necessary. Disposition information is documented in previous reports and referred to in the "Additional Report" statement.

REPORTS		
DATE EFFECTIVE 08-14-2015	APPROVING AUTHORITY QUALITY ASSURANCE MANAGER	PAGE 127 OF 162

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Revision History:

February 9, 2010 – Initial version of procedure.

January 6, 2011 – Information required in DNA reports (Section A.3.d) was amended to allow the loci tested and/or amplification test kit used.

July 16. 2012 – LIMS-specific statements were added; examples in Section G were shortened and evidence item numbers were modified to be LIMS-compliant; some extraneous explanatory statements were removed to streamline the document.

October 1, 2012 – (1) Removed requirement to report negative results from comparisons of suspect samples to the local databases, except in specific circumstances (one time search, where sample was submitted specifically for comparison to databases); (2) Added a bolded cautionary statement regarding evidentiary case report identifiers in the body of suspect reports; (3) Added a statement that case reports must state when DNA profiles are suitable for entry into a DNA databank, including which databank(s) are eligible.

April 1, 2013 – Due to how LIMS generates report dates (at administrative review when the final report is created), the requirement in the manual that a suspect report should be dated later than an evidence case report is removed from the procedures. Revisions occur in Section B. Minor changes are made to this section to be consistent with the process of notification to DAO's after suspect sample comparison to an evidence file.

May 1, 2015- Added notation as to when to use the CASE RECORDS REVIEW-PREVIOULSY REPORTED RESULTS form. Section B updated to indicate that pseudo-exemplars that yield mixtures will be reported as "not suitable for comparison"

August 14, 2015 – Removed reference to" start date" that is no longer added to report headers, and updated examples and procedures to reflect the new LIMS report template and new reporting guidelines.

Technical Review

GUIDING PRINCIPLES AND SCOPE

Technical review is an evaluation of reports, notes, data, and other documents to ensure that there is an appropriate and sufficient basis for the scientific conclusions. The Department of Forensic Biology uses a program of technical review for case reports issued by the Department in order to ensure that all appropriate testing was conducted, that reports accurately reflect the results of testing, and that all opinions are based upon objective scientific observations.

This document describes the technical review procedure of the Department.

Managers may establish additional requirements for technical review within their work groups; however, such requirements may not be less stringent than the requirements described in this procedure.

If differences of opinion arise during the technical review process and cannot be resolved by the analyst, reviewer, their supervisor(s), and/or manager(s), the "*Discrepancies in Interpreted Results*" procedure in the *Administrative Manual* must be followed.

PROCEDURE

During technical review, the functional reports, notes, data, and other documents are checked to verify that the Department's analytical, case management and QA/QC procedures were followed; data was interpreted correctly; and the final case report accurately reflects the supporting data. Technical review is performed on all cases prior to the release of the report, except for those that are eligible for Administrative Completion (see the "Administrative Completion of Cases" procedure).

The hard copy case file pulls together the case documentation needed for technical review. Prior to submitting a case for technical review, the reporting analyst should ensure that all necessary technical and administrative records have been printed and placed into the hard copy case file. See the "Case File" procedure for further details on the technical and administrative records that are needed.

A. Technical Reviewer Requirements

1. The reporting analyst cannot perform a technical review of their own case. Technical reviews may not be performed by the author or co-author of any examination records within the associated case record.

2. The technical reviewer must be or have been an analyst qualified in the methodology being reviewed.
   a. "Analyst" includes those whose sole analytical responsibility is technical review.

3. **Criminalist II or above may technically review:** Serology cases; DNA cases where no DNA testing past the quantitation step is attempted.

4. **Criminalist III or above may technically review:** All of the above, as well as cases that proceed to DNA amplification and typing.

B. Elements of Technical Review

There are two basic types of case technical review, full technical review and limited scope technical review.

1. **Full technical review.** At a minimum, a full technical review includes the following steps. Some steps will not be applicable to technical review of serology cases or DNA cases that do not proceed past the quantitation step.
   a. The case report and records in the case file are reviewed to ensure that:
      i. All submitted items are accounted for in the case report and testing conforms to proper technical procedures and applicable laboratory policies and procedures.
      ii. The reported results and conclusions are accurate and supported by the technical records:
         1. DNA profiles are consistent with the raw or analyzed data (e.g., electropherograms, sample sequences).
         2. All required controls and allelic ladders (including appropriate controls from reworked samples) are accounted for. Inclusions,

exclusions, and results reported as inconclusive comply with Department guidelines

a) Associations must be properly qualified in the case report with either a quantitative or qualitative statement as appropriate.
b) When no definitive conclusions can be reached, the case report must clearly communicate the reason(s).

3. Examination notes and supplemental records meet Department requirements with respect to dates of examination and analyst and case identifiers.

b. The case report is reviewed for accuracy of spelling and grammar.

(**Note**: This step is a part of the Administrative Review process that has been incorporated into the Technical Review process)

c. The following elements are verified as present in the report:

- FB case number
- Description of the evidence
- Description of the DNA technology
- Description of the DNA loci or amplification system
- The results and conclusions
- A quantitative or qualitative interpretative statement
- The disposition of evidence
- The signature and title of the analyst of record
- Other pertinent case information as applicable, e.g., name of victim, NYPD complaint number
- A location for documentation of administrative review

d. The chain of custody is reviewed

e. The statistical analysis (if applicable) is reviewed

f. A database review is completed if not already done (**See Section E**)

2. **Limited scope technical review.** A limited scope technical review is the verification of the most critical elements of a case, including:

a. The informative DNA typing results, including review of controls
b. The comparisons made
c. The conclusions which are relayed in the case report

3. Problems identified during technical review must be corrected. The majority of corrections are the responsibility of the reporting analyst; however, technical reviewers have discretion to make minor administrative corrections that do not alter the results and/or conclusions (e.g., writing an FB number on a page).

C. Update NYPD DEMP (DNA Evidence Management Program)

The Department of Forensic Biology has agreed with the NYPD to check their DNA Evidence Management Program (DEMP) for additional evidence that may exist pertaining to a sexual assault case currently undergoing technical review by the Department of Forensic Biology. It has been further agreed that DEMP will be updated before completion of the technical review of that case. This is the only situation where a tech reviewer <u>must</u> check and update DEMP.

1. If the goals of the case have not been met by testing the kit (e.g. no semen has been found or no male profile has been developed), the technical reviewer needs to check DEMP for the existence of additional evidence pertaining to that case.

   a. If there is additional evidence, select ***"send to OCME if the case is still active"*** and update the LIMS communication log for that case to indicate that this request was made.

      For kits, if there is a listed suspect, attempt to contact the assigned ADA to determine if additional evidence still warrants testing.

   b. If DEMP indicates that there is no additional evidence for that case, update the LIMS communication log for that case to indicate that DEMP was checked and no additional evidence exists.

