

## FORENSIC BIOLOGY PROTOCOLS FOR FORENSIC MITOCHONDRIAL DNA ANALYSIS

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#### MITOCHONDRIAL DNA GUIDELINES

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## **Mitochondrial DNA Guidelines**

PURPOSE: Guidelines for mitochondrial DNA testing to ensure clean laboratory practices, unambiguous sample identification, and relevant control runs.

### A. <u>General Procedures:</u>

To reduce the possible contamination in the laboratory that could occur: (i) between the analyst and the samples (ii) from one sample to another, or (iii) from extraneous sources of DNA within the laboratory.

- 1. Lab coat, gloves, and mask, eye protection, and on face shield, must always be worn while in the exam and pre-amplification room. Lab coat, gloves, eye protection must be worn in the post amplification area. All gowning must be done in the vestibules of exam, pre-amp or post amp rooms.
- 2. Lab coats can be reused for a period of one week. Afterwards, they should be thrown out. Masks/face spields can also be reused for a period of one week. Goggles can be exposed to V light in the Stratalinker to extend their time of use.
- 3. When working in the exam or pre-amplification laboratory, gloves must be rinsed in 10% bleach before each procedure and in-between the handling of separate samples.
- 4. Pipettes must be wiped down with 10% bleach before each procedure, and between the pipetting of separate samples.
- 5. All hoods must be wiped down with 10% bleach before and after each procedure, followed by 70% Ethyl Alcohol rinse, and UV light, if available, should be applied for 39 minutes before and following each procedure.
- 6. All racks tube-openers and any other plastic implements (but <u>not</u> the pipettes) must be exposed to UV light in the Stratalinker for a minimum of 30 minutes before they can be used for amplification or extraction.
- 7 Any 96-well tube racks taken from the pre-amp room to the post-amp room must be placed into the post-amp bleach bath, rinsed, and dried prior to being returned to the pre-amp room.
- 8. All 1.5ml and 0.2ml tubes can be kept in plastic Nalgene boxes or comparable containers, and should only be removed with bleached and dried gloves while fully gowned. Prior to placement of tubes into these containers, the tubes used for, washing, extraction and amplification must be exposed to UV light in the Stratalinker for 30 minutes.

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9. Counters, sinks, refrigerator/freezer handles and door handles inside the laboratory and gowning room should be wiped down with 10% bleach on a monthly basis.

#### **B.** Nomenclature

The following are suggested naming conventions for use throughout the sample processing. The goal of this nomenclature is to ensure that sample names are unique identifiers.

- 1. Samples re-extracted for the purposes of duplication (new cutting): The suffix : "dup" will be added to the sample name to separately identify the re-extraction sample from the original, and this suffix will be applied to these duplication samples throughout the processing
- 2. Samples reamplified in order to improve on the quality of the results or for other purposes: The suffix "reamp" will be added to the sample name. If multiple reamplifications are necessary, the numeral 1, 2, 3, etc. will be added to the suffix.
- 3. At the 3130xl run step:
  - The suffix "recyc" wilk added to each sample name for samples that are resequenced (e.g. sample-recyc). If multiple re-cycle sequences are necessary, the numeral 1, 2, Setc. will be added to the suffix.
  - The suffix "cont" will be added to each sample name for samples that are resequenced to confirm sequence or length heteroplasmy (e.g. sample-conf). If multiple confirmatory sequences are necessary, the numeral 1, 2, 3, etc. will be added to the suffix.
  - The uffix "reinj" will be added to each sample name for samples that are reinjected (e.g. sample-reinj). If multiple reinjections are necessary, the numeral 1, 2, 3, etc. will be added to the suffix.
  - The primer used will be added as suffix to each sample name. This suffix will always be added last, e.g. sample-B4, sample-recyc-1-B4, sample-conf-2-B4, sample-reinj-3-B4.
- 4. Contig name:
  - A contig name should be: FBYY-12345-HVI, or FBYY-12345-HVII, or FBYY-12345-HVI dup, FBYY-12345-HVII dup

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- In certain cases more than one sample will be typed and identifiers could be added after FBYY-12345, e.g. FBYY-12345(V)-HVI, FBYY-12345-PM7-HVI, FBYY-12345-PM1-HVI, FBYY-12345-Q1-HVI, FBYY-12345-Q2-HVI
- 5. Sequencher ID
  - The sequencher ID of an analyzed run will be identical to that run ID, e.g. SYY-123.
  - The sequencher ID of a case will be identical to the FB case number, e.g. FBYY-12345.
  - The sequencher ID for a Missing person case will be the FB# space MP (e.g. FBYY-12345 MP) 1724120

#### С. **Repeat Analysis of Samples**

Repeat testing of a sample can start at different ages, as listed below. Appropriate controls must be used.

- Extraction stage: A new extraction regative control must be run. 1.
- Amplification stage: New amplification negative and positive control must be 2. The extraction negative control does not need to be repeated if it included. previously passed.
- 3. Cycle sequencing: Positive and negative controls must be tested for each primer used. The original extraction negative does not have to be repeated if it passed for all needed sequences. The original amplification negative does not have to be repeated if it passed for all needed sequences; a cycle sequencing negative (cAN) should then be used (20 µl H<sub>2</sub>O) for each primer used. The original positive control should be used and suffixed recyc for each primer used; however, any positive ontrol can also be used as long as the contig of interest can be built with that positive control. Note that if a sample needs to be re-sequenced with a primer because the positive control at that primer failed, then every control or sample in that run needs to be re-sequenced with that primer.

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### **D.** Batching and Duplication Guidelines

Duplication of samples is only necessary from when samples are batched.

Exemplar samples batched and extracted for nuclear DNA may be duplicated with a second nuclear DNA extraction and STR typing.

For mtDNA, duplication of a given sample can be accomplished by running one informative primer for that sample in either HVI or HVII.

- 1. Evidence samples
  - a) Batching of evidence samples will be allowed at all steps of mtDNA analysis including the DNA extraction stage. When batching evidence samples at the extraction stage, a maximum number of five samples can be batched. Duplication at the extraction level can be done for case-related reasons (see supervisor).
  - b) Identical mtDNA profiles in olving at least one evidence sample (two evidence samples or one evidence sample plus an exemplar) within a case are considered duplicated for the evidence sample.
  - c) Duplication of sample at the quantification level is not required. Evidence samples may be duplicated if they do not match any other sample in the case at the discretion of a supervisor.
  - d) Duplication of evidence samples may begin at the amplification or cycle sequencing steps if there is no additional evidence material for extraction or amplification, respectively.
- 2. Exemplar samples
  - a) Batching of exemplar samples from different cases will be allowed at all steps of mtDNA analysis including the DNA extraction stage.
  - b) HVI-HVII amplification and sequencing of exemplar samples from the same case (e.g. family members, duplication samples) should be performed at least once separately.
  - c) Suspect exemplars will be duplicated if that sample matches an evidence sample.

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- d) Victim exemplars will be duplicated if they do not match any other sample in the case and if that exclusion is informative.
- e) Missing Persons' exemplars and unidentified remains do not need to be duplicated.
- f) Any exemplar may be duplicated for case related reasons or to streamline testing.
- 3. Exemplar with Evidence samples

With the exception of quantification evidence and exemplar samples must always be tested separately in time and/or space. Batching of evidence with exemplar samples is allowed during the DNA quantitation step. Batching of evidence with exemplar samples is also allowed during Agilent matysis provided that sample aliquots are done on each sample type (evidence or exemplar) at separate times. Quantification steps do not need to be duplicated.

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Revision History:

July 24, 2010 – Initial version of procedure.

February 28, 2011 – Removed "product gel" from Paragraph D.3.

July 16, 2012 - Minor revisions in content to generalize terminology for LIMS.

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April 1, 2014 – Modified section D (Batching and Duplication Guidelines). Batching of evidence in now allowable at all steps of mDNA analysis. Policy for duplication of evidence has been modified to be at the discretion of the supervisor if sample results are not duplicated in the case.

#### HAIR EVIDENCE EXAMINATION

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## Hair Evidence Examination

#### **General Guidelines**

Refer to Evidence and Case Management Manual for general laboratory guidelines for evidence examination, note-taking, itemization, and preparation for evidence examination.

#### A. <u>Hair Evidence Examination</u>

- 1. Record all packaging documentation and open packaging a dead-air hood (preferred) or comparable (e.g. enclosed space).
- 2. Document the hair examination. Note the hair approximate length and whether or not the hair is mounted.
- 3. If hair is <1 cm in length, see supervisor. If the hair will be consumed indicate in case notes that the sample coll be consumed for testing and proceed.
- 4. For hairs that are loose, proceed with the 5. For hairs that are mounted, proceed with demounting (See "Washing Hairs for Mitochondrial and Nuclear Testing", part A) and then return to step 5.

Note: It is at the analyst's discretion to photo document hair mounted on a slide at this step. In this case follow step 5 below prior to demounting hair.

- 5. Take a picture of the full fair:
  - Digital or Mideo pipture can be made.
  - If the hair is uncounted, it can be placed in a weigh boat.
  - Place hair appropriate background for photo documentation. Brown, black, or darker colored hairs should be placed on a white sheet of clean paper. Blonde, white or light colored hairs should be placed on a darker background.
  - Take a digital/Mideo photograph of the full hair, including a ruler/measurement in the frame. For digital pictures, be sure the digital camera is set to Macro (flower) and the flash is off before taking the picture. For Mideo pictures, see Mideo Macro/Microscopic Digital Imaging System below (see part B).
    - i. Save /export pictures as the LIMS attachments.
    - ii. Print digital and Mideo images for case file (see part C).

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### B. Mideo Macro/microscopic digital imaging system

- 1. Make sure the computer is on and all of the proper cables are connected between the Firewire camera and the computer.
- 2. Double-click on the desktop shortcut **EZDocPlus**.
- 3. The main program screen will appear. Click on "Camera" and select "Micro Cam M". The QCam Microcam Control Panel will appear.
- 4. Make sure at this point that the stereo microscope is on, the light source is active, and the specimen is in focus. When viewing solid, dark objects, it is best to use the ocular light ring to illuminate the sample. When viewing slides or thin tissue samples, use the direct light from the lamp base of the microscope.
- 5. On the **Microcam Control Panel shows to the right**), perform the following:
  - a. Click the **Live** button
  - b. Adjust the binning so that the setting is 3 for both the horizontal approvertical.
  - c. Check the **Flip Image** box.
  - d. Click the **Auto Opposure** button.
  - e. Adjust the intensity of the light and click Auto Exposure if the image is too bright or too dark.

**NOTE:** To the background color is not white or off white, place a sheet of paper in view of the lens and click on the White Balance button. Repeat step 5d once completed.

QCam Macrocam	×		
Basic Exposure White B	alance Advanced		
Auto Expose	White Balance		
Camera Default	Clip To Rect		
Binning	Cooling		
Horizontal 1	Flip Image		
Vertical 1	Load Settings		
Adjust Exposure when binning changes	Save Settings		
Live Grab			
Close			

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- 6. Once the image on the screen is in focus and there is proper contrast, click the **Grab** button on the control panel. This will freeze the image on the screen.
- 7. Under the **Tools** menu, select **Overlays**. Once the panel opens up, perform the following:
  - a. Click on the **Measure** tab.
  - b. Click the **Load Calibration** button.
  - c. Select the calibration based on the current microscope magnification level.
  - d. FOR LINEAR OBJECTS
    - 1) Click on the **Length** button.
    - 2) Select any of the length tools to measure the length of the imaged object.
  - e. FOR NON-LINEAR OBJECTS
    - 1) Click on the **Multilength** button
    - 2) Trace the non-linear object length by left-clicking the mouse at desired turns and corners. Hit "Enter" on the keyboard when finished.



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- 8. Save the image by going to the File menu and selecting Export Image.
- 9. Save image with case identifying name (e.g. FB07-04117 Item 1A-1).
- 10. Import the saved image into the LIMS as an attachment for the evidence item.

### C. Printing digital and mideo images for case file

- 1. Open Microsoft PowerPoint.
- Go to File menu and select Page Set-up. Change slide origination from landscape 2. to portrait.
- 3. Import pictures
- 4. Add Sample ID. Add comments if needed.
- Save as FB# in Photo Archives 5.

**Revision History:** 

July 24, 2010 - Initial version of procedure.

July 16, 2012 - Minor revisions in content to generalize terminology for LIMS.

WASHING HAIR FOR MITOCHONDRIAL OR NUCLEAR DNA TESTING

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## Washing Hair for Mitochondrial or Nuclear DNA Testing

PURPOSE: To prepare hairs for DNA extraction.

## A. Demounting

- 1. If the hair is loose, then proceed to the appropriate hair washing procedure. If a "possible root" is observed, the sample should be cut and washed for nuclear DNA testing extraction (see part C).
- 2. If the hair is mounted:
  - Process only one mounted slide at a time. i.
- 12412 Turn on the heat plate and adjust the heat dial between 100-110°C. Place ii. the slide on a heat plate until the mountant softens and using forceps remove the cover slip. The prountant oftens quickly and hairs will scorch if left on the heat plate too we.
  - The hair will be attached to either the coverslip or the slide. Remove hair iii. and place into a xytene bath for up to 5 minutes or until the mountant completely dissolver. Was and slides/coverslip containing hairs can be kept in the xylene bath for longer than 5 minutes if necessary.
  - Using clean forceps carefully remove the hair from the xylene bath iv.
  - It is at the discretion of the analyst to make a picture of the full hair at this v. time.
  - Proceed to the appropriate hair washing procedure. vi.

## B. Washing the hair for mtDNA testing extraction

- Using Oceps and a scalpel cut a 2 cm region of the hair or hair shaft. A picture 1. of the cutting should be taken at this time. If the hair is also to be tested for nuclear DNA, the mitochondrial DNA cutting should be away from the root. Place the unused portion of the hair onto the backing of a post-it note and return to the packaging
- 2. If "possible tissue" attached to hair is observed, see your supervisor. In some cases the hair will not be washed, proceed to step 11 and enter N/A as **TergAZyme and Saline lot #.**
- 3. Prepare 5% TergAZyme solution by adding 15ml of GIBCO water to 0.75g of TergAZyme. Mix well. Record TergAZyme lot #.
- Using clean forceps, place the hair fragment cutting into a 1.5 ml tube with 1 ml 4.

#### WASHING HAIR FOR MITOCHONDRIAL OR NUCLEAR DNA TESTING

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of 5% TergAZyme solution. Vortex the tube for 1 minute at high speed, and place into the sonicator for 15 minutes. After sonication, vortex the sample again for 1 minute at high speed.

- 5. Prepare a 50 ml Falcon tube and filter cup. Label the tube and filter cup tab with the sample name. Pre-wet the filter cup membrane with 1 ml of Gibco  $dH_2O$ .
- 6. Remove the hair from the TergAZyme with clean forceps, and place the hair into the filter cup in the center of the membrane.
- 7. Wash the hair with 1 ml of Gibco  $dH_2O$ . Allow the liquid to pass through the filter.
- 8. Wash the hair with 1 ml of 0.85% saline. Allow the liquid to pass through the filter. Record Saline Lot #.
- 9. Wash the hair with 1 ml of 100% ethanol. Allow the iquid to pass through the filter.
- 10. Remove the filter cup containing the hair and place on a Kimwipe to let the ethanol evaporate. Once the filter membrane is dry, the hair will be dry as well.
- 11. Transfer the cut hair fragment to the bottom of a clean 1.5 ml tube. Label the tube.
- 12. Store the tube containing the hair tragment in the appropriate "To Be Extracted" cryobox in the pre-amplification aboratory freezer.
- 13. Proceed to Mitochondrial extraction for mitochondrial DNA testing procedure.

## C. <u>Washing the hair for nuclear NA testing extraction</u>

1. For nuclear DNA extractions, using forceps and a scalpel cut up to 1.5 cm of the proximal region of the hair, including the root. Place the unused portion of the hair onto the backing of a post-it note and return to the packaging. A picture of the root should be taken at this time.

# If "possible tissue" attached to hair is observed, see your supervisor. In some cases the hair will not be washed, proceed to step 11 and enter N/A as Saline lot #.

- 2. Prepare a 50 ml Falcon tube and filter cup set by labeling the tube and filter cup tab with the sample name. Pre-wet the filter cup membrane with 1 ml of 0.85% saline. Document Saline lot #.
- 3. Using clean forceps, place the cut hair into the filter cup in the center of the membrane.
- 4. Wash the hair with 1 ml of 0.85% saline. Allow the liquid to pass through the filter. Repeat that step.
- 5. Wash the hair with 1 ml of 100% ethanol. Allow the liquid to pass through the filter.

