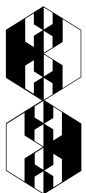# TrueAllele® Casework Process

## Standard Operating Procedures

**Cybergenetics**

**TrueAllele® Casework Process: Standard Operating Procedures**

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# 1 Process Overview

The casework process shows how a case moves from the initial agreement to the case report and preparation for trial.  The process is divided into six distinct steps: Agree, Obtain, Plan, Process, Confirm, and Report.  This overview section describes the general process used at Cybergenetics, which can be adapted and integrated into an external lab's process.

The modular design of the casework process allows a lab to fit the process into their specific workflow and site.  A small lab may have one person performing all six steps; larger labs may have groups responsible for specific steps.  Regardless, the casework process flow is the same.

The six casework process steps are briefly described below:

**Agree**

The process starts with an agreement to process a case for a client.  Through discussion, the scope, cost, personnel, goals, points of contact, payment arrangement, etc. for the case are determined.  This information is documented for later use in the process.  Once both parties agree about what is to be done, the case continues in the casework process.

**Obtain**

In this step, the data is received.  After confirming data receipt, the data is inventoried to verify that everything needed for processing is present.  If data or information is missing, the sender is contacted to obtain the missing items.  Usually, once all of the case information and materials have arrived and are documented, the case moves to the next step.

**Plan**

After data receipt, an analyst reviews the data and develops a plan that describes how the case will be processed. The plan includes information from the agreement and is determined based on the data received. Plans may be brief or lengthy, depending on the case. The ultimate goal of the plan is to ensure that processing answers the questions asked by the client. If desired, the plan is shared with the client. Typically, once the plan is reviewed/approved, data processing begins.

**Process**

Following planning, a trained TrueAllele® operator (who has completed the "Solving Cases" Operator courses) processes the data on a TrueAllele computer system. The initial processing results are assessed and documented relative to the plan. After this initial processing is complete, preliminary results are sent to the client. The casework process may pause at this step while waiting on the client's response for how they would like to proceed.

**Confirm**

If the client requests a case report or further processing, the case is reviewed to see if further processing is necessary. Additional processing may not be needed in every case. Once all processing is complete, the case moves to the final step in the casework process.

**Report**

Typically, the final step of the casework process is the generation of a case report or other requested materials. During this step, the report is drafted, verified, reviewed by a reporting scientist or an administrator, and then sent to the client. Besides the report, additional materials (e.g., demonstrative aid, case packet, etc.) may be produced as needed.

# 2  Agree

At the beginning of the process, the client and Cybergenetics discuss using TrueAllele Casework to process a case.  The data, the extent of the processing, and the output of the process, such as a report or other materials, are discussed.  The client may decide to focus on specific items within a case where there could be highly probative information.

The client and Cybergenetics provide each other with appropriate contact information.  They may also discuss invoicing and whether expert witness testimony will be required.  Once the two groups agree, the client begins sending materials to Cybergenetics.

## 2.1  Discuss

The client and Cybergenetics discuss the case to determine what is to be done, the approximate completion date, and the final output.  Cybergenetics sends the client an intake form to be completed and returned with case data.

<u>Procedure:</u>

- Discuss the case with the client to determine:
  - The specific case items to be considered.
  - The amount of data to be examined.
  - The nature of the data.
  - The case context and forensic questions.
  - The amount of processing that may be required.
  - The format of the output.
  - The case invoicing (as needed).

- The estimated trial date and if expert witness testimony is required.
- Document the information and provide relevant details to the obtainer, who is the person responsible for acquiring the case materials (see Section 3 - Obtain).
- Send client the intake form to be filled out and returned with case data.

# 3 Obtain

Once an agreement exists for a case, the obtainer (the person or persons responsible for acquiring the case materials) begins gathering the information and items needed to process the case. The obtainer begins preparing a case page to store the information about the case, inventories the data and documentation, and determines if any additional information is needed. The obtainer provides a chain of custody for all items, and may organize the data into evidence and reference folders. Usually, once the data and documents are in place, the obtainer moves the case to the planning step.

## 3.1 Check

When case materials arrive, the obtainer checks if the case is new or if the materials are part of an existing case. If it is part of an existing case, the materials are documented on that case's case page. If it is a new case, then process proceeds as described.

Though rare, it is possible that a conflict can arise when:
- Cybergenetics has already analyzed a case for a client, then is asked to process it again for the opposing client.
- Two clients independently send the same case at the same time.

When a possible conflict is identified, the obtainer alerts the casework supervisor for resolution. The case is not processed until the conflict is resolved.

Procedure:

- Briefly review the case materials:
- Check against past cases to see if the case is new, existing, or in conflict:

- New cases proceed as normal.
- Existing cases (when not in conflict) are processed as additions to the initial case submission.
- Conflict cases are flagged for resolution.  No work is done until the conflict is resolved.

## 3.2  Prepare

When data for a case arrives, the obtainer begins preparing a case page for documenting and storing the case information.  At Cybergenetics the case page is a wiki page.  Other examples of a case page include LIMS or a physical case folder.  The obtainer uses a case page template to standardize the placement of specific information.  This standardization allows others to find information and lets the obtainer see what information is currently available.

**Create the case page**

The obtainer starts a case page using a template.  They add the case to the case status page and case tracking page to begin progress tracking.

Procedure:

- Create a new page for the case:
  - Link the new case to the case status page to begin progress tracking.
  - Add a link to the page to the existing client's page (when available).
  - Copy and paste the case page template to structure the page.
- Add a case card to the casework tracking website.
  - Add any relevant information to the card, such as operator and deadline.

## 3.3 Inventory

A client sends data and case documentation (including the intake form) to Cybergenetics. When the obtainer receives this information, they inventory what was received and acknowledge data receipt. They place the data files on a fileserve for secure storage. Physical media is placed in a locked filing cabinet.

**Acknowledge receipt**

When any data or case information arrives, whether by email, electronic data transfer, or as physical media, the obtainer lets the sender know that they received the data and information. The obtainer uses the data received message template (found on the Case Communications page) as a guide for confirming data receipt.

Procedure:

- Send client an email message indicating that Cybergenetics received the case data and documentation.

**Inventory information**

The obtainer lists the data and documentation received in a spreadsheet file. This file list allows the obtainer to see what information is available and what more may be required.

Procedure:

- In a spreadsheet, list all files (*.fsa*, *.hid*, documents, etc.) that were received, and annotate what each file is (e.g., evidence, reference, document, etc.) along with relevant identifiers for evidence and reference items.
  - Use the three column headers to inventory the files:
    - *File*: The file names pasted in from Finder.

- o  *Type*: Indicate whether the file is a folder, document, or relevant sequencer file (evidence or reference).
- o  *Item*: For evidence and reference files, provide the item identifier.
- o  *Used in inference <optional>*: When more than one data file exists for an item, use this column to indicate which data were used.
- o  *Kit <optional>:* When more than one data file exists for an item processed by more than one kit (e.g., Profiler Plus® and COfiler®), use this column to indicate which kit corresponds to which data file.
- At the bottom of the list, indicate when and by whom the list was prepared.  This annotation allows this information to be readily visible in the case packet, later in the process.
- Add the file list to the case page.


**Move data**

The obtainer moves the data and documentation files to a secure fileserve computer for storage.


Procedure:


- On the fileserve, create a parent folder for the case/client (as needed) named as the case/client/lab/group.  Note that a parent folder may already exist for a case/client.
- Within this parent folder, create a folder named as the date when the data and documentation files were received.  This naming shows what information was received on that date.
  - Use the format DDmonYY when naming the folder.
  - Copy all files that were received into this folder.

# 3.4 Document

Once the data and documentation are inventoried, the obtainer records the chain of custody information to show the source of the case materials. If the obtainer determines that more case information is required, they contact the client and request that information.

**Add chain of custody**

The obtainer documents the source of the data and case documentation.

Procedure:

- Record the following:

| | |
|---|---|
| *Sender* | The person that sent the data/information |
| *Organization* | The sender's organization, lab, or affiliation |
| *Date* | The date on which the data/information was received |
| *Time* | The time at which the data/information was received |
| *Mode* | The manner in which the data was sent (e.g., email, link, etc.) |
| *Receiver* | The person that receives the data/information |
| *Description* | A brief description of the received materials |
| *Action* | The disposition of the received data/information following receipt |

- Other relevant chain of custody files, such as copies of data receipts, tracking information, email messages and the file list are included on the case page.

**Request missing information**

If case information, such as data or documentation, is missing, the obtainer contacts the client and requests the data or documentation.

Important information to receive from the client may include:

- The case intake form, with a completed page 3 listing the items of interest.
- The client's reason for sending their data to Cybergenetics.
- How each item relates to the case and other case context.
- The forensic question being asked of each item.
- If any deadlines exist and when/what that deadline is.

**Initial case page documentation**

For a preliminary analysis, the obtainer documents the administrative information, case numbers, casework form, kit, and software information on the case page.  Structuring this information on the case page allows others to more readily understand the case.

Procedure:

- For preliminary analysis, add administrative information to the case page, sourcing the information as needed (see General Guidelines, Section 10.1 – Case Page).
    - If case is proceeding directly to the Report stage, complete the entire case page (see General Guidelines, Section 10.1 – Case Page).

# 4  Plan

Before the start of case processing, the planner reviews the data in the context of the case materials to create an initial processing proposal.  Once the planner has a sense of the case and understands the relevant forensic questions, this person prepares a plan that describes how the case processing will proceed.

This plan may describe the requests that are created, what the termination conditions may be, and the timeframe for the results.  After creating the proposal, the planner may review the proposal with other staff.  Case processing begins after the processing plan is reviewed, either by the planner or other staff.

The processing plan ensures that the case results are ready when needed, making the reporting process easier.  Also, the plan focuses resources appropriately by determining what is needed to answer the client's questions.

## 4.1  Review

The planner reviews the case information to understand the case and to determine the requests to create.  This case information may be found in the intake form, in lab reports, in client correspondences, or in other case documentation.

The planner checks for specific processing requested by the client.  They determine what case processing is needed before the deadline (if present).  The planner summarizes the case information, and, after assessing the data, uses it to propose a processing plan.

Procedure:

- Review the case information.
- If information is missing, the client is contacted to acquire it.

## 4.2 Assess

To assess the data, the planner processes the sequencer (*.fsa* or *.hid*) files through the Analyze module and uploads this information to a TrueAllele World.  (The obtainer, while inventorying the data in the Obtain step, may also perform the Analyze step.)  In the Request module, the planner examines the evidence data in detail to prepare the processing plan.

Procedure:

- Collect the electronic data files (*.fsa* or *.hid* files).
- Process the electronic data files through the Analyze module.
    - Analyze the data at 0 rfu.
    - For AB 3500 sequencer data, analyze data using the 3500 rescale feature if multiple peak height values exceed 10,000 rfu.
- Copy the processed DataDisk to the fileserve.
    - Archiving the DataDisk as a ZIP file is preferable as it preserves file permissions.
- Upload the peak information to the TrueAllele World using the Data module.
    - Create a new World as needed using the Tools module, adding relevant lab and client information on the World (see General Guidelines, Section 10.2 – TrueAllele World).
- Assess the evidence data in the Request module.
    - Download the evidence lanes.
    - Review the data as an overview and by locus.

- Estimate the number of contributors.  Some methods to estimate the number of contributors include:
    - Counting the number of peaks present at each locus.
    - Reviewing peak height ratios.
    - Reviewing known contributors to the data (e.g., for intimate samples) along with peak heights.
- Check for possible differential degradation.
    - Use the Dye mode to view the data across all dyes.
    - Determine if the contributor number is changing as size increases.

## 4.3 Propose

When the case documentation review and data assessment is complete, the planner prepares a processing plan.  This plan proposes evidence requests and shows the name, assumptions, options, and processing parameters used for each request.

The planner's preparation considers the agreed-upon end materials and the reporting scientist's needs for reporting the case.  By preparing for the end materials in the initial plan, the planner ensures that the reporting scientist can issue a report in the expected timeframe.

Once the planner documents the processing plan, they may discuss it with senior staff. Once the plan is documented, the planner moves the case to the Process step.

Procedure:

- Create a processing plan, using screening parameters when indicated by the data and deadline.

- For each evidence item, propose one or more requests as indicated by the case review and data assessment (see General Guidelines, Section 10.3 – Request Naming).
- Propose one or more replicate requests for each condition.
- Document the plan by exporting a Request *.req* file for operator review.
- Discuss and finalize the plan with the casework supervisor (as needed).
  - Update the plan as needed.
- Once plan is finalized, indicate that the case is ready for processing.

## 4.4 Replan

After reviewing initial results, the plan may have to be updated, if additional processing is needed.  Also, a new plan may have to be created if additional case data or information arrives after the case processing has started.  Many cases may need an updated plan.

Regardless of whether the operator, reviewers, or scenario proposes an update to the plan, the protocol is the same.  The proposed updates are documented and may be discussed with the casework supervisor.  Once the updated plan is documented, new processing can begin.

# 5 Process

This section defines an operator, provides an overview of the operator process, and describes the purpose of the operator process in the casework protocol.

**Purpose**

An operator is the person or persons responsible for implementing the processing plan. They use the Visual User Interface (VUIer™) software to ask questions of the data and to review the computer's answers. After assessing the results, the operator determines when the case processing has finished or what more may need to be done.

The operator's purpose is to:

- Understand the data processing plan.
- Implement the plan.
- Generate results for reporting.

The operator process starts with raw data from a DNA laboratory, and ends with reportable concordant genotypes. Genotype concordance factors are given in Genotyping Guidelines, Section 11.5 - Genotype Concordance.

**Processing Plan**

The processing plan describes how the data will be processed. This plan (which can be long or short, depending on the case) may contain information about the case and the data, such as the possible number of contributors to the mixture or if the DNA is visibly degraded. This information helps to explain the specific assumptions, options, and parameters used in the data processing.

The plan shows the requests to be created or reviewed by the operator. From this plan, the operator uses VUIer to create or review the requests for the case. The plan also

lets the operator know when materials are needed, guiding the operator's actions accordingly.  Once the operator assesses the initial results, they can propose updates to the processing plan, which may be discussed with the casework supervisor (see Section 4 - Plan).

## 5.1 Prepare

Before creating requests, the operator becomes familiar with the case by reviewing the case form, as necessary.  The operator reviews the data, case context, case notes, and processing plan.  Once the operator understands what is expected from the processing step, the operator begins using VUIer.

Procedure:

- Add the CYB operator's name and any additional administrative information to the case page.
- Review the data, case context, notes, and processing plan.
  - Examine the data in the following context:
    - o Data
    - o Mixture
    - o Degradation
- Discuss any questions with the casework supervisor regarding processing assumptions, options, or parameters before proceeding as needed.

## 5.2 Process

In the process step, the operator creates the evidence and reference requests described in the plan.  Using the contributor assumptions, options, and processing parameters set in the interpretation requests, the computer separates genotypes from the data.  An operator then assesses these genotype results.

**Evidence requests**

Creating the evidence requests is an important part of the process step. These evidence requests drive all further review.

The operator loads each evidence sample into the Request module, reviews the data, and creates the requests as specified in the processing plan. These evidence requests range from simple to complex, depending on the data. More processing time may be needed for complex samples. The operator sets the request processing parameters in each request's setting tab (see General Guidelines, Section 10.4 - Request Processing). The operator then assesses the results once the computer solves the requests.