2. If the goals of the case have been met by testing the kit (e.g., a male profile was developed), the technical reviewer still needs to check DEMP for the existence of additional evidence pertaining to that case.

   a. If there is additional evidence, select ***"do not send to OCME"*** and update the LIMS communication log for that case to indicate that this request was made..

b. If DEMP indicates that there is no additional evidence for that case, update the LIMS communication log for that case to indicate that DEMP was checked and no additional evidence exists.

D. Number of Technical Reviews

1. One full technical review is sufficient for most cases; however, ***enhanced technical review*** is required in some circumstances. Enhanced technical review is:

   a. One full technical review conducted by a manager OR
   b. Two technical reviews, including at least one full technical review, conducted by Criminalist Level IIIs or above.

2. **An enhanced technical review is required for:**

   a. Cases that require kinship analysis or paternity analysis
   b. Cases that require partial match analysis (suspect to case only, not within a case)
   c. Cases that require the calculation of a likelihood ratio
   d. Cases where a comparison of the DNA profile of a suspect, victim, elimination sample, or other known/deduced donor to a sample results in an inconclusive result ("no conclusion can be drawn").

   e. Cases containing mixtures that exhibit more than one "Z" or "INC" in the deconvoluted profile (unless the "Z" or "INC" is due to dropout/degradation rather than ambiguity in the deconvolution)

   The requirement for enhanced technical review does not apply to cases that contain only mixtures where the DNA profile of the deconvoluted contributor is unambiguous. Characteristics of simple DNA mixtures may include:

   - The presence of a clear major contributor with the addition of just a few other called alleles
   - A completely deconvoluted major contributor with no more than one "Z" or "INC"
   - A completely deconvoluted major or minor contributor, with no more than one "Z" or "INC", obtained by assuming a contributor to the mixture

Note: An analyst or technical reviewer may request an enhanced technical review of any case.

E. Documentation of Technical Review

1. Technical review is officially documented either (1) on the applicable Scheduled Analysis sheet with the reviewer's initials and the date (pre-LIMS cases) or (2) within the LIMS.
   a. Pre-LIMS cases: The technical review completion dates should also be entered into the electronic case logbook.
      i. The "Tech review III/IV" field should be used for the first technical review completion date.
      ii. The "Review AD" field should be used for the second technical review completion date (if applicable).
2. Tech review approval should be recorded in LIMS only when corrections, if any, have been made.
3. DNA cases with completed technical reviews are ready for administrative review.

F. Database Review

1. DNA profiles that are eligible for CODIS and/or LINKAGE must undergo a database review by a Criminalist III or above. One database review by a Criminalist III or IV is sufficient in most circumstances; however, one review by a manager or two reviews by Criminalist III/IV's or above are required for:
   a. Mixture profiles resulting from complex mixtures, and
   b. Single-source (complete or partial) profiles deduced from complex mixtures
2. Database review can be included as part of a full or limited-scope technical review or it can be conducted as a stand-alone review in order to expedite profile entry into a database.
3. Database review of LINKAGE-eligible profiles may be completed before or after their entry into LINKAGE.

4. At a minimum, a database profile review includes:

   a. A review of the database profile and interpretation (LIMS) or the "DNA Profile Evaluation Form" or "Missing Persons DNA Profile Evaluation Form" (pre-LIMS, as applicable) and supporting documentation to ensure that:

      i. All required fields within the form have been completed
      ii. The DNA profile(s) is accurate
      iii. The specimen identification number is correct
      iv. The positive and negative control results are acceptable
      v. The DNA profile(s) is eligible for entry into the applicable database(s)

   b. Verification that profiles were correctly entered into LINKAGE (if applicable)

5. The database review is documented with the reviewer's password-verified electronic signature (post-LIMS evidence) or on the Scheduled Analysis form (pre-LIMS evidence).

   a. Pre-LIMS evidence: The Access database contains fields named "Database review" (in the Suspect Logbook) and "CODIS review" (in the Case Logbook). These fields are not used for official documentation of database reviews; however, dates entered into the fields (e.g., Suspect log book—date profile entered into LDIS; Case log book—date of database review) can be useful for casework metrics as a close approximation of the date that the profile is entered into LDIS:

6. **Corrections to DNA Profile Evaluation Forms prior to entry into CODIS.**
   a. Corrections to database profiles are shown to the reporting analyst, who verifies the changes prior to entry into LDIS.
   b. If the profile is needed for immediate upload and the reporting analyst is not available, the corrections can be approved by a Criminalist III or above. The corrected database profile is later shown to the reporting analyst.

7. **Corrections to DNA Profile Evaluation Forms after CODIS entry.**
   a. Corrections are made by the CODIS group.
   b. The CODIS group will involve the reporting analyst as necessary, particularly if doing so provides training value to the reporting analyst.

Revision History:

February 9, 2010 – Initial version of procedure.

September 24, 2010: Clarify enhanced technical review requirements for mixtures; add Proficiency Tests to case types that require enhanced technical review: exempt suspect profiles from requirement for database review *prior* to entry into LDIS; clarify that Access logbook fields pertaining to database review are useful for casework metrics, but are not official documentation of database review; add procedures on modification of DNA Profile Evaluation forms to Section E (Database Review).

March 28, 2011 - Specified the technical review requirements set forth in the 2011 version of the ASCLD/LAB-*International* Supplemental Requirements; revised procedure to indicate that technical review is performed on all cases prior to the release of the report.

July 16, 2012 – Changes to language on documentation of Technical Review to account for simultaneous existence of pre-LIMS evidence and case reports tech reviewed in LIMS.

April 1, 2014 – Procedure revised such that Criminalist Level III analysts are allowed to conduct technical review of DNA positive cases. "Guiding Principles and Scope" section revised to clarify procedure when unresolved discrepancies occur.

May 30, 2014 – Section C.2, requirements for an enhanced technical review, was revised to specify the type of cases that require an enhanced technical review and the type of cases that do not require it.

June 16, 2014 – Revised requirements for Enhanced Technical Review.

September 1, 2014 – changed the name of the "Unresolved Discrepancies" procedure to "Discrepancies in Interpreted Results". Also noted that the "Discrepancies in Interpreted Results" procedure has moved to the Administrative Manual.

October 1, 2014 - Section C added pertaining to checking/updating of DEMP (DNA Evidence Management Program) before final technical review of sexual assault case files/reports.

May 1, 2015 – Updated Section D of the Technical Review section to clarify requirements for an "enhanced" review.

August 14, 2015- Clarified in Section C. that if there is a suspect listed, the ADA should be contacted before requesting additional evidence be sent to the OCME.

Administrative Review

GUIDING PRINCIPLES AND SCOPE:

An administrative review is the final evaluation (editorial review) of the report and case file documentation (examination and administrative) and must be completed prior to the distribution of the report. Reports cannot be issued without a completed administrative review; this includes high priority ("rush") cases.