#### WASHING HAIR FOR MITOCHONDRIAL OR NUCLEAR DNA TESTING

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- 6. Remove the filter cup containing the hair and place on a Kimwipe to let the ethanol evaporate. Once the filter membrane is dry, the hair will be dry as well.
- 7. Transfer the cut hair fragment to the bottom of a clean 1.5 ml tube. Label the tube.
- Store the tube containing the hair fragment in the appropriate "To Be Extracted" 8. cryobox in the pre-amplification laboratory freezer.
- . th .ig the . .NA testing pre ARCHINED mator WAARAA 9. Within the LIMS system, indicate the cutting was made on the evidence item and schedule the appropriate DNA extraction procedure using the sample creation wizard.
- 10. Proceed to Mitochondrial extraction for nuclear DNA testing procedure.

**Revision History:** 

July 24, 2010 – Initial version of procedure.

July 16, 2012 – Minor revisions in content to generalize terminology for LIMS.

ORGANIC EXTRACTION FOR MITOCHONDRIAL OR NUCLEAR DNA TESTING

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## Organic Extraction for Mitochondrial or Nuclear DNA Testing

Refer to the current *Protocols for Forensic STR Analysis* manual for extraction, quantitation, amplification, and STR procedures currently on-line for other Nuclear DNA Operations.

<u>PURPOSE:</u> To isolate nuclear or mitochondrial DNA from the hair using an enzymatic digestion of the hair followed by an organic extraction.

## A. Extraction for Mitochondrial and Nuclear DNA testing

- 1. Prepare hair for digestion by removing the appropriate microcentrifuge tube from the "To Be Extracted" cryobox. Record the Organic Extraction documentation.
- 2. Prepare the incubation solution in a 1.5ml tube using the following table. Label this tube with the extraction date and time as CNEGDDMMYY-HHMM.

Reagents	1 hair + extraction negative		
Proteinase K (20mg/ml)	30 µl (15*2)		
DTT (1M)	75 μl (37.5*2)		
20% SDS	7.5 µl (3.75*2)		
Organic Extraction Buffer	188 µl (94*2)		

- 3. When extracting clumps of hair, or multiple hairs together, the total volume of the incubation solution can be increased 2- to 10-fold, to accommodate the size of the sample. Adjust the reagent volumes to accommodate these changes. Be sure to record such volume changes in the documentation.
- 4. Have the extraction tube set-up witnessed.
- 5. Aliquot 150  $\mu$ l of the incubation solution into the 1.5ml tube containing the hair and leave the remaining solution in the original 1.5ml tube as the negative control.
- 6. Incubate samples for 30 min. in a 1400 rpm shaker at 56°C. Record the number of the thermal mixer , the thermal mixer temperature setting and actual temperature in the documentation.
- 7. After 30 min., hairs should be dissolved. If not, incubate for a total of 1-2 hours. If hairs have not dissolved, add 1µl of 1M DTT and incubate overnight. Be sure to record this on the extraction documentation, if performed. Hairs and control

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samples should be both treated the same way. After overnight incubation, record the thermal mixer setting and temperature in the documentation.

- 8. When the hair sample is completely dissolved, proceed with the extract to the purification step (see part B)
- 9. The hair sample might not completely digest even after the overnight incubation. If the hair is chemically treated, straightened, or dyed, it might resist digestion. The incubation process might remove the pigment or coloring from a hair and leave it opaque. If this happens, record this observation in the documentation. Centrifuge the sample for 3-5 minutes at full speed. Collect the supernatant (extract) in a new tube, carefully without disturbing the peller. Add the suffix "– R" to the sample name and label on the original tube correlation the hair remain (pellet). Hair remains will be stored with the other sample. Proceed to purification step with the extract (see part B).

## **B.** Purification of DNA for Mitochondrial and Nuclear DNA testing

- 1. During the incubation, prepare and label for each sample: one Eppendorf Heavy Phase Lock Gel (PLG) tube, one microson filter, three microcon collection tubes, and one 1.5 ml tube for final extract. PLG tubes can be centrifuged for 30 seconds at maximum speed prior to sample addition.
- 2. After incubation, have the purfication tube set-up witnessed.
- 3. Transfer each extracted sample to appropriate labeled PLG tube. PLG tubes make the phase separation between organic and aqueous layers of an organic extraction easier. To each PLG tube add an equal volume of Phenol: Chloroform: Isoamyl Alcohol (25:24:1 PCIA). The PCIA volume to be added should be 150µl unless the extraction volume has been increased in step A3. PCIA is an irritant that is toxic. Its use should be confined to a certified fume hood. Gloves and a mask should be worn.
- 4. Shake obriefly vortex the tube to achieve a milky emulsion.
- 5. Centrifuge the tube in a microcentrifuge for 2 minutes at maximum speed.
- 6. Insert Microcon DNA Fast Flow filter cup (blue) into labeled microcon tubes for each sample.
- 7. Prepare the Microcon concentrator by adding 100  $\mu$ l of TE<sup>-4</sup> to the filter side (top) of the concentrator.
- 8. Transfer the aqueous phase (top layer) from the PLG tube to the prepared Microcon concentrator. Do not disturb the PLG layer. Discard the PLG tube containing the organic layer into the organic waste bottle in the fume hood.
- 9. Spin the Microcon concentrator for 25 minutes at 500 rcf.
- 10. Transfer the Microcon filter cup into a new labeled Microcon tube and add 400 µl

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of TE<sup>-4</sup> to the filter side (top) of the concentrator.

- 11. Spin again at 500 rcf for 20 minutes. After this spin, if liquid is still observed on the membrane, spin again at 500 rcf for an additional 6 minutes. After this spin, if liquid is still observed on the membrane, continue spinning for a longer time.
- 12. Add 20  $\mu$ l of TE<sup>-4</sup> to the filter side (top) of the concentrator.
- 13. Invert the blue concentrator cup and place into appropriate microcon collection tubes. Spin at 1000 rcf for 3 minutes to collect samples.
  - For mitochondrial DNA testing,
    - Using a pipetter, measure volume collected and record it.
    - Transfer samples to a 1.5 ml microcentrifuge tube for sparage.
    - Adjust samples volume to 50  $\mu$ l using TE<sup>-4</sup> record (hese volumes.
    - Proceed with HVI-HVII amplification with 20µVor samples.
  - For nuclear DNA testing,
    - Using a pipetter, measure the volume collected
    - The volume should be close to 20ul, in control and hair samples. If the volume is  $>30\mu$ l, prepare a new microcon filter and tube (see part 6 above) and spin at 500 rcf, control and half samples, for an additional 6 minutes. After this spin, if liquid is sold observed on the membrane, continue spinning for a longer time.
    - Measure the final volume elected and record it.
    - Transfer samples to a siml microcentrifuge tube for storage
    - $\circ$  Send 2.5 µL of samples (neat) for nuclear quantification. If quantitation results show an insufficient amount of nuclear DNA for STR testing, the extract may then be used for mtDNA analysis.

**Revision History:** 

July 24, 2010 – Initial version of procedure.

November 4, 2010 – Added instruction for thermal mixer documentation.

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July 16, 2012 - Minor revisions in content to generalize terminology for LIMS.

December 31, 2012 – YM100 microcons were discontinued by the manufacturer. The manufacturer is now producing the DNA Fast Flow Microcons. All references to the YM100's have been revised. Spin times in Section B, Steps 11 and 13 have been revised for the new microcons.

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#### DUPLEX MITOCHONDRIAL DNA PCR AMPLIFICATION

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## **Duplex Mitochondrial DNA PCR Amplification**

<u>PURPOSE:</u> To increase the amount of available mtDNA for the purposes of analysis, by performing an *in vitro* replication of template DNA using oligonucleotide primers, thermostable DNA polymerase and deoxynucleoside triphosphate bases (dNTPs) within a thermal cycler.

#### PROCEDURE:

A positive control, an amplification negative, and an extraction negative control (if applicable) should be included with each batch of samples being amplified to demonstrate procedural integrity. The positive control is a laboratory grade cell line, for which the mtDNA type is known.

Follow the mtDNA pre-amplification guidelines for mandling the tubes and cleaning of the work surfaces. The following steps have to be performed in the oppropriate dedicated areas. Evidence samples and exemplar samples should not be handled in the same time.

## A. Preparing the DNA aliquits for HVI-HVII amplification

- Amplification can be performed with either Roche or Homebrew reagents.
   Homebrew reagents should be used for Missing Person's testing only.
- When amplifying extracts which have nuclear DNA quantification data, the target amount of extract to be amplified is:
  - 1000 when using Roche reagents
  - **A pg** when using Homebrew reagents
- When amplifying samples that have not been quantified (e.g., hair shaft samples), use 20ul of the extract and Roche reagents, only.
- Table I refers to the preparation of the control samples for the amplification.

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#### Table I – Control samples for amplification.

Sample	DNA (extract)	TE <sup>-4</sup>
HL60 Positive Control DNA (100 pg/20 µl)	20 µl	
Amplification Negative Control		20 µl
Extraction Negative Control,(s) when sample amplified neat	20 µl	
Extraction Negative Control (s) when a dilution/concentration of sample extract is amplified	Submit 20 µl of the extraction negative at die same dilution/concentration factor or more concentrated than the sample	

#### **Amplification Setup B**.

- JEW HIRator For each amplification set, for the ot numbers and samples in the 1. documentation. Label Q 2011 PCR eaction tubes with sample label name and with date and time for the positive and negative controls.
- If samples require dilution prepare the aliquots in UV'ed 1.5mL tubes, and place 2. the neat samples back into storage.
- 3. Master mix preparation:
  - For Amplification using Roche reagents: a)
    - Prepare a Master Mix with Reaction Mix and Primer Mix, The following calculations are used:
      - Reaction Mix: number of samples N x 20 µl Reaction Mix 0  $= \mu l$
      - Primer Mix: number of samples N x 10  $\mu$ l Primer Mix = 0 \_\_ µl

**Note:** For  $\leq 6$  samples, use N, for  $\geq 6$  samples, use N+1. To save on reagents, individual aliquots of Reaction and Primer Mix can be made.

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- Add Reaction Mix and Primer Mix together to prepare Master Mix.
- Vortex the Master Mix and centrifuge briefly.
- Aliquot 30 µl of the Master Mix into the bottom of each labeled 0.2 ml reaction tube.
- b) For amplification with Homebrew reagents:
  - Prepare Reaction Mix and Primer Mix master mixes according to Homebrew amplification documentation. The following amounts of reagents per sample are used:

Reaction Mix Reagents	Volume per sample	Primer Mix Reagents	Volume per sample
Irradiated dH2O	3.7 μ <b>l</b>	Aradiated dH2O	6 µl
GeneAMP 10X PCR Buffer	5 µir	10μM HVIF	1 µl
2.5mM dNTPs	γµl	10µM HVIR	1 µl
25mM MgCl <sub>2</sub>	4.8 <b>Q</b> I	10µM HVIIF	1 µl
5U/µL AmpliT Q Gold DNA Polymerase	2.5 μl	10µM HVIIR	1 µl
Total Reaction Mix volume per sample	20 µl	Total Primer Mix volume per sample	10 µl

The following calculations are used:

- Reaction Mix: number of samples + 1 (N + 1) x Reaction Mix Reagent Amount =  $\mu$ l
- Primer Mix: number of samples + 1 (N + 1) x Primer Mix Reagent Amount =  $\__ \mu l$
- Vortex the Reaction and Primer Mix and centrifuge briefly
- Aliquot 20 µl of the Reaction Mix and 10ul of the primer mix into the bottom of each labeled 0.2 ml reaction tube.

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- 4. Add samples into the 0.2ml tubes. Use a sterile filter pipette tip for each sample addition. Open only one tube at a time for sample addition. The final aqueous volume in the PCR reaction mix tube will be 50 µl. Transfer the appropriate volume of target DNA or TE<sup>-4</sup> to each respective sample tube. After the addition of the DNA, cap each sample before proceeding to the next tube. If necessary, spin down the tubes at 1000 rcf for a few seconds.
- 5. When finished, place the rack with the 0.2ml tubes in the pre-amp room 112412014 dumbwaiter. Send the samples up to the post-amp room.

#### **Thermal Cycling** С.

- Turn on the Perkin Elmer 9700 Thermal Cycler. 1.
- 2. Use the following settings to amplify the sample

9700 Thermal Cycler	The amonffication file is as follows-
	Soakat 94°C for 14 minutes
User: mtDNA	- Denature 92°C for 15 seconds
	Anneal at 59°C for 30 seconds
File: lamtdna	- Extend at 72°C for 30 seconds
	Incubation at 72°C for 10 minutes
C	Storage soak at 4°C indefinitely

- Place the tubes the tray in the heat block, slide the heated lid over the tubes. 3. and fasten the hid by pulling the handle forward. Place the microtube rack used to set up the samples for PCR in the post-amp room bleach bath
- 4. Start the run by performing the following steps:
  - The main menu options are RUN CREATE EDIT UTIL USER. To a. select an option, press the F key directly under that menu option.
  - Verify that the user is set to "mtDNA" if not, select the USER option (F5) b. to display the "Select User Name" screen.
  - Use the circular arrow pad to highlight "mtDNA." Select the ACCEPT c. option (F1).

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d	Press the RUN button (F1) and select the "lamtdna	," file.
е.	Verify that the reaction volume is set to 50 $\mu$ l and	the ramp speed is set to
f	9600 (very important).	
Ι.	The run will start when the heated cover reaches 10 then display a flow chart of the run conditions. A the step being performed, hold time is counted dow indicated at the top of the screen, counting up.	03°C. The screen will flashing line indicates vn. Cycle number is
g.	Be sure to record the use of the thermal cycler in the appropriate instrument name.	▶ he documentation under
h.	Upon completion of the amplification, press the ST until the "End of Run" screen is dtsplayed, and ren Select the EXIT option (K5). Wope any condensati with a Kimwipe and pull the d closed to prevent of the heat block. Turn the instrument off.	ΓOP button repeatedly nove your samples. ion from the heat block dust from collecting on

i. After removing your samples, place them in the appropriate 2-8 °C refrigerator for storage. Samples should be separated according to sample type (exemplat, evidence, or quality control). Record the date and time of when samples were amplified on the cover of the 0.2 mL PCR storage box.

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#### **IMPORTANT**:

Turn instruments off **ONLY** when the Main Menu is displayed, otherwise there will be a Power Failure message the next time the instrument is turned on. It will prompt you to review the run history. Unless you have reason to believe that there was indeed a power failure, this is not necessary. Instead, press the STOP button repeatedly until the Main Menu appears.

In case of a real power failure the 9700 thermal cycler will automatically resume the run if the power outage did not last more than 18 hours. The Uninterruptible Power Supply (UPS) present in the amplification room will power the thermal cyclers for about 2-3 hours in the case of a total power outage. The history file contains the information at which stage a the cycling process the instrument stopped. Consult with the QA team and/or the Technical Leader on how to proceed.

**Revision History:** 

July 24, 2010 – Initial version of procedure.

December 22, 2010 – Added procedure for Homebrew amplification. Changed title of procedure. July 16, 2012 – Minor revisions in content to generalize terminology for LIMS.

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#### **QUANTITATION USING AGILENT 2100 BIOANALYZER**

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## **Quantitation using Agilent 2100 Bioanalyzer**

To quantify the amplified product of the mitochondrial hypervariable regions I PURPOSEand II, in order to establish the input of DNA for linear array analysis and/or cycle sequencing. The DNA 1000 assay is capable of analyzing amplified DNA fragments in the range of 25-1000 bp, and in the concentration range of 0.5-20 ng/uL.

### A. Preparing the documentation:

- a. Prepare a new Agilent Test Batch, and select samples for analysis
- b. Exemplar samples and positive controls should be run at 2 fold (d2) and 5-fold (d5) dilutions. Hair and evidence samples should be due d1 (neat) and d2. Negative controls should be run d1 (neat). Prepare output samples accordingly.
- c. Exemplar and evidence samples may be quantitated on the same Agilent run; however, they must be aliquotted for mantitation separately.
- d. Prepare the plate record, and manually link the samples into the associated plate
- e. Download the plate record, and confirm the .CSV file is saved in the appropriate network location.