Procedure:

- Set up the initial evidence requests.
  - For each evidence sample, create an item and requests as specified in the processing plan.
  - Follow the request-naming scheme (see General Guidelines, Section 10.3 - Request Naming).
  - Use the contributor assumptions, options, and parameters described in the plan.
  - If the plan is documented as a Request *.req* file, review the requests proposed in that file and update those requests as needed.
- Document the Request session by exporting a Request *.req* file. Add this file to the case page with the operator name/initials and date. This file documents evidence requests for a case.
- After exporting the Request *.req* file, verify the request naming and processing parameters in the pre-upload table, and upload the requests to the case World.

**Reference requests**

The operator typically creates reference requests in a separate Request session.  This separate session reaffirms the computer's objectivity.  (The TrueAllele inference process is already completely objective.)

Typically, reference requests are set up at least one day after the initial evidence requests creation.  Once the system infers genotypes for the reference requests (within minutes), the operator uses them for comparison to evidence genotypes.  The system uses the evidence, reference, and population genotypes to calculate likelihood ratio (LR) match statistics.

Procedure:

- Set up the reference requests as specified in the processing plan.
    - Use the request naming scheme.
    - Upload text profiles to the case World as needed via the Data module; add the case number and reference roles to the case via the Request module, when necessary.
- Document the Request session by exporting a Request *.req* file.  Add this file to the case page with name/initials and date.  This file documents reference requests for a case.
- After exporting the Request *.req* file, upload the reference requests to the case World.

## 5.3 Assess

In the casework process, the operator spends most of their time assessing the results.  They may review the data, mixture weights, degradation curves, inferred genotypes, etc. to understand the results.  The operator can use the operator process questions to

guide their assessment and to document the observations about the results. Once the operator understands and documents the results, they move to the iteration step.

**Evidence genotypes**

The operator reviews the evidence-inferred genotypes, using the assessment questions as a guide (see Report, Section 7.4 - Genotyping Considerations). The questions help the operator review the evidence genotypes methodically and to standardize the order of their observations. The operator uses this review to determine the next action in the data processing.

Procedure:

- Download the evidence-inferred genotypes into the Report module.
- Assess the results using the questions listed in the General Guidelines section as a guide.

**Reference genotypes**

The operator assesses the reference genotypes to ensure that their genotypes are as expected based on the data or documentation.

Procedure:

- Download the reference genotypes into the Report module
- Assess the reference genotypes in Report.
  - For inferred genotypes, verify that:
    - The genotype for each locus has one allele pair value at 100% (unless the reference contains a tri-allele).
    - Any microvariants/rare alleles are observed in the data and are not from sizing issues.

- For uploaded reference profiles, compare the genotype with the source documentation.

**Population frequencies**

For preliminary results, a generally applicable population frequency set is preferably used to calculate LRs.  The operator downloads this population into the Report module. Note that most populations are preloaded on the World for convenience.

Procedure:

- Download the population frequencies into the Report module.
  - Click the Add button to view a list of populations.
  - When appropriate, use the NIST1036_2017_ALL population.  Note that the CYB population can also be downloaded as needed for error rate calculations.

**Match statistics**

To calculate the preliminary TrueAllele match statistics, the operator has to have evidence, reference, and population genotypes downloaded in the Report module. These preliminary match statistics are documented on the case page.

Procedure:

- With evidence, reference, and population genotypes downloaded into the Report module, assess the genotype and match results.
- Export the Report session by creating report spec files and match tables, and add these files to the case page. Document the date of upload and initials of the person uploading the files.

## 5.4 Iterate

After assessing the results, the operator determines what actions to take next.  The operator usually determines these actions using the processing plan, the results, and/or the genotyping algorithm.  The operator uses the results to help explain why an action is proposed or when no further action is necessary.

Once the operator determines the action, they propose updating the plan (see Plan, Section 4.4 - Replan) and may discuss this update with other staff.  After review, the operator continues with processing (as needed).

Procedure:

- Determine actions by reviewing the processing plan, the results, and/or the genotyping algorithm.  Use the results to help explain the reason for the actions.
    - Replicate requests to establish genotype concordance as needed.
    - Increase the request processing time to better separate contributors.
    - Create new evidence requests using different assumptions, options, and parameters.
    - Use references as known contributors in evidence requests when indicated.
        - Verify reference genotypes prior to using them in subsequent inferences.
    - Create additional requests between data lanes (e.g., joint amp, joint item) to use more data in the inference.
    - Reset a request when one of the following conditions occurs:
        - An artificially large MW standard deviation (>1) is displayed.
        - Identical results are observed (e.g., same answers recorded twice for replicate requests).
- Document the plan when proposing new actions.
- Discuss the updated plan with other staff as needed.

- Implement the updated plan, iterating through the process until results are reproducible, reliable, and reportable.
  - As needed, use the genotyping algorithm to determine when case processing has concluded.

## 5.5 Record

After initial case processing is complete, the operator prepares preliminary screening results to provide the client with the match information present in their case. These preliminary screening results consist of a document with the approximate match statistics, when appropriate. These statistics are provided to the client in an email message. Another analyst verifies the preliminary results (as well as the information posted to the case page) before the preliminary screening results are sent to the client.

The preliminary screening results email message is usually divided into several sections:
- *Brief introduction* that describes the current processing status (e.g., completed initial screening, completed processing, etc.)
- Informal summary of the *match information* that provides the inclusionary or exclusionary information. This summary does not use formal reporting language.
- *Follow on* that defines what further action is available (e.g., TrueAllele case report, additional processing, MiniFiler™ testing, review of additional evidence items, etc.).

The preliminary screening results table includes:
- A *Match table* that records the approximate match statistic values between evidence and reference (or evidence) items in the case. These values can be taken from the *Match Screening Table,* when appropriate.
- *Table information* that describes different attributes of the match table.

The case form accompanies the preliminary results, and provides a list of the evidence and reference items shown in the table.

Procedure:

- Review the case results in the Report module.
- Prepare the preliminary screening results table, when appropriate.
  - Open the *CASE_preliminary_results.xls* template file.
  - Fill in the Match table information with the evidence and reference item numbers.
  - Add the approximate inclusionary/exclusionary log(LR) values for the case comparisons.
    - **Inclusionary** match statistics are taken from the *Match Screening Table*, or calculated by averaging log(LR) values from concordant genotypes that gave the maximal LR within a request, relative to a specific reference.
      - Inclusionary match statistics can be calculated by averaging log(LR) values from concordant genotypes.
    - **Exclusionary** match statistics are provided when necessary to answer the forensic question.
      - Exclusionary statistics can be calculated by averaging log(LR) values from concordant genotypes. These concordant genotypes are generally not statistically associated with other case references.
  - Provide information about **unknown contributors** as needed.
    - When reporting unknown contributors, verify that the inferred genotype is not artefactual (e.g., product of major contributor's stutter peaks, etc.).
    - Calculate the unknown contributor's average KL value from concordant genotypes to provide the expected match statistic. List this average KL value in bold in the Match table.
    - When not relevant to the forensic question, information specific to unknown contributors is not necessary.
  - Save the completed table as a PDF file for attaching to the client message.

- In some cases (e.g., only exclusionary results to a new reference), this table may not be needed.
- Prepare the informal summary of the preliminary results.
  - Use the Preliminary TrueAllele screening results message template found on the Case communications page as a guide.
- Send preliminary screening results message, table and case form to another staff member for verification.  Include the relevant report spec file, Report module *Match Table,* and *Match Screening Tables* for the other analyst's review as needed (see Section 8 - Verifying a Case Report for guidelines).
- Once the preliminary screening results message is verified and approved, send to the client.

## 5.6 Conclude

Once preliminary screening results are sent, the operator concludes the process by documenting the current state of the case.  This documentation step allows for independent confirmation of the processing and the results.

Procedure:

- Update the case page.
  - Verify that the relevant Request *.req* files are present.
  - Ensure that the report spec files and match tables include the current results.
  - Review the assessment notes and updates to the processing plan (as needed).
  - Add preliminary screening results (once sent) to the case page.
    - Include the email message and preliminary results PDF file to the case page.
    - Indicate the date the results were sent, who sent the results, and to whom they were sent.
- Update the case status page with the date when the preliminary screening results were sent.

## 5.7 Exploratory Processing

In some cases, the client may be interested in identifying more information about their case data and results before requesting a case report. The client requests that Cybergenetics do additional exploratory processing for the evidence data and summarize those results. To perform exploratory processing, an operator assesses the preliminary TrueAllele results and determines what actions to take next, using the genotyping algorithm as needed.

Once the operator determines the next actions, they propose updating the plan (see Plan, Section 4.4 - Replan) and may discuss this update with other staff. After review, the operator then conducts this additional computer processing to elicit more identification information from the evidence data (see Process, Section 5.4 - Iterate).

Procedure:

- Review the data and results for the items of interest (as noted by the client).
- Follow the procedure outlined in the Iterate section of this protocol to conduct the additional computer processing (see Process, Section 5.4 - Iterate)

**Record**

When exploratory processing is finished, the operator prepares the exploratory processing results to update the client about the items of interest. The exploratory processing results consist of a document with approximate match statistics and an email message describing these results. Another staff member verifies these results (as well as the information posted to the case page), before the results are sent to the client.

The exploratory processing results email message is divided into several sections:

- *Brief introduction* that describes the current processing status (e.g., completed exploratory processing, etc.)
- Informal summary of the *match information* that provides the inclusionary or exclusionary information for items of interest.
- *Follow on* that defines what further action is available (e.g., TrueAllele case report, MiniFiler™ testing, examining additional evidence items, etc.).


The exploratory results document is divided into sections:
- *Administrative information* that includes case identifiers*.*
- *Item information* that includes evidence and reference identifiers.
- *Match table* that records the approximate match statistic values between evidence and reference (or evidence) items in the case.
- *Table information* that describes different attributes of the match table.


Procedure:


- Review the case results in the Report module.
- Prepare the exploratory results table.
   - Open the *CASE_exploratory_results.xls* template file.
   - Fill in the Administrative information with case identifiers.
   - Fill in the Item information with the evidence and reference item numbers and descriptions.
   - Add evidence and reference item numbers to the Match table.
   - Add the approximate inclusionary/exclusionary log(LR) values for the case comparisons.
      - **Inclusionary** match statistics are taken from the *Match Screening Table*, or calculated by averaging log(LR) values from concordant genotypes that gave the maximal LR within a request, relative to a specific reference.
         - Inclusionary match statistics can be calculated by averaging log(LR) values from concordant genotypes.

- o **Exclusionary** match statistics are provided when necessary to answer the forensic question.
  - ♦ Exclusionary match statistics can be calculated by averaging log(LR) values from concordant genotypes. These concordant genotypes are generally not statistically associated with other case references.
- Provide information about **unknown contributors** as needed.
  - o When reporting unknown contributors, verify that the inferred genotype is not artefactual (e.g., product of major contributor's stutter peaks, etc.).
  - o Calculate the unknown contributor's average KL value from concordant genotypes to provide the expected match statistic. List this average KL value in bold in the Match table.
  - o When not relevant to the forensic question, information specific to unknown contributors is not necessary.
- Save the completed table as a PDF file for attaching to the client message.
- Prepare the informal summary of the exploratory results.
  - Use the Exploratory TrueAllele results message template found on the Case communications page.
- Send exploratory results message and table to another staff member for verification. Include the relevant report spec file, Report module *Match Table* and *Match Screening Tables* for the other analyst's review as needed (see Section 8 - Verifying a Case Report for guidelines).
- Once the exploratory results message is verified and approved, send to the client.
- Once the exploratory results are sent, add these results to the case page.
  - Include the email message and exploratory results PDF file to the case page.
  - Indicate the date the results were sent, who sent the results, and to whom they were sent.
- Update the case status page with the date when the exploratory results were sent.

# 6 Confirm

When the client requests a case report, the case proceeds to the confirmation step.  In this step, an operator takes a second look at the case to determine if the case is ready for reporting.  The operator may have to consider new information provided by the client and see if additional processing is needed.  If more processing is needed, the operator will propose updating the plan.  When no additional processing is needed, the case can move to the Reporting step.

## 6.1 Review

The operator performs a complete assessment of the case.  This assessment includes both the case documentation (pre- and post-processing) and the results.  Once the operator completes the assessment, they determine if the case needs any additional processing.

**Documentation**

The operator examines the case documentation to confirm the data processing and results.  This confirmation includes review and completion of the case page information – lab reports, client correspondence, operator notes – as needed.  The operator checks the page so that all necessary information is available (see General Guidelines, Section 10.1 - Case Page for more information).

Procedure:

- Open the case page and review its contents.
  - Confirm the Administrative section information.
    - Add lab reports and other files.

- o Add the case context and forensic question under the appropriate page header.
- Complete the Data section of the page.
  - o Fill in evidence and reference tables.
  - o Add population citation(s).
- Verify that the Files section includes the Request and Report module files and that these files are up to date.
- Expand the Notes section with all processing plan tables:
  - o List the request name.
  - o Provide the assumed number of known and unknown contributors.
  - o Note if any options are used (e.g., degraded DNA).
  - o State the processing parameters.
- Complete Communications and Correspondence sections.

**Results**

The operator assesses the results using the case information and may refer to the operator process questions and/or the genotyping algorithm (see Report, Section 7.4 - Genotyping Considerations and Genotyping Guidelines, Section 11.1 - Algorithm). The case information includes the forensic questions. The genotyping algorithm and the operator process questions can help to guide the results assessment.

Procedure:

- View the results in the Report module.
- Refer to the operator process questions and the genotyping algorithm for additional guidance.

## 6.2 Confirm

If the operator determines that no more processing is necessary after assessing the results, they move the case to the Reporting process.

When the operator determines that more processing is necessary, they propose updating the plan.  The operator may discuss the proposal with other staff.  After review, the operator updates the plan.  The operator then performs the additional processing (following the operator process) and assesses the new results.  Once the operator confirms the results (initial and additional), they move the case to the Reporting process.

**Determine**

The operator assesses the results to determine what happens next.  If no conditions were observed (see Genotyping Guidelines, Sections 11.1 - Algorithm and 11.3 - Condition), the operator indicates that no further action is required and moves the case forward in the process.

Procedure:

- Determine the case status.
    - If the results are confirmed, move the case to the Reporting step.
    - If the results are not confirmed, review the results to determine what additional processing may be needed.

**Replan**

If the results are not confirmed, the operator proposes additional actions and interpretation requests to confirm the genotype and match results.  The operator documents the proposal, describing the conditions and actions that can confirm the

results.  The operator may discuss the proposal with other staff.  Following review, the operator updates the processing plan.

Procedure:

- Propose updating the processing plan.
  - Describe the request changes or additions to be made.
- Discuss the proposal with other staff as needed.
- Once the proposal is approved, update the processing plan.

**Perform**

The operator uses the updated processing plan to continue the case processing.  They follow the Process procedures (Section 5) to create new requests and assess new results.  Once the new processing has concluded, the operator confirms the case results.

Procedure:

- Using the updated plan and the Process procedures, the operator begins data processing.
  - The operator follows the Process steps (Section 5), including assessing the genotype and match results.
- Once the operator finishes data processing, they begin confirming the case.
  - If the results are confirmed, the operator moves it to the Reporting step.
  - If the results are not confirmed, the operator meets with other staff to determine the next action.

# 7 Report

This section describes how the report drafter uses the case page and case results to prepare a TrueAllele case report. The report drafter is the certified reporting scientist who provides the first signature on the case report. The process includes documenting the data and results so that details can be recalled later during testimony. After the report drafter finishes the report, they send it to other analysts for verification. Once verified, the report is sent to the client.

## 7.1 Gather Information

To start, the report drafter gathers the materials they need to review the case.

**Assemble files**

Before reporting, the report drafter may create a case folder on their computer that will contain documents and files needed to prepare the report. This case folder allows the report drafter to be organized when drafting the report.