A program of administrative review for reports issued by the Department of Forensic Biology helps to ensure that reports and case file documentation are in compliance with the guiding principles and procedures in the Department's management system.

This procedure describes the administrative review and report distribution process for the Department.

PROCEDURE:

Administrative reviews can be performed by the Forensic Biology Administrative Team as well as by Criminalists and other titles. The Administrative Review Checklist shall be referenced by the administrative reviewer to ensure that all aspects of the Administrative Review Procedure have been completed. The Administrative Review Checklist is summary of all key points of the Administrative Review Procedure. The Checklist does not replace the need to follow the Administrative Review Procedure detailed in this manual, but instead acts to enhance the administrative review process. The electronic signature of the administrative reviewer in LIMS indicates completion of the administrative review and signifies that all aspects of the Administrative Review Procedure, and by extension the Administrative Review Checklist, have been adhered to.

The author of a test report may <u>not</u> conduct an administrative review of their own report and its associated records.

A. Administrative Review

Administrative review is conducted on the draft copy of the report in LIMS (this may be printed out to aid administrative review).

1. Ensure the following key information is accurate and complete in the report:

a) Title block: FB# or proficiency test # / victim name / suspect name / complaint # / ME # / arrest # / NYSID # / / ME name & date of autopsy

b) Header: FB#, the victim's or supect's name and, if applicable, an ME#. The header must appear on all pages except the first page.

c) Text: Check page numbering; ensure the report is signed. For LIMS-created case reports, this signature is electronically validated. Case reports created outside of the LIMS contain a handwritten inked signature.

d) Evidence received and disposition:

Check for correct evidence itemization, voucher # and date evidence received.

2. Review all hard copy administrative and examination records in the paper case file to ensure that the records are uniquely identified according to laboratory policy and/or procedure.
   a) Check examination notes for analyst's initials, FB# and page #.
   b) Ensure that the FB# appears on all pages of administrative documentation.

   Note: The review of the report for spelling and grammatical accuracy is an element of the Administrative Review process that is conducted during Technical Review.

3. The case file is routed back to the analyst if major corrections to the case file are needed, such as changes to the report. When minor problems are noted, such as missing page numbers or initials, report distribution can be completed prior to routing the case file back to the analyst for corrections.

4. Document the administrative review. For case reports created outside of LIMS (pre-LIMS cases), the administrative reviewer signs in the designated area on the hard copy of the report.

5. Case reports created outside of the LIMS are scanned to .pdf format and distributed to the appropriate customers. (See Sections E and F for details.) The

LIMS-created reports are generated as .pdf documents when the "Final Report" button is selected. Report distribution should be done on the same day as the administrative review.

6. A copy of the case report .pdf must be saved to a location on the FBio server to allow for distribution to the NYPD's ECMS system and other agencies (as necessary).

B. Additional Information on Administrative Reviews

a. For pre-LIMS evidence where an **Amended Report** without any more work has been issued, the administrative review is documented only in the case file, not in the electronic Case Log Book ("Access database"). There is an additional Administrative Review database for cases received prior to January 1st, 2007. This database is named Admin Review Through 2006 form and can be found under Admin Review Forms in the Forensic Biology Access Main Switchboard.

b. For **Administrative Completion of Cases** (a case file is closed out without issuing a technical report on the findings; for example after a stop testing request) a report is written and submitted for administrative review only; no technical review is required.

C. Scanning of report(s) utilizing the scanner (Fujitsu ScanSnap S1500)

For cases that contain reports generated outside of the LIMS system, the following procedure should be followed to digitize the signed report into a .pdf document.

1. Check the bottom right hand corner of the computer screen where the application icons are located. The scanner is ready if a blue circle with a white "S" is displayed.
2. Place report face down and upside down on the scanner. Only one report can be scanned at a time. A route sheet is for internal purposes and will not be scanned.
3. Press the blue (scan) button to scan the report.
4. Select "scan to folder".
5. In the "specify file name" dialog box change the pdf file name from date & time to the appropriate FB# (e.g., 10S0034; 1000263; 0906754a).

6. In the "specify destination folder" dialog box save the pdf file in the appropriate reports directory via the browse button. (e.g., M:\FBIOLOGY_MAIN\ Reports\Suspect\FB10-S).
7. Select "Save". "Files were saved successfully" is displayed.
8. To cancel the scan, select "Cancel" and close out the dialog box. Select "yes" to delete the file.

D. Report Distribution

1. For case generated prior to LIMS, the Forensic Biology Report Route Sheet indicates where the report needs to be sent. For case reports generated within the LIMS system, the report recipients will be automatically designated.

2. All reports with a complaint number are uploaded to NYPD Enterprise Case Management System (ECMS). All reports needed for Medical Examiner identification purposes are sent to OCME Case Management System (CMS). The following reports (.pdf files) are sent to the DA's Offices using email:

   - Homicides
   - Sexual Assaults
   - All other crime types where there is a "hit" in a DNA database (local, state or national).
   - All other crime types where an arrest is indicated on the 61 form or other paperwork.

3. All crime types where the 61 form or other submitted paperwork does not indicate that an arrest has occurred are not routinely sent to the DA's Offices; this includes property crimes, assaults, and criminal possession of a weapon.

4. For the case reports generated prior to LIMS, the completion of the report distribution must be documented by initialing and dating the Report Route Sheet.

Note: The original of the report is maintained in the Forensic Biology case file.

5. OCME CMS (via electronic upload)

   a) From the OCME Intranet site, click on the "UVIS-CMS" tab at the top of the page.
   b) Click on the line that states "Click Here to Access the UVIS-CMS Application".

c) A pop-up window will appear asking you to "Please Click on My Silos to Select Silos", click OK.
d) Type the ME# for the case report you are uploading into CMS into the search box at the top right hand side of the screen that states "Type Case No."
e) Uncheck the box at top right side of the screen that states "Last One Year Case" if the case is older than the current year.
f) Hit enter to search for case.
g) Click on the case number when the case entry appears on the screen.
h) From the drop-down menu under the "Documents" tab select "Forensic Biology report".
i) Click the "Upload Files" button.
j) Click the "Browse" tab at the bottom of the screen.
k) Search for and select the case report you need to upload into CMS from the folder where Forensic Biology reports are kept in PDF format. You can browse and select multiple case reports for upload to CMS as needed.
l) Click the "Upload" button at the bottom of the screen.
m) A PDF icon of the case report should appear on the screen. Click "Open" to view the report to ensure the correct report was uploaded to CMS. Click "Open" when the pop-up window appears asking if you want to open or save the PDF.
n) Click the "Update" button on the bottom right hand side of the screen to ensure the report has been uploaded to CMS.