### **B.** Preparing the samples

- a. Follow the documentation to prepare dilutions. Add  $H_2O$  first in all tubes where needed.
- b. Vortex and certifications between serial dilutions
- c. Aliquot all volumes less than 2  $\mu$ l using a 2  $\mu$ l pipette.
- d. When pireting sample for dilution or quantitation, pick up from the top of the solution directly on the meniscus) to avoid carrying sample on the outside of the tip.
- e. Use 1µl for quantification. Vortex and centrifuge every tube before use.

### **C. Procedure**

- a. If the Gel-Dye mix is not prepared, proceed to SECTION A.
- b. If the Gel-Dye mix is already prepared, proceed to SECTION B.
- c. For analysis of data only, proceed to SECTION C.

#### **QUANTITATION USING AGILENT 2100 BIOANALYZER**

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#### POWDER-FREE GLOVES ARE REQUIRED FOR THE HANDLING OF AGILENT CHIPS. POWDER FROM LATEX GLOVES COULD CLOG THE MICRO-CHANNELS ON A CHIP.

#### Section A- Preparing the gel-dye mix

- 1. Allow the DNA dye concentrate (blue tube) and the DNA gel matrix (red tube) to come to 37°C in the heat block.
- 2. ALWAYS PROTECT THE DYE CONCENTRATE FROM THE LIGHT. Vortex the DNA dye concentrate (blue tube) and spin down. Add 25 µl of the dye concentrate (blue tube) to the DNA gel matrix vial (red tube).
- 3. Vortex the mixture for 10 seconds to ensure complete mixing, and transfer the entire mixture to the top receptacle of a spin filter.
- 4. Centrifuge for 15 minutes at 6000 rpm. Discard the filter and label the gel-dye mix tube with the lot numbers of the DNA dye concentrate, the DNA gel matrix, and your initials and the date.
- 5. One tube of gel-dye mix is enough for 10 runs, and will last for 4 weeks. Discard the geldye mix 4 weeks after the date of poparation. Protect the gel-dye mix from light, and store at 4°C. Record the creation of the gel-dye mixture in the LIMS.

#### Section B- Loading and running of the Agilent Bioanalyzer 2100

2100 Expert System Setting veft inside of the window, click on system) are saved by default as:

- 1. Data Files Name, verial number, data, time are checked.
- 2. Data Files directory: "Create Daily subdirectories" is checked.
- 3. Data File format: "Binary format" is checked.
- 4. Nothing is checked in "Run and Results", "Auto Export," and, "Default Export Directories".

## ALL PIPETTING INTO THE CHIP MUST BE DONE DIRECTLY ON THE GLASS AT THE BOTTOM OF THE WELL, NEVER ON THE SIDES OF THE WELL.

1. Allow the gel-dye mix to equilibrate to room temperature.

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- 2. Have a witness check samples and worksheet. Record the run name, the lot#, analyst, date, time, and the Agilent machine, in the documentation. Open a new DNA chip
- 3. Pipette 9  $\mu$ l of gel-dye mix into the bottom of the well marked . Make sure there are no bubbles, if any use a 1 $\mu$ l pipette tip to remove them. Place it in the priming station, and fill out usage log. Make sure the base plate of the station is set to position C, and the clip on the syringe trigger is set to the lowest position. Make sure the syringe piston is pulled back to the 1 ml mark, and close the lid of the priming station. (Listen for the "click.")
- 4. Grab the syringe with your index fingers under the fins on the syringe body and thumbs on the plunger. Swiftly and steadily, press down on the plunger until it locks under the silver trigger. Make sure your thumbs are not in the way of the trigger lock or it will not work. Let the chip pressurize for 60 seconds.
- 5. Release the syringe with the trigger, and make sure the syringe comes back to 0.3-0.4 ml. Wait for 5 seconds, pull slowly the syringe back to 1 ml, and open the chip priming station. Turn the chip over and inspect the capillaries for proper filling.
- 6. Pipette 9  $\mu$ l of gel-dye mix into the two were marked **G**. Make sure there are no bubbles, if any use a 1 $\mu$  tips to remove them.
- 7. Vortex and spin down the DNA packer (green tube), and pipette 5 μl of marker into each of the 12 sample wells and ladder well. Each well must be filled, even if it will not be used.
- 8. Vortex and spin down the DNA ladder (yellow tube), and pipette 1  $\mu$ l of ladder into the lower right well, married with the ladder symbol.
- 9. Add 1  $\mu$ L of amplified DNA to each well. If a well is not used, add 1  $\mu$ l of dH<sub>2</sub>O into the well.
- 10. Place the chip in the IKA vortexer and vortex at ~2200 rpm for 60 seconds.
- 11. Run chips within 5 minutes.
- 12. Start the collection software by clicking on the symbol on the desktop.

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- 13. Click on "instrument" on the left panel and place the cursor in one cell of the Sample Name column, click on the right button of the mouse, select import, choose the .CSV text file that was created for the run (see A7). The software might give a warning "failed to import the text file." Ignore, and press OK.
- 14. Once the machine is highlighted in the upper left-hand corner of the screen, open the lid. The icon should now show the lid open as well. Insert the DNA 1000 chip and carefully close the lid. The machine icon will now change to a blue chip on the screen. Make sure the "Assay Class" in the "Assay Details" panel (middle right panel) is "DNA 1000". If the assay class is different than DNA 1000 see a supervisor before starting the run.
- 15. Adjust the sample # in the Data Acquisition Parameters field, if necessary.
- 16. Click on the START button. The run will begin with a pre-heat and should take to proximately 35-40 minutes for a full chip.
- 17. The ladder sample will process first. It is good idea to monitor this sample to make sure the upper and lower markers come out correctly (15 bp and 1500 bp).
- 18. **Immediately** after the run (less chan 5 minutes), remove the sample chip. The electrodes need to be cleaned with the clear electrode cleaner chip within 5 minutes after the run. To do this, begin by filling one of the large wells with 350 μl of deionized water. Place the electrode cleaner in the Agilent 2100 Bioanalyzer and close the lid for 10 seconds (and **not more than 10s**). Open the lid, remove the electrode cleaner chip, and let the pin set dry for another 10 seconds (and **not more than 10s**), then close the lid. Drain and dry the electrode cleaner chip.

#### Section C- Data collection, analysis, electronic filing

When the Bioanalyzer 2100 run is complete, go to the Data & Assay field. The main window will show the gel image, sample list, and chip summary. Any problems detected by the software will be indicated with yellow triangles above the lanes in the gel image (see troubleshooting).

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#### 1- Ladder:

Select the Ladder sample on the sample list. The main window should show the the following peaks (11 ladder peaks plus lower-LM- and upper-UM- markers):

Lower Marker 15bp 25bp Ladder Ladder 50bp 100bp Ladder 150bp Ladder 200bp Ladder

200bp Ladder 300bp Ladder 400bp Ladder 500bp Ladder 700bp Ladder 700bp Ladder 1000bp Ladder 1500bp Upper Marker 2—Samples: Click on the individual sample on the sample list. One positive control and sample lanes should show two peaks, indicating the HVIL and HVI amplified products (around 420-490 bp) for samples amplified with HVI and HVII multiplex primers. All samples should have the lower samples amplified with HVI and HVII multiplex primers. All samples should have the lower marker (~15bp) and upper marker (~1500to).

#### **3-Manual editing:**

If the upper marker (UM) or the marker (LM) is present but not labeled properly, right click on the peak cell "size bp" in the table and select "manually set upper marker" or "manually set lower marker," respectively.

If a ladder peak, HVI and/or HVII are present but not labeled or if an extra peak is present: right click on the peak, select "manual integration", add or remove peak at that position (bp).

Smaller amplified product peaks in samples with severely unbalanced HVI and HVII peak heights due to potential length heteroplasmy may be manually edited. Be sure to record any and all edits within the run documentation.

#### **4-Export data to the network:**

The data are automatically saved in a "yyyy-mm-dd" folder as "DES547045xx\yyyy-mm-dd\_hhmm-ss.xad" (a shortcut on the desktop). If from AG1: DES547045xx is DES54704515, if from

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#### AG2:DES547045xx is DES54704524.

**a**- Open the yyyy-mm-dd\_hh-mm-ss.xad file, make edits if necessary, save the .xad file as DES547045xx\yyyy-mm-dd\_hh-mm-ss-**analystinitials.**xad. Transfer the .xad file (s) in M:\MITO\_DATA\Agilent Archive\yyyy\ yyyy-mm-dd-hh-mm-ss folder.

**b-** Create a PDF file by going to the "file" menu and selecting "print." When the print window opens, select "Run Summary", "electropherograms" and "Results Table", choose "all wells" if it is a full chip, or fill in the well numbers of used wells for a partial chip. Select "Include Ladder", one per page, PDF. Click on "… " to select the drive. Select the appropriate folder on the network. Add analystinitials before ".pdf" in the path name. Click save.

c- Check that PDF and xad file (s) are present in M:\MITO\_DATA

Archive\yyyy\ a new yyyy-mm-dd-hh-mm-ss folder.

## 2100 expert software

If analysis or review is done at a different time than the run of from another computer, open the 2100 Expert software.

Select "data" in the "contexts" column on the left side of the window.

Go to file Open

Select the folder with the run you want review analyze in M:\MITO\_DATA\Agilent

Archive\YEAR\xxxxxxxxxx

Select the appropriate.xad file of the run Click open

After analysis/review: IF ANY DITS/CHANGES ARE MADE, do not forget to re-save the .xad file with **-reviewerinitian** at the end of its name. Create a new PDF file. Print and initial.

## Section D- Data Entry, Review, Filing, Rerun

#### DATA TAB ENTRY

Open the appropriate Agilent batch to review and edit, as necessary.

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bp \* : peak position manually called

bp \*\* : peak position edited out manually

bp ^ : spikes position manually removed

LM\*: sample lower maker manually called UM\*: sample upper maker manually called

Samples

HVII and HVI peaks should be discrete and approximately 400 to 500bp respectively or the

peak will be inconclusive. Samples with multiple peaks or peak imbalance due to potential sequence length heteroplasmy may be manually edited.

The "Vol, Used" refers to the volume aliquotted of the original amplified sample. *Sample edits*:

If a sample is edited, enter the location in bp followed by one of the symbols from the table above. If special edits are needed, document them in the sample edits column. Indicate if editing was necessary for any sample, including the tabler, and if so, record the edits in the documentation.

Once the editing is complete in the Agiest Software, save the file, and export the final results to the appropriate network location.

Import this Agilent data file into the LINS system against the Agilent batch data. This will automatically update the dilution factors, and input the HVI and HVII initial values. This, in turn, will calculate the value of HVI and HVII, and output the final "Conc, Mean HVI-HVII" value for each sample in the bach.

## REVIEW TAB ENTRY

Fill the "Intrepretation" following the guidelines in the table below:

	one dilution			
HVII	HVI			Comments
[0.5-20]	[0.5-20]	HVII and HVI mean concentration	ation will be used for further testing	USE
INC	[0.5-20]	non-INC peak concentration value will be used for further testing		USE
[0.5-20]	INC	non-INC peak concentration value will be used for further testing		USE
INC	INC	Rerun		RQ
2 dilutions				
Comments				
dilution	A pass dil	ution A within $\pm$ 2.5 X dilution	use lower value	USE

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dilution B pass	В		-
dilution A pass	dilution A outside $\pm 2.5$ Xdilution	Rerun	RQ
dilution B pass	В	Rerun	RQ
dilution A pass	2/2	use for further testing	USE
dilution B INC	II/a	n/a	-
dilution A INC		n/a	<b>. .</b> -
dilution B pass	II/a	use for further testing	USE
If both dilutions a	re INC	AL	
dilution A INC	<b>n</b> /a	Rerun at appropriate dilution	RQ, dx
dilution B INC	II/ a	Rerun at appropriate dilution	RQ, dx
appropriate diluti	on example 1		
dilution 2 <0.5	n/a	Reven at appropriate dilution	RQ, d1
dilution 5 <0.5	ii/a	Rerun a appropriate dilution	RQ, d1
appropriate diluti	on example 2	<u> </u>	
dilution 2 >20	n/a	Recon at appropriate dilution	RQ, d10
dilution 5 >20	10 a	Kerun at appropriate dilution	RQ, d100
<b>XOI I III I</b>			

If both dilutions are INC for any other reason than concentration value out of range, see supervisor

INC = sample inconclusive

USE = concentration will be sued for further testing

RQ = sample will be requantified

dx = sampel will be requantified at dilution x

• If the ladder (e.g., discrete bands) or upper or lower markers are not present (e.g., can't be edited) the run is inconclusive, all samples have to be requantified, indicate as such in each sample Interpretation cell.

• If one or both markers are not called, the run is inconclusive, all samples have to be requantified, indicate as such in each sample Interpretation cell.

• If a sample peak concentration value is out of range it will appear as INC

If a sample was called INC for any other reason than the value range it will appear as INC. A comment can be added to explain why the peak was called INC in the "notes" of the review sheet. In both cases the concentration of only one peak could be used for further testing instead of the mean concentration of both peaks and **USE** added in the comments column (see table above).

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- If the ladder fails manually select "fail" as the "Ladder Result", if not select "Pass".
- If the ladder marker (s) fail(s) circle "fail" as the "Ladder Result", if not select "Pass".

#### REVIEW

The reviewer will review the documentation, as well as any comments based on the parameters in section D.

After review, the reviewer will indicate the appropriate samples for the next process step, as indicated by the Interpretation results of each sample.

#### RERUNS

1. After review, the analyst will set up a new Agilent batch for the necessary samples that were indicated as reruns.

were indicated as reruns.

**Revision History:** 

July 24, 2010 – Initial version of procedure.

July 16, 2012 – Minor revisions in content to generalize terminology for LIMS.

#### MITOCHONDRIAL DNA LINEAR ARRAY ANALYSIS

DATE EFFECTIVE 07-16-2012

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## **Mitochondrial DNA Linear Array Analysis**

#### **PURPOSE**

For the detection of sequence variation targeting 18 positions within the hypervariable regions I (HVI) and II (HVII) of the human mitochondrial DNA (mtDNA) genome. Large sample sets can be screened using immobilized oligonucleotide strips via a biotin/streptavidin-linked hybridization assay (Roche Linear Array Mitochondrial DNA HVI/HVII Region-Sequence Typing Kit is used), allowing the identification and comparison of questioned samples and 124120 known samples.

#### **PROCEDURE**

The following procedure will take approximately 2-2.5 hours. Make sure before beginning the procedure that sufficient amounts of Linear Array, Wish Buffer, Citrate Buffer, and Chromogen are available. If not, contact the QA team to make or order more. The Linear Array procedure can accommodate 24 samples per tray, and no vore pich two trays can be run simultaneously in one shaking waterbath. If less than 24 samples are being run, leave empty wells between samples whenever possible to avoid spillover contamination. A single tray should contain only exemplar samples or evidence samples. Do not run exemplars and evidence together in the same tray. Do not run evidence or exchiplar sample types from the same case in one Linear Array experiment (e.g. staggering the run of 2 trays in one Linear Array experiment; one tray contains evidence from a given case, the other tray contains an exemplar sample from the same tase).

## Hybridization A.

- 1. Turn on the shaking water bath to 55°C, at 50-70 rpm. Do not leave uncovered. Be sure that there is enough water covering the base of the bath before proceeding.
- 2. Turn on the circulating stationary water bath to 45°C. Warm the Wash Buffer.
- 3. Remove samples from storage, vortex and spin down in a centrifuge. Arrange your amplified samples in a tube rack, and record the Linear Array documentation.
- 4. Using forceps, remove an appropriate number of Linear Array strips; arrange on a kimwipe, and label the clear end with a pen containing non-soluble ink so that the

#### MITOCHONDRIAL DNA LINEAR ARRAY ANALYSIS

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**black bar is on the left side** of the strip. Place the array strips in the 24-well tray in the same orientation. Cover the tray with the lid. Take care not to touch the stripes on the strips with gloves or scrape with forceps.

- 5. Label an appropriate number of 1.5 ml microcentrifuge tubes.
- 6. Have a witness check the set up.
- 7. Add: 15 μl of Denaturation Solution
   Up to 21.4 μl of PCR product

Whenever possible, the target amount of 75 ng of amplified mtDNA should be used for the Linear Array assay.

If the concentration of amplified DNA in an extract is < 10ng / 4 µl (< 2.5ng / µl), do not use for Linear Array. Reamplify the sample with more input DNA or proceed directly to DNA sequencing.