Procedure:

- If needed, create a case folder on the computer.
  - Name the folder with the case name. If that folder already exists, create a subfolder within named as 'report'.
- Download the report spec files and match tables from the case page into the folder.
- Copy the *CASE_report.doc* template into the folder.
  - Rename the case report template by pasting the CYB case name over 'CASE'.
- Download *CASE_signature_page.doc* template into folder.

- Rename case signature page template by pasting the CYB case name over 'CASE'.

**Review case documentation**

To become acquainted with the case, the report drafter does an independent assessment by reviewing the case context and the results. This review includes checking that the relevant administrative attributes are available as well as reviewing the match results summary. In addition, the report drafter verifies that the case processing protocol was followed and that all necessary processing is completed.

Procedure:

- Review the case page contents:
  - Confirm that all relevant administrative attributes are posted.
    - o If any information is missing, add it to the case page (see the case page template or General Guidelines, Section 10.1 - Case Page for more information).
  - Review the case and item identifiers in the Data section.
    - o Verify that all items have been accounted for.
    - o Confirm that a specific population set is cited.
    - o Verify that all VUIer and Server software version numbers used to process the case are documented.
  - Review the Files section.
    - o Check that Request and Report files are present.
    - o If needed, create the report spec and match table files for each item that is being reported.
  - Review the Notes section:
    - o Check that the notes are complete.
    - o Confirm that evidence item requests include replicates.

o   Check that the number of considered contributors includes the lab's assumptions (from the case information) when informative.

- Review the Communications and Correspondence sections:
    o   Check that all pertinent communications are present and documented.

## 7.2 Prepare Report

**Begin Report**

The report drafter begins the report by filling in the relevant fields of the case report template, except for the match statistics to be reported.  This step allows the report drafter to ensure that all the administrative and case context information is available to produce a complete report.

Procedure:

- Open the *CASE_report.doc* template.
- Fill in the Header fields:
    • Report date.
    • Case identifiers
        o   CYB name.
        o   Lab and agency numbers.
- Fill in Administrative fields:
    • Person requesting report.
    • Agency address:
        o   Note that the address includes the person's agency, city, state, and ZIP code.
        o   This address is not meant to be a mailing address.
- Fill in the Case context fields:
    • Victim(s), Suspect(s), Defendant(s), Other references (as needed):
        o   List the person's last name first, in all caps, followed by their first name with just the first letter capitalized.

- o Order the names by role (victim, elimination, suspect, etc.), then alphabetically.

- Evidence item/exhibit numbers and descriptions.

  o Order numerically by item/exhibit number.

- Reference item/exhibit numbers and descriptions.

  o Order numerically by item/exhibit number.

- Complete the Methods fields:

  - STR kit(s) used.

  - DNA lab/agency that produced lab report and the lab report type.

  - Population source(s).

  - Theta value.

  - VUIer version.

  - Use optional statements as needed.

- Add a Results paragraph for each item/exhibit.

  - When more than one evidence item/exhibit is being reported, add a title with the item/exhibit number and description above the Results paragraph.

- Add a match statement sentence for the case comparisons to be included.

  - Fill in the item/exhibit description and number.

  - Fill in the reference name and number.

  - Edit the ethnic population names as needed.

  - List the match statement sentences numerically by reference item/exhibit number.

  - Ensure that the evidence description is the same as the Results paragraph title.

- Fill in the DNA Match Tables section with item/exhibit names and descriptions.

  - Ensure that the evidence item/exhibit description is the same as the description in the Results section.

  - Indicate the total number of population subgroups in the statement at the page bottom.

- As needed or if requested, append an Item/Exhibit Naming table to the case report to document multiple names or numbers for items/exhibits.
- Complete the *CASE_signature_page* template:
  - Complete the header information (case identifiers) by copying and pasting the information from the report.
  - Determine which analysts are reviewing the report, and copy and paste their names and degrees below the signature lines.
  - Save the file as PDF.

## 7.3 Survey Genotypes

**Survey**

Before match statistics are reported, the report drafter surveys all relevant genotypes and match statistics for a case, starting with the match table.  This table summarizes information about the case.  Afterwards, the report drafter focuses on a specific set of genotypes and matches to review and report.  This set of genotypes are those with the largest log(LR) values relevant to a specific reference.  The LR is a numerical summary of the statistical support in evidence data for a hypothesis.

With a reasonably accurate data model, the LR cannot overstate evidential support. (More complete statistical models can generally derive more information from data.) When making a comparison to a specific person's reference genotype, the LR hypothesis is that the person left their DNA in the evidence.  Therefore, whether within or between requests, genotypes with the largest LR values should be used, since they are most relevant for a comparison with the person.

Procedure:

- Open the VUIer Report module.
- Load the case report spec file (by item).

- Open Preferences.

  • Set appropriate co-ancestry coefficient (when applicable).

- Open the *Match Table*.

  • Review all matches.

  • Review the KLs, mixture weights, and standard deviations.

    o Ensure suitable and reproducible values for each criterion.

- Identify the genotypes for the comparison(s) to be reviewed.

  • Enable the reference genotype of interest in the *Genotype Selector*. Disable other reference genotypes.

  • Consider KLs, mixture weights, and standard deviations for the requests as needed for selecting the genotypes.

  • For **inclusionary** match statistics:

    o Use the 'Max within Request' feature to identify the evidence genotypes having maximal log(LR) values for a reference. An agreement set may be noted. Identify a concordant set from these genotypes.

    o Uncheck (in the *Genotype Selector*) the evidence genotypes where the reference genotype was used as a known.

  • For **exclusionary** match statistics:

    o Identify evidence genotypes that do not match other case references that are in agreement. An agreement set may be noted. Identify a concordant set from these genotypes.

  • For **unknown contributor** genotypes:

    o Identify evidence genotypes that do not match any case references and give a maximal KL value for the request. An agreement set may be noted. Identify a concordant set from these genotypes.

    o Use the 'Max within Request' feature to help to identify the maximal KL values for non-matching evidence genotypes.

## 7.4 Genotyping Considerations

A report drafter may carefully consider the following ten topics when preparing a case report and notes.  Considering the questions for each topic entails a comprehensive review of the data, mixtures, genotypes, and match statistics in a case.

*Data*

What does the data look like?  How tall are the peaks?  How low are the peaks?  Are there any peak morphology issues?  What is the peak height allele balance like?  Is there low-level background contamination?

*Mixture*

Does this data suggest a DNA mixture?  How many contributors are present (more than one hypothesis is permitted)?  Which loci support your contributor hypotheses (repeat for each number hypothesized)?  Why?

*Degradation*

Does the data suggest DNA degradation?  Was TrueAllele run with this option turned on?  What do the decay curves show?  Does the computer modeling suggest differential degradation of the DNA contributions?

*Separation*

How well separated are the contributor components?  How does the number of assumed contributors affect this separation?  How is this separation demonstrated in the mixture weight Markov chain (histogram and history)?

*Convergence*

How well did the mixture weight Markov chains converge?  What can you determine from the Markov chain history visualization?  What does the Gelman-Rubin convergence statistic show for the different computer runs and their individual contributors?

*Genotype inference*

What is the quality of the genotype inferences?  How well separated are the inferred genotypes from the population genotype (as probability distributions)?  What do the Kullback-Leibler divergence statistics indicate?

*Genotype separation*

Within a computer run, how well differentiated are the genotypes?  Do different contributors show similar probability distributions?  Do some genotypes resemble the population genotype?

*Genotype concordance*

Between different computer runs, how concordant are the genotypes?  How many independent computer runs were done?  Do these runs accumulate probability at the same allele pair values?  Are the runs concordant under different assumptions (e.g., number of contributors, degraded options)?

*Genotype statistics*

For a matching genotype, what can you say about its contributor?  Is this a major or minor contributor?  What is the contributor's mixture weight average?  What about the standard deviation?

*Match statistics*

How did you identify which inferred evidence genotype to report?  What factors made this genotype a representative choice?  Why do you believe that you are not overstating the match results?

## 7.5 Document Observations

The report drafter documents their observations on the case page.  Each observation is concise, typically taking just one line per observation.  These observations include statistics (where appropriate) to support the objective findings.

The report drafter copies the standard headers (found on the Protocols page) onto the case page before beginning the review.  Following each header, on the same line, the report drafter states their observations as they use the VUIer program.  They may use the questions as a guide when needed (see Report, Section 7.4 - Genotyping Considerations).

**Data**

*Concept*
DNA data observations describe the TrueAllele input.

*TrueAllele tools*
An analyst can use the *Data View* interface in a VUIer software module to review the data input. There are different ways to view data.
The data can be viewed at all loci, some loci, or one locus at a time. A peak height cutoff display value can be set for easier data review. The interface permits data display by Lane, Sample, or Dye. A Peak Table is available with detailed data information.

*Fact recorded*
In the Data section, the peak height rfu range is recorded. The TrueAllele processing peak height (e.g., 5 rfu) and other data descriptors (raised baseline, spikes, etc.) are recorded here when needed.

**Mixture**

*Concept*

DNA data can provide support for how many people contributed their DNA to a mixture.

*TrueAllele tools*

An analyst can use the *Data View* interface in a VUIer software module to review how many contributors appear in the data. There are different ways to view data.

The data can be viewed at all loci, some loci, or one locus at a time. The interface permits data display by Lane, Sample, or Dye.

*Fact recorded*

In the Mixture section, loci that support particular contributor numbers are recorded.

**Degradation**

*Concept*

DNA data can provide information regarding both overall and differential DNA degradation.

*TrueAllele tools*

An analyst can use the *Genotype Selector* 'Max within Request' feature to help in identifying a genotype from each request.

An analyst can use the *Data View* interface in a VUIer software module to examine DNA data degradation. There are different ways to view data.

The data can be viewed at all loci globally, or by dye. The interface permits data display by Lane, Sample, or Dye.

*Fact recorded*

In the Degradation section, qualitative observations regarding both overall and differential degradation are recorded.

**Separation**

*Concept*

DNA mixture weight information provides knowledge about separation of inferred DNA contributors within a mixture.

*TrueAllele tools*

An analyst can use the *Genotype Selector* 'Max within Request' feature to help in identifying a genotype from each request.

An analyst can use the *Mixture View* interface in a VUIer software module to review how different contributor fractions are from one another. The interface permits mixture weight display by Histogram, History, or in tabular form (Weight, Variance).

The *Match Table* shows sets of mixture weight statistics.

*Fact recorded*

In the Separation section, a qualitative observation of the mixture separation of each inferred contributor fraction is recorded.

**Convergence**

*Concept*

Mixture weight convergence statistics provide information regarding how thoroughly the statistical sampling search was for a computer run.

*TrueAllele tools*

An analyst can use the *Genotype Selector* 'Max within Request' feature to help in identifying a genotype from each request.

An analyst can use the *Mixture View* interface in a VUIer software module to review the mixture weight Markov chains. The interface displays convergence information by Histogram, History, or in tabular form (Convergence).

The *Match Table* shows sets of mixture weight convergence statistics.

*Fact recorded*

In the Convergence section, a qualitative assessment of the number of mixture weight GR statistics for mixture requests at different levels is recorded.

**Genotype inference**

*Concept*

A genotype posterior probability distribution summarizes a contributor's log(LR) match information when making all possible reference genotype comparisons.

The Kullback-Liebler (KL) statistic gives the expected average value of this posterior information distribution. KL describes how an inferred genotype differs from the population prior.

*TrueAllele tools*

An analyst can use the *Genotype Selector* 'Max within Request' feature to help in identifying relevant genotypes.

An analyst can use the *Genotype View* interface in a VUIer software module to review the divergence of the inferred genotype from the population. An analyst can view

genotypes at all loci, some loci, or one locus at a time. The interface lists KL information in tabular form.

The *Distribution* interface and tables permit review of prior and posterior genotype distributions.

The *Match Table* shows sets of KL statistics.

*Fact recorded*
In the Genotype inference section, a qualitative assessment of how different the inferred genotype is from the population is recorded, along with the average KL statistic calculated on the agreement set.

**Genotype separation**

*Concept*
Genotype probability distributions show the difference between inferred contributor genotypes from a mixture.

*TrueAllele tools*
An analyst can use the *Genotype View* interface in a VUIer software module to compare or contrast the genotype probability distributions for different contributors. Genotypes can be viewed at all loci, some loci, or one locus at a time. This interface also provides genotype information in tabular form.

The *Distribution* interface and tables permit simultaneous review of genotype information for different contributors from the same computer run.

The *Match Table* shows mixture weight statistics for genotype separation.

*Fact recorded*

In the Genotype separation section, a qualitative assessment of how different inferred genotypes from a mixture are from one another is recorded.

**Genotype concordance**

*Concept*

Genotype probability distribution and statistic similarities for an inferred contributor across multiple independent computer runs show genotype concordance and reproducibility.

*TrueAllele tools*

An analyst can use the *Genotype Selector* 'Max within Request' feature to help in identifying the concordant set.

An analyst can use the *Genotype View* interface in a VUIer software module to compare probability distributions between different computer runs. An analyst can view genotypes at all loci, some loci, or one locus at a time. This interface also provides genotype information in tabular form.

The *Distribution* interface and tables show genotype information for an inferred contributor from different computer runs, helping to assess concordance.

The *Match View* and *Match Table* can help assess genotype information and match statistics regarding concordance and reproducibility.

*Fact recorded*

In the Genotype concordance section, a qualitative assessment of the genotype concordance is given, along with a listing of genotypes included in the concordant set for a reported contributor.

**Genotype match**

*Concept*

Genotype mixture weight, mixture weight standard deviation, and KL statistics together summarize the contributor fraction, search broadness, and genotype information present for inferred evidence genotypes. Allele tables and moderate match estimate (MME) values give information regarding searching non-matching evidence genotypes CODIS.

*TrueAllele tools*

An analyst can use the *Genotype Selector* 'Max within Request' feature to help in identifying the concordant genotypes.

An analyst can use the *Mixture View* interface in a VUIer software module to view mixture weight and mixture weight standard deviation information. The interface permits display by Histogram, History, or in tabular form (Weight, Variance).

An analyst can use the *Genotype View* interface to view genotype information, including posterior probability and KL statistics, both visually and in tabular form.

The *Distribution* interface and tables permit review of posterior genotype distributions.

The *Match Table* shows sets of mixture weight, mixture weight standard deviation, and KL statistics.

The *Profile View* interface in a VUIer module allows an analyst to export allele tables for inferred contributor genotypes. An analyst can use a spreadsheet to calculate MME values.

*Fact recorded*

For reported evidence genotypes, the inferred mixture weight, mixture weight standard deviation, and KL are recorded. These statistics can be recorded as average values across a set of concordant genotypes, representative statistics from an identified representative genotype, or both.

A representative genotype database specification can be recorded.

When reporting a non-matching evidence genotype, the evidence genotype table is recorded. An allele list and moderate match estimate (MME) value can be recorded as well.

**Reported match**

*Concept*

Likelihood ratio (LR) match statistics give the comparison match information between two genotypes, relative to a prior probability. The probability of misleading evidence (PME) statistic gives the error rate for a reported match statistic.

*TrueAllele tools*

An analyst can use the *Genotype Selector* 'Max within Request' feature to help in identifying the concordant genotypes.
An analyst can use the *Match View* interface in a VUIer software module to view LR or log(LR) match statistics. An analyst can view match statistics at all loci, some loci, or one locus at a time. This interface also provides match information in tabular form.

The *Distribution* interface and tables permit review of prior and posterior genotype distributions with log(LR) comparisons and provide error rates in tabular form.

*Fact recorded*

For reported genotype to genotype comparisons, the log(LR) match statistics and error rate PME statistics are recorded. These statistics can be recorded as average values across a set of concordant genotypes, representative statistics from an identified representative genotype, or both.