6. NYPD ECMS (via electronic upload)

a) Click on the Internet Explorer icon and navigate to URL: http://10.152.144.123/ecms. This is the log in screen.
b) On the Log in screen: enter the Login ID and Password. Then click on the "Login" button. During an initial log in, the user will be prompted to change their password.
c) After successful log in, the NYPD ECMS Screen will appear. To upload a new Forensic Biology report, click on the "DNA Attachment" button (bottom right corner).
d) Another NYPD ECMS screen will appear. Fill in the following information: the identification date (the date that a report is being scanned and uploaded); the Forensic Biology number (format: FB09-00001); OCME number and EU number are optional (can be left blank), and the complaint number (format: year – precinct – number).
e) Click on the "View Complaint" button to compare the complaint to the one in the file. Verify that the information corresponds.

f) To attach the file (Forensic Biology report), click the "Upload" button. This will open a file browser. Browse for the file, highlight the pdf version, and click open.

g) The uploaded file can be viewed by clicking on the "View" button. If an incorrect file was uploaded then click on the "Upload" button again, browse for the correct file and click open. This will overwrite the previous attachment.

h) Once the correct report is uploaded, click on the "Save" button located at the bottom right corner of the screen. At this point, the entry will be forwarded to the case folder and a system message "The Forensics Entry is successfully inserted" appears. Click on the "Close Window" button.

i) The entry must be approved prior to being forwarded to the NYPD system. Click on the "Action" button to the right of the entry to approve. Select either the "View" option or view the entry and approve using the "Approve" button on the bottom right.

j) To delete the entry and not approve, select the "Delete" option from the "Action" button. At this point, the entry will not be forwarded to the case folder and a system message "The Forensics Entry is deleted successfully" appears. Click on the "Close Window" button.

7. DA(s) Offices (via email)

Non-LIMS reports:

a) Click on the inbox for the DNALab mailbox.

b) From the top menu, click on "New". This will open a "New" e-mail message.

c) Click on "Send" from the top menu of the new e-mail message. On the "Send" toolbar, click the "Options" drop down menu button and select "From". This step only needs to be done the first time. Afterwards, the "From" line should appear upon clicking "New". Now place the cursor on the "From" line and type "DNALab" to send from the DNALab mailbox. Otherwise, the e-mail will be sent from the user's own mailbox.

d) Place the cursor on the "To" line and type in the designated DA Office e-mail address.

e) Place the cursor on the "Subject" line and type in the offense type and the victim's or suspect's name (e.g., Homicide / (S) Goethals Bridge). Click on the paper clip icon (top toolbar) to attach the pdf file.

f) Replace a personal e-mail signature block with the FB Dept. e-mail signature block. Do this by copying and pasting from a previous sent e-mail in the "Sent Items Archive" of the DNALab mailbox.

Department of Forensic Biology
Office of Chief Medical Examiner
421 East 26th Street
New York, New York 10016
Tel: 212-323-1200
Fax: 212-323-1590
Email: DNALab@ocme.nyc.gov
Web: www.nyc.gov/ocme

g) No text is needed in the body of the e-mail. There is one exception – if the report is meant for a specific Assistant District Attorney, the report is still sent to the main email address, but "ATTN: ADA ……name here…." Is added in the body of the email in bold block letters.

h) E-mails that are sent to DA's Offices are automatically placed in the "Sent items" of the e-mail inbox. To archive these e-mails, move the sent e-mails from the "Sent items" of the mailbox to the "Sent Items Archive" of DNALab mailbox.

LIMS generated reports will be automatically e-mailed to any DA's office in the Distribution List tab for that case report.

8. Other (e.g., outside jurisdiction, corporation counsel, AUSA)

a) Follow the instructions on the route sheet if the report can be sent via email.

b) Notify the A team if the report needs to be faxed or mailed as a hard copy.

E. Case file routing

1. Unless minor corrections are necessary, or additional testing needs to be scheduled, the file should be placed in a "to be filed" bin.

2. Use the Forensic Biology Internal File Route Sheet to indicate any destinations other than the filing bin and affix this sheet to the outside of the file. Unless there are exigent circumstances, do not use sticky notes.

3. Prepare an out-guide stating the initials of the receiving Forensic Biology staff member, team, or CODIS for all files that are not routed to the filing bin. Place all out-guides in the filing bin.

F. Troubleshooting

1. Open an IT help desk ticket for any scanner related problems.

2. ECMS will suspend user accounts after three unsuccessful logins. In the event this happens or there are any issues with accounts, please contact the designated FBio liaison for ECMS.

3. A supervisor of the Administrative Team can help with any questions regarding report distribution or file routing. For case specific questions, consult your supervisor.

ADMINISTRATIVE REVIEW		
DATE EFFECTIVE 08-14-2015	APPROVED BY QUALITY ASSURANCE MANAGER	PAGE 144 OF 162

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Revision History:

February 9, 2010 – Initial version of procedure.

May 13, 2010 – Updated the procedure to include the evaluation of a case file to determine if it is ready for an Administrative Review (Section A); updated the Administrative Review Procedure (Section B and C); added the steps necessary for report distribution (Section D and E); and added procedures to be followed post-report distribution (Section F). Section G inserted to address troubleshooting.

December 13, 2010 – Revised Section C (Administrative Review Additional Information) to include updated procedures for reviewing a Proficiency Test.

March 28, 2011 – Specified the administrative review requirements set forth in the 2011 version of the ASCLD/LAB-*International* Supplemental Requirements; reorganized procedure and separated out the Administrative Review and Recording Productivity Metrics process.

July 16, 2012 – Substantial rewrite of the procedure to accommodate changes caused by LIMS implementation. Section C was left mostly unchanged.

December 30, 2013- Addition of procedure on how to electronically upload to OCME CMS added to the "Report Distribution" section.

February 2, 2015- Addition of use of Administrative Review Checklist added to section. Procedure modified to remove obsolete/ unnecessary reviews of information during administrative review.

August 14, 2015- Removed references to the pre-LIMS case productivity form that is no long in use. Removed references to recording pre-LIMS case metrics as all metrics are now pulled from LIMS.

Subcontracting

GUIDING PRINCIPLES AND SCOPE

Subcontracting is the utilization of another laboratory to provide services within the Department's scope of accreditation. It does not pertain to situations in which the Department uses an external laboratory to conduct a specific analysis using a technology that the laboratory is not qualified to perform or when the Department will not take or retain ownership of the data. For example, using another laboratory to provide mitochondrial DNA testing is "subcontracting" since our laboratory provides mitochondrial DNA testing services. However, the utilization of another laboratory to provide RFLP work is not "subcontracting" since our laboratory does not provide RFLP services.

A sub-set of subcontracting is **outsourcing**, which is the utilization of a vendor laboratory to provide DNA services in which the Department takes or retains ownership of the DNA data for entry into CODIS, when applicable.