- 8. Add 3 ml of pre-warmed **Wash Buffer** Weach Linear Array strip.
- Add the denatured samples to the liquid within each appropriate well.
   Do not add the sample directly onto the strip.
- 10. Mix by rocking gently, over the tray with the lid, foil, and add two weights on the top. Place in the backing water bath for **15 minutes**.

When **5 minutes** are left on the previous step, prepare the **Enzyme Conjugate** solution using the following formula:

Number of samples x 3.3 ml Wash Buffer Number of samples x 12 µl Enzyme Conjugate

Swirl to mix, cover with foil, and add a weight to the top to prevent from tipping over. Place in the circulating water bath to keep warm.

11. Remove the tray from the shaking water bath, uncover, and pour off the Wash Buffer from the labeled end of the strips. Wipe the condensation from the lid and edges of the tray.

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- 12. Add 3 ml of pre-warmed **Wash Buffer** to each strip. Rinse by carefully rocking for 10 seconds and pour off from the labeled end of the strips. Wipe the condensation from the lid and edges of the tray.
- 13. Add 3 ml of the **Enzyme Conjugate** solution to each strip with a disposable pipette.
- 14. Cover with lid and foil, add weights, and place the tray in the shaking water bath for **5 minutes**.
- 15. Remove the tray from the shaking water bath, uncover, and our off the Enzyme Conjugate solution from the labeled end of the strips. Note the condensation from the lid and edges of the tray.
- 16. Add 3 ml of pre-warmed **Wash Buffer** to each strip. Rinse by rocking for 10 seconds, and pour off from the labeled end of the strips.
- 17. Add 3 ml of pre-warmed **Wash Buffer(b)** each strip.
- 18. Cover with lid and foil, and weights, and place in the shaking water bath for 12 minutes.
- 19. Remove the tray from the shaking water bath, uncover, and pour off the Wash Buffer from the labeled end of the strips. Wipe the condensation from the lid and edges of the tray.
- 20. Add 3 ml of pre-warmed **Wash Buffer** to each strip. Rinse by rocking for 10 seconds, and pour off from the labeled end of the strips.
- 21. Add 3 ml of **Citrate Buffer** to each strip.
- 22. Cover with lid and foil, add weights and shake at **Room Temp for 5 minutes** at 100 rpm.
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23. **In a glass container**, prepare the **Color Development** solution using the following formula:

Number of samples x 3.3 ml Citrate Buffer Number of samples x 4  $\mu$ l 3% Hydrogen Peroxide Number of samples x 0.15 ml Chromogen

Swirl to mix and use immediately.

- 24. Remove the tray from the room temperature shaker, uncover, and pour off the Citrate Buffer from the labeled end of the strips. Wipe the ondensation from the lid and edges of the tray.
- 25. Add 3 ml of the **Color Development** solution to each strip by using a disposable pipette.
- 26. Cover with lid and foil, add weights, and shake at **Room Temperature for a minimum of 10 minutes** at 100 rpm. Ofter 10 minutes, briefly check color development. If strip is not fully de cloped, continue development for an additional 5 minutes. Color development is normally complete after 15 minutes; however, further incubation can be done at the analyst's discretion. Color development must be stopped if there is any indication of the appearance of blue non-specific background staining. Record the total time of color development on the Linear Array documentation.
- 27. Remove the tray from the room temperature shaker, uncover, and pour off the Color Development solution from the labeled end of the strips. Wipe the condensation from the lid and edges of the tray.
- 28. Stop the color development by adding  $5 \text{ ml of } dH_2O$  to each strip. Rinse by rocking for 20-30 seconds.
- 29. Pour off the  $dH_2O$  from the labeled ends of the strips. **Repeat the dH\_2O rinse process twice more.** When finished, either immediately proceed to the photography stage (preferred) or store the strips in a hybridization tray filled with  $dH_2O$  (not more than several hours) and photograph later. Record the date, time and a brief description of samples on the lid.

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30. Clean trays with ethanol or isopropanol and rinse with  $dH_2O$ . If after rinsing with ethanol or isopropanol and the dye is still present, repeat the cleaning, but let stand for half an hour, and then rinse.

### **B. Photography**

Using forceps, arrange the developed Linear Array strips on an acrylic tray, using the supplied ruler from Roche as a guide. The black bar on the left side of the strip should be used to align the strips to the ruler. Be sure to keep the strips moist.

No more than 12 strips should be photographed at a time. If there are more than 12 strips present, the second photograph needs to include a positive and a (amplification or extraction) negative control strip taken from the first set of strips.

- 1. Once arranged on the tray, place the tray onto the copy stand. Turn on spotlights as necessary.
- 2. Attach the digital camera to the copy sound by screwing it in place. Adjust the height and focus of the camera so that all of the strips and ruler are visible and clearly focused. Optimal settings incluce setting the camera to the macro mode (which is the flower image beneath the OK outton); manual focusing the image by pressing half way down on the shutter rolease button; and by also adjusting the white balance by selecting Menu: White balance: White Bal. Preset, select Measure, and then frame the reference object (such any light sources turned on) and press OK.
- 3. Connect the canora to the computer, open MS Powerpoint and insert the image into a blank slide. Using a text box label the image with the picture's reference number as LAmmddy, hhmm from the associated Linear Array worksheet date and time. Save .ppt file to into M:\MITO\_DATA\Photo Archives\Linear Array Photo Archive folder using the picture's reference number. Export the image as a .JPEG file, and save into the same network location. Attach this .JPEG file to the LIMS Linear Array test batch. Print image, initial and date the picture, and proceed to interpret the results.

## MITOCHONDRIAL DNA LINEAR ARRAY ANALYSIS

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## **<u>C</u>**. Interpretation of Results

- A Allele Calling
  - 1. All interpretations must be made from the photo documentation of the Linear Array strips.
  - 2. Fill in the corresponding bands on the Linear Array documentation based on the ruler markings.
  - 3. Weak bands are considered any bands that have an intensity significantly less than the other bands within the same hypervariable region on the same strip. All weak bands should be recorded as "wX", where X is the actual probe signal.
  - 4. In the case where two bands are present at one probe location, record both bands as "X/Y" where X is the first band numerically and Y is the second. The weak band rule may still apply (such that "wX/wY", "wX/Y" and "X/wY" are all the possibilities.
  - 5. If no bands are present at a probe location, enter "0" for that location in the spreadsheet. If no bands are present in any of the probe locations, all locations should be marked with Qlash "-".
- B. Control Sample Guidelips
  - 1. Check the populative controls to make sure there are no bands present.
  - 2. The Hoo positive control, run with each amplification set, should yield the following probe signals:

Probe	16093	1A	1C	1D	1E	IIA	IIB	IIC	IID	189
HL60	1	1	1	2	2	2	6	1	1	1

- 3. See <u>"INTERPRETATION GUIDELINES GUIDELINES FOR CONTROLS</u>" on how to proceed if there are any problems.
- C. Interpretation and further testing strategy

#### MITOCHONDRIAL DNA LINEAR ARRAY ANALYSIS

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- 1. See "INTERPRETATION GUIDELINES - LINEAR ARRAY" for comparison of allele calls.
- 2. Based on the case context, the following samples need to proceed to cycle sequence analysis:
  - Included exemplars
  - One representative sample for all probative evidence
  - Samples with partial profiles
  - All negative and positive controls if any sample from the batch is being 101 112A120 sequenced

No sequencing is required for:

- Excluded exemplars
- Apparent mixtures \_
- Redundant evidence samples

**IMPORTANT**: if any linear array re-tayoridization is required, make sure sufficient amplification product for cycle sequencing is preserved. This is especially valid for the negative controls and samples with Www DNA yields that cannot easily be reamplified.

Depending on the case it might be becessary to omit the linear array repeat.

#### Sequence concordance D.

- For all single Surce samples with probe signals, the linear array results are 1. correlated to the underlying sequence variants for concordance checking.
- 2. This is one in an automated fashion using the Linear Array Summary & Stats spreadsheet found on the network.
- 3. On the first page of the spreadsheet, fill in the sample name.
  - A. Fill in the probe signals interpreted from the previous section into the corresponding cells.

The following rules must be applied:

1) Input weak bands with a "w" followed by the numerical type.

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- 2) Input multiple bands, e.g., x/y, on two separate sheets, one with the "x" and one with the "y," with the following exception. If a w2/w3 call is present at 1C, then enter "w2/w3" at this location.
- 3) Input null bands with a zero.

B.Print out the spreadsheet to include in the casefile.

C. Print out the results to a pdf document, and attach the pdf to the LIMS for the Linear Array test batch.

4. The spreadsheet will provide the following sequence for the HL60 positive control:

	Probe Designation	Sequence Variation
	16093	16093 T
	1A 🔥	16126 T
		16129 G
		16304 T
HVI	$\beta$ , $\gamma$	16309 A
	· <u>`</u> (O`	16311 T
	TD	16362 C
	IE 1E	16270 C
	ð.	16278 T
	IIA	73 G
J.	IIB	146 T
		150 T
$\bigcirc$		152 C
нуш	IIC	189 A
11 V 11		195 T
		198 C
		200 A
	IID	247 G
	189	189 A

4.Assay results can be translated into sequencing results based on the spreadsheet calculations, and compared against the other samples. Null alleles are not convertible.

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5.For reference, the probe designations and sequence variations are presented below.

	Probe Designations	Sequence Variation Detected
	16093 1 16093 2	16093 A T T T C • • C • •
	1A1 1A2 1A3	16126       16129         T       G       T       A       C       G       T         •       •       •       •       •       •       •       •         •       •       •       •       •       •       •       •       •
IVH	1C1 1C2 1C3 1C4 1Cw2/w3	16304       16309       1631         A       G       T       A       G       A       C         •       •       C       •       •       •       •       •       •         •       •       •       •       •       •       •       •       •       •         •       •       •       •       •       •       •       •       •       •         •
	1D1 1D2	
	1E1 1E2 1E3	$\begin{array}{c} 16270 \\ C \\ T \\ \cdot \\ \cdot \\ T \\ \cdot \\ \cdot \\ T \\ \cdot \\ \cdot \\ \cdot$
	ПА 1 ПА 2	
ПЛН	IIB1 IIB2 IIB3 IIB4 IIB5 IIB6 IIB7	146       150       152         C       T       C       T       C       T         ·       C       T       C       T       A       T         ·       ·       ·       ·       ·       ·       ·       ·         ·       ·       ·       ·       ·       ·       ·       ·       ·         ·       ·       ·       ·       ·       ·       ·       ·       ·         ·       ·       ·       ·       ·       ·       ·       ·       ·         ·       ·       ·       ·       ·       ·       ·       ·       ·         ·       ·       ·       ·       ·       ·       ·       ·       ·         ·       ·       ·       ·       ·       ·       ·       ·       ·         ·       ·       ·       ·       ·       ·       ·       ·       ·       ·         ·       ·       ·       ·       ·       ·       ·       ·       ·       ·         ·       ·       ·       ·       ·       ·       ·
	IIC1 IIC2 IIC4 IIC5	189       195       198       200         G       A       C       A       T       A       C       T       A       A         •       <
	IID1 IID2	247 T T G A A • • A • •

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			189						195
189 1	G	A	А	С	A	Т	А	С	C/T*
189 2	•	•	G	•	•	•	•	•	•

\* Both 189 1 and 189 2 probes are degenerate at position 195 with respect to the presence of either a C or T base.

# **TROUBLESHOOTING**

# Problem: No bands on a Linear Array strip where there should be.

Possible causes	Solutions
Quality of reagents is inappropriate	Check expiration dates on all reagents, and make new if necessary. Make sure Enzyme Conjugate and Color Development Solutions were not made more than 5 minutes prior to use.
All of the proper reagents were not added	Make sure that Citrate and Wash buffers were not switched at any steps.
No DNA present	Check quantitation assay. Check other strips: problem may be isolated to one well or PCR sample.
Temperature	Check temperature of water bath, and ensure that all steps were done at the proper temperature.
DNA was not denatured properly	Make sure Denaturation Solution was added to sample. Make or purchase new Denaturation Solution.
DNA degradation	Do not allow DNA to incubate with

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Denaturation Solution for more than 60
minutes.

### Problem: High Background

Possible causes	Solutions
Color Development step not performed at room temperature or temperature of the room is too high.	Repeat typing and ensure that color development step is performed on an orbital shaker at room temperature between +15 and +25 °C.
Insufficient or improper water washes following Color Development.	Ensure that the strips were washed 3 times for at least 20-30 seconds per wash: wash times can be increased or additional washes can be performed.
Excess Color Development Solution remaining in tray following aspiration of pouring-off of solution.	Ersure Cotor Development Solution is adequately removed.
Developed strips exposed to strong light and /or not kept wet during interpretation of imaging.	Defionized water can be applied with a squirt bottle during photography if necessary. Align all strips prior to turning on photography lights.
Inadequate agitation of the strips during Hybridization, Conjugation, and or Wash steps.	Check speed of rotating water bath (50-70 rpm). Verify that solutions are washing over strips. Repeat typing.
Excess Amount of Enzyme Conjugate: SA- POD added to Enzyme Conjugate Solution.	Check calculations and repeat typing, ensuring correct amount of Enzyme Conjugate:SA-POD added to Enzyme Conjugate Solution.
Tray not properly cleaned prior to use.	Ensure trays were not cleaned with detergents or bleach; thoroughly clean and dry the affected trays. Clean trays with ethanol or isopropanol and rinse with dH <sub>2</sub> O. Discard tray if discolored even after proper cleaning.
Wash bottles are contaminated.	Thoroughly clean and dry wash bottles.

#### MITOCHONDRIAL DNA LINEAR ARRAY ANALYSIS

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Revision History:

July 24, 2010 – Initial version of procedure.

September 3, 2010 – Revised version of procedure: Paragraphs B3 and B4 have been rewritten into one paragraph B3 only to reflect our current procedure

July 16, 2012 - Minor revisions in content to generalize terminology for LIMS.

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#### **EXO-SAP-IT SAMPLE CLEANUP**

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# **EXO-SAP-IT Sample Cleanup**

<u>PURPOSE:</u> Prior to cycle sequencing, unincorporated primers and nucleotides present in the amplification reaction are deactivated by the addition of ExoSAP-IT.

### PROCEDURE:

- 1. Create a new ExoSAP-It test batch in the LIMS system, and fill in the necessary documentation.
- 2. Confirm the tube label and sample description for each sample. Every run should include a positive control and an amplification negative control. Note: It is very important for these entries to be in 3130xl format; do not use spaces or the following characters: | /:\* "><|? ')
- 3. Based on each sample's previous runs, the appropriate values for each column in the ExoSAP-It batch will be automatically filled in. The "Vol, Misc" must be entered by the analyst, and then the batch should be saved. This will trigger the automatic values to populate in the data, and the calculations for the ExoSAP-It volume and the new concentration will automatically execute.

For a detailed description of the calculations performed in this spreadsheet, refer to Appendix D – Detailed CysSeq/3130xl Spreadsheet Calculations.

There should be the of ExoSAP-IT added for every 5ul of sample in the amplification type.

4. Use the following settings to incubate the samples:

9700 Thermal Cycler	The ExoSAP-IT file is as follows:
User: mtDNA	- Soak at 37°C for 15 minutes - Soak at 80°C for 15 minutes
File: exosap-it	Storage soak at 4°C indefinitely

#### **EXO-SAP-IT SAMPLE CLEANUP**

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- 5. Place the tubes in the tray in the heat block, slide the heated lid over the tubes, and fasten the lid by pulling the handle forward.
- 6. Start the run by performing the following steps:
  - a. The main menu options are RUN CREATE EDIT UTIL USER. To select an option, press the F key directly under that menu option.
  - b. Verify that the user is set to "mtDNA." If not, select the USER option (F5) to display the "Select User Name" screen.
  - c. Use the circular arrow pad to highlight "mtDNA." Select the ACCEPT option (F1).
  - d. Select the "exosap-it" file, and press the RUN button (F1).
  - e. Verify that the reaction volume is set to 50 µl and the ramp speed is set to 9600 (very important).
  - f. If all is correct, select the TART option (F1).

The run will start when the heater cover reaches 37°C. The screen will then display a flow chart of the run condition. A flashing line indicates the step being performed; the hold time is counted down, cycle number is indicated at the top of the screen, counting up.