A representative match *Locus Table* can be recorded.

## 7.6 Complete Report

After reviewing the data, mixture weight, genotypes, and match information, the report drafter is able to complete the Results section of the *CASE_report.doc* template and provide match information.

Procedure:

- Fill in the Results section of *CASE_report.doc* template.
  - Fill in evidence name and item numbers in the results paragraph, where indicated.
  - Add the number of contributors:
    - Include all assumptions.
    - Remove the word 'unknown' when a reference was used as a known contributor in the inference.
  - When applicable, indicate the use of known contributors using the standard language found in the case report template.
  - When applicable, note any options used with the standard language found in the case report template.
  - Ensure there is singular or plural language agreement.
  - Fill in the specific reference name and item number for each match statement as needed.

- When reporting the **average** match statistic from the concordant set:
  - Enable one population in the *Genotype Selector*.
  - Paste in the average LR match statistic across the concordant set for this population, copied directly from the *Match Table*.
  - Repeat the above steps for each population to be reported.
  - Calculate and insert the composite error rate for every reported match statistic:
    - Ensure that only loci included in both the evidence and reference or other comparison genotypes are enabled when calculating error rates.
    - Calculate the composite error rate for the population that produces the average log(LR) value closest to zero using the VUIer *Distribution* feature.
- When reporting a **representative** genotype:
  - Paste in the LR match statistics, copied directly from the Locus Table for the genotype match.
  - Calculate and insert the error rate for every reported match statistic:
    - Ensure that only loci included in both the evidence and reference or other comparison genotypes are enabled when calculating error rates.
    - Calculate the error rate for the population that produces the log(LR) value closest to zero using the VUIer *Distribution*, *Non-contributor,* or *Contributor* feature.
- Where applicable, include statements about **unknown contributor** genotypes.
  - Fill in evidence name and item numbers, where indicated.
  - Calculate the expected LR from the KL, and paste both values into the report, where indicated.
  - Include the allele list paragraph with MME value, when requested.
- When providing a comparison statement with no statistic:
  - Include the general match comparison statement.
  - Use this statement to show a comparison without a statistic.
- Complete the DNA Match Tables section of report template.
  - Fill in the item names and numbers as needed.

- Add the minimum LR and log(LR) values for the reported comparisons.
- Provide the number of ethnic populations used.
- Complete the Alleles List section for unknown contributor genotypes, when requested.
- Verify that the TrueAllele Casework Method section is up to date.
- Leave the last page blank (for inserting the signature page).
- Complete the signature page PDF:
  - Electronically sign the signature page.
  - Add the date on which the report draft was completed.

## 7.7 Verify Report

After the draft report is finished, the report drafter sends it to another staff member for independent review and verification (see Section 8 - Verifying a Case Report for more information on the verification process).  This step ensures that all information in the report is reviewed and inspected for accuracy before the case report is issued.  The verification process also allows the report drafter to make any changes to the report before sending the case report for a final review.  More than one analyst may review a case report.

Procedure:

- Send the report to at least one other Cybergenetics reporting scientist for independent review and verification.
  - Include the case page link, the item report specs and match tables, and a draft email message to the client.  Use the TrueAllele case report message template found on the Case communications page.
- If necessary, make any changes to report based on reviewer's comments.
- The reporting scientist signs and dates the signature page once they complete their review.
- Once the report is complete, the reporting scientist saves it as a PDF file.

## 7.8 Final Review

Before sending the case report to the requesting person/agency, a reporting scientist performs an administrative review of the case report, results, notes, etc. This review can be the final step before the report is sent. An administrative review may be done as needed. The report drafter sends the report and other materials to the person performing the administrative review. Once this review is completed, one of the report signers (usually the report drafter who is the first signature) sends the report to the client.

Procedure:

- Send the report to a reporting scientist for administrative review as needed.
    - Include the case page link, the item report specs and match tables, and a draft email message to the client.
- If necessary, make any changes to report based on the reviewer's comments.
- This reporting scientist signs and dates the signature page once they complete their review.
- Complete the report:
    - If not already done, save the report as a PDF file.
    - Add the signature page PDF to the report PDF.
- Send the report to the requesting person/agency along with the reporting scientist's CV and Cybergenetics trials list, and jurisdictions documents.
- Post the case report PDF to the case page, indicating when and to whom it was sent.
- Update the case status page with date when the report was sent.

## 7.9 Follow-up

Once a case report has been sent, Cybergenetics follows up with the client to determine if any additional case materials are needed (e.g., supplemental report, case packet, demonstrative aid, trial testimony, etc.). This follow-up should be done regularly to ensure that no deadlines are missed.

## 7.10 Secondary Review

When a TrueAllele analyst who did not sign the original report is needed to testify to that report, a secondary review is performed. The analyst follows the review steps of the reporting and verification processes outlined in sections 7 and 8. This independent review includes examining all reports, results, notes, etc. The analyst completes the secondary review letter and sends it to the client, along with the analyst's CV, the original TrueAllele report, and this SOP document.

Procedure:

- Independently review reports, results, notes, etc. following the review procedures.
- Complete the secondary review letter template:
  - Add the date, client name, address, case identifier, and the original report date.
  - Save as a PDF file.
- Electronically sign the letter.
- Send the review letter to the requesting person/agency along with CV, original TrueAllele report, and SOP document.
- Add the letter PDF to the case page.

# 8  Verifying a Case Report

A case report is verified for accuracy before it is sent to the client.

The report drafter sends the case report to another reporting scientist for review and verification (see Report, Section 7.7 - Report Verification).  The report drafter includes the case page link, the case report, the relevant report specs, and match tables as well as a draft email message to the client.

The person verifying the report thoroughly checks each section of the report.  The verifier can use the worksheet to ensure complete verification of the report.

The verifier uses the case page to confirm the report information.  This person also verifies that the case page information is accurate and properly sourced.

## 8.1  Administrative section

The Administrative section of the report contains the header information, requesting agency and agency contact information, all relevant case identifiers, and the names and list of all evidence and reference items included in the report.  All of these subsections are checked for accuracy and completeness.

Procedure:

*Header*
- Confirm the Cybergenetics logo and contact information.
- Verify the current date.
- If more than one page exists, check the second page header for date and case identifiers.

*Agency*

- Confirm the title and name of the person who requested the report (e.g., prosecutor, defender, etc.).
- Verify the client's agency and address (agency, city, state and zip code). Note that the address is not intended as a mailing address.

*Case identifiers*

- Confirm the CYB case identifier.
- Verify any case identifiers used by other organizations.
- If the report contains a second page, confirm the case identifiers in the page header.

*Reference names*

- Check each reference name and its associated role.
- Verify that the reference names are alphabetized within each role set.
- Confirm that singular and plural headers are used appropriately.

*Evidence items*

- Verify the item number and description of each evidence and reference item.
- Check that items are in numerical order, where references follow evidence items.

## 8.2 Methods section

The Methods section of the report summarizes how match results were produced. It lists information on the processing, the STR kit, the lab report type, the agency that produced the data, the population subgroups used, the theta value, and the VUIer version used for the match calculations. The bullet points in this section are all verified for accuracy and completeness.

Procedure:

- Verify the STR kit(s) used to amplify the data. Ensure that the appropriate trademark symbols are used and formatted.
- Verify the report type that is the source of the case information, where the type typically appears as the document's title.
- Check that the proper name of the agency issuing the case information is used.
- Confirm the standard processing statement is accurate.
- Confirm that the population source(s), theta value, and VUIer version used for match statistic calculations are documented.
- Check that the optional bullet points are included as appropriate.

## 8.3 Results section

The Results section provides the processing parameters and match information for each evidence item and associated reference match. The paragraph preceding the match statements are verified for the number of assumed contributors, evidence and reference item numbers, proper use of plural words, and any optional statements needed. The match statements are checked for accuracy and completeness of the item names and numbers as well as the proper match statistic for each population group.

Procedure:

For each reported evidence item:
- Verify that the item name and number are correct in the paragraph and match statement.
- Refer to the processing and make sure all contributor assumptions are listed, including indication of known and unknown contributors.
- Ensure that optional statements are used as needed.
- Confirm that additional processing options are recorded.

- Ensure that all reference item numbers for the comparison are listed in the results paragraph.
- When conducting an evidence to evidence comparison, ensure that evidence item numbers are listed in the results paragraph.
- Where necessary, confirm the correct usage of singular/plural terms.
- For each match statement, confirm that the correct reference or evidence name and number are listed.
- Verify the LRs being reported using the VUIer software and the item report spec file.
- Ensure the reported LRs sync up with the appropriate population subgroup.
- Verify error rate statements and values.
- When multiple evidence items are included in the report, check any match statement headers.
- Verify unknown contributor information, including item names and numbers, expected LR and KL values. Verify MME values when appropriate.
- The Signature page should also be verified to ensure the correct names and titles of all listed persons (analysts, technical reviewers, reporting scientist, etc.).
- Verify the Signature page's header information.

## 8.4 DNA Match Tables

Providing tables with match statistics in the report helps summarize the information. The likelihood ratio is presented in both words and the log(LR) values. The DNA Match Tables section is verified for accuracy of the evidence and reference item names and numbers as well as the match statistics and number of populations used.

Procedure:

- Confirm that the optional statements are included, as appropriate.
- Check that all reported evidence and reference items are included.
- Verify each item number and description.

- Verify both the LR and log(LR) values.
- When unknown contributors are reported:
  - Check that the optional paragraph is included.
  - Verify the expected LR and KL values, as appropriate.
- Check that the asterisked statement at the bottom includes the correct number of population groups used.

## 8.5 Item Naming (Optional)

At times, it is necessary to include an Item/Exhibit Naming table if there are many different item names in a case.  This table maps multiple item names contained in the report.  This table is verified using the information on the case page for accuracy.

## 8.6 Case Page

Verification includes both the report and the case page information.  This step includes reviewing the data and match results and verifying the report drafter's notes about the reported items.

Procedure:

- Check that the information recorded on the case page is complete, accurate, and sourced.
- Independently review the Report notes following the data and results review procedures outlined in Report, Sections 7.3 - Survey Genotypes, 7.4 - Genotyping Considerations, and 7.5 - Document Observations.

When finished, the reviewer informs the report drafter that the report is verified, and if any updates are needed before sending.

## 8.7 Verification Worksheet

The verification worksheet below is used as a guide when verifying case reports and other case information.  The use of this worksheet is optional.

| | | |
|---:|:---:|:---|
| **Administrative** | ☐ | Cybergenetics logo and CYB contact information |
| | ☐ | Current date |
| | ☐ | If more than one page exists, check page 2 header for current date |
| | ☐ | Title and name of person who requested the report |
| | ☐ | Person's agency and address |
| | ☐ | CYB and other case identifiers indicated |
| | ☐ | If more than one page exists, check page 2 header for case identifiers |
| | ☐ | References by role |
| | ☐ | Evidence item list with description |
| | ☐ | Reference item list with description |
| **Methods** | ☐ | Kit |
| | ☐ | Report type |
| | ☐ | Agency producing report |
| | ☐ | Population source |
| | ☐ | Theta value |
| | ☐ | VUIer and software versions |
| | ☐ | Optional statements |
| **Results** | ☐ | Match statement (one for each evidence item) |
| | ☐ | Item number |
| | ☐ | Contributor assumption number |
| | ☐ | Unknown contributor assumption (where applicable) |
| | ☐ | Optional statement assuming known reference (item roles and numbers) |
| | ☐ | Optional degraded DNA option statement |
| | ☐ | Optional joint data analysis statement |
| | ☐ | Reference item numbers |
| | ☐ | If multiple, pluralize statement |
| | ☐ | Match statement evidence name, number and reference name, number |
| | ☐ | Match statistics by population |
| | ☐ | Error rate statement and values |
| | ☐ | Unknown contributor paragraph information (expected LR, KL, MME) |
| **Tables** | ☐ | Optional second sentence |
| | ☐ | Evidence item numbers and descriptions |
| | ☐ | Reference names and numbers |
| | ☐ | LR and log(LR) values, expected LR and KL values |
| | ☐ | Population number statement at bottom |
| **Allele list** | ☐ | Item names/descriptions (when needed) and allele list |
| **Documentation** | ☐ | Documentation on case page |
| | ☐ | Report notes |
| **Completion** | ☐ | Notify Reporter |

# 9  Trial Materials

Once the case report has been sent, Cybergenetics staff follows up with the client to determine if the case is going to trial.  When a case is set to go to trial, the reporting scientist will need trial materials available for court testimony.  These materials can include a TrueAllele case packet, a demonstrative aid, and the TrueAllele case DVD.

This section describes the trial materials typically produced for court.  After the materials are created, each document is reviewed and verified by another trained analyst before the materials are sent to the client.  Sections 10.5, 10.6, and 10.7 of the General Guidelines describe the detailed steps used to create these materials.

**Case packet**

The case packet provides all information used to reach the conclusions described in the case report.  Case packets can be lengthy documents and are divided into sections that focus on a part of the process.  Each section is verified before being added to the final packet.

Procedure:

- Create the case packet following General Guidelines, Section 10.5 - Case Packet.
- Send the case packet (in sections) to another analyst for verification.
- After each section is verified, assemble the sections into one document and add page numbers.
- Once the case packet is approved and sent to the client, post the final version to the case page.
- Update the case status page with date when the case packet was sent.

**Demonstrative aid**

The demonstrative aid helps the reporting scientist explain the basic concepts of DNA analysis and TrueAllele results to a lay jury, judge or other lawyers.  This PowerPoint presentation is used for explaining the DNA results, and is prepared with teaching in mind.  The demonstrative aid is verified before sending it to the client.

Procedure:

- Create the demonstrative aid following General Guidelines, Section 10.6 - Demonstrative Aid.
- Send the demonstrative aid to another analyst for verification.  A verification checklist is found in Section 10.6.
- Once the demonstrative aid is approved and sent to the client, post the final version to the case page.
- Update the case status page with date when the demonstrative aid was sent.

**Case DVD**

The TrueAllele Case DVD provides a wealth of information regarding TrueAllele and case specific results to both prosecution and defense attorneys.  This ~ 4 GB of content provides education materials, validation studies, the VUIer software, and every case specific file produced in the case.  This DVD can be used to answer questions lawyers may have regarding the TrueAllele analysis of a case.  It also allows them to explore the results themselves.

Procedure:

- Create the case DVD following General Guidelines, Section 10.7 - Case DVD.
- Have another analyst verify the DVD contents.
- Once the DVD contents are approved, send the DVD via Dropbox.
- Alternatively, burn two physical copies, and send via courier (e.g., FedEx).

- If a physical copy is sent with no Dropbox link, store the case's final DVD contents on a dedicated hard drive.

# 10  General Guidelines

The following sections provide general guidelines for a variety of topics.

## 10.1 Case Page

The case page is typically a wiki page.  All information, documentation, and results pertaining to a specific case can be found on this page.  This section provides guidelines for adding information to the case page.  The bolded sections below are the main section headers from the Case Page template.  Guidelines are provided below each header.  All information (e.g., evidence and reference descriptions) should be sourced for easier verification.

**Administrative**

- Add CYB name, lab, agency and other numbers.
- Add Offense, Evidence, Victim, and Suspect/Defendant.
- Add location information.
- Add CYB Operator name(s).
- Add contact information (e.g., Prosecutor contact, Lab contact, etc.)
  - Include the person's title, full address, office information, and email address.
- Add names of people to send reports to.
- Add chain of custody information (see Obtain, Section 3.3 - Inventory).
  - Include a file list describing file, type, and item numbers for all files received.
- Add case context, if known.
  - Cite source of context (e.g., from intake form, email, from phone conversation, etc.)
- Add lab reports or other case documentation in appropriate section (e.g., intake form, lab reports, lab EPGs, case information, etc.