It is not the usual practice of the Department of Forensic Biology to subcontract/outsource work. Should the need arise; however, the Department would use only competent subcontractors. This document describes the general process for establishing a subcontracting agreement that meets the requirements of ISO 17025 and the FBI Quality Assurance Standards for Forensic DNA Testing Laboratories.

PROCEDURE

In the event that the Department of Forensic Biology needs to subcontract work, the Department notifies the affected customers, e.g., the NYPD and/or District Attorney's Offices, in writing. In most cases the Department requests the customer to provide their approval, preferably in writing.

The Department seeks subcontractors that it believes to be appropriate for the tests to be conducted.

- If a subcontractor is selected by the Department, then the Department is responsible to the customer for the subcontractor's work.

- If a subcontractor is selected by the customer, the Department follows all steps in the subcontractor qualification process. The Department informs the customer of the results of the results of that process, and the ramifications of using vendor laboratories that do not meet the Department's requirements.

A. General Requirements for Subcontractor Qualification

1. A subcontractor must be accredited, preferably to ISO/IEC 17025.

2. The Quality Assurance Unit maintains a register of the subcontractors that the Department of Forensic Biology uses for tests, as well as the records that support subcontractor competence, for example, accreditation certificates and audit documents.

    i. The records include the date on which the subcontractor was approved.

B. DNA Subcontractor Qualification

1. The appropriate Technical Leader determines whether an external laboratory is competent to act as a subcontractor for the Department. The minimum requirements for DNA laboratory competence are:
    i. Compliance with the FBI Quality Assurance Standards for Forensic DNA Testing Laboratories, as verified by a review of the vendor laboratory's external audit document report, the vendor laboratory's responses, and/or follow-up actions to any findings detailed in the report.
    ii. Compliance with federal accreditation requirements.

2. Where the vendor laboratory will perform DNA analysis for the Department (and not for a law enforcement agency or entity other than the Department), the appropriate Technical Leader reviews and approves the technical specifications of the subcontracting agreement prior to the awarding of any agreement.

3. Prior to the initiation of analysis under a subcontracting agreement, the following steps take place:
    i. The appropriate Technical Leader or designee performs an initial on-site visit to subcontracting laboratory.
        - The employee performing the visit is a qualified or previously qualified analyst in the technology, platform, and DNA typing kit used to generate the DNA data.
        - It is not necessary to conduct a full DNA audit during this visit, but at a minimum the visit must include an assessment of the work site and documentation of the subcontractor's ability to perform analysis on the outsourced work.

ii. The appropriate Technical Leader documents in writing that the Department accepts ownership of the subcontractor's DNA data. A copy of the approval is provided to the subcontractor.

4. Subcontracting agreements that extend beyond one year require an annual on-site visit to the subcontractor laboratory.
   i. An on-site visit conducted by another NDIS laboratory using the same technology, platform, and DNA typing kit is acceptable. The records provided to the appropriate Technical Leader must include:
      - The date of the visit
      - A summary of the visit
      - Documentation of the qualified personnel who performed the visit.

   The Technical Leader documents their review and acceptance of the records of the on-site visit.

   A new "initial visit" is required when renewals or re-awards involve gaps in the agreement of greater than 6 months, or where there are changes to the technical specifications.

C. Data Integrity

All data and/or reports generated by a subcontractor as well as any vendor-generated profiles uploaded to or searched in CODIS by the Department are technically reviewed in the same manner as data and reports generated wholly within the Department. See the TECHNICAL REVIEW procedure for details.

Revision History:
February 9, 2010 – Initial version of procedure.

Administrative Completion of Cases

GUIDING PRINCIPLES AND SCOPE

Under certain circumstances it may be advantageous to complete a case file without issuing a technical report on the findings. Many cases submitted to the Department of Forensic Biology are resolved without relying on the data generated from the evidence. For example, plea agreements, recanted complaints, or investigative results that indicate no crime was committed are all reasons why testing results on submitted evidence may not be needed. In many of those situations cessation of testing, report writing, and/or technical review will prevent unnecessary expenditure of Forensic Biology resources.

This document describes the process to administratively close a case.

PROCEDURE

1. Cases are eligible for administrative closure if both of the following are true:

   - An appropriate entity, e.g., ADA, NYPD Liaison Unit, has provided written confirmation (letter, e-mail) that a Forensic Biology report is no longer needed. If the written or oral confirmation has come from the NYPD, follow up with the District Attorney's Office is necessary to ensure that the case can be administratively closed.
     - The documentation is retained in the case record.
   - Any DNA profiles that might potentially be generated from testing the evidentiary items would not be CODIS-eligible (as per the usual rules for determining CODIS eligibility).

   Unless no crime occurred, testing on items of evidence that might produce a CODIS-eligible profile testing must continue and a report must be issued.

2. The Criminalist IV supervisor responsible for the case evaluates whether the case qualifies for administrative close-out.

   - For major crimes it may be preferable to finish a report and the technical review even if the case qualifies for administrative closure. This is because the case may be re-opened, for example after an appeal, and it would be a challenge to finalize the initial results at a later date.

3. The Criminalist IV should perform the following actions before approving an administrative close-out of a case:

   - The Criminalist IV reviews the written documentation to confirm that a DNA report with technical results is not needed.
   - The Criminalist IV documents their approval in the case communication log.

4. Securing data and evidence

   Depending on the status of the testing, different steps are required before the case can be closed.

   a. <u>Evidence was examined, no extraction</u>
      - Remove samples from any pending extraction batches.
      - Reunite clippings with retained stains or evidence items before the evidence is returned. However, if the evidence was swabbed with 0.01% SDS the swab is extracted and tested to avoid degradation issues.

   b. <u>Samples were extracted and/or quantitated</u>
      - Extracts of biological fluid stains and other HSC samples are saved.
      - Extracts for low level DNA items, such as a touched object, are amplified and run, but the data is not interpreted.

   c. <u>Samples were amplified</u>
      - The STR typing steps, including run analysis and editing, are completed, but the data is not interpreted.

   d. <u>Samples were run</u>
      - Electropherograms are included in the case record, but the data is not interpreted.

5. Administrative Report

   - All technical pages are numbered and initialed
   - The productivity worksheet (pre-LIMS evidence only) is filled out to capture the completed analytical steps
   - The report contains the header and the evidence disposition section, but no results. The first page should contain a sentence such as:

"Testing was suspended and no technical results will be reported on the submitted evidence items. This case can be reactivated upon request. Further analysis will require approximately 60 days."

6. Administrative Review and Report Distribution

- **The case is submitted to administrative review.**
- **If the case is less than one year old the report is distributed in the usual manner. If the case is older than one year, the report is maintained in the case record, but is not distributed.**

Revision History:

May 13, 2010 – Initial version of procedure

July 16, 2012 – Minor changes to terminology to account for LIMS implementation, e.g., "communication log" rather than "case contacts"; removed requirement in section 5 to enter "Admin only" into communication log.