Upon completion of the amplification, remove samples and press the STOP button repeatedly until the 'End of Run' screen is displayed. Select the EXIT option (F5). Wipe any contensation from the heat block with a Kimwipe and pull the lid closed to prevent dust from collecting on the head block. Turn the instrument off.

7. When the batch is complete, the new concentration value must be "pushed" to the ExoSAP-It'd DNA sample within the LIMS system. From this point forward, the ExoSAP-It'd DNA sample will be the point of all cycle sequencing testing for mtDNA analysis.

**Revision History:** 

July 24, 2010 – Initial version of procedure.

July 16, 2012 – Minor revisions in content to generalize terminology for LIMS.

#### **CYCLE-SEQUENCING**

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# **Cycle-Sequencing**

<u>PURPOSE</u>: Following the duplex mtDNA amplification, the samples identified as probative will be sequenced to determine the mtDNA profile. The Sanger method is used to cycle sequence the mtDNA in question using fluorescent dideoxynucleoside triphosphate bases chain terminators. The Applied Biosystems Big Dye Terminator Cycle Sequencing Kit is used.

#### PROCEDURE:

- 1. The cycle sequencing reactions are done in a 96-well plate. Prepare the samples and reagents needed for cycle sequencing and be witnessed according to the sample names and order listed on the Cycle Sequencing documentation.
- 2. The amount of template DNA and water needed for each sample is calculated by the LIMS system. This calculation takes into account the total volume and concentration of amplified product present in the sample rube following the ExoSAP-IT procedure.

The target amount for cycle sequencing is ng of amplified product.

The following formula is then used to reate each sample for cycle sequencing

4  $\mu$ l of Big Dye Terminator Reaction Mix + 2  $\mu$ l of Sequencing Buffer + 3.2  $\mu$ l Primer (1  $\mu$ M concentration  $\rightarrow$  mtDNA template + Water = 20  $\mu$ l total volume.

Samples with less than  $\log$  of amplified product in  $3\mu l$  may be cycle-sequenced using  $3\mu l$  of the sample.

3. If a dilution of template DNA is necessary, it will be indicated on the cycle sequencing documentation as "x @ 1/10th" where x is the input volume. If no dilution is necessary, the the notation will be "neat." The amount of water sufficient to make  $20\mu$ l reaction volume is then calculated. If a sample is a negative control sample, the mtDNA concentration of zero will result in a default template input of  $3\mu$ l, with the notation of "control"attached to the sample The documentation cannot indicate dilution factors greater than 1/10. For situations where the amount of DNA indicated is less than  $1\mu$ l @ 1/10 dilution, calculate the volume of extract required @ 1/100 dilution (multiplication by 10), and use this volume of a 1/100 dilution. Also calculate, by subtraction, the correct volume of water to add to the reaction. Note the correct aliquots on the documentation as a deviation of the procedure.

### **CYCLE-SEQUENCING**

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For a detailed description of the calculations performed in this spreadsheet, refer to Appendix D- Detailed Cycle Sequencing/3130xl Spreadsheet Calculations.

- 4. A *master mix for each primer* can be made with the following formula:
  - a. For (N+2) samples, add:
    - 4 µl x (N+2) Big Dye Terminator Ready Reaction Mix
    - 2 µl x (N+2) Sequencing Buffer
    - 3.2 µl x (N+2) primer (1uM concentration)

A *master mix for each sample DNA* can be made with the following formula:

- b. For N samples, add:
  - $X \mu l x$  (N) mtDNA sample DNA, where X is the amount of mtDNA needed as calculated by the system.
  - Y  $\mu$ l x (N) Water, where Y is the amount of water needed as calculated by the system

Note: The calculations for the two master mixes mentioned above are done by the LIMS system. They are located by clipting on the "Reagents" tab.

- c. Include all controls for each primer that is used for a sample. If a sample is repeated starting at the cycle sequencing step the original negative controls do not have to be repeated if the first test was successful.
- d. The re-cycle sequencing step requires the following:
  - A new cycle sequencing amplification negative control for each primer used in re-cycle sequencing to account for the cycle sequencing reagent.
  - A positive control, for each primer used in re-cycle sequencing to report on the integrity of the reaction.
  - Samples can be re-cycle sequenced with more (-recych) or less (-recycl) input DNA if necessary. Based on validation, up to 90ng of DNA can be used for recych. If recych sample volume would be more than 3μL, see supervisor.

## **CYCLE-SEQUENCING**

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5. Use the following settings to amplify the cycle sequencing samples:

9700 Thermal Cycler	The cycle sequencing amplification file is as follows:
User: mtDNA	Soak at 96°C for 1 minute
File: BDT cycle seq	<ul> <li>Denature 96°C for 15 seconds</li> <li>Anneal at 50°C for 1 seconds</li> <li>Extend at 60°C for 1 minutes</li> </ul> Storage soak at 4°C indefinites
Document	ARCHINE Dinator Mile

#### Revision History:

July 24, 2010 – Initial version of procedure.

July 16, 2012 - Minor revisions in content to generalize terminology for LIMS.

#### SDS CLEANUP

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# **SDS** Cleanup

<u>PURPOSE:</u> To help separate the primers from the cycle-sequenced DNA with the addition of 2% SDS to the samples, prior to Centri-Sep filtration.

PROCEDURE:

Do not refrigerate the 2% SDS tubes. This will cause the SDS to precipitate out of solution. Store the 2% SDS tubes at room temperature. Ensure that there is no precipitate in the tube before adding to samples.

- 1. Add  $2\mu l$  of 2% SDS to each tube of cycle-sequenced DNA. Vortex and spin down the plate(s) in a centrifuge.
- 2. Place the tubes in a thermal cycler, using the following conditions-



3. When the tubes are back room temperature following the 25°C soak, proceed to the Centri-Sep purification.

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#### **CENTRI-SEP SAMPLE FILTRATION**

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# **Centri-Sep Sample Filtration**

<u>PURPOSE:</u> Prior to sample electrophoresis, sequenced products must be purified in order to remove unincorporated dye terminators.

## A. Procedure for Single Columns

- 1. Gently tap columns to insure dry gel material has settled to bottom of spin column. Remove top column cap and add 800  $\mu$ L of sterile dry O to one column for each sequencing reaction.
- 2. Replace top cap and mix thoroughly by inverting column and vortexing briefly. It is important to hydrate all of the dry gel. Allow columns to hydrate for at least 2 hours at room temperature. As the columns are hydrating you will need to label one sample collection tube (1.5 mL microcent) fuge tube) for each sequencing reaction. You will also need one wasn tube for each hydrated column. These do not need to be labeled.
- 3. Once the columns are hydrated, remove any air bubbles by inverting the column and sharply tapping the column, allowing the gel to slurry to the opposite end of the column. Stand the column upright and allow the gel to settle while in a centrifuge tube rack.
- 4. Once the gel is settled, remove first the top column cap, and then remove the column end stopper from the bottom. Allow excess column fluid to drain into a wash tube by first gently tapping the column into the wash tube then allowing to sit for approximately 5 minutes. Remove the column from the wash tube, discard the liquin and reinsert the column into the wash tube.
- 5. Spin the assembly at 700 x g for 2 minutes to remove interstitial fluid. Be sure to note the orientation of the columns. At this point the columns should be used as soon as possible for the loading of cycle-sequenced DNA product.
- 6. Load entire sequencing reaction volume (20  $\mu$ L) to the top of the gel. Be careful to dispense sample directly onto the center of the gel bed without disturbing the gel surface.
- 7. Place column into labeled sample collection tube and spin at 700 x g for 2

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minutes maintaining original orientation. The purified sample will collect in the bottom of the tube.

8. Discard the column and dry the sample in a vacuum centrifuge (approximately 15-20 minutes). Do not over dry samples.

## **B.** Procedure for Centri-Sep 8 Strips

- 1. Determine how many strips are necessary to filter the amplified samples. Separate the desired number of strips by cutting the follower the strips with scissors.
- 2. Open the well outlets on each strip by cutting off the bottom edge with scissors. Cut at the narrowest part of the bottom of the tube.
- 3. Peel off the top foil and arrange the steps evenly on deep-well centrifuge plates. Spin the plates at 750 rcf for 2 minutes to remove the liquid.
- 4. Arrange the newly drained stops on a new 96-well plate. Add the amplified sample to each column.
- 5. Once all of the samples are loaded, place the 96-well plate with the Centri-Sep 8 Strips into the centrifuge, and spin at 750 rcf for 2 minutes.
- 6. Confirm that all of the samples passed through the strip into the wells of the 96well plate and discard the Centri-Sep 8 Strip.
- 7. Evaporate the samples in the 96-well plate at 75°C in a thermalcycler with the lid open.
- 8. If the samples are not going to be loaded immediately, they should be stored as dried pellets at 4°C for no longer then 14 days. When ready, proceed to 3130xl setup.

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# ABI 3130xl Sequencing

<u>PURPOSE</u>: The 3130xl 16-capillary array system is used to electrophoretically analyze samples following cycle sequencing and cleanup. The system uses 96-well plates containing the samples of interest, and can process 16 separate samples with each injection. Sequence data is generated at the end of the run for downstream sequencing analysis.

## A. Setting up a 3130xl Run

- 1. Turn on the computer. Make sure computer is fully booted to the Windows desktop. To login, the User should be "ocmelims" and the password should be "passw0rd". If the instrument is not on, turn it on. The status bar light will change from solid yellow (indicates instrument is booting) to blinking yellow (indicates machine is communicating with computer) and then to solid green (indicates instrument is ready for command).
- 2. On the desktop, click on the shortcut for the respective instrument's data file. The main path to this data file is

E:\Applied Biosystems\VDC\data collection\data\ga3130xl\*Instrumentname* 

- 3. Once there, create a master file using the following format: *"InstrumentnameYeac-bun Number* Files" (e.g. Batman08-015 Files) within the appropriate archive folder (e.g. Batman 2008). Move the 3130xl mtDNA files into this master file.
- 4. Open the 300*xl* Data Collection v3.0 software by double clicking on the desktop Icon of Start > All Programs > AppliedBiosystems > Data Collection > Run 3130xl Data Collection v3.0 to display the Service Console.

By default, all applications are off indicated by the red circles. As each application activates, the red circles (off) change to yellow triangles (activating), eventually progressing to green squares (on) when they are fully functional.



# NOTE: This process could take several minutes. The Service Console must <u>not</u> be closed or it will shut down the application.

Stop All

Once all applications are running, the **Foundation Data Collection** window will be displayed at which time the **Service Console** window may be minimized.

Restart All

5. Check the number of injections on the capillary in the LIMS and in the **Foundation Data Collection** window by clicking on the **ga3130xl** > *instrument name* > **Instrument Status**. If the numbers are not the same, update the LIMS system. If the number is  $\geq 140$ , notify QC. Proceed only if the number of injections you are running plus the usage number is  $\leq 150$ .

Foundation Data Collection Version	sion 3.0 · No User is logged				60
File View Service Tools Wizards Help		×			
		1			RA -
Ach hatruments     Constant Scoop     Database Manager     Salt 30:1     Protocol Manager     Monoger     Monode Manager     Monode Manager	GA Instruments > ga3130x1 yr yw y Status Overview Instrument 0 Wan Maria Status : kde	Sensor Values	Everts	Array Serial Number: Array Length: Array Usage: Polymer Type:	36B01476 36 cm 12 POP4
Event Log Statist Run Scheckle Capitares Viewer Capitares Viewer Schutz Viewer Marual Control Service Log	Eser: Off Oven Off Oven Off Front Doors: Closed Oven Door Closed Autosempler: Return	200         kV         600.0         µA           15.0         400.0         400.0         400.0           10.0         400.0         400.0         400.0           10.0         400.0         400.0         400.0           10.0         400.0         400.0         400.0           10.0         400.0         400.0         400.0           10.0         400.0         400.0         400.0           10.0         400.0         400.0         400.0           10.0         400.0         400.0         400.0           10.0         400.0         400.0         400.0           10.0         400.0         400.0         400.0           10.0         400.0         400.0         400.0           10.0         400.0         400.0         400.0           10.0         400.0         400.0         400.0           10.0         400.0         400.0         400.0           10.0         400.0         400.0         400.0           10.0         400.0         400.0         400.0           10.0         400.0         400.0         400.0           10.0         400.0         400.0	13:46:50 System status: Inie 13:46:50 System Status: Diagnostic state. 13:43:45 System Status: Diagnostic 13:43:43 Requested to entr into diagnostics state. 13:43:41 Requested to exit diagnostics state. 13:42:34 System Status: Diagnostic 13:42:34 Requested to entr into diagnostics state.		

6. Check the LIMS to see when the POP6 was last changed. If it is >7 days, proceed with POP6 change (See part F of this Section) and then return to Step 9.

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7. Check the level of POP6 in the bottle to ensure there is enough for your run (approximately  $600 \ \mu l$  is needed per injection). If there is not, proceed with POP6 change (See part F of this section) and then return to Step 9.



- 8. If you are the first run on the Distrument of the day, proceed with steps 9 17. If a run has already been performed on the instrument that day, skip to "**Creating a Plate ID**"
- 9. Close the instrument doors and press the tray button on the outside of the instrument to bring the autosampler to the forward position.
- 10. Wait un the autosampler has stopped moving and then open the instrument doors.
- 11. Remove the three plastic reservoirs from the sample tray and anode jar from the base of the lower pump block and dispose of the fluids.
- 12. Rinse and fill the "water" and "waste" reservoirs to the line with Gibco® water.

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- 13. Make a batch of 1X buffer (45 ml Gibco® water, 5 ml 10X buffer) in a 50mL conical tube. Record the lot number of the buffer, date of make, and initials on the side of the tube. Rinse and fill the "buffer" reservoir and anode jar with 1X buffer to the lines.
- 14. Dry the outside <u>and inside rim</u> of the reservoirs/septa and outside of the anode jar using a Kimwipe and replace the septa strip snugly onto each reservoir. **If these items are not dry, arcing could occur thus ruining the capillary and polymer blocks.**
- 15. Place the reservoirs in the instrument in their respective positions, as shown below:



- 16. Place the anode jar at the base of the lower pump block.
- 17. Close the instrument doors

# B. Creating a Plate D

- 1. Click of the **Plate Manager** line in the left window.
- 2. Select **Import** from the bottom of the screen. Find the text file that was previously saved in the master file for the 3130xl run data (e.g. B08-015.txt file present in the **Batman08-015 files** folder)
- 3. Click on **OK**.

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# C. <u>Preparing the DNA Samples for Sequencing</u>

Arrange amplified samples in a 96-well rack according to how they will be loaded into the 96- well reaction plate. Sample order is as follows: A1, B1, C1, D1... G1, H1, A2, B2, C2... G2, H2, A3, B3, C3, etc. Thus the plate is loaded in a columnar manner where the first injection corresponds to wells A1 to H2, the second injection corresponds to wells A3 to H4 and so on. Label the side of the reaction plate with the name used for the Plate ID with a sharpie.

4. Remove the Hi-Di formamide from the freezer and allow it to thaw. Add 10µl of formamide to each dried sample and mix to bring the ample into solution.

#### Once formamide is thawed and alignoted, discard the tube. Do not re-freeze opened tubes of Hi-Di formamide

- 5. If single Centri-Sep columns were used, load the entire  $10 \ \mu$ l of the resuspended samples into the 96-well tray in the uppropriate wells. The injections are grouped into 16 wells starting with A1, B1, and so on moving down two columns ending with 2G, 2H, for a total of 16 vells. Fill any unused wells that are part of an injection set (eg. containing <16 samples) with 10 \mu l of Hi-Di formamide.
- 6. Once all of the samples have been added to the plate, place the 96-well septa over the reaction plate and firmly press the septa into place. Spin plate in the centrifuge for one minute.
- 7. Remove the reaction plate from the base and heat denature samples in the 95°C heatblock for 2 minutes followed by a quick chill in the 4°C chill block for 5 minutes. Centrifuge the tray for one minute after the heat/chill.
- 8. Once denatured, place the plate into the plate base. Secure the plate base and plate with the plate retainer.

# **IMPORTANT:** Damage to the array tips will occur if the plate retainer and septa strip holes do not align correctly.

Do not write on the septa with pen, markers, sharpies, etc. Ink may cause artifacts in samples. Any unnecessary

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# markings or debris on the septa may compromise instrument performance.