- Be sure to indicate when and how these documents were received (e.g., with data, via email, etc.).
- Use OCR software to convert documents into searchable PDFs.
- Do not leave empty section headers.

**Data**

- Add evidence and reference information to appropriate tables (copy and paste when possible).
  - Indicate the information's source (e.g., from lab report)
  - Include all relevant item numbers.
    - Include a CYB name when it differs from the lab item or other number present.
  - Include the exact description from case documentation (typically from a lab DNA report).
  - Include date received when data is received on multiple days.
  - When manual profiles are uploaded, document the genotype source, *.txt* file, and when/who uploaded it below the reference table.
- List population (with link to population page) and population citations.
- List kit, sequencer, VUIer software version, and TrueAllele server version used.

**Files**

- Add all request files created with date/person who posted them.
- Add all report spec and match table files created with date/person who posted them.
  - Add one set of files for each item.
  - Upload a file that includes all items as needed.

**Notes**

- Add date, person, and role (obtainer, planner, operator, etc.) as a header for each section of notes.
  - Include only one header per day for the same person/role.

- Add short, descriptive case notes for each Request table (e.g., Reviewed data in Request to develop initial processing plan, Following review with person, uploaded requests assuming known references, etc.).
- Fill in Request table(s) for all requests created.

**Results**

- Add preliminary results (as a header in the section) once sent.
  - Include date sent, mode (e.g., via email), sender, and recipient(s).
  - Include email message with attachment(s).
- Add the report section header when drafting case report notes.
  - Include all relevant report notes, database spec lines, and locus tables.
  - Add the case report once it has been sent.
    - Be sure to include date sent, mode (e.g., via email), sender, and recipient(s).
- Add the case packet and demonstrative aid once they have been sent.
  - Be sure to include date sent, mode (e.g., via email), sender, and recipient(s).

**Communications**

- List all germane communications pertaining to the case.
  - Note as: date, email from X to X regarding content.
  - Include data emails, report emails, context emails, etc.
  - Document phone conversations.

**Correspondence**

- Add all germane correspondence pertaining to the case.
  - Copy and paste communications list.
  - Add messages under appropriate communications line.
  - Include data emails, report emails, context emails, etc.
  - Summarize phone conversations.

## 10.2 TrueAllele World

Typically, a new TrueAllele World is created when a case is received. Multiple cases can also be solved on the same TrueAllele World. This section contains guidelines for annotating and creating a TrueAllele World for a case using the VUIer software.

**Create World**

Using the Tools module, the obtainer, planner, or operator creates a TrueAllele World. The date the case is received is generally included in the World Information window (TrueAllele World > Information).

**Add Client**

A client name is added to the World. This name is typically a shortened acronym of the client's office name (e.g., Allegheny County District Attorney's Office client name is ACDA). Any name can be used, however. Contact information can be added, if known. These additional fields can be left blank.

**Add Lab**

A lab name is added to the World. This name is typically a shortened acronym of the lab's name (e.g., Pennsylvania State Police lab name is PSP). Any name can be used, however. Contact information can be added, if known. These additional fields can be left blank.

## 10.3 Request Naming

**Overview**

When creating a request, the planner or operator may name a request using the fields in the listed order. This order standardizes the request name regardless of which fields are used. Note that each field is separated by the underscore '_' symbol in the request

name.  This standardized naming allows features like the *Match Screening Table* to group requests.

**Case name**

The case name can be used when multiple cases are on the same World.  If the World contains only one case, the case name can be omitted from the request name.

**Item name**

The item name may or may not be the sample/lane/exhibit name.  Typically, the VUIer DNA item name and the Request item name are identical.

Optional item name fields are available and follow the item name in the indicated order:

- lab name
- kit name
- well number
- amplification number
- injections number

If multiple items are joined in a request (whether known reference or other evidence), the planner/operator can separate each item with the plus sign '+' symbol.  Try to avoid using the underscore "_" separator character within item names.

For some older cases, data processed above 0 rfu may be indicated by having the peak height level added to the request name (e.g., 5rfu).  This field follows the item name and is usually separated by an underscore.

For cases where only some of the evidence data is rescaled, add "_rsc" after the item name (e.g., Q1_rsc) to indicate that the 3500 rescale feature was used for this item.

**Number of contributors**

When creating the request, the planner or operator indicates the total number of contributors assumed to be present in the evidence using the following field where # is replaced with the actual numeric value.

- ncon#

**Options**

When an option is used, such as the degraded DNA feature, the option may be indicated using the code below:

| Option | Code |
|--------|------|
| Off ladder - Medium | OL2 |
| Off ladder - Large | OL3 |
| Differentially degraded mixture | dgrd |
| Sort contributors | sort |

**Number of cycles**

The planner/operator may indicate the cycling parameters where the # character is replaced by the numeric value(s) for the thousands of cycles used.

- #K

**Request naming example**

Case LB2011 has three evidence items 1A, 2B, and 3C. Items 1A and 2B contain 2 total contributors. As item 1A is an intimate sample, the reference K1 can be used in the genotype inference. Item 2B is amped twice in wells A12 and H09. The number of contributors in item 3C may be two or three, and this item was analyzed using the 3500 rescale feature. Each request was processed with a cycle time of 50,000/50,000. The example case naming is shown in the table below.

| Request name | Description |
|---|---|
| LB2011_1A+K1_ncon2_50K | Item 1A with reference K1 as a known contributor |
| LB2011_2B_A12_ncon2_50K | Item 2B in well A12 |
| LB2011_2B_H09_ncon2_50K | Item 2B in well H09 |
| LB2011_3C_rsc_ncon2_50K | Item 3C, rescaled, assuming two total contributors |
| LB2011_3C_rsc_ncon3_50K | Item 3C, rescaled, assuming three total contributors |

## 10.4 Request Processing

This section describes processing guidelines to consider when creating evidence requests during the Plan or Replan steps of the casework process. This table offers guidelines for an analyst when setting processing parameters. The table serves as a guide, as cases may require or use other processing parameters based on the case context, data, or time.

| Number of unknown contributors | Total number of contributors | Differential degradation | Suggested cycles |
|---|---|---|---|
| 1 | 1 | NA | 25K |
| 1 | 2 | | 50K |
| 1 | 2 | yes | 100K |
| 2 | 2 | | 50K |
| 2 | 2 | yes | 100K |
| 3+ | 3+ | | 100K |
| 3+ | 3+ | yes | 100K |

# 10.5 Case Packet

*To start, download the Case Packet template ZIP file from the wiki.*

**Overview**

The case packet provides all of the information used to reach the conclusions described in the case report. Case packets can be lengthy documents, and are first assembled in discrete sections for efficiency. Each of these sections focuses on one part of the process, and typically involves just one main interface. Each section is verified before being added to the completed packet.

**Materials**

- To get started, download the following files from the case page:
  - report spec files
  - match table files
  - locus tables (if available)
  - case report (to help with ordering items)
  - VUIer™ (Be sure to use the latest released VUIer™ version)
- To aid in gathering and reviewing the case packet information, create a report spec file with only the reported evidence genotype database coordinates, reference genotypes, and populations.

**Title page**

- Open the *01_Title.docx* file:
  - Add the name of the prosecuting body; *e.g., Commonwealth of Pennsylvania*
  - Add the name of the defendant(s).
  - Add the date packet is prepared (Use Month Day, Year format unless international, then use Day Month Year).
- Save as *01_Title.pdf*.
- Send to another analyst to verify.

**Table of contents**

- Open the *02_Table of Contents.doc* file:

    • Verify that all materials for all sections (e.g., lab EPGs) are present.

- Save as *02_Table of Contents.pdf*.

- Send to another analyst to verify.


**Case**

*Case notes*

- Before assembling the case information, verify that the information on the page is accurate and complete.

- In a web browser, save the case page as a PDF:

- Click Printable version from sidebar. Use File > Print; save as PDF.

    • Leave all headers and footers option blank on the main print dialog box before saving.

    • Select PDF > Save as PDF… to save case page.

    • Use PDF Pen application "Correct text" feature from toolbar to remove any links (e.g., to case page, match table files, etc.) including "Retrieved from" link.

        o Highlight text, select Format > Correct text, then delete.

    • Remove "Last modified" date and save.

        o Highlight text, select Format > Correct text, then delete.


*Case page*

- Open the *Case_page.docx* file.

    • Verify that the information is correct.

- Save as *Case_page.pdf*.


*Case PDF*

- Assemble the Case PDF by combining the case notes PDF with Case_page.pdf.

    • Start by opening the case_page.pdf file, then insert the case notes after first page.

---

- Add file list(s) as PDF after case notes.
- Add preliminary results PDF(s) after file list.
- Save as *03_Case.pdf*.
- Send completed section to another analyst to verify.


**Data**

*Data page*

- Open the *Data_page.docx* file.
  - Verify that the information is correct.
- Save as *Data_page.pdf*.


*Peak table*

- For each evidence and reference data item, use *Data View* in the VUIer Report module to save the peak table.
  - For evidence data, turn on the peak labels and ensure that the peak height cutoff value is set to 0 rfu or lowest rfu value analyzed, e.g., 5 rfu.
  - For reference data, turn on the peak labels and ensure that the peak height cutoff value is set to 10 rfu.
  - Select Table > Peak and save.
- Open the table in Excel. Resave the table as a spreadsheet *.xls* file (instead of text *.txt* or a MATLAB *.xls* file).
  - Replace the TrueAllele-generated title with the evidence or reference name from the case report and make left-aligned, bold, Arial font size 12 pt.
    - For example, replace *Data Peak: CYB C3_ncon1_50K_rep1* with **Item C3**
    - If the item is amped using more than one STR kit, indicate the STR kit name after the item name. (i.e., PowerPlex® 16, Identifiler®, MiniFiler™).
      - If the kits used are variations of a single name (e.g., Identifiler® Plus and Identifiler® Direct), do not specify this difference. If they are absolutely different kits (e.g., Identifiler® and PowerPlex® 16), specify the kit used.

- o For references, replace the default name with **Reference role #** (e.g., **Suspect G**).

- Make the table Arial font size 12 pt.

- Center align the template and track columns.

- Right align the design, length, height and area column headers.

- Check that the table print with Layout = portrait.

- Save the formatting changes, then save as PDF (see image below as an example).

  - o Be sure all columns save as a single page wide.

**Item C3**

| template | track | locus | desig | length | height | area |
|:---:|:---:|---|---:|---:|---:|---:|
| 1 | 1 | AMELO | 0.4 | 103.966 | 20 | 13 |
| 1 | 1 | AMELO | 1 | 105.898 | 497 | 259 |
| 1 | 1 | AMELO | 2 | 112 | 95 | 55 |
| 1 | 1 | CSF1PO | 10 | 336.702 | 221 | 146 |
| 1 | 1 | CSF1PO | 11 | 340.613 | 175 | 106 |
| 1 | 1 | CSF1PO | 12 | 344.605 | 108 | 61 |
| 1 | 1 | D13S317 | 9 | 176.899 | 80 | 36 |
| 1 | 1 | D13S317 | 11 | 185.1 | 11 | 5 |
| 1 | 1 | D13S317 | 12 | 188.9 | 120 | 58 |
| 1 | 1 | D13S317 | 13 | 192.898 | 173 | 84 |
| 1 | 1 | D16S539 | 9 | 280.101 | 35 | 21 |
| 1 | 1 | D16S539 | 11 | 288.101 | 95 | 54 |
| 1 | 1 | D16S539 | 12 | 292.103 | 58 | 33 |
| 1 | 1 | D16S539 | 13 | 296.303 | 101 | 65 |
| 1 | 1 | D18S51 | 12 | 305.788 | 12 | 7 |
| 1 | 1 | D18S51 | 13 | 309.708 | 117 | 74 |
| 1 | 1 | D18S51 | 14 | 313.55 | 20 | 13 |

*Data Table*

- Assemble the Table document with the *Data_page.pdf* first, followed by the data table PDFs in report item order.
- Save as *Table.pdf* in the Data folder.

*Data EPG*

- In the *EPG_page* document under the **EPG** heading, list the evidence and reference (when STR data is available) items in the order of the report and indicate the STR kit(s) used (when more than one is available).

- If a single item is amped using more than one STR kit – indicate kit name after the item name and list each amp. For example:
    - Item C3 (Profiler Plus®)
    - Item C3 (COfiler®)
- For reference items, list as Reference role # (e.g., Suspect G).
- Save as *EPG_page.pdf*.

- For each data item (both evidence and reference), capture an image of the data (see image below as an example).
    - Open *Data View* for the reported request and select the View Sample mode (S button). Depending on monitor size, adjust window accordingly.
    - Show eight tracks at a time for kits with 16 loci; Show all lanes for smaller kits (MiniFiler, SGMplus, Profiler Plus/COfiler, etc.)
        - For Fusion or other 20+ kits, save 3 images (e.g., 8 loci, 8 loci, 7 loci).
    - Set a reasonable peak height cutoff (rfu) value to remove baseline artifacts, if necessary. Make sure that the rfu value does not remove labels from peaks of interest.
    - Reduce the side track 'purple' area to increase the white data image region.
    - If desired, increase text size.
    - Save the image as JPEG using the Save button in the upper left corner of the window. For kits with more than 10 locus tracks, scroll down to the second set of loci and save the second (and third) image.
    - Save all images using the same window and purple region sizes.
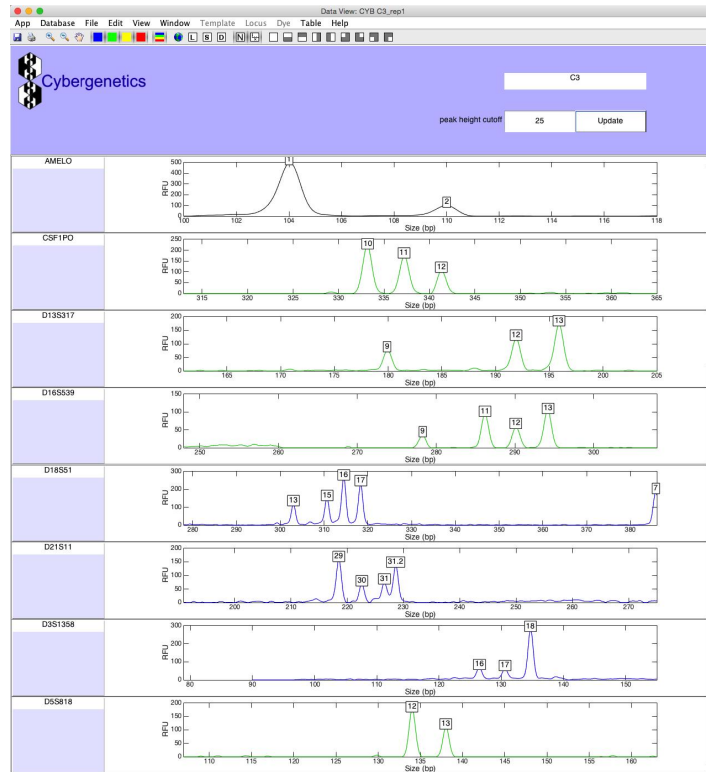
- Assemble the EPG document with the *EPG_page.pdf* first, followed by the EPG images in report item order. Be sure to include all images in order.
- Save as *EPG.pdf*.