September 1, 2014 – statement added that follow up with DAO's office is necessary if the NYPD states that a case can be administratively closed.

November 24, 2014 – Changed step 3 in the procedure indicating that a Criminalist IV no longer requires approval from an assistant director for administrative close-out of cases.

Abbreviations

The following are the commonly used abbreviations in the Department. While these abbreviations are typically used as suffixes within sample identifiers, they may be used independently in case notes as well.

Abbreviation	Description
, #	STR rerun due to poor/no size standard
, 1/10 dil	STR rerun at 1/10 dilution
, confirm OL	STR rerun to confirm off-ladder allele
_0.0000001	1/10,000,000 Dilution
_0.000001	1/1,000,000 Dilution
_0.00001	1/100,000 Dilution
_0.0001	1/10,000 dilution
_0.000167	1/6000 Dilution
_0.00025	1/4000 Dilution
_0.0003	1/3000 Dilution
_0.0004	1/2500 Dilution
_0.0005	1/2000 Dilution
_0.001	1/1000 Dilution
_0.0025	1/400 Dilution
_0.005	1/200 Dilution
_0.008	1/125 Dilution
_0.01	1/100 Dilution
_0.015625	1/64 Dilution
_0.02	1/50 Dilution
_0.03125	1/32 Dilution
_0.04	1/25 Dilution
_0.05	1/20 Dilution
_0.0625	1/16 Dilution
_0.1	1/10 Dilution
_0.1_a	1/10 dilution for sample a replicate
_0.1_b	1/10 dilution for sample b replicate
_0.125	1/8 Dilution
_0.166	1/6 Dilution

Abbreviation	Description
_0.2	1/5 Dilution
_0.25	1/4 dilution
_0.5	1/2 Dilution
_0.78	Suffix used for QA sensitivity test
_1	Sequential number identifier
_10	Sequential number identifier
_11	Sequential number identifier
_12	Sequential number identifier
_13	Sequential number identifier
_14	Sequential number identifier
_15	Sequential number identifier
_150	Suffix used for QA sensitivity test
_16	Sequential number identifier
_17	Sequential number identifier
_18	Sequential number identifier
_19	Sequential number identifier
_1a	Sequential number identifier for sample a replicate
_1b	Sequential number identifier for sample b replicate
_1c	Sequential number identifier for sample c replicate
_1H	Sequential number identifier for high dilution
_2	Sequential number identifier
_20	Sequential number identifier
_21	Sequential number identifier
_22	Sequential number identifier
_23	Sequential number identifier
_24	Sequential number identifier
_25	Sequential number identifier
_25	Suffix used for QA sensitivity test
_26	Sequential number identifier
_27	Sequential number identifier
_28	Sequential number identifier
_29	Sequential number identifier
_2a	Sequential number identifier for sample a replicate
_2b	Sequential number identifier for sample b replicate

Abbreviation	Description
_2c	Sequential number identifier for sample c replicate
_2H	Sequential number identifier for high dilution
_3	Sequential number identifier
_30	Sequential number identifier
_31	Sequential number identifier
_32	Sequential number identifier
_33	Sequential number identifier
_34	Sequential number identifier
_35	Sequential number identifier
_36	Sequential number identifier
_37	Sequential number identifier
_38	Sequential number identifier
_39	Sequential number identifier
_3H	Sequential number identifier for high dilution
_4	Sequential number identifier
_40	Sequential number identifier
_41	Sequential number identifier
_42	Sequential number identifier
_43	Sequential number identifier
_44	Sequential number identifier
_45	Sequential number identifier
_46	Sequential number identifier
_47	Sequential number identifier
_48	Sequential number identifier
_4H	Sequential number identifier for high dilution
_5	Sequential number identifier
_50	Suffix used for QA sensitivity test
_5H	Sequential number identifier for high dilution
_6	Sequential number identifier
_6.25	Suffix used for QA sensitivity test
_6H	Sequential number identifier for high dilution
_7	Sequential number identifier
_8	Sequential number identifier
_9	Sequential number identifier

Abbreviation	Description
_a	Sample a
_a_low	Sample a replicate amplified at a lower than optimal DNA amount
_A1	A1 mtDNA primer
_A2	A2 mtDNA primer
_A4	A4 mtDNA primer
_abc	Pooled comparison samples
_aH	Sample a replicate at a high dilution for STR plates
_AM	Bottle mouth swabs/samples with possible saliva suffix
_b	Sample b
_b_low	Sample b replicate amplified at a lower than optimal DNA amount
_B1	B1 mtDNA primer
_B4	B4 mtDNA primer
_bH	Sample b replicate at a high dilution for STR plates
_BL	Bloodstain suffix
_c	Sample c
_c_low	Sample c replicate amplified at a lower than optimal DNA amount
_C1	C1 mtDNA primer
_C2	C2 mtDNA primer
_CB	Cigarette Butt suffix
_cH	Sample c replicate at a high dilution for STR plates
_conf	Confirmatory run for mtDNA cycle sequencing
_conf_A1	A1 Confirmatory primer for mtDNA cycle sequencing
_conf_A2	A2 Confirmatory primer for mtDNA cycle sequencing
_conf_A4	A4 Confirmatory primer for mtDNA cycle sequencing
_conf_B1	B1 Confirmatory primer for mtDNA cycle sequencing
_conf_B4	B4 Confirmatory primer for mtDNA cycle sequencing
_conf_C1	C1 Confirmatory primer for mtDNA cycle sequencing
_conf_C2	C2 Confirmatory primer for mtDNA cycle sequencing
_conf_D1	D1 Confirmatory primer for mtDNA cycle sequencing
_conf_D2	D2 Confirmatory primer for mtDNA cycle sequencing
_conf_M13	M13 Confirmatory primer for mtDNA cycle sequencing
_conf2	2nd Confirmatory run for mtDNA cycle sequencing
_conf2_A1	2nd A1 Confirmatory primer for mtDNA cycle sequenicng
_conf2_A4	2nd A4 Confirmatory primer for mtDNA cycle sequencing

