BATCH PAPERWORK & ANALYSIS

Analyst

1) Bring all data files into GeneMarker and analyze using F6C_CT-DSS_29 or F6C-CT-DSS_Knowns template.
2) Save GeneMarker project to file folder that FSA files are in (U:\3130 NUCLEAR DNA CASEWORK & QC\To Be Analyzed).
3) Analyze samples, adding comments for all click-offs in evidentiary (forensic unknown) samples. Click-offs should mostly be dye-artifacts, raised baseline, and pullup peaks.
4) If a sample needs to be re-injected, or if for another reason you are not reporting out a sample, disable the sample by right-clicking on the file name in the left panel and note the reason on QR-300.
5) Re-save GeneMarker file when all click-offs have been made and all samples have been disabled.
6) Print out e-grams from samples and controls.
7) Export report as a text file to your “Analysis Export File” in your to be analyzed folder (This text file is used by the Concordance Checker, Cross-Comparison/Staff Search, Contributor Estimator, and Allele Table macros).
8) Run concordance checker (QR-37) if positive controls are present, using text file created.
9) Repeat steps 1 thru 8 if there are multiple injection sheets. For known sample batches, skip to step 17.
10) For each evidentiary (forensic unknown) sample project, start a new project by bringing in the same data files into GeneMarker, and analyze them using F6C_CT-DSS_29_STRmix template. Save GeneMarker project with identical name as before, but with “STRmix” added to the end.
    - **OR** you can re-analyze your data from the current project by pressing the green play button again. A message will come up asking if you want to re-call the size standard. You want to check the box for “Call Size Again” and click on “Apply to all”. Don’t forget when you save this file to save it with STRmix added to the end.
11) Using your analysis on the egram peak tables as a guide, click off all the same peaks you just clicked off with exceptions (that will all come up as non-concordances when you run your project comparison, but just note it in the comments section):
    - If you clicked off a stutter peak because pullup contributed to it, leave this peak in your STRmix project. Provided that the peak is still greater than 50 rfu, with pullup subtracted, and the pullup is not responsible for the majority of the peak height.
    - If you clicked off a peak as high stutter, leave this peak in your STRmix project.
    - Same goes if any of these peaks are a combo of N+1 and N-1 stutter
        - There might be exceptions to this, for example, if the subtraction of pull-up brings the stutter peak below 50rfu, STRmix should not see this peak, and if the

pull-up contribution adds an unusually large amount of height to the stutter peak, it might be better for STRmix not to see such a high peak. Ask for assistance if you are unsure.

12) Disable all samples that you disabled in the previous project.
13) Re-save GeneMarker file when all edits have been made and all samples have been disabled.
14) Export report as a text file, same location as file created in step 7.
15) Run project comparison macro, QR-301, using the exported text files for your fully analyzed project and your STRmix project.
    - If there are any discrepancies not accounted for in your analysis, you must correct them in the appropriate GeneMarker project. Then re-save the GeneMarker projects AND re-export the text files AND re-run project comparison Macro.
    - Keep repeating this until the number of discrepancies can be explained by your analysis.
    - Print out this sheet for the batch paperwork; you only need the final copy in your batch.
16) Create a contributor # estimation (QR-302) sheet for each sample with results. Remember that you should generally use any non-artifact peaks below AT (25-49 rfu) for this worksheet. If it's a single source sample, or you feel you don't need the macro to assist you in determining number of contributors, you still need this sheet, but add notes to the comments area as to your determination of number of contributors.
    - Check the box in the Notes section if you used peaks below AT.
    - Note minimum number of male contributors on designated line.
    - Note: Peaks below the AT at Y-STR loci may be used to assist in assessment of overall contributor number. However, the minimum number of male contributors is based only on peaks at or above the AT.
17) Initial and date QR-4A (Batch Paperwork Review Worksheet).
18) Give batch to Technical Reviewer to review changes.