*Lab EPG (when available)*

- In *LabEPG_page.docx* under the **Lab EPG** heading, list the items and indicate the STR kit(s) used (when more than one kit is available).
  - If the item is amped using more than one STR kit, indicate kit name after the item name.
  - Ensure that the item order is the same as for the EPGs above;
  - Save as *LabEPG_page.pdf*.
- Assemble the LabEPG PDF document with the *LabEPG_page.pdf* first followed by the lab EPG images in item order.
- Save as *LabEPG.pdf*.

*Data PDF*

- Combine the Table, EPG, and LabEPG PDFs, in order.

- Save as *04_Data.pdf*.

- Send completed section to another analyst to verify.


**Request**

*Note that the Request 'list' and 'timing' ordering should sync with the request ordering in the match tables.*


*Request list*

- Open the *Request.docx* file:

- Provide the list of requests along with the specific assumptions and parameters for each evidence item.

  - List the requests, ordered by name.

    o Ensure that the request order matches the match table order (in the Match section) and remains consistent throughout the document.

    o In the Word table, insert the request name, the total number of assumed contributors, any known references used in the inference, any options used, and number of cycles used.  The request information is taken directly from the case page (when available). Be sure column headers and information match those in the Case notes section of the case page (e.g., Degraded DNA instead of options, entries should say 'on')

    o Add horizontal lines as needed for clarity.

    o Only include requests used for reporting. Omit screening requests.


*Request timing*

- Use the first database query to gather the start date, the finish date, and duration times for the requests:

  - Open a terminal window.

  - Connect to the server.

- Login to the case World: psql <worldname>.
- Enter the password at the prompt.
- Enter the database query below.
  - Replace the dash, quotes, and/or commas as needed for the command to work properly.

select name, date(started) as started, date(finished) as finished, date_trunc('minute', finished-started) as duration from req where process not like 'reference' order by name;

- Copy and paste output into Excel.
- Add the times in table format to the Timing description page, ensuring that the request order is the same as in the Request list.
  - Use the Text-to-Columns function in Excel to separate the table copied from the terminal window.
- Change the date columns to the day-month-year format (e.g., 1-Jan-2014) in Excel as needed.
  - May need to remove extra spaces before the request name and the date columns in order to properly edit the values.
- Be sure formatting is consistent. Note: some requests can finish in less than a day. Only include requests used for reporting. Omit screening requests.
- Add horizontal lines as needed for clarity (make sure they are consistent with Request listing table).
- Copy and paste timing information from Excel into *Request.docx* file.
- Use the database query to gather the total duration time (in days, fractions of hours) for the requests used for reporting:
  - If needed, log in to case World in terminal following steps above.
  - Enter the database query:

select extract(epoch from (select sum(finished-started) from req where name like '%req names%')/3600/24) as total_days;

- Paste the results into a spreadsheet program.
- Calculate hours using the following formula:

= round((MOD(total_days,1)*24),0)

- Copy and paste the days and hours output into the duration total field of *Request.docx* file.
- Enter \q to quit PostgreSQL.
- Enter exit to close the server connection.

*Request PDF*
- Save the completed *Request.docx* file as *05_Request.pdf*.
- Send completed section to another analyst to verify.

## Genotype
*Evidence genotype*
- If not already identified (i.e., when reporting the average genotype and match statistic values for a comparison), identify a representative evidence genotype from the concordant set with the log(LR) value closest to the average.  Then, follow the steps below using this representative genotype.
- In the Report module *Genotype View*, save the genotype for the reported genotype(s) for each item:
  - Use a 99% genotype confidence level.
  - In Preferences, set the number of decimal places to at least 4 so that no probability values appear as zero.  Increase the number of decimal places as needed when values appear as 0.0000.
- Open the file in Excel and resave as a spreadsheet *.xls* file;
  - For the genotype information, set the font to Arial size 12 pt.
  - Right or center align the allele1, allele2, and probability columns.
  - Expand column widths as needed (e.g., set to 1.2").

- To change the widths, highlight all columns, right click top of column, select 'Column width'.

- Above the request title, add a row and indicate the specific match ("Item <name/number in report> vs. <reference role> <reference name/number in report) and make this title bold, Arial font size 12 pt. Do not include the word "item" after reference role (e.g., **Item C3 vs. suspect G**).

- Save the spreadsheet for each evidence genotype as a PDF file (see image below as an example).

**Item C3 vs. suspect G**
C3_rep1 contributor 2

| locus | allele 1 | allele 2 | probability |
|---|---|---|---|
| AMELO | 1 | 1 | 1.0000 |
| CSF1PO | 10 | 11 | 0.8648 |
| | 11 | 12 | 0.0774 |
| | 10 | 12 | 0.0578 |
| D13S317 | 12 | 13 | 0.9340 |
| | 9 | 13 | 0.0429 |
| | 13 | 13 | 0.0155 |
| D16S539 | 11 | 13 | 0.9890 |
| | 12 | 13 | 0.0078 |
| D18S51 | 16 | 17 | 1.0000 |
| D21S11 | 29 | 31.2 | 1.0000 |
| D3S1358 | 18 | 18 | 0.9981 |
| D5S818 | 12 | 13 | 0.8442 |
| | 12 | 12 | 0.1540 |
| D7S820 | 8 | 9 | 0.4113 |
| | 8 | 10 | 0.3220 |
| | 9 | 10 | 0.2667 |
| D8S1179 | 12 | 12 | 0.9999 |
| FGA | 21 | 23 | 1.0000 |
| Penta_D | 13 | 14 | 0.9934 |
| Penta_E | 13 | 13 | 1.0000 |
| TH01 | 6 | 7 | 0.9781 |
| | 7 | 9.3 | 0.0165 |
| TPOX | 8 | 9 | 0.7656 |
| | 8 | 8 | 0.2344 |
| vWA | 16 | 19 | 0.9992 |

*Reference genotype*

- In the Report module *Genotype View*, export the genotype for each case reference included in case report.

- Open the file in Excel and resave as a spreadsheet *.xls* file instead of a tab-delimited text *.txt* file.

- Add the reference's name and role and name/number, as indicated in the case report, in the first row of the spreadsheet and make the title bold; Do not include the word "item" after reference role (e.g., **John Smith, suspect G**).

- Change font to Arial font size 12 pt.

- Expand column widths as needed (e.g., set to 1.2").
   - To change the widths, highlight all columns, right click top of column, select 'Column width'.

- Right or center align the allele1, allele2, and probability columns (see image below as an example).

**John Smith, suspect G**

| locus | allele 1 | allele 2 | probability |
|-------|---------|---------|-------------|
| AMELO | 1 | 2 | 1 |
| CSF1PO | 12 | 12 | 1 |
| D13S317 | 9 | 13 | 1 |
| D16S539 | 9 | 12 | 1 |
| D18S51 | 13 | 15 | 1 |
| D21S11 | 30 | 31 | 1 |
| D3S1358 | 16 | 17 | 1 |
| D5S818 | 12 | 12 | 1 |
| D7S820 | 10 | 10 | 1 |
| D8S1179 | 8 | 11 | 1 |
| FGA | 21 | 22 | 1 |
| Penta_D | 12 | 14 | 1 |
| Penta_E | 7 | 14 | 1 |
| TH01 | 9 | 9.3 | 1 |
| TPOX | 8 | 8 | 1 |
| vWA | 15 | 18 | 1 |

- Save the spreadsheet for each reference as a PDF file.
- Assemble the Reference PDF in the item order of the report.
- Save as *Reference.pdf.*

*Population genotype*
- Download the population PDF from the population page.
- If a case packet-ready population PDF file is not available, download the population files used in the case from the population page linked to the case page and save each as a spreadsheet file.

- Format the files as described below.
  - Add two rows to the top of each spreadsheet and in the top row put the name of the population (e.g., United States FBI Caucasian population) in bold Arial font size 12 pt.
  - Change the table data to Arial font size 12 pt.
  - Expand column widths as needed (e.g., set to 1.2").
    - To change the widths, highlight all columns, right click top of column, select 'Column width'.
  - Right align the design and count columns.
  - Save the file as PDF.
- Assemble the Population PDF in alphabetical order by population name and save as *Population.pdf*.


*Genotype PDF*
- Verify that all phrasing in *Genotype_page.docx* is correct and save as PDF.
- Assemble the Genotype PDF.
  - Combine the Evidence, Reference, and Population PDFs, in order.
    - Insert each after the page in the *Genotype_page.docx* that describes it.
- Save as *06_Genotype.pdf*.
- Send completed section to another analyst to verify.


**Match**

*Match table*
- Use the match tables for each item downloaded from the case page.
  - Confirm that the tables contain match information for all requests.
  - Be sure that the requests appear in the same order as listed in the Request section.
  - Insert two rows above the "Evidence" header and add the Item # as a header in bold Arial font size 12 pt. (see image below as an example).
    - Add horizontal lines as needed for clarity.

- To ensure that the tables look the same, in Excel select both spreadsheet tabs and format the column widths if needed.
- Highlight the row for the identified representative match statistic in both tabs.
  - Include the Evidence, Contributor, N contrib, Weight, Std Dev, KL, and reported match statistic columns. Do not highlight the match statistics to other references.
- Save both the "all" and ">1" worksheets in each workbook as PDF files. Each evidence item can have at least two tables.
  - When the tabs contain the same information (e.g., only inclusionary match statistics), only one table is needed.
- Assemble the Match table PDF file.
  - Order the match table PDFs by item, with the ">1" file first for each item.
  - Save as *Match_table.pdf*.

**Item C3**

| Evidence | Contributor | N Contrib | Weight | Std Dev | KL | A | G |
|---|---|---|---|---|---|---|---|
| C3_rep1 | 1 | 2 | 0.33 | 0.04 | 19.01 | | 16.69 |
| C3_rep1 | 2 | 2 | 0.67 | 0.04 | 19.07 | 18.19 | |
| C3_rep2 | 1 | 2 | 0.32 | 0.03 | 19.08 | | 16.98 |
| C3_rep2 | 2 | 2 | 0.68 | 0.03 | 19.15 | 18.28 | |
| C3_rep3 | 1 | 2 | 0.33 | 0.04 | 19.08 | | 16.70 |
| C3_rep3 | 2 | 2 | 0.67 | 0.04 | 19.04 | 18.13 | |

*Locus table*

- Use the locus tables for each reported match downloaded from the case page.
- If locus tables not available, save them for each reported match from the VUIer *Match View* interface.
  - If not already identified (i.e., when reporting the average genotype and match statistic values for a comparison), identify a representative evidence genotype from the concordant set with the log(LR) value closes to the average. Then, follow the steps below using this representative genotype.

- In Excel, increase the column sizes as needed so that all values are visible (e.g., a Column width set to 1.25" or larger).

- Set values to 4 decimal places.

- Set font to Arial size 12 pt.

- Center align the population columns.

- Remove any zero rows (e.g., loci not included in MiniFiler™).

- Add a row to the top of the spreadsheet and add a title in bold: Item <name/number from report> vs. <reference role> <reference name/number from report>.  Do not include the word "item" after reference role (e.g., **Item C3 vs. suspect G**)

- Save each locus table as a PDF file (see image below as an example).

**Item C3 vs. suspect G1**
C3_rep1 contributor 1 vs. C0020_G1

| locus | US+PP16_BLK | US+PP16_CAU | US+PP16_HIS |
|---|---|---|---|
| CSF1PO | 0.3984 | 0.4461 | 0.3666 |
| D13S317 | 1.7921 | 1.7349 | 1.4851 |
| D16S539 | 1.0295 | 1.0156 | 1.0620 |
| D18S51 | 1.6932 | 1.4477 | 1.3911 |
| D21S11 | 1.4299 | 1.4572 | 1.4806 |
| D3S1358 | 0.4970 | 0.2556 | 0.2437 |
| D5S818 | 0.4944 | 0.5645 | 0.7406 |
| D7S820 | 0.5149 | 0.6465 | 0.6501 |
| D8S1179 | 2.8913 | 2.2783 | 2.6660 |
| FGA | 1.3662 | 1.1559 | 1.3161 |
| Penta_D | 1.9850 | 1.4517 | 1.6983 |
| Penta_E | 1.8326 | 1.6412 | 1.6532 |
| TH01 | 1.3906 | 0.9211 | 1.1531 |
| TPOX | 0.6896 | 0.4508 | 0.6893 |
| vWA | 1.1197 | 1.2279 | 1.3481 |
| | | | |
| Total | 19.1245 | 16.6949 | 17.9441 |
| Joint | 1.33192E+19 | 4.95379E+16 | 8.79148E+17 |
| Words | 13.3 quintillion | 49.5 quadrillion | 879 quadrillion |

- Assemble the Locus table PDF.

- Order by item and reported match.

- Save as *Locus_table.pdf*.
- Verify that all phrasing in *Match_page.docx* is correct and save as PDF.


*Contributor analysis (as needed)*

- Add the contributor analysis information using the Report *Distribution* or *Contributor* feature for reported exclusionary match statistics. Use the composite calculation when reporting an average match statistic.
  - Create one chart per match using the population that produces the match statistic closest to zero (value observed in *Match Table)*.
  - Follow steps outlined in Non-contributor analysis section below for formatting.


*Non-contributor analysis (as needed)*

- Add the non-contributor analysis information using the Report *Distribution* or *Non-contributor* feature for reported match statistics. Use the composite calculation when reporting an average match statistic.
  - Create one chart per match using the population that produces the minimum match statistic across the populations (see image below as an example).
    - Use reasonable x-axis labels to center histograms.
    - Enable the histogram and the 'pink' region (which may not always be visible).
    - Increase interface font to the largest size possible.
    - Add 2 units to each side of the x-axis labels.
    - Save image as JPEG from the *Distribution* or *Non-contributor/Contributor* interface using appropriate population.
    - Insert the image into the Word template. Size the width to 3".
  - Title the non-contributor graph page using the appropriate item, reference role and number.
  - Include the stats tables below the graph (see image below as an example).
    - Use the mean and standard deviation statistics for the population used to create the histogram image.

- Add all tail probabilities from all populations and ensure all numbers use the same formatting (e.g., 1 x 10$^{-4}$).
- For all values, display 4 digits after the decimal.
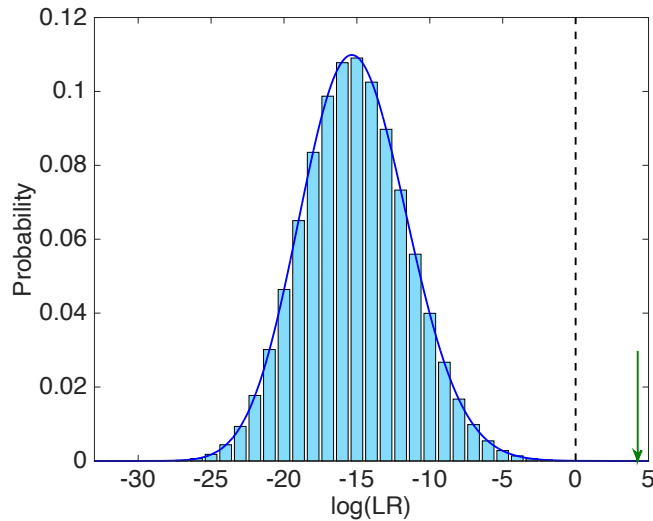


| Statistic | Value |
|---|---|
| mean | -15.1083 |
| std dev | 3.6093 |

| LR | log(LR) | Tail probability | One in … | Ethnicity |
|---|---|---|---|---|
| 79.6 thousand | 4.9010 | 2.6348 x 10$^{-8}$ | 38 million | African-American |
| 144 thousand | 5.1579 | 1.6958 x 10$^{-8}$ | 59 million | Caucasian |
| 17.9 thousand | 4.2531 | 1.6796 x 10$^{-7}$ | 5.95 million | Hispanic |

*Distribution (as needed)*

- Add the non-contributor and contributor analysis information using the Report *Distribution* feature for reported match statistics. Use the composite calculation when reporting an average match statistic.
  - Create one chart per match that includes both the contributor and non-contributor distributions.
    - For inclusionary match statistics, use the population that produces the minimum match statistic across the populations.