Abbreviation	Description
_conf2_B1	2nd B1 Confirmatory primer for mtDNA cycle sequencing
_conf2_B4	2nd B4 Confirmatory primer for mtDNA cycle sequencing
_conf2_C1	2nd C1 Confirmatory primer for mtDNA cycle sequencing
_conf2_C2	2nd C2 Confirmatory primer for mtDNA cycle sequencing
_conf2_D1	2nd D1 Confirmatory primer for mtDNA cycle sequencing
_conf2_D2	2nd D2 Confirmatory primer for mtDNA cycle sequencing
_conf3	3rd Confirmatory run for mtDNA cycle sequencing
_conf3_A1	3rd A1 Confirmatory primer for mtDNA cycle sequencing
_conf3_A4	3rd A4 Confirmatory primer for mtDNA cycle sequencing
_conf3_B1	3rd B1 Confirmatory primer for mtDNA cycle sequencing
_conf3_B4	3rd B4 Confirmatory primer for mtDNA cycle sequencing
_conf3_C1	3rd C1 Confirmatory primer for mtDNA cycle sequencing
_conf3_C2	3rd C2 Confirmatory primer for mtDNA cycle sequencing
_conf3_D1	3rd D1 Confirmatory primer for mtDNA cycle sequencing
_conf3_D2	3rd D2 Confirmatory primer for mtDNA cycle sequencing
_D1	D1 mtDNA primer
_d1	Neat for Agilent
_d1_HB	Amplification at neat in homebrew
_d10	10-fold dilution for Agilent
_d10_HB	Amplification at 1/10 dilution in homebrew
_d100	100-fold dilution for Agilent
_d100_HB	Amplification at 1/100 dilution in homebrew
_D2	D2 mtDNA primer
_d2	2-Fold dilution for Agilent
_d2_HB	Amplification at 1/2 dilution in homebrew
_d5	5-Fold dilution for Agilent
_d5_HB	Amplification at 1/5 dilution in homebrew
_dup	Sample duplication
_dup_hi	Duplicate amplification at higher than optimal DNA amount
_dup_hr	Duplicate amplification at higher than "hi" DNA amount
_dup_reamp	Sample duplication reamplification
_dup_recut	Duplicate of a recut sample
_dup_rerun	Sample duplication rerun
_EC	Epithelial Cell Fraction

Abbreviation	Description
_FN	Fingernail suffix
_Ha	Sample a at a high dilution for ID28 STR plates
_HB	mtDNA Amplification Homebrew sample
_Hb	Sample b at a high dilution for ID28 STR plates
_HB_reamp	Mito homebrew sample reamp
_Hc	Sample c at a high dilution for ID28 STR plates
_hi	Amplified with higher than optimal DNA amount
_high_HB	Amplification with higher than optimal DNA amount in homebrew
_Hr	Amplified with higher than the "hi" DNA amount
_Ht	Amplified with the maximum DNA amount
_lo	Amplified with lower than optimal DNA amount
_lwr	Amplified with lower than the "lo" DNA amount
_M13	M13 mtDNA primer
_max	Amplified with the maximum DNA amount
_mcon	Microcon
_mcon1	Microcon 1
_mcon2	Microcon 2
_nd	No Dup
_nd	No duplication of sample needed
_neat	Neat
_opt	Amplified with the optimal DNA amount
_PT	Touched items swabbed by NYPD suffix
_R	Remains from Extraction
_reamp	Re-amplification
_reamp_hi	Reamplification at higher than optimal DNA amount
_reamp_Hr	Reamplification at higher than "hi" DNA amount
_reamp_Ht	Reamplification at highest DNA amount
_reamp_lo	Reamplification at lower than optimal DNA amount
_reamp_opt	Reamplification at optimal DNA amount
_reamp2	2nd Re-amplification
_reamp2_hi	2nd reamplification at higher than optimal DNA amount
_reamp2_lo	2nd reamplification at lower than optimal DNA amount
_reamp2_opt	2nd reamplification at optimal DNA amount
_reamp3	3rd Re-amplification

Abbreviation	Description
_recut	Recut
_recut2	2nd Recut
_recut3	3rd Recut
_recyc	Re-cycle sequencing for mtDNA
_recyc_A1	A1 primer for mtDNA re-cycle sequencing
_recyc_A4	A4 primer for mtDNA re-cycle sequencing
_recyc_B1	B1 primer for mtDNA re-cycle sequencing
_recyc_B4	B4 primer for mtDNA re-cycle sequencing
_recyc_C1	C1 primer for mtDNA re-cycle sequencing
_recyc_C2	C2 primer for mtDNA re-cycle sequencing
_recyc_D1	D1 primer for mtDNA re-cycle sequencing
_recyc_D2	D2 primer for mtDNA re-cycle sequencing
_recyc2	2nd Re-cycle sequencing for mtDNA
_recyc2_A1	2nd A1 primer for mtDNA re-cycle sequencing
_recyc2_A4	2nd A4 primer for mtDNA re-cycle sequencing
_recyc2_B1	2nd B1 primer for mtDNA re-cycle sequencing
_recyc2_B4	2nd B4 primer for mtDNA re-cycle sequencing
_recyc2_C1	2nd C1 primer for mtDNA re-cycle sequencing
_recyc2_C2	2nd C2 primer for mtDNA re-cycle sequencing
_recyc2_D1	2nd D1 primer for mtDNA re-cycle sequencing
_recyc2_D2	2nd D2 primer for mtDNA re-cycle sequencing
_recyc3	3rd Re-cycle sequencing for mtDNA
_recyc3_A1	3rd A1 primer for mtDNA re-cycle sequencing
_recyc3_A4	3rd A4 primer for mtDNA re-cycle sequencing
_recyc3_B1	3rd B1 primer for mtDNA re-cycle sequencing
_recyc3_B4	3rd B4 primer for mtDNA re-cycle sequencing
_recyc3_C1	3rd C1 primer for mtDNA re-cycle sequencing
_recyc3_C2	3rd C2 primer for mtDNA re-cycle sequencing
_recyc3_D1	3rd D1 primer for mtDNA re-cycle sequencing
_recyc3_D2	3rd D2 primer for mtDNA re-cycle sequencing
_recych	Re-cycle sequencing for mtDNA, High
_recych_A1	A1 primer for mtDNA re-cycle sequencing, High
_recych_A4	A4 primer for mtDNA re-cycle sequencing, High
_recych_B1	B1 primer for mtDNA re-cycle sequencing, High