# D. Placing the Plate onto the Autosampler (Linking and Unlinking Plate)

Autosampler holds up to two, 96-well plates in tray positions A and B. To place the plate assembly on the autosampler, there is only one orientation for the plate, with the notched end of the plate base away from you.

- 9. In the tree pane of the Foundation Data Collection v3.0 software click on GA Instrument > ga3130xl > *instrument name* > Run Scheduler > Plate View
- 10. Push the tray button on the bottom left of the machine and wait for the autosampler to move forward and stop at the forward position.
- 11. Open the doors and place the tray onto the autosampler in the correct tray

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position, A or B. There is only one orientation for the plate.

12. Ensure that the plate assembly fits flat in the autosampler. Failure to do so may allow the capillary tips to lift the plate assembly off the autosampler.

When the plate is correctly positioned, the plate position indicator on the **Plate View** page changes from gray to yellow. Close the instrument doors and allow the autosampler to move back to the home position.

NOTE: When removing a plate from the autosampler be careful not to hit the capillary array. Plate B is located directly under the array, so be especially careful when removing this tray.

Linking/Unlinking the Plate record to Plate

- 13. On the plate view screen, click on the plate ID that you are linking. If the plate ID is not available click **Find All**, and select the plate ID created for the run.
- 14. Click the plate position for B that corresponds to the plate you are linking.

# NOTE: It may take a minute for the plate record to link to the plate depending on the size of the sample sheet.

If two plates are being run, the order in which they are run is based on the order in which the plate were linked.

Once the plate has been linked, the plate position indicator changes from yellow to green when linked correctly and the green run button becomes active.

15. To unlink a plate record just click the plate record you want to unlink and click "**Unlink**".

## E. Viewing Run Schedule and Starting Run

- In the tree pane of the Foundation Data Collection software, click GA
   Instruments > ga3130xl > instrument name > Run Scheduler > Run View.
- 2. The **RunID** column indicates the folder number(s) associated with each injection

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in your run (e.g. *Batman-2008-0114-1600-0197*). The folder number(s) and the run ID should be recorded in the **LIMS**.

- 3. Click on the run file to see the Plate Map or grid diagram of your plate on the right. Check if the blue highlighted boxes correspond to the correct placement of the samples in the injections.
- 4. NOTE: Before starting a run, check for air bubbles in the polymer blocks. If bubbles are present, click on the <u>Wizards</u> tool box on the top and select "Bubble Remove Wizard". Follow the wizard until all **bubbles** are removed.
- 5. Click on the green **Run** button in the tool bar when you are ready to start the run. When the **Processing Plate** dialog box opens (You are about to start processing plates...), click **OK**.
- 6. To check the progress of a run, click on the Cap/Array Viewer or Capillaries Viewer in the left window. The Cap/Array Viewer window will show the raw data of all 16 capillaries at once. The Capillaries Viewer window will show you the raw data of the capillaries you select to view.

**IMPORTANT**: Always existing from the Capillary Viewer and Cap/Array Viewer windows. During a run, do not leave these pages open for extended periods. This may cause unrecoverable screen update problems. Leave the Instrument Status window open.

The visible setting should be: EB voltage 12.2 kV Daser Power prerun 15 mW Laser current (no set value)

EP current (no set value) Laser Power during run 15mW Oven temperature 50°C

Expected values are: EP current constant around 40-60  $\mu$ A starting current EP current constant around 70-80  $\mu$ A running current Laser current: 5.0 A  $\pm$  1.0 A

It is good practice to monitor the initial injections in order to detect problems.

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## F. Water Wash and POP Change

Refer to Section A, pg. 2 for schematic of 3130*xl* while proceeding with the water wash and POP change procedure.

- 1. Remove a new bottle of POP6 from the refrigerator.
- 2. Select Wizards > Water Wash Wizard
- 3. Click "Close Valve"
- 4. Open instrument doors and remove the empty POP bothe
- 5. With a dampened Kimwipe<sup>®</sup>, wipe the polymer upply tube and cap. Dry.
- 6. Replace POP bottle with the water for the file to the top with Gibco® Water.
- 7. Remove, empty, and replace the anode Suffer jar on the lower polymer block.
- 8. Click "Water Wash." This procedure is will take approximately 4 minutes.
- 9. When the water wash is finished click "Next"
- 10. Select "Same Lot" or "Different Lot"
- 11. Remove water on the lower polymer block. Dry supply tube and cap with a Kimwipe
- 12. Replace with a new bottle of room temperature POP.
- 13. Click "Next."
- 14. Click "Flush." This will take approximately 2 minutes to complete.
- 15. Inspect the pump block, channels, and tubing for air bubbles.
- 16. Click "Next."

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# **3130xl Genetic Analyzer Troubleshooting**

#### **Instrument Startup**

Observation	Possible Cause	<b>Recommended Action</b>
No communication between the instrument and the computer (yellow light is blinking).	Instrument not started up correctly.	Make sure the oven door is closed and locked and the front doors are closed properly. If everything is closed properly, start up in the following sequence: a. Logout of the computer. b. Turn off the instrument. c. Boot up the computer. d. After the computer has booted completely, turn the instrument on. Wait for the green status light to come on. e. Launch Data Collection software.
Red light is blinking.	Incorrectionstart up procedure.	<ul> <li>Start up in the following sequence:</li> <li>a. Log out of the computer.</li> <li>b. Turn off the instrument.</li> <li>c. Boot up the computer.</li> <li>d. After the computer has booted completely, turn the instrument on. Wait for the green status light to come on.</li> <li>e. Launch the Data Collection Software.</li> </ul>

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Observation	Possible Cause	Recommended Action
Computer screen is frozen.	Communication error. This may be due to leaving the user interface in the Capillary View or Array View window.	There will be no loss of data. However, if the instrument is in the middle of a run, wait for the run to stop. Then, exit the Data Collection software and restart as described above.
Autosampler does not move to the forward position.	Possible communication error, OR Oven or instrument door is not closed.	Restart the system, and then press the Tray button. OR a. Close and lock the oven door. b. Close the instrument doors. c. Press the Tray button.
Communication within the computer is slow.	Database is full.	Old files need to be cleaned out of the database. Follow proper manual procedures described in the ABI Prism 3130xl Genetic Analyzer User's Manual.
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### **Spatial Calibration**

Observation	Possible Cause	<b>Recommended</b> Action
Unusual peaks or a flat line for the spatial calibration.	The instrument may need more time to reach stability. An unstable instrument can cause a flat line with no peaks in the spatial view.	Check or repeat spatial calibration.
	Improper installation of the detection window.	Reinstable the detection window and make sure it fits in the proper position.
	Broken capillary resulting in a bad polymer fill	Check for a broken capillary, particularly in the detection window area. If necessary, replace the capillary array using the Install Array Wizard.
	Dirty detection window.	Place a drop of METHANOL onto the detection window, and dry. Use only light air force.
Persistently bad spatial calibration results.	Bad capillary array.	Replace the capillary array, and then repeat the calibration. Call Technical Support if the results do not improve.

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## **Spectral Calibration**

Observation	<b>Possible Cause</b>	<b>Recommended Action</b>
No signal.	Incorrect preparation of sample.	Replace samples with fresh samples prepared with fresh formamide.
	Air bubbles in sample tray.	Centrifuge samples to remove air bubbles.
If the spectral calibration fails, or if a message displays "No candidate spectral files found".	Clogged capillary	Refill the capillaries using manual control. Look for crogged capillaries during capillary fill on the cathode side.
	Incorrect parameter files and/or run modules solected.	Correct the files and rerun the calibration.
	Insufficient filling of array.	Check for broken capillaries and refill the capillary array.
Internet	Expired matrix standards	Check the expiration date and storage conditions of the matrix standards. If necessary, replace with a fresh lot.
Spike in the data.	Expired polymer.	Replace the polymer with fresh lot using the change Polymer Wizard.
	Air bubbles, especially in the polymer block tubing.	Refill the capillaries using manual control.
	Possible contaminant or crystal deposits in the polymer.	Properly bring the polymer to room temperature; do not heat to thaw rapidly. Swirl to dissolve any solids. Replace the polymer if it has expired.

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#### **Run Performance**

Observation	Possible Cause	<b>Recommended</b> Action
No data in all capillaries	Bubbles in the system.	Visually inspect the polymer block and the syringes for bubbles. Remove any bubbles using the Change Polymer Wizard. If bubbles still persist, perform the following: a. Remove the capillary array. b. Clean on the polymer bottle. c. Replace polymer with fresh polymer.
No signal.	Dead space at bottom of sample tube. Bent capillary array	Centrifuge the sample tray. Replace the capillary array Repeat reaction.
	Cracked or broken capillary	Visually inspect the capillary array including the detector window area for signs of breakage.
Low signal strength.	Poorevality formamide.	Use a fresh lot of formamide Vortex the sample thoroughly, and then centrifuge the tube to
	Weak amplification of DNA Instrument/Laser problem	Re-amplify the DNA. Run instrument diagnostics.

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Observation	Possible Cause	<b>Recommended</b> Action
Elevated baseline	Possible contamination in the	Wash the polymer block with
	polymer path.	hot water. Pay particular
		attention to the pump block, the
		ferrule, the ferrule screw, and
		the peek tubing. Dry the parts
		by vacuum pump before
		replacing them onto the
		instrument.
	Possible contaminant or crystal	Bring the polymer to room
	deposits in the polymer.	temperature, swirl to dissolve
		any deposits. Replace polymer
	<u> </u>	n'expired.
	Poor spectral calibration	Perform new spectral
		calibration.
	CX. No	
	Detection celes dirty.	Place a drop of methanol onto
		the detection cell window.
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Observation	Possible Cause	Recommended Action
Loss of resolution.	Too much sample injected.	Dilute the sample and reinject.
	Poor quality water.	Use high quality, ultra pure water.
	Poor quality or dilute running buffer.	Prepare fresh running buffer.
	Poor quality or breakdown of polymer.	Use a free of polymer.
	Capillary array used for more than 150 injections.	Replace with new capillary array.
	Degraded formamide.	Use fresh formamide and ensure correct storage conditions.
	Improper injection and un conditions.	Notify QA to check default settings.
Poor resolution in some capillaries.	Insufficient filting of array.	Refill array and look for cracked or broken capillaries. If problem persists contact Technical Support.
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Observation	Possible Cause	<b>Recommended Action</b>
No current	Poor quality water.	Use high quality, ultra pure water.
	Water placed in buffer reservoir position 1.	Replace with fresh running buffer.
	Not enough buffer in anode reservoir.	Add buffer up to fill line.
	Buffer is too dilute.	Prepare new running buffer.
	Bubbles present in the polymer	Pause run and inspect the
	block and/or the capillary and /or	instrument for bubbles. They
	peek tubing.	tubing.
Elevated current.	Decomposed polymer.	Open fresh lot of polymer and store at 4°C.
	Incorrect butter dilution.	Prepare fresh 1X running buffer.
	Arcing in the gel block.	Check for moisture in and
	ent	around the septa, the reservoirs, the oven, and the autosampler.
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Observation	Possible Cause	<b>Recommended</b> Action
Fluctuating current	Bubble in polymer block.	Pause the run, check the polymer path for bubbles, and remove them if present.
	A slow leak may be present in the system.	Check polymer blocks for leaks. Tighten all fittings.
	Incorrect buffer concentration.	Prepare fresh anning buffer.
	Not enough buffer in anode.	Add butfor up to the fill line.
	Clogged capillary.	Rechl capillary array and check for clogs.
	Arcing.	Check for moisture in and around the septa, the reservoirs, the oven, and the autosampler.
Poor performance of capillary array used for	Poor quality formatrice	Prepare fresh formamide and reprep samples.
Tewer than 150 runs.	Incorrect buffer.	Prepare new running buffer.
	Poor reality sample, possible cleared needed.	Desalt samples using a recommended purification
Migration time becomes progressively slower.	Leak in the system.	Tighten all ferrules, screws and check valves. Replace any faulty parts.
	Improper filling of polymer block.	Check polymer pump force. If the force needs to be adjusted, make a service call.
	Expired polymer.	If necessary, change the lot of polymer.

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Observation	Possible Cause	<b>Recommended</b> Action
Migration time becomes progressively faster.	Water in polymer bottle resulting in diluted polymer.	Replace the polymer, making sure the bottle is clean and dry.
Arcing in the anode – lower polymer block.	Moisture on the outside of the lower polymer block.	Dry the lower block. If damaged, replace lower polymer block.
Error message, "Leak detected" appears. The run aborts.	Air bubbles in the polymer path. Pump block system is the polymer path. loose/leaking.	Check for bubbles and remove it present, then check for leaks. Make sure all ferrules, screws, and tubing is tightly secure. Ferrule in capillary end of block may be positioned wrong or missing. Check for this ferrule.
	Lower pump block has burnt out. When there is condensation in the reservoir (s) this will cause electrophroresis problems and burn the lower block	Replace the lower block.
Buffer jar fills very quickly with polymer	Lower polymer block is not correctly mounted on the pin valve.	Check for bubbles and remove if present. Then, look for leaks. Check to make sure the metal fork is in between the pin holder and not on top or below it.
# ABI 3130xl SEQUENCING

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Observation	Possible Cause	<b>Recommended Action</b>
Detection window pops out while replacing the capillary array. Replacing the window in the correct orientation is difficult.	Tightening of the array ferrule knob at the gel block causes high tension.	Loosen the array ferrule knob to allow the secure placement of the window. Re-tighten and close the detection door.
Detection window stuck. It is difficult to remove when changing the capillary array.	ARCHIVED Inator	To loosen the detection window: a. Undo the array ferrule knob and put the polymer block towards you to first notch. b. Remove the capillary comb from the holder in the oven. c. Hold both sides of the capillary array around the detection window area, and apply gentle pressure equally on both sides. d. Release.
QC	oument cont	

### Revision History:

July 24, 2010 – Initial version of procedure.

July 16, 2012 - Minor revisions in content to generalize terminology for LIMS.

### MITOCHONDRIAL DNA SEQUENCING ANALYSIS

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# **Mitochondrial DNA Sequencing Analysis**

<u>PURPOSE</u>: To compile the sequence data generated by the ABI 3130xl into a project for analysis, by editing the sequence data and compiling a consensus sequence that can be compared with the revised Cambridge Reference Sequence (rCRS) to determine the mitochondrial DNA type.

### PROCEDURE:

The data following the 3130xl run will be saved on the local 3130xl computer in separate injection folders. These folders, along with the run statistics and the run theets will be saved into a folder in the Mito\_Data drive. The run data is also copied into an Aralysis Folder in the Mito\_Data drive for analysis. Samples run using the ABI Big Dyc Terminator kit will need to be processed using ABI Sequence Analysis software for the basecalis to be assigned. Once the files have been processed with Sequence Analysis, they will be imported into the GeneCodes Sequencher software alignment program for conservus sequence analysis and interpretation of the mitochondrial DNA type.

# A. Transfer of the 3130xl rundata into the master file

1. On the desktop, click on the shortcut for the respective instrument's data file. The main path to this data file is:

E:\Applied Biosystems\UDC\data collection\data\ga3130xl\Instrumentname

Once there, identify the injection folders of the runs you wish to analyze.

- 2. Copy the injection folders into the master file (e.g. Batman08-015 files) that was created earlier making sure that all of the run statistic files and log files are included.
- 3. Also copy the newly created run files into the respective archive files in the MITO DATA directory.

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# **B.** Sequence Analysis

- 1. Open the Sequence Analysis program by double clicking on the icon. Login using your username and password.
- 2. Click on the import samples icon in the upper left of the screen, or go to Add Sample(s) under the File menu.
- 3. In the new window that pops up, locate the master file of the run that you wish to analyze. Click on the individual run files within the master file, and for each one click **Add Selected Samples>>** at the bottom of the winnow. As this is done, a list in the right of the window will populate with the stamples from the run. Click **OK** when finished importing samples.
- 4. The **Add Sample Status** window will indicate the progress of importing the samples. When this finishes, the samples will appear in the top window of the screen. Maximize this area by dragging the center divider bar to the bottom of the window.
- 5. The samples should all have the boxes under **BC** (base calling) checked. Click on the **Green Arrow** at the top, of the screen to begin the analysis of the samples.
- 6. The Analysis Status work of will indicate the progress of analyzing the samples. As samples are analyzed, the BC column will display a green, blue or yellow box around the check fox indicating the quality of the base calling:
  Green: Ordicates a successful base calling for that sample Blue : Indicates a problem in base calling the data for that sample Yellow: Indicates that there is no data to be analyzed for that sample
- 7. If the sequencing analysis is successful, click the yellow floppy-disk icon in the top left of the screen to **Save All Samples**, or click on **Save All Samples** under the File menu.