- o For exclusionary match statistics, use the population that produces the match statistic closest to zero (value observed in *Match Table)*.
- Include both contributor and non-contributor statistics.
- Follow steps outlined in Non-contributor analysis section above for formatting.

*Match PDF*

- Combine the *Match_page.pdf*, *Match_table.pdf* and *Locus_table.pdf*.
- Insert the Match table and Locus table PDFs after each page that describes the sections.
- Save as *Match.pdf*.
- Send completed section to another analyst to verify.

**Case packet**

- Assemble the case packet:
  - After each section has been verified, combine the Title Page, Table of Contents, Case, Data, Request, Genotype, and Match PDFs in order.
  - Save as *<case name>_ case_packet.pdf*.
- Add page numbers to all pages using PDF numbering software, such as PDFpen.
- Have the completed case packet reviewed briefly for section ordering and page numbering.
- Once case packet is reviewed and approved, send to the client.
  - Use the TrueAllele trial materials message template found on the Case communications page as a guide.

## 10.6 Demonstrative Aid

**Overview**

A demonstrative aid is often needed for court to explain the science and results of the TrueAllele® Casework system.  This demonstrative aid is a PowerPoint presentation that is created using a template.  The presentation teaches the jury about the TrueAllele

science and what the case results mean.  This section describes the procedures and thought process behind preparing a demonstrative aid.

**Procedure**

The demonstrative aid begins with a PowerPoint template. To prepare the case specific demonstrative aid, the reporting scientist can choose a locus, capture data and interface images, and prepare each slide, as outlined below.

**Locus selection**

Choosing a locus involves reviewing the data, genotypes, match statistics, and forensic questions.  A representative locus easily shows how TrueAllele works and fits with the proposed number of contributors.  This locus is used throughout the presentation to illustrate what a DNA mixture looks like and the TrueAllele genotype inference process.  Exceptions can be made to the locus selection procedure for ease of creating a demonstrative aid useful for teaching.

Procedure:

- In the VUIer Report module, load the case's report spec file or reported genotypes of interest.
- Select the reported request, reference of interest, and the associated (or minimum) population.
  - If not already identified (i.e., when reporting the average genotype and match statistic values for a comparison), identify a representative genotype from the concordant set with a log(LR) closest to the average for demonstrative purposes.
- Open the *Data View* window for the reported request.
- Open the *Genotype View* and *Match View* interfaces.
- Examine each locus for the following criteria:
  - A clearly explained pattern and number of peaks that fits the contributor assumption reported on.

- Good allele separation and balance.
- Only a few inferred evidence genotype possibilities (if there are many, use a confidence level of 0.95 or lower as needed) with reasonable probability on the reference of interest's genotype.
- For inclusionary match statistics, good information gain (but not the highest or lowest locus LR).
- For exclusionary match statistics, reasonable ratio between genotype brown and blue bars.
  o Ensure reference allele pair is included at the set confidence level.
- If choosing a representative locus is difficult, discuss the locus choices with the reporting scientist or other staff to determine which example best represents the case.

**Title slide**

The *Title slide* introduces the case name, the date, the location of the trial, and the person that is presenting the demonstrative aid.

Procedure:

- Replace <Prosecution> with the name of the prosecuting body.
- Replace <Defendant> with the first and last names of the defendant(s) from the Cybergenetics case report.
- Replace <Month> with the month in which the trial will take place. Verify that the correct year is indicated.
  - If the trial month is unknown, list the month and year the aid is being prepared.
- Replace <City> and <State> with the city name and state abbreviation where the trial will take place.
- Replace <Reporting Scientist> with the name of the person testifying with their associated <Degrees> following the name.
- Center the text boxes as needed.

**DNA biology**

The *DNA biology* slide explains the basics of cell biology and where DNA is found in a cell. A locus is described as well.

Procedure: This slide does not change.

**Short tandem repeat**

The *Short tandem repeat* slide explains the concept of locus repeat units (alleles).

Procedure: This slide does not change; Replace with the UK version as appropriate.

**DNA genotype**

The *DNA genotype* slide explains a genetic locus, alleles, and genotypes. It also explains why a person's genotype is unique.

Procedure: This slide does not change.

**DNA evidence interpretation**

The *DNA evidence interpretation* slide provides a basic outline of how easily single source DNA evidence is analyzed, interpreted, and compared to a reference. This is a good introduction before mixtures complicate matters.

Procedure: This slide does not change.

**DNA mixture interpretation**

The *DNA mixture interpretation* slide describes how mixtures complicated interpretation and are not as easy as single source DNA. Probabilities are also introduced.

Procedure: This slide does not change.

**Computers can use all the data**

The *Computers can use all the data* slide is the first time any EPG case data appears in the presentation. It explains what DNA data looks like at a locus and that there is a pattern associated with the peaks.

Procedure:

- Open the *Data* window for the reported/representative request (from the report notes).
- Go to the locus that was selected for the demonstrative aid.
- Turn on the peak and axis labels if they are not already visible.
- Increase the font size to the maximum value.
- Make the window a small square in the corner of the screen using the view buttons.
- Increase the display cutoff to remove baseline labels as needed.
- Use the Zoom tool to focus on the peaks of interest (including any stutter peaks), leaving about a peak's width of space on either side.
- Using a screenshot tool, select the portion of the window containing the data, axes and labels and save the image.
- Insert the image into the PowerPoint slide.
- Resize it to a height of 5", align it to the bottom, and center it horizontally.
- Indicate what is meant by peak height and peak size using the arrows and labels
  - Choose a lower peak near the center of the image.
  - Arrows should not cross through any peak labels.
  - Arrows should touch and center on the peak label box.
- Change <locus> to the full name of the locus that was used.

**People may use less of the data (optional)**

The *People may use less of the data* slide explains how DNA data is interpreted using human methods. This slide is used when a non-TrueAllele match statistic will also be presented at the trial; otherwise, it is typically removed.

Procedure:

- Copy data image from previous slide and paste onto this slide.  This should place the image in the same position on the slide.
- Move the red line so that it is at the stochastic threshold used by the laboratory that generated the data, and move the text 'Threshold' next to it.  If this value is unknown, use 100 or 150 rfu (or some other reasonable value).
- Place a red 'x' over the peak labels below the red line.
- Place the solid blue boxes below the line on the peaks over threshold, and align them horizontally.  Make these boxes to fit between the threshold and bottom of the peaks.
- Place blue circles around the peak labels over the line, centering the label inside the circle.
- Use the blue arrows to point from the "Over threshold…" text box to the blue circles.
- Use the purple arrows to point from the "Under threshold…" text box to the red x's.
- If needed, move the "All-or-none…" and "Under threshold…" text boxes so they do not cover the peaks or axis labels.

**How the computer thinks (Good explanation)**

This *How the computer thinks* slide explains how TrueAllele interprets the DNA evidence using a good explanation of the data.  The computer considers every genotype solution and tries to explain the peak pattern.

Procedure:

- Copy data image from previous slide and paste onto this slide.  This should place the image in the same position on the slide.
- If needed, arrange the text boxes (except the title and subtitle) so that they do not cover the peaks and axis labels.
- Indicate which alleles belong to the first contributor (who the story is focuses on):

- Move the first set of colored boxes (usually blue) so that they encompass the contributor's alleles and align them horizontally so that they are just touching the baseline (if possible).  The boxes should be the same height.
- For exclusionary match statistics, the person of interest's allele pair does not have to be included.
- Indicate which alleles belong to the second contributor.  When possible, add additional contributors in decreasing mixture weight.
  - Move the second set of colored boxes so that they encompass the second contributor's alleles and align them horizontally as above.  The boxes should be the same height.
- Indicate which alleles belong to the third contributor.
  - Move the third set of colored boxes so that they encompass the third contributor's alleles and align them horizontally as above.  The boxes should be the same height.
- Add boxes for additional contributors as needed.
- Once all boxes are added, create the "animation" by copying and pasting this slide before itself and removing contributor boxes one by one until there are as many slides as the contributor assumption.
  - For example, with 3 contributors, copy and paste the slide and remove the third set boxes leaving only the first two. Then, copy and paste that slide and remove the second set of boxes leaving only the first. There are now 3 slides that add up to the final proposal (i.e., all 3 colored boxes present).


**How the computer thinks (Worse explanation)**

This *How the computer thinks* slide shows a worse explanation of the data that TrueAllele may consider.  This slide visually shows a different explanation of the data than previously seen.

Procedure:

- Copy data image from previous slide and paste onto this slide. This should place the image in the same position on the slide.
- Create a proposed pattern that does not resemble the data (stacked rectangles have different heights than the data peaks).
    - Create a pattern that is feasible and reasonable, but unrelated to the data. Some rectangles should be placed where there is no or little data. However, use actual allele positions, not off-ladder sizes. The 'evidence genotype' slide may provide helpful allele pair options for contributor 1.
    - Change the genotype for contributor 1 (blue rectangles, person of interest in match statistic) to a different allele pair.
    - Change other contributor genotypes. Move the allele pairs around.
    - Change the rectangle heights (contributor quantity).
- If needed, arrange the text boxes (except the title and subtitle) so that they do not cover the peaks, colored rectangles, and axis labels.

**Evidence genotype**

The *Evidence genotype* slide introduces the genotype probability distribution inferred by TrueAllele from the data presented in the previous slides. It also explains that the process is completely objective.

Procedure:

- In the VUIer Report module, uncheck all genotypes.
    - Enable the representative genotype.
    - Download and enable CYB_placeholder population (system60, World placeholder). This population will allow the blue bars in *Genotype View* to appear narrower for continuity with the following slides.
- Set the appropriate co-ancestry coefficient, if necessary.

- Open the *Genotype* window.
- Increase the font size to the maximum value and turn on the axis labels.
- Make the window a small square in the corner of the screen using the view buttons.
    - If there are many genotypes, it may be necessary to use a lower confidence interval or resize the window to remove some of the white space above them.
    - Using a screenshot program, select the portion of the window containing the genotypes, axes and labels and save the image. Do not close the *Genotype* window.
- Insert the image into the PowerPoint slide, align it to the bottom of the slide, center it, and resize it to a height of 5".
- In the VUIer Report module, open the evidence genotype table and find the probabilities for each allele pair possibility at that locus and list them as whole number percentages above the allele pair probability bar on the slide.

**DNA match information**

The *DNA match information* slides introduces the reference genotype. It explains how a comparison is made and how match information is determined at a locus.

Procedure:

- In the VUIer Report module, turn on one population.
    - Use the population that gave the minimum match statistic, or the one that gives the log(LR) closest to zero.
    - Use a screenshot program in the *Genotype* window to select the same portion of the window from the previous slide and save the image.
- Insert the image into the PowerPoint slides, keeping it in the same position as the image on the Evidence genotype slide.
- On the first DNA match information slide, copy and paste the allele pair probabilities from the Evidence genotype slide, keeping them in the same position.

- On the second DNA match information slide, keep only the probability of the blue bar at the reference of interest's allele pair.
  - On this same slide, type the probability of the allele pair in the reference population near the brown bar at the suspect's allele pair. This value is found in the composite genotype table by enabling the population frequency in the Report Preferences window.
  - Place the red box around the two bars at the suspect's allele pair.
  - Divide the blue bar percentage by the brown bar percentage and type the (rounded) ratio into the <ratio> field, and move it near the red box, preferably centered on the top of the red box.
  - Adjust the blue arrow so it points from "Prob(evidence match)" to the top corner of the blue bar.
  - Adjust the brown arrow so it points from "Prob(coincidental match)" to the top of the brown box.
  - Copy and paste the equation text boxes onto the first DNA match information slide, keeping it in the same position.
  - Note: If the comparison is made to the victim or other reference, change "suspect" in the subheading to "victim" or other reference role.

**Match information at # loci**

The *Match information at # loci* slide explains that what was done for the locus in the previous slide is done at all loci, and that the product of the ratios forms the match statistic.

Procedure:

- Change the number of loci in the slide title to reflect the total loci used.
- In the VUIer Report module, enable the reference genotype of interest, keeping enabled the previously selected evidence and population genotypes.
- In the *Match* window, select Display linear scale.

- Open the locus table and copy the loci and locus scores for the population used in the DNA match information slide and paste into the upper left of the "locus_strength" Excel spreadsheet.
- Save the chart as a picture by right-clicking within the plot.
- Insert the image into the PowerPoint slide and center it horizontally and align it to the bottom.
- Move the red box to the locus used in the previous slide and adjust it so that the box encompasses the entire bar and locus label.

**Is the reference in the evidence?**

The *match statement* slide contains the statement from the case report for the evidence-to-reference match.  The only match statement listed is the one that goes along with the data and genotype story told in the previous slides.

Procedure:

- Replace <suspect> in the title to the appropriate reference label.
- Replace <evidence> with the evidence item description.
- Replace <reference> with the name of the reference as it appears in the case report.
- Replace <BLKLR>, <CAULR> and <HISLR> with the appropriate match statistics as listed in the report.
- For inclusionary match statistics, remove the '< >' from around the word <more>.
- For exclusionary match statistics, replace <more> with the word *less* (italicized).
- Ensure proper population names are listed.
- If only one population is reported, delete the other statements.

**Match statistics**

The *Match statistics* slides provide the match table found in the case report, which summarizes all of the matches (positive and negative) in the case.

Procedure:

- Create tables as found in the case report.  Include both positive and negative match statistics as needed for clarity.
- Add this table to the slides.
- Order slides with LR first and log(LR) second, unless otherwise told.
- Indicate positive associations as blue text and negative associations as red text.

**Non-contributor/Contributor analysis**

The *Non-contributor/Contributor Analysis* slide shows the error rate graph with no reference arrow.

Procedure:

- Use the *Distribution* or *Non-contributor/Contributor* feature in the Report module to produce the graph with as described in General Guidelines, Section 10.5 - Case Packet.
  - Turn off reference arrow.
  - Make font largest size in VUIer.
  - Adjust the axes as needed.
  - Save image using save icon in interface.
- Insert image into the slide.

**Error Rate**

The *Error Rate* slide shows the error rate graph and one in value for the genotype used in the preceding match statement.

Procedure:

- Use the *Distribution* or *Non-contributor/Contributor* feature in the Report module to produce the graph as described in General Guidelines, Section 10.5 - Case Packet.
  - Turn on reference arrow.
  - Make font largest size in VUIer.
  - Adjust the axes as needed.
  - Save image using save icon in interface.
- Add the appropriate one in value to the statement on slide.
- Add reported LR and log(LR) values near reference arrow.

## Verification

- Send the completed demonstrative aid to another analyst to verify.  The verification checklist below may be helpful during verification.
- Once demonstrative aid is reviewed and approved, send to the client.
  - Use the TrueAllele trial materials message template found on the Case communications page as a guide.