Abbreviation	Description
_recych_B4	B4 primer for mtDNA re-cycle sequencing, High
_recych_C1	C1 primer for mtDNA re-cycle sequencing, High
_recych_C2	C2 primer for mtDNA re-cycle sequencing, High
_recych_D1	D1 primer for mtDNA re-cycle sequencing, High
_recych_D2	D2 primer for mtDNA re-cycle sequencing, High
_recych2	2nd Re-cycle sequencing for mtDNA, High
_recych2_A1	2nd A1 primer for mtDNA re-cycle sequencing, High
_recych2_A4	2nd A4 primer for mtDNA re-cycle sequencing, High
_recych2_B1	2nd B1 primer for mtDNA re-cycle sequencing, High
_recych2_B4	2nd B4 primer for mtDNA re-cycle sequencing, High
_recych2_C1	2nd C1 primer for mtDNA re-cycle sequencing, High
_recych2_C2	2nd C2 primer for mtDNA re-cycle sequencing, High
_recych2_D1	2nd D1 primer for mtDNA re-cycle sequencing, High
_recych2_D2	2nd D2 primer for mtDNA re-cycle sequencing, High
_recych3	3rd Re-cycle sequencing for mtDNA, High
_recych3_A1	3rd A1 primer for mtDNA re-cycle sequencing, High
_recych3_A4	3rd A4 primer for mtDNA re-cycle sequencing, High
_recych3_B1	3rd B1 primer for mtDNA re-cycle sequencing, High
_recych3_B4	3rd B4 primer for mtDNA re-cycle sequencing, High
_recych3_C1	3rd C1 primer for mtDNA re-cycle sequencing, High
_recych3_C2	3rd C2 primer for mtDNA re-cycle sequencing, High
_recych3_D1	3rd D1 primer for mtDNA re-cycle sequencing, High
_recych3_D2	3rd D2 primer for mtDNA re-cycle sequencing, High
_reinj	Re-injection of sample for mtDNA
_reinj	Reinjection
_reinj_A1	A1 primer reinjection for mtDNA cycle sequencing
_reinj_A4	A4 primer reinjection for mtDNA cycle sequencing
_reinj_B1	B1 primer reinjection for mtDNA cycle sequencing
_reinj_B4	B4 primer reinjection for mtDNA cycle sequencing
_reinj_C1	C1 primer reinjection for mtDNA cycle sequencing
_reinj_C2	C2 primer reinjection for mtDNA cycle sequencing
_reinj_conf_A1	A1 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf_A4	A4 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf_B1	B1 Confirmatory primer reinjection for mtDNA cycle sequencing

Abbreviation	Description
_reinj_conf_B4	B4 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf_C1	C1 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf_C2	C2 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf_D1	D1 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf_D2	D2 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf2_A1	2nd A1 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf2_A4	2nd A4 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf2_B1	2nd B1 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf2_B4	2nd B4 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf2_C1	2nd C1 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf2_C2	2nd C2 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf2_D1	2nd D1 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf2_D2	2nd D2 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf3_A1	3rd A1 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf3_A4	3rd A4 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf3_B1	3rd B1 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf3_B4	3rd B4 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf3_C1	3rd C1 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf3_C2	3rd C2 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf3_D1	3rd D1 Confirmatory primer reinjection for mtDNA cycle sequencing
_reinj_conf3_D2	3rd D2 Confirmatory primer reinjection for mtDNA cycle sequencing

Abbreviation	Description
_reinj_D1	D1 primer reinjection for mtDNA cycle sequencing
_reinj_D2	D2 primer reinjection for mtDNA cycle sequencing
_reinj_recyc_A1	A1 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc_A4	A4 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc_B1	B1 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc_B4	B4 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc_C1	C1 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc_C2	C2 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc_D1	D1 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc_D2	D2 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc2_A1	2nd A1 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc2_A4	2nd A4 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc2_B1	2nd B1 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc2_B4	2nd B4 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc2_C1	2nd C1 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc2_C2	2nd C2 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc2_D1	2nd D1 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc2_D2	2nd D2 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc3_A1	3rd A1 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc3_A4	3rd A4 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc3_B1	3rd B1 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc3_B4	3rd B4 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc3_C1	3rd C1 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc3_C2	3rd C2 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc3_D1	3rd D1 primer reinjection for mtDNA re-cycle sequencing
_reinj_recyc3_D2	3rd D2 primer reinjection for mtDNA re-cycle sequencing
_reinj_recych_A1	A1 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych_A4	A4 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych_B1	B1 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych_B4	B4 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych_C1	C1 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych_C2	C2 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych_D1	D1 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych_D2	D2 primer reinjection for mtDNA re-cycle sequencing, High

Abbreviation	Description
_reinj_recych2_A1	2nd A1 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych2_A4	2nd A4 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych2_B1	2nd B1 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych2_B4	2nd B4 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych2_B4	2nd B4 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych2_C1	2nd C1 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych2_C2	2nd C2 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych2_D1	2nd D1 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych2_D2	2nd D2 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych3_A1	3rd A1 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych3_A4	3rd A4 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych3_B1	3rd B1 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych3_B4	3rd B4 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych3_C1	3rd C1 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych3_C2	3rd C2 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych3_D1	3rd D1 primer reinjection for mtDNA re-cycle sequencing, High
_reinj_recych3_D2	3rd D2 primer reinjection for mtDNA re-cycle sequencing, High
_reinj2	2nd Re-injection of sample for mtDNA
_reinj2	2nd reinjection
_reinj2_A1	2nd A1 primer reinjection for mtDNA cycle sequencing
_reinj2_A4	2nd A4 primer reinjection for mtDNA cycle sequencing
_reinj2_B1	2nd B1 primer reinjection for mtDNA cycle sequencing
_reinj2_B4	2nd B4 primer reinjection for mtDNA cycle sequencing
_reinj2_C1	2nd C1 primer reinjection for mtDNA cycle sequencing
_reinj2_C2	2nd C2 primer reinjection for mtDNA cycle sequencing
_reinj2_D1	2nd D1 primer reinjection for mtDNA cycle sequencing
_reinj2_D2	2nd D2 primer reinjection for mtDNA cycle sequencing
_reinj3	3rd Re-injection of sample for mtDNA
_reinj3	3rd reinjection
_reinj3_A1	3rd A1 primer reinjection for mtDNA cycle sequencing
_reinj3_A4	3rd A4 primer reinjection for mtDNA cycle sequencing
_reinj3_B1	3rd B1 primer reinjection for mtDNA cycle sequencing
_reinj3_B4	3rd B4 primer reinjection for mtDNA cycle sequencing
_reinj3_C1	3rd C1 primer reinjection for mtDNA cycle sequencing

ABBREVIATIONS

Abbreviation	Description
_reinj3_C2	3rd C2 primer reinjection for mtDNA cycle sequencing
_reinj3_D1	3rd D1 primer reinjection for mtDNA cycle sequencing
_reinj3_D2	3rd D2 primer reinjection for mtDNA cycle sequencing
_rerun	Rerun
_rerun_0.05	Rerun at 1/20 dilution
_rerun_0.1	Rerun at 1/10 dilution
_rerun_0.2	Rerun at 1/5 dilution
_rerun_hi	Rerun at high parameter
_rerun2	2nd rerun
_rerun3	3rd rerun
_S	Scrapings suffix
_S(2)	Scrapings suffix resubmission
_SF	Sperm Cell Fraction
_SW	Items swabbed
_SWR	Swab Remains Fraction
_T	Touched items swabbed by OCME suffix
_Y	Y-STR suffix
2	Sequential number identifier
H	High for positive controls in ID31 STRs
-HVI	HVI Contig
-HVI_dup	Duplication of HVI contig
-HVII	HVII Contig
-HVII_dup	Duplication of HVII contig

Revision History:

April 1, 2014 – Initial version of procedure.