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- 8. Print the analysis report page. Click on the **Analysis Report** button at the top of the page (white button with <sup>A</sup><sub>R</sub>; A is in red and R in blue), or select **Analysis Report** under the Analysis menu at the top of the screen. When the report page opens, right click on the column headings for the analysis report. Deselect the following options- *PP Status, Peak 1, Base Spacing, # Low QV, # Med QV, # High QV, Sample Score, CR Start, and CR Stop.* The visible column headings will show the following- **BC Status, Well, Cap #, LOR, 'A' S/N, 'C' S/N, 'G' S/N, 'T' S/N, Avg S/N**. To ensure that all sample identification fits onto one row, deselect "Fit Columns to Window" (lower left of screen), select size "8" font, and increase the width of "Sample File Name" column.
- 9. Create a PDF file of the Analysis Report by clicking **Print** and send the file to **Adobe PDF**. Be sure the page set-up is set to portrait before creating the PDF file. Check the PDF file to make sure that the complete Sample Names and Sample Descriptions are present (e.g., not car off). If necessary, make formatting adjustments, resend Adobe PDF file, and recheck. Following the successful creation of the PDF file, save in the out folder (e.g., save in *B08-040* with run name *B08-040 Analysis Report*) that contained within the Analyzed Archive.
- 10. Attach the PDF Analysis Report to the LIMS for the cycle-sequencing batch. Close the PDF Analysis Report and the Analysis Report screen.
- 11. Click **Exit** under the **File** menu to close out the Sequencing Analysis program.
- 12. The Analysis report will be placed together with the run review sheet, the 3130xl run sheet, and the 3130xl cycle-sequencing worksheet for review and archiving

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# C. Sequencher

Before you begin Sequencher, make sure that the USB key is fully inserted in a local USB port on the computer, and the computer fully recognizes the key. If successful, the computer will make a "Ding-Dong" sound. Starting Sequencher without this USB key will cause the program to lock out all editing capabilities.

1. Open Sequencher. Under the **Contig** menu, select **Consensus to Forensic Standards**. This only needs to be done after opening Sequencher for the first time. Once set, it will remain until the program is closed. Also, check to make sure that the Assembly parameters used to create contigs are set to the proper settings. Click on the box in the upper left-hand corner that is marked "Assembly Parameters". The following settings should be selected:

Assembly Algorithm.	Disconstant (redial hystop)
Assembly Algorithm:	J Druy Data (radial button)
Optimize Gap Placement:	ReAligner (check box)
	Prefer 3' Gap Placement (check box)
Minimum Match Percentere:	85% (slide bar)
Minimum Overlap:	20 (slide bar)
Assemble By Name:	not Enabled (deselected)

- 2. Under the **File** menu, go to **Import** and select **Sequences**.
- 3. Find the sequence files that were copied to the Analyzed Archive. To simplify, under File of type select "With Chromatogram Sequences." To select all of the files press and hold the Shift key, and click on the last file. Once the files are selected click **Open.** Maximize the analysis window to view all of the samples and sample data.
- 4. Import the appropriate reference sequence into the project for every contig that needs to be built. The reference files (HVI.spf or HVII.spf) are located on the Forensic Biology network (Mito Data/Reference Seqs).

### These files can be saved to the desktop or local hard drive for easier access.

5. Holding down the Shift or the Control key, click on imported rCRS file, and the forward and reverse sequence files that will make up the contig.

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- 6. At the top of the screen, click on the **Assemble to Reference** button. If the samples contain viable data, the contig will be formed. If the samples do not contain quality data, they will not import into the contig. Name the contig according to the sample name and hypervariable region sequenced. (e.g.- Hair 1A HVII)
- 7. Select the new Contig icon by clicking on it once. In the **Contig** menu at the top of the screen, select **Trim to Reference Sequence**.
- 8. Double click on the Contig icon. When the contig diagraph window opens, click on the **Bases** button at the top left of the screen.

A new window will open showing the individual sequence files above the rCRS reference sequence at the top of the window and the consensus sequence at the bottom of the window. Individual sequences, including the reference sequence can be moved up or down by placing the cursor on the name of the sequence in the apper left box and dragging the sequence up or down.

Under the consensus sequence is a series of "•" and "+" symbols. The "•" symbols highlight base call disagreements from the rCRS and the "+" symbols highlight ambiguities in the consensus sequence.

- 9. To view the chromatogram data and the sequence data together, highlight a base in the consensus sequence and click the **Show Chromatograms** button at the top of the screen. This will open a second window showing the chromatogram data for all of the sequences in the contig. Notice that the reverse primer sequence has been reversed and compiled in the process of building the contig. Adjust the position of the two screens so that all of the sequence data is visible along with the chromatogram data, and so all of the base positions can be reviewed. Use this display and review all sequence positions.
- 10. To quickly move from one ambiguity to the next in the consensus sequence, click on the first base in the sequence and then press **Control-N** simultaneously on the keyboard. This will jump both the sequence data and chromatograms to the next ambiguous position. To find only the instances where the contig is in disagreement between the strand data, click on the sequence data and press **Control-D**.

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<u>IMPORTANT</u>- In the instances where length and/or sequence heteroplasmy is present and yields single-stranded DNA regions and/or ambiguous bases, or un-editable N calls are present, the consensus setting on the Sequencher program must be set to Plurality mode to analyze that particular sample.

- 11. Within the LIMS, create the appropriate contig samples, and indicate which primer samples are associated with each appropriate contig. All edits, trims, and modifications to the contig sequence must be recorded within the LIMS documentation.
- 12. To edit a base call, click on the base in question in the consensus sequence or individual sequence, and press the appropriate letter on the keyboard according to the following:



\*See Nomenclatore section of this manual for further discussion.

- 13. **To delete a base ch**ck on the base in question and do one of the following:
  - a. To have the bases fill in from the left side of the strand, press the delete
  - b. **(b)** have the bases fill in from the right side of the strand, press the **backspace** key, and follow the on-screen instructions.
- 14. **To insert a base**, press the **Tab** key and follow the on-screen instructions.
- 15. **To shift the entire strand,** place the cursor over the strand in question and press and hold the **Ctrl** key. The cursor will turn into a open hand icon. Click and hold using the icon and the hand will "grab" the strand, allowing you to move the entire strand left or right.
- 16. To move a single base, place the cursor over the base in question and press and

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07-16-2012 MITOCHONDRIAL DNA TECHNICAL LEADER 80 OF 121	DATE EFFECTIVE	APPROVED BY	PAGE
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hold the **Alt** key. The cursor will turn into a lasso icon. Click and hold using the icon and the lasso will "grab" the base, allowing you to move the base.

17. **To highlight a section of the sequence**, click on the beginning base in the sequence you wish to highlight, and then move the cursor to the last base in the sequence section, press and hold the **Shift** key, and click on the final base.

### 18. To review edits press and hold Ctrl E.

- 19. When the sequencing analysis and editing are completed the contigs that were built need to be archived in the appropriate folders. To archive contigs, hightlight contigs that are to be archived together, go to file → export → selection as subproject. Click on Browse button and selectronder for contig to be archived. Make sure that the format is set to 'Sequencher Project'. Click the Export button. Enter project name, e.g. PCddmrow-hhrder for positive control contigs and FBXX-12345 for sample contigs
  - Positive Control contigs should be achived as follows: M:/MITO\_DATA/PC Archive/year/PCmmddyy-hypm.
  - Samples contigs should be archived as follows: M:/MITO\_DATA/Project Archives/*sample type/FBXX* 2345. Sample type should be 'Casework' for evidence and associated exemplars and should be 'Missing Person cases' for all Missing person samples

From this point forward, the saved contigs can be further modified with additional primer runs, edited, and resaved as outlined above.

The following procedures should only be done once the analysis of the contig is complete and the contig is ready for review.

- 20. Once contigs have been exported and archived, open appropriate project, go to the **Contig** menu and click on **Compare Consensus to Reference**. If necessary, widen the contig name column to view the entire contig name. To print, select **Reports, Entire Table, Open Report, and Print**. Select **portrait** as the orientation, and print.
- 21. Print the **Compare Consensus to Reference** page again, but this time send the

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file to **Adobe PDF**. Click **Print.** Save the PDF file in the master run file, named as the sample name eg. "FB05-0005m hair 1 HVI" Close the Adobe window. Close the Difference Review window. Attach this PDF to the LIMS system within the contig sample.

- 22. At the top of the sequence comparison page, click on the **Summary** button. When the **Summary View** window opens, click on **File**, **Print Setup**, and select "landscape." Then click on the **Ruler** button at the top of the page and adjust the margins (triangles on ruler) and adjust column spacing as needed to print entire sample ID.
- 23. Print the **Summary** page. To do this, select the **File** ment and select **Print**.
- 24. Print the **Summary** page again, but this time send the file to **Adobe PDF**. Click **Print.** Save the PDF file in the master run file, named as the sample name plus "sum," eg. "FB05-0005m hair 1 HV sum? Close the Adobe window. Attach this PDF to the LIMS within the carrie sample.

- 25. Click on the Overview button. In the Contig Diagram, double click on the individual sequence files. The sequence window of the file will open. Click on the Show Chromatogram button at the top of the screen. A new window will open. In the upper left corner is a slider bar, the four-color bases and two buttons: a dot and a vertice bar. DO NOT CLICK THE VERTICAL BAR, AS THIS WILL ERASE THE HEADER FROM THE PRINTED PAGE. Print this chromatogram as edited data, trimmed to the hypervariable region of interest. Fo do this, select the File menu and select Print Setup. Select landscape as the orientation, and print.
  - a. If you are printing the forward strand, under **Page Range** select **the FIRST four (4) pages** of the chromatogram.
  - b. If you are printing the reverse strand, under **Page Range** select **the LAST four (4) pages** of the chromatogram.

### Repeat step 25 for every separate chromatogram file.

26. Create an Adobe PDF file for this chromatogram as edited data, trimmed to the hypervariable region of interest. To do this, select the **File** menu and select **Print** 

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Setup. Select landscape as the orientation, and print to Adobe DPF from the drop-down list. Click OK. Under the File menu, select Print.

- If you are printing the forward strand, under Page Range select the a. FIRST four (4) pages of the chromatogram.
- If you are printing the reverse strand, under Page Range select the LAST b. four (4) pages of the chromatogram.

Confirm that the Adobe PDF is selected, and click Print. Note the PDF file in the master run file, named as the sample name plus the proper, e.g. "FB05-0005m hair 1 HVI A4." Close the Adobe window. Attach this PDF to the LIMS within the contig sample.

# Repeat step 26 for every separate chromatogram file.

- 27.
- Click on the **Overview** button. The lines at the top of the diagram indicate the forward and reverse strands in 28. relation to the rCRS sequence, and the green bar below the lines indicates which areas of the rCRS are covered by the available sequence data. If the sequence is present in both the forward and reverse strand, the bar will be green with thin white strips on the top and bottom. If there is a partial coverage in only one direction, the bar will ontain a light blue pattern.
- Print out the Covering Diagram. Under the File menu, select Print Setup. Select 29. landscape as the orientation, and print (select printer from the drop-down list). Click QK Under the File menu, select Print. Confirm that the appropriate printer is selected and click **Print**.
- 30. Print the **Contig Diagram** page again, but this time send the file to **Adobe PDF**. Select landscape as the orientation, and click **Print.** Save the PDF file in the master run file, named as the sample name plus "map," eg. "FB05-0005m hair 1 HVI map." Close the Adobe window. Attach this PDF to the LIMS within the contig sample.
- 31. The final step of Sequencher analysis is to prepare the export data file from Sequencher for the LIMS. This will allow the contig data to import into the contig sample within the LIMS. To do this, open the contig and select "Compare

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Consensus to Reference" from the Contig menu. Click on the "Reports" button at the top of the screen. Select the radio button for "Entire Table" and from the drop down menu, select the report format as "Variance Table Report." Save the variance table as a text file to the appropriate network location and import into the LIMS for the appropriate contig.

32. After the import is completed in the LIMS, and the contig data is saved, the analyst can run the reports for the mtDNA Run Review and Positive Control Reviews, and print these reports as necessary for review.

### **File Output and Construction** D.

Arrange the paperwork in following order, from bottom to

- a.
- b.
- Run/rerun review sheets Control review sheets Sequencher Chromatogram printouts (Pnecessary)- landscape c.
- Contig Diagram- landscape d.
- Summary View- landsc e.
- f. **Editing Sheet**
- Compare Consensus to Reference- portrait g.

Landscape pages should be arranged in the file so that the right side of the landscape view faces the top edge of the file, and the left side of the landscape view faces the bottom side of the file.

### Data Review E.

- 1. Once all of the Sequencher data has been completed and the file have been archived, pass the entire set of sample printouts for one 3130 run to another IA for data review.
- 2. For the IA performing the review, the following steps must be performed.
  - Open the respective file from the appropriate archive located in the a. MITO\_DATA directory. Review all sequencher files.
  - For each sample, including Positive Control(s), ensure that all edits b.

### MITOCHONDRIAL DNA SEQUENCING ANALYSIS

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reflected in the editing documentation are valid and accounted for within the data set.

- c. For positive controls, ensure that the proper type is displayed on the Compare Consensus to Reference page.
- d. For negative controls, open the bases and chromatogram windows for each primer for each sample to ensure that no base calling data is present. If necessary, attempt to re-build a contig using questionable negative controls.
- e. Ensure for every sample that the documentation is assembled in order and reflects the entire project and sample names.
- 3. If a problem is found, mark the occurrence within the documentation and return the documentation to the original analyst.

# F. Archiving the Sequencher Bath

Data will be archived in **BINDERS**, **ASEFILES**, and **ELECTRONIC FILES**.

# ARCHIVED IN BINDERS:

Instrument binders (e.g. Barman) 3130xl report, original Analysis report, original Editing reports for Neg controls that could build into a contig, original Run review reports, original

### PC Binder

<u>For each positive control:</u> Positive control review report Contig diagrams, original Sequence summaries, original Editing reports, original Difference review sheets, original

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### FB CASEFILES:

3130xl report, copy Run review report(s), copy Positive control review report, copy Positive control editing report, copy FB sample contigs, originals Contig diagrams

### ARCHIVED IN ELECTRONIC FILES:

--U15) -port Aun review reports Analyzed run sequence files Neg controls that could build in the config ives (e.g. PC\_053108-1306) 'C Sequencher file C editing report - review report archive (e.g. FPAMEN Sequench-- dit: Analyzed run files (e.g. B08-015)

PC archives (e.g. PC\_053108-1306)

FB project archive (e.g. FB08 FB Sequencher f FB editing repor

> NOTE: If a positive CTR is sequenced twice (e.g., during QC tests), the name will stay the same as in PCmmddyy-hhmm but a lettered suffix will be added after each new sequencing as in PC-mmddyy-hhmm-A, PC-mmddyyhhmm-B....

A backup of all of the sequencing data contained in the MITO\_DATA directory will be archived by DOITT.

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**Revision History:** 

July 24, 2010 – Initial version of procedure.

July 16, 2012 - Minor revisions in content to generalize terminology for LIMS.

Controlled versions of Department of Forensic Biology Documents only exist electronically on the Forensic Biology network. All printed versions are non-controlled copies.

### SEQUENCE NOMENCLATURE AND ALIGNMENT

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# **Sequence Nomenclature and Alignment**

Nucleotide positions are designated according to the standard one-letter code based on the nomenclature system adopted by the International Union of Pure and Applied Chemistry (IUPAC; see table below). Note that an "N" is used to denote unresolved sequence ambiguities where N can be any one of the four bases. IUPAC codes that designate two possible bases should only be used in instances of sequence heteroplasmy.

IUPAC code	Base designation	IUPAC code	<b>Base designation</b>
G	Guanine	R	A or G
А	Adenine	Y	C or T
Т	Thymine	K	G or T
С	Cytosine	↓ × M	A or C
Ν	G, A, T, or C	diffic s	C or G
		W	A or T
ng Sequencher 4.	<u>9</u> Arolo		

# **A.Using Sequencher 4.9**

- 1. Sequence differences between the questioned sample and the revised Cambridge Reference Sequence (CRS) are generated and printed out from the Comparison Report file in Sequencher. These differences are organized by hypervariable region (eg., difference review file is generated for each HVI and HVII tifferences are listed in order of occurrence on the mtDNA region). molecule
- In most cases, the alignment of a given mtDNA sequence with that of rCRS is 2. straightforward. However, care must be taken in the placement of insertions and deletions in reference to that of rCRS according to the following standard nomenclature:
  - Characterize profiles using the least number of differences from the a. reference sequence. Align the 310 T base in the rCRS with a T whenever possible.