Technical Reviewer

1) Review all batch paperwork.
2) Open the Analyst's fully analyzed (non-STRmix) project.
3) Review samples, note any differences to the 1st Analyst. Check that:
    a. Correct analysis template is used.
    b. Analyst's assessment of size standards, ladders, controls, and potential contamination are appropriate (see SOP sections 31.5.2 and 31.5.3 and WI-35 Steps 6-7 under Creating a Project).
    c. All called peaks appear to be true alleles.
    d. All deletions/edits made are appropriate.
    e. For database samples, confirm that Specimen Categories are assigned correctly.
    f. If applicable, check that project concordance as documented on QR-301 is acceptable.
4) Initial and date QR-4A.

5) Give batch to Administrative Reviewer.

Administrative Reviewer

1) Review all batch paperwork.
2) Initial and date QR-4A.
3) Give batch back to Analyst.

Analyst

1) Review & make any corrections.
    a. If additional click-offs need to be made, or click-offs need to be undeleted, do so in both STRmix and Allele Report project. Re-save both GeneMarker files. Re-export both text files and re-run project comparison Macro.
2) Initial and date QR-4A. Return batch to Technical Reviewer.

Technical Reviewer

1) Review any changes made by 1st analyst.
2) Add batch name to spreadsheet on U-drive.
3) Initial and date QR-4A.
4) Return batch to Analyst.

Analyst

1) Make photocopies of injection sheets for case jackets in batch. Original Q/K sample e-grams & original contributor estimator are just for case jackets, not to be in batch paperwork.
2) Scan batch paperwork (not containing Q/K sample e-grams & contributor estimator sheets) & save PDF file to u-drive.
3) Move FSA and project files from “To Be Analyzed” to “Completed” folder on U-drive.
4) Give batch paperwork to Technical Reviewer to review.

Technical Reviewer

1) Ensure all pages scanned and PDF file on u-drive is complete and accurate.
2) Ensure FSA folders have been moved to U:\3130 NUCLEAR CASEWORK & QC\Completed.
3) Add initials to batch paperwork spreadsheet.

CASEWORK

Analyst

1) Enter all possible profiles into CODIS.
2) Make comparisons of all knowns to all Q's in case.
    a. Does a sample have 5+ contributors?
        i. If so, do any of the knowns CBE to the sample warrant being conditioned? If yes, does that bring it down to 4 unconditioned contributors?
            1. Yes – can interpret.
            2. No – inconclusive or elimination.
    b. Samples that are clear eliminations are not run through STRmix, "Eliminate by Analyst" in report macro.
    c. Comparisons that are not clear eliminations, are run through STRmix.
        i. Reported out comparison based on LR calculated.
    d. If reporting out a statistic for a comparison, deconvolute in STRmix with appropriate knowns conditioned to profile.
        i. Report out comparison based on LR calculated.
        ii. If not reporting out a statistic (i.e. intimate sample with no suspect known submitted, single source sample when known expected on sample), no need to run STRmix, enter "assumed" in report workbook.
    e. Does a sample only have results at one locus? → inconclusive or elimination by analyst
    f. Are you unable to determine the number of contributors with reasonable scientific certainty? → inconclusive or elimination by analyst
    g. Is there a problem with the deconvolution discovered Re: 2nd diagnostics that can't be resolved? → inconclusive or elimination by analyst
3) If a sample is deconvoluted through STRmix:
    a. The file will automatically save onto the server, under F:\results.
    b. Print out pages 1 and 3 of the advanced report.
    c. Scrutinize advanced reports for any problems with the deconvolution.
        i. Fill out QR-303 for the 2nd diagnostics for each deconvolution.
    d. Move the file in the F:\results folder to your folder in F:\ results.
    e. Create a folder in your folder for this case, named with the case number in format DSS-XX-XXXXXX, and move that folder into this newly created case specific folder.
4) Review case jacket, write report.
5) Give case jacket to TR.