## Verification checklist

This worksheet may be used when verifying a demonstrative aid to ensure that all information is accurate.  The use of this checklist is optional.

| Computer Interpretation of Quantitative DNA Evidence | ☐ Names of the parties involved |
|---|---|
| | ☐ Month and year |
| | ☐ City and state |
| | ☐ Reporting Scientist and degrees |
| | ☐ Text boxes centered and in middle of slide |
| DNA biology | ☐ No changes made |
| Short tandem report | ☐ Use US/UK slide as appropriate |
| DNA genotype | ☐ No changes made |
| DNA evidence interpretation | ☐ No changes made |
| Computers can use all the data | ☐ Correct locus indicated |

| | | |
|---|---|---|
| | ☐ | Image fonts are large |
| | ☐ | Image, heading, and subheading are centered |
| | ☐ | Image appears clean and crisp (arrows don't cross, etc.) |
| **People may use less of the data - optional** | ☐ | Verify that this slide is needed |
| | ☐ | Data image does not 'move' when flipping between this and previous slide |
| | ☐ | Correct threshold value is used and line doesn't cross peak labels |
| | ☐ | X's and circles are centered on labels |
| | ☐ | Blue boxes are same size and aligned |
| **How the computer thinks (Good explanation)** | ☐ | Data image does not 'move' when flipping between this and previous slide |
| | ☐ | Genotypes proposed include known references and make sense |
| | ☐ | Reference of interest listed as first contributor |
| | ☐ | Bottoms of boxes touching the x-axis are aligned |
| | ☐ | Text boxes do not obscure any peak or axis labels |
| | ☐ | Data image does not 'move' when flipping between this and subsequent slides |
| **How the computer thinks (Worse explanation)** | ☐ | Contributor 1 genotype changes |
| | ☐ | Heights of rectangles change |
| | ☐ | Pattern does not resemble data, but no off-ladder alleles are represented |
| | ☐ | Bottoms of boxes touching the x-axis are aligned |
| | ☐ | Text boxes do not obscure any peak or axis labels |
| | ☐ | Verify all genotypes are present |
| **Evidence genotype** | ☐ | Image fonts are large |
| | ☐ | Correct probabilities assigned that add up to confidence level used |
| | ☐ | Probabilities centered above bars |
| | ☐ | Image fonts are large |
| **DNA match information 1** | ☐ | The image and probabilities do not 'move' when flipping between this and the previous slide. |
| | ☐ | Correct probabilities are copy and pasted from previous slide. |
| | ☐ | The equation text box does not 'move' when flipping between this and the subsequent slide. |
| **DNA match information 2** | ☐ | The correct genotype is indicated |
| | ☐ | The evidence and population probabilities are correct |
| | ☐ | The ratio value is correct |
| | ☐ | The reference role is accurate |
| **Match information at # loci** | ☐ | Loci are in alphabetical order |
| | ☐ | The number of loci is correct |
| | ☐ | Correct locus is indicated |

| | | |
|---|---|---|
| | ☐ | Graph shows the reported match result |
| | ☐ | Verify role of reference indicated |
| **Is the reference in the evidence?** | ☐ | Evidence description is correct |
| | ☐ | Reference name is correct |
| | ☐ | Correct populations present |
| | ☐ | Match statistics are those listed in case report |
| | ☐ | One in value is correct |
| **Match tables** | ☐ | Item numbers, descriptions, and reference columns match those found in the case report |
| | ☐ | LR and log(LR) values match those found in the case report |
| | ☐ | Blue fonts show positive match stats, red negative, and grey neutral |
| **Non-contributor/Contributor analysis for reference** | ☐ | Correct graph used |
| | ☐ | Item and reference numbers, descriptions are accurate |
| **Error Rate** | ☐ | Correct graph (with arrow) is used and does not 'move' when flipping between this and previous slide |
| | ☐ | Error rate, LR, and log(LR) values are correct |

## 10.7 Case DVD

*Overview*

The TrueAllele Case DVD provides a wealth of information regarding TrueAllele and case specific results to both prosecution and defense attorneys. This ~ 4 GB DVD provides education materials, validation studies, the VUIer software, and every case specific file produced in the case. This DVD can be used to answer any question lawyers may have regarding the TrueAllele analysis of a case. It also allows others to explore the results themselves.

*Materials*

The following outline provides instructions for the typical DVD.

Procedure:

- On Dropbox, make a copy of the *TrueAllele_DVD* folder.

- Append Cybergenetics case name to the end of the *TrueAllele_DVD* folder.

  • This creates a *TrueAllele_DVD_CASE* folder.

- In the *TrueAllele_DVD_CASE* folder.

  • Update top level *0-ReadMe.docx* with case specific information and the date. Save this document as a PDF, and delete the *.docx* file from folder.

  • Verify that the *1-Reliability* folder is up to date.

  • Verify that the *2-Validation* folder is up to date.

  • Review *3-Tutorials* folders for completeness and double-check against ReadMe file.

  • Add license key to *4-VUIer* folder:

    o Obtain a VUIer read-only license key (found on Case DVD page).

    o Paste the license key (hyphenating every 4 characters) to the *License.docx* file located in the *4-License* folder.

    o Save *License.docx* as *License.pdf.*

    o Delete *.docx* file after creating PDF.

  • In the *5-Case* folder:

    o Copy sequencer files to *1-Sequencer files* folder (files located on fileserve; information found on case page).

    o Add the TrueAllele case report(s) to *2-TrueAllele report* folder (from case page).

    o Add CVs of all analysts who signed the report to *3-Curriculum Vitae* folder (See CV Dropbox).

    o Add Case packet to the *4-Case packet* folder (from case page).

    o Add demonstrative aid to the *5-Demonstrative aid* folder when available (from case page).

    o Generate VUIer report *.tas* files for every report spec file found on the case page (including screening runs), and add to *6-VUIer files* folder. Ensure the CYB population is present/enabled when necessary.

    o Add all other files not contained in one of the above folders to the *7-Process files folder*, structured by case page section (e.g., Chain of custody,

Casework form, lab reports, lab EPGs, Request files, Report files, Results files, etc.). Add, change, and remove subfolders as needed.

- o Update *0-ReadMe.docx* with every file name that was added to the appropriate folder section.
- o Save *0-ReadMe.docx* as a PDF.
- o Delete *.docx* file from folder.
- Have another person verify *TrueAllele_DVD_CASE* folder before sending the DVD contents to the client.

*Verification*

Once the DVD materials are assembled, have another analyst verify the contents for accuracy.

Procedure:

- Verify that all ReadMe documents are filled in properly.
- Check that all files and supporting documentation are included in the *5-Case* folder.
- Ensure a valid license key is present.
- Check all VUIer report *.tas* files to ensure that they load.
    - Check that the CYB population is present (when necessary).

*Completion*

Once the DVD materials are verified, send these materials to the client.

Procedure:

- Once verified, send DVD Dropbox link to the client.
    - Use the TrueAllele trial materials message template found on the Case communications page as a guide.
- When physical DVD copies are needed:

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- Download the *TrueAllele_DVD_CASE* folder.
  - o Use a Windows computer when possible.
- Ensure no temporary files are present.
- Delete temporary files as needed.
-  Burn *TrueAllele_DVD_CASE* folder to 2 DVDs from a Windows computer:
  - o Disc title – CYB case name.
  - o Use default burning options.
  - o Label DVD as follows:
    - ♦ TrueAllele Case DVD
    - ♦ CASE NAME
    - ♦ Date
    - ♦ Initials
  - o Put burned DVD into case.
  - o Have someone verify the DVD once burn is complete.
  - o Typically, 2 DVDs are burned: 1 for the prosecution and 1 for the defense.
  - o Copy completed DVD folders to dedicated external hard drive in the Case DVDs folder.
- Edit and print DVD cover letter found on Case DVD page.
  - o Have another person verify this cover letter.
- Ship DVD to appropriate contact person via courier (e.g., FedEx).
  - o Courier account and shipping information found on Case DVD page.
    - ♦ Print shipping label.
    - ♦ Have another person verify this information.
    - ♦ Drop shipping envelope into courier box.

# 11  Genotyping Guidelines

The following sections provide additional details about genotype review.

## 11.1 Algorithm

The following diagram outlines the algorithm that may be used for the Iteration step of the operator Process.

**Algorithm**

ITERATE until termination

   % if a condition is recognized, then do action

   % one iteration may respond to multiple conditions with multiple actions
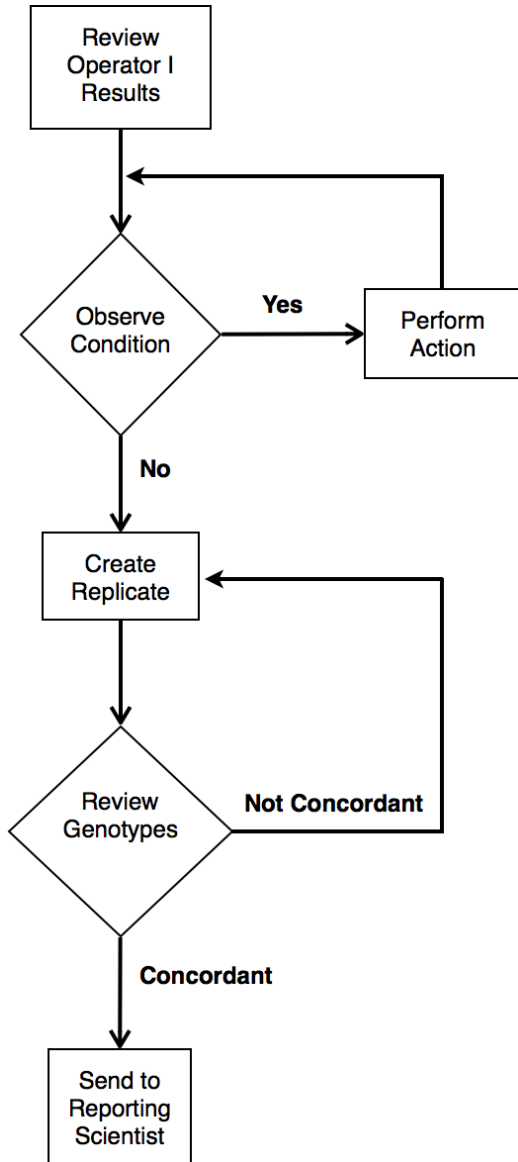
 IF SEE condition1 THEN DO action1

   ELSEIF SEE condition2 THEN DO action2

   ELSEIF SEE condition3 THEN DO action3

   …

   ELSEIF SEE conditionN THEN DO actionN

   END

## 11.2 Action

The following table provides descriptions of the processing actions an analyst may perform.

| *name* | *purpose* | *mechanism* |
|---|---|---|
| run a request longer | to provide the system with additional sampling | set request to run for a greater number of cycles |
| make a different contributor number assumption | provide the system more contributor freedom to explore the solution space | change request process to assume a different number of contributors |
| replicate a request | to demonstrate reproducibility | replicate the request |
| combine data | to provide additional information for the system to consider | create joint amp or item requests |
| assume degradation | to account for decreasing contributor mixture weights across the sample | create a request using the degraded DNA option |
| deactivate artifacts | to remove non-data peaks that may influence the inference | deactivate data peaks or loci in the Request module |
| provide case documentation | to provide case processing information to relevant individuals | annotate case notes according to protocol and provide case files |

## 11.3 Condition

The following table provides descriptions of possible data conditions an analyst may observe.

| name | symptom | possible cause |
|---|---|---|
| non-data artifacts peaks | non-data peaks are represented in the inferred genotypes | sequencer or chemistry issues |
| differential degradation of contributors | mixture weight ratios appear to change at higher molecular weight loci or number of contributors decreases as size increases | DNA deposited at different times or exposed to elements |
| uncertainty in contributor number | not all loci support a contributor assumption | data issues such as drop-in, drop-out, allelic overlap and degradation |
| mixture weight may not have converged | based on data review, unexpected distribution or mixture weight chains appear to still be searching | data issues, such as peak imbalance, can complicate the inference of the mixture weight |
| broad mixture weight histogram | based on data review, unexpectedly broad weight distribution | data issues, such as peak imbalance, or contributor assumption, can complicate the inference of the mixture weight |
| mixture weight unexpectedly sharp | based on data review, unexpected small standard deviation or rope-like chains | Markov chain may not have fully explored |
| ratio changing across loci | mixture weight ratios appear to change at higher molecular weight loci or number of contributors decreases as size increases | DNA deposited at different times or exposed to elements |

| | | |
|---|---|---|
| genotype not concordant across replicates | inferred genotype distributions do not appear similar | different contributor assumption, not enough sampling |
| LR values below 1/100 at one or more loci | matching allele pair is not represented in genotype distribution | additional sampling may be needed, alleles not present in data |

## 11.4 Condition > Action

The following table describes which processing actions may address specific data conditions.

| *condition* | *action* | *applicability* |
|---|---|---|
| non-data artifacts peaks | deactivate artifacts | non-data peaks are seen in the inferred genotypes |
| differential degradation of contributors | assume degradation | mixture weight ratios appear to change at higher molecular weight loci |
| uncertainty in contributor number | make a different contributor number assumption | client context suggests different contributor assumptions |
| mixture weight may not have converged | run a request for additional cycles | data has not received longer processing time yet time is available before results are required |
| broad mixture weight histogram | run a request for additional cycles | data has not received longer processing time yet time is available before results are required |
| | make a different contributor number assumption | client context suggests different contributor assumptions |
| | assume degradation | mixture weight ratios appear to change at higher molecular weight loci |

| | | |
|---|---|---|
| mixture weight unexpect-edly sharp | run a request for additional cycles | mixture weight has very tight histograms with a very low standard devia-tion |
| ratio changing across loci | assume degradation | mixture weight ratios ap-pear to change at higher molecular weight loci |
| genotype not concordant across replicates | replicate a request | additional replicates may be required |
| LR values below 1/100 at one or more loci | run a request for additional cycles | data has not received longer processing time yet time is available before re-sults are required |

## 11.5 Genotype Concordance

Below are some genotype concordance factors that may be helpful.

| *concordance* | *feature* |
|---|---|
| concordant | similar genotype probabilities inferred across independ-ent replicate requests |
| | replicate matching genotypes have similar mixture weights |
| | replicate genotype log(LR) match statistics are similar (for example, within 2 ban) |
| | replicate genotype LR contributor distributions form a single cluster |
| possibly non-concordant | different genotype probabilities inferred across inde-pendent replicate requests |
| | replicate matching genotypes have dissimilar mixture weight |

replicate genotype log(LR) match statistics are different (for example, not within 2 ban)

replicate genotype LR contributor distributions form multiple clusters

# 11.6 Assigning Genotypes

When assigning genotypes to matches, one of two algorithms is used, depending on the context of the results. Note that, regardless of algorithm used, concordance is assessed for all replicate genotypes.

**Algorithm 1, no reuse of genotypes**

This algorithm is used with validation studies and most casework. In this algorithm, each inferred genotype is used only once.

- Determine the greatest match between the inferred and reference genotypes across all references.
- Note the reference genotype for this match.
- In the replicate request, identify the greatest match between the inferred genotypes
- and this reference.
- Remove these inferred genotypes (and reference) from the set and repeat until all references are matched.

**Algorithm 2, with reuse of genotypes**

This algorithm is used with casework when considering kinship where an inferred genotype can be used more than once. As kinship genotypes are similar, they may, in some circumstances, produce positive matches to the same inferred genotype.

- Determine the greatest match between the inferred and reference genotype.
- Note the inferred genotype.

- In the replicate request, identify the greatest match between the inferred genotypes and this reference.
- Remove this reference from the set and repeat.

## 11.7 Case Documentation

The following table describes documentation typically included in a case record.

| document | feature |
|---|---|
| client case context | lab documentation indicating the items of interest and providing item context |
| client case report | original documentation of case processing from lab; may contain conclusions |
| data | sequencer files for data interpretation |
| TrueAllele results | inferred genotypes and matches stored on a TrueAllele World |
| request file | interpretation request record |
| report spec file | case import specification file for the Report module |
| match table | log(LR) statistics table for the inferred evidence geno-types vs. comparison genotypes |
| case notes | notes of the casework process |
| case communications and correspondence | Relevant communications and correspondence germane to case (e.g., case context, data receipt, etc. not about scheduling) |