Technical Reviewer

1) Review case jacket, comparisons and report as you normally would.
    a. If you disagree with an eliminated comparison, the 1st Analyst will have to run this sample through STRmix.
2) If you need to review more of the Advanced Report than is in the case jacket, you can find it on the STRmix server, F:\Results in the Analyst's folder, in the folder specific to this case

3) Give case jacket to AR.

Administrative Reviewer

1) Review case jacket, comparisons and report as you normally would.
    a. If you disagree with an eliminated comparison, the Analyst will have to run this sample through STRmix.
2) If you need to review more of the Advanced Report than is in the case jacket, you can find it on the STRmix server, F:\Results in the Analyst's folder, in the folder specific to this case
3) Give case jacket back to Analyst.

Analyst

1) Make all appropriate corrections to report and case jacket.
2) If either the TR or the AR disagreed with one of your elimination calls, you must run that sample through STRmix, print out appropriate pages and fill out QR-303.
    a. The report will have to be re-worked:
        i. If it is still an elimination, it is now "elimination by STRmix", and not "elimination by analyst", report wording will be different.
            1. If it is no longer an elimination, report out result based on LR.
3) Print out final copy of report.
4) If there are STRmix results, move the folder for this case from your folder on the server's F-drive to F:\results\Completed.
5) Give case jacket to TR for correction check.

Technical Reviewer

1) Ensure all corrections are accurate.
2) If additional deconvolution work needed to be completed, make sure new wording in report is accurate and review all additional paperwork.
3) If there's STRmix data, check to make sure the folder has been moved to F:\results\Completed.
4) Give case jacket to AR for correction check.

Administrative Reviewer

1) Ensure all corrections are accurate.
2) If additional deconvolution work needed to be completed, make sure new wording in report is accurate and review all additional paperwork.
3) Give case jacket back to analyst.

CODIS

Analyst

1) If there is a CODIS hit for a sample of yours, you will be notified by the CODIS administrator/alternate or their designee.
2) If a deconvolution of this sample has already been completed, the case jacket can be brought to the CODIS administrator/alternate or their designee.
3) If a deconvolution of this sample has not yet been completed, deconvolute the sample, making sure to condition any knowns that you assumed when writing the report.
    a. Print out page 1 of the advanced report, fill out QR-303, and give the case jacket to your TR to review the additional paperwork. You can check, initial, and date next to 3.D. on QR-4.

Technical Reviewer

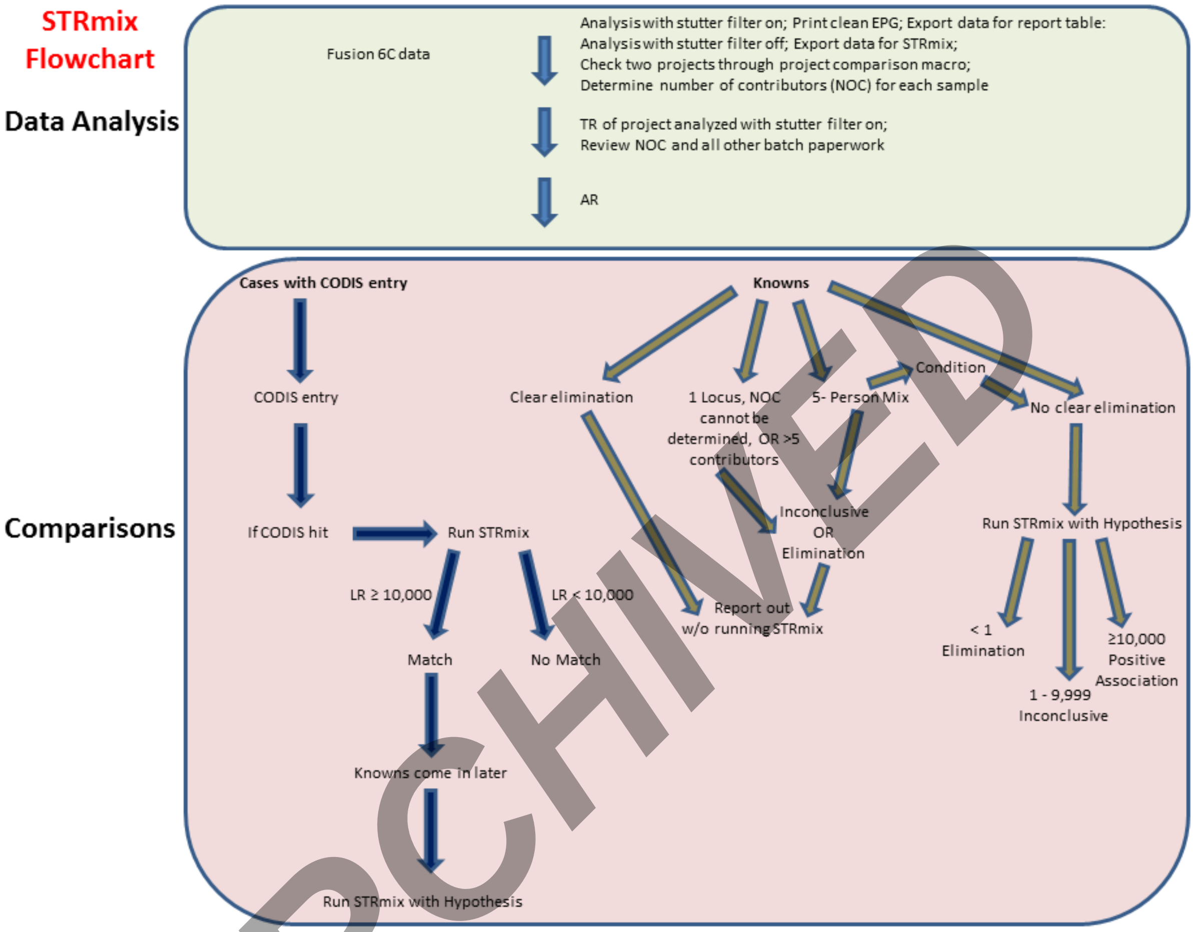
1) Review additional paperwork in case jacket.
2) Check, initial and date next to 3.D. on QR-4.
3) Give case jacket to the CODIS administrator/alternate or their designee.

Analyst

1) When you receive your case jacket back for initials, move your STRmix folder to F:\results\completed. Check, initial, and date that you did so on QR-4.

OTHER

1) If a known comes in later on that warrants being conditioned, all deconvolutions need to be repeated with a new deconvolution, and a new statistic is calculated.
2) If a known comes in later that's not clearly eliminated regarding a sample that has already been deconvoluted, use the "LR to previously analysis" function of STRmix, and do not repeat the deconvolution.
3) Similarly, if you have a Q in the case, and two knowns are CBE to that sample, only deconvolute the sample once. For the 2nd known, use the "LR to previous analysis" function of STRmix.


STRmix Flowchart
Data Analysis
Fusion 6C data
Analysis with stutter filter on; Print clean EPG; Export data for report table:
Analysis with stutter filter off; Export data for STRmix;
Check two projects through project comparison macro;
Determine number of contributors (NOC) for each sample
TR of project analyzed with stutter filter on;
Review NOC and all other batch paperwork
AR
Comparisons
Cases with CODIS entry
CODIS entry
If CODIS hit
Run STRmix
LR ≥ 10,000
LR < 10,000
Match
No Match
Knowns come in later
Run STRmix with Hypothesis
Knowns
Clear elimination
1 Locus, NOC cannot be determined, OR >5 contributors
5- Person Mix
Condition
No clear elimination
Inconclusive OR Elimination
Report out w/o running STRmix
Run STRmix with Hypothesis
< 1 Elimination
1 - 9,999 Inconclusive
≥10,000 Positive Association