### SEQUENCE NOMENCLATURE AND ALIGNMENT

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- b. If there is more than one way to maintain the same number of differences with respect to the reference sequence, differences should be prioritized in the following order: (i) substitutions: transitions are favored over transversions, (ii) insertions/deletions (indels).
- c. Insertions and deletions should be placed furthermost 3' to a homopolymeric region, with respect to the light strand of rCRS. Insertions and deletions should be combined in situations where the same number of differences to the reference sequence is maintained. In situations involving the "AC" motif, treat this motif as a homopolymeric region with respect to indels in the AC repeat region. Alignment rules a, b, and c are described in Budowle, et al, 2002. For casework samples where alternative alignment following the brerarchy of Wilson, et al, 2002a,b, is also possible, the alternative alignment does not need to be included in the case file.
- 3. Insertions (INS) should be listed to the right of a particular nucleotide position. Insertions are documented by first noting the site immediately 5' to the insertion followed by a point and a "1" for the first insertion, a "2" if there is a second insertion, and so on.
- 4. Deletions (DEL) should be isted exactly where the known base in the reference sequence is missing in the sample sequence to minimize the number of differences between the questioned sample and the rCRS reference sequence. Deletions are noted by a ":" on the Sequencher printout in the consensus sequence.
- 5. **Sequence reteroplasmy** (also known as point or site heteroplasmy) occurs when a single cample contains at least two mtDNA sequences that differ at one or two nucleotide positions. The appropriate one-letter IUPAC code will be used during the editing of a given site that shows sequence heteroplasmy. This designation will be reflected in the Sequencher Comparison Report. In addition, the presence of sequence heteroplasmy at the given nucleotide position for the respective heteroplasmic bases will be recorded on the sequence editing documentation.

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- 6. **Length heteroplasmy** occurs in regions that contain many tandem C nucleotides. These regions are commonly referred to as polycytosine or C-stretch regions. Length heteroplasmy refers to a sample that has at least two types, each one differing by the total number of C nucleotides at a given C-stretch.
  - a. It will be noted if a given casework sample has length heteroplasmy in HVI. The number of C residues, however, in the area with HVI length heteroplasmy will not be recorded. Length heteroplasmy in HVI most commonly arises when there is a substitution of a C for a T at position 16,189. The reference type in HVI is  $C_5TC_4$ . Sequences showing length heteroplasmy in HVI will be truncated to fit the CTC<sub>4</sub> format including the T to C change at position 16,189.
  - b. It will be noted if a given casework sample has length heteroplasmy in HVII. Length variants in HVII are commonly observed in the number of C residues preceding a T regione at position 310. It is often possible to determine unambiguously the dominant length variant in this region. The profile used for further analysis on Sequencher should be composed of only the major type as the profile by the analyst.

# B.<u>Using Sequencher 4.1.4</u>

1. Sequence differences between the questioned sample and the revised Cambridge Reference Sequence (rCRS) are generated and printed out from the Difference Review file in Sequencher. These differences are organized by hypervariable region (eg., one difference review file is generated for each HVI and HVII region). The differences are listed in order of occurrence on the mtDNA molecule. "Ref" (reference) and "Con" (consensus) indicate what bases are present in the rCRS and the questioned sample, respectively, at the designated mtDNA sequence positions.

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- 2. In most cases, the alignment of a given mtDNA sequence with that of rCRS is straightforward. However, care must be taken in the placement of insertions and deletions in reference to that of rCRS according to the following standard nomenclature:
  - a. Characterize profiles using the least number of differences from the reference sequence. Align the 310 T base in the rCRS with a T whenever possible.
  - b. If there is more than one way to maintain the same number of differences with respect to the reference sequence, differences should be prioritized in the following order: (i) substitutions: transitions are favored over transversions, (ii) insertions/deletions (indels).
  - c. Insertions and deletions should be placed furthermost 3' to a homopolymeric region, with respect to the light strand of rCRS. Insertions and deletions should be combined in situations where the same number of differences to the reference sequence is maintained. In situations involving the "AC" motif, treat this motif as a homopolymeric region with respect to indeps in the AC repeat region. Alignment rules a, b, and c are described in Budowle, et al, 2007. For casework samples where alternative alignment following the hierarchy of Wilson, et al, 2002a,b, is also possible, the alternative alignment does not need to be included in the case file.
- 3. Insertions (INS) should be listed to the right of a particular nucleotide position. Insertions are documented by first noting the site immediately 5' to the insertion followed by a point and a "1" for the first insertion, a "2" if there is a second insertion, and so on.
- 4. Deletions (DEL) should be listed exactly where the known base in the reference sequence is missing in the sample sequence to minimize the number of differences between the questioned sample and the rCRS reference sequence. Deletions are noted by a ":" on the Sequencher printout in the consensus sequence.

### SEQUENCE NOMENCLATURE AND ALIGNMENT

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- 5. **Sequence heteroplasmy** (also known as point or site heteroplasmy) occurs when a single sample contains at least two mtDNA sequences that differ at one or two nucleotide positions. The appropriate one-letter IUPAC code will be used during the editing of a given site that shows sequence heteroplasmy. This designation will be reflected in the Difference Review. In addition, the presence of sequence heteroplasmy at the given nucleotide position for the respective heteroplasmic bases will be documented on the editing sheet.
- 6. **Length heteroplasmy** occurs in regions that contain many tandem C nucleotides. These regions are commonly referred to as polycytosine for C-stretch regions. Length heteroplasmy refers to a sample that has at least two types, each one differing by the total number of C nucleotides at a given C-stretch.
  - a. It will be noted if a given casework sample has length heteroplasmy in HVI. The number of C residues, however, in the area with HVI length heteroplasmy will not be recorded. Length heteroplasmy in HVI most commonly arises when there is a substitution of a C for a T at position 16,189. The reference type in HVI is  $C_5TC_4$ . Sequences showing length heteroplasmy in HVI will be truncated to fit the  $C_5TC_4$  format including the T to C change at position 16,189.
  - b. It will be noted if a given casework sample has length heteroplasmy in HVII. Length variants in HVII are commonly observed in the number of C residues preceding a T residue at position 310. It is often possible to determine thambiguously the dominant length variant in this region. The profile read for further analysis in Sequencher should be composed of only the major type as determined by the analyst.

**Revision History:** 

July 24, 2010 – Initial version of procedure.

July 16, 2012 – Minor revisions in content to generalize terminology for LIMS.

### **EDITING GUIDELINES**

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# **Editing Guidelines**

Sequencher base calls can be modified if the underlying data support it. The analyst can change an "N" call into a base determination, insert an additional base, remove a position, or trim a sequence. A base call must not be edited without proper justification.

Reasons for base removal are:

- Extra base inserted due to broad peak, peak artifact, or analysis default spacing

Reasons for base insertion are:

- Base omitted however authentic peak is present
- To maintain proper spacing

Reasons for changing a base to an "N" or to a degenerate IUPAC code

- Ambiguous bases are detected
- Dye or electrophoretic artifact interference
- Due to sequence or length heteroplasmy

Reasons for changing an "N" call to a base is

- rdinator - Base omitted or called "N", how er authentic peak is present
- Dye artifact or electrophoretic interference
- Neighboring peak interference

Reasons for trimming a sequence:

- Trimmed to remove end sequence (sequence tail removal)
- Trimmed rCRS and sequences to other (shorter) sequence position for duplication

Editing for other reasons should be documented with a comment explaining the edit.

Many software calls and be easily resolved and corrected by the analyst. However, ambiguous situations should not be edited. If an electrophoresis problem is suspected, this sample should be re-injected. Sequence information at each base position should be confirmed by data from both DNA strands when possible. Single-stranded regions present due to length heteroplasmy, must be confirmed by confirmatory sequencing of the same strand in the same direction. The Sequencher complementary strand alignment will flag conflicts between the two sequencing directions for all strands imported into the contig.

**Revision History:** 

July 24, 2010 - Initial version of procedure.

July 16, 2012 - Minor revisions in content to generalize terminology for LIMS

### **INTERPRETATION GUIDELINES**

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# **Interpretation Guidelines**

# **GUIDELINES FOR CONTROLS**

### A. Negative controls

Negative controls are considered negative if there is no detectable DNA based on the quantitation procedure and no "readable" sequence is seen after 3130xl electrophoresis. For DNA sequencing analysis, the controls are also considered negative if sequence was obtained, but it cannot align to the reference sequence.

A "readable" sequence from a negative control run is a sequence that can be aligned to the rCRS for >90 consecutive bases with no more than  $4^{\circ}$  N° calls within any 10 consecutive bases.

Two negative controls are associated with each sample: the extraction negative (ext neg or e neg) and the amplification negative (amp neg) controls. The former tests for potential DNA introduced during extraction through amplification, while the latter tests for the presence of any background DNA that was introduced during the amplification, or present in the amplification reagents. Both of these controls need to be processed for all sequencing primer sets.

Flow charts for passing, failing or retesting negative controls is as follows:

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\* If confirmed, the following actions should be taken:

- For extraction negative controls
  - Re-amplify to confirm presence of DNA, samples can proceed if re-amplification is clean.
  - If the extraction negative control still yields a peak following re-amplification, it is preferable to re-extract if more sample is available. If sample amount is limiting, analyst may proceed with caution. The results are only valid if the sequence detected for the amplification negative courfol does not match any of the associated samples or any of the samples in the case.
  - If the amount of DNA present in the extraction negative control exceeds 10% of any associated sample (DNA amounts determined by Agilent), that sample is invalid.
- For amplification negative controls
  - Re-amplify sample set.
  - If sample amount is limiting, it is left to the analyst's discretion to proceed with the amplification set since this result indicates that the background DNA is limited to the amplification control tube rather than being ubiquitous in all samples. The results are only valid if the sequence detected for the amplification negative control does not match any of the associated samples or any of the samples in the case.
  - If the amount of DNA present in the amplification negative control exceeds 10% of any associated sample, that sample is invalid.

Note: Any failed negative controls may be sequenced for quality control purposes.

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### 2. Linear array



- \* If confirmed, the following actions should be taken:
  - For extraction negative controls
    - Re-amplify and re-providize to confirm presence of DNA. 0 Samples on be interpreted and sequenced if the reamplification does not yield linear array signals.
    - If amount of extract available is limited, proceed to sequencing and do no interpret linear array
  - For amplification negative controls
    - Re-applify sample set. 0
    - K sample amount is limiting, it is left to the analyst's discretion 0 where the data of this amplification set since this result indicates that the background DNA is limited to the amplification control tube rather than being ubiquitous in all samples. The results are only valid if the linear array type detected for the amplification negative does not match any of the associated samples or any of the samples in the case.

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### 3. Sequencing results



^ If sequence data is present for an extraction or amplification negative control, but does not have base calls assigned, an analyst should manually assign base calls to determine if the sequence data can be aligned to the rCRS and if it is a "readable" sequence.

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\* If an extraction or amplification negative control contains a "readable" sequence, the results should be confirmed by recycle-sequencing. If confirmed, then the test fails and retesting must start at the point of sample re-extraction or amplification. If the amount of original sample present is limiting, the DNA extract is limiting or the re-amplification yields the same results, then sample results can be interpreted and reported if the sequence is different from all associated samples in the case. The determined sequence for the extraction or amplification negative control must contain "readable" sequence in order to be used in sequence comparisons with case samples.

If both extraction and amplification negative control from the same test contains "readable" sequence, the extraction negative cannot be interpreted because the amplification may have introduced a contaminant. The test fails and all samples and the extraction negative must be re-amplified and resequenced

\*\*If an extraction or amplification negative controls contain sequence data that can be aligned to the rCFS for < O consecutive bases, the test passes however the results should be confirmed by recycle-sequencing. If confirmed, see a mtDNA supervisor before proceeding with further testing. The following testing can be done if further testing is deemed necessary:

- For an extraction regative control, re-amplification of the negative control in question followed by re-extraction of associated samples if necessary.
- For an amplification negative control, re-amplification of the entire amplification set.

**NOTE:** If it is necessary to re-sequence a casework sample from the cycle sequence step, a new cycle sequencing amplification negative control (CAN) must be created for this round of cycle sequencing. This negative control must yield a negative result for the results to be valid.

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### **B. Positive controls**

The positive control (HL60) is included for each amplification and must produce sequence that is consistent with the known polymorphisms. The positive control sample must yield results for the full read length of the associated sample contig, but at a minimum, HVI, 16024-16365, HVII, 73-340, or both. In addition, the positive control serves as the run control. Therefore, in order to be valid, every run must have a positive control that passes specification.

This sequence will produce the following linear array type:

										_
Probe	16093	<b>I</b> A	1C	1D	1E	IIA	IIB	IIC	IID	189
HL60	1	1	1	2	2	2	6	1	1	1

If the positive control fails to produce the expected result, all samples associated with this control fail. If the suspected that the problem is not related to the amplification but could stem from a subsequent step, the positive control and all of the samples can be retested starting either at the cycle sequencing or the 3130xl injection step.

In cases of dye interference or electrophoretic artifact, some N calls in the positive control will be allowed as follows:

1. A maximum number of 4 "N" calls within any 10 base stretch for any primer strand used to build the contig will be allowed for either HVI or HVII region provided that the calls on the complementary strand are unambiguous and not contradictory to the questioned nucleotide position(s)

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2. Any positions that have ambiguous N calls on both complementary strands that cannot be resolved through retesting will result in the failing of the positive control and all of the associated sample runs.

# **Guidelines for Reporting**

### A. Linear array interpretation

- 1. A sample will not be used for comparisons if:
  - The sample displays a suspected partial profile (generally faint signals, more than 3 weak probe signals and/or the presence of 4 or more blank regions indicate the presence of a partial profile)
  - The sample consists of a mixture of LNA (more than 2 apparent heteroplasmic types could be caused by a mixture)
- 2. The numeric probe signed alls are the basis for linear array interpretation. Conclusions are as follows:

Consistent (cannot exclude)	All numerical calls match and no locus is inconclusive
Inconclusive	The two types show one difference or one or more of the regions are inconclusive (see below)
Exclusion	Two or more differences that show no evidence of heteroplasmy

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3. Heteroplasmy, weak probe signals or type 0 signals are treated as follows:

Weak probe signal	Weak call versus normal call; different probe signal	Difference
	Weak call versus normal call; same probe signal	Inconclusive
	Weak call versus type 0 probe signal	Oconclusive
	Type 0 signal call versus normal call	Difference
Type 0 probe signal	Type 0 signal call versus weak probe signal	Inconclusive
	Type 0 signat call versus type 0 signal call	Consistent if no evidence of a partial profile
	Both samples display heteroplasmy at the same region	Consistent
Heteroplasmy	One cample displays heteroplasmy; one of these probe signals is also present in the other sample	Consistent
Docume	One sample displays heteroplasmy; the probe signals are not present in the other sample	Difference

# B. Sequencing: Reporting of Base Calls

- 1. Sequence data should be determined from both complementary strands of DNA for mtDNA regions HVI and HVII. Only under special circumstances (see 2. below) can sequence be reported for confirmed data from a single-strand.
  - a. All good quality data that shows concordance for both complementary DNA strands or confirmed single-strand data can be reported. A list of reported differences from the rCRS must be accompanied by the range of

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nucleotides of the region that was sequenced. All possible alternative alignments are not reported.

- b. For sequence where an ambiguous calling situation occurs for one strand, it must be left unresolved and called an "N". No more than 4 uneditable N calls are acceptable within any 10 base stretch of strand sequence data.
- c. If an "N" base call is made on one of the DNA strands (eg., due to an electrophoretic artifact), this base position can still be reported as a base in the plurality consensus sequence as long as (i) the data on both strands are not in conflict with each other, and (ii) the data generated from the complementary or confirmatory DNA strand is clean and there is no question regarding its base call.
- d. A minimum read length of 20 contiguous base pairs of double-stranded or confirmed data that forms a contig will be valid for interpretation and for generating weight assessment.
- f. A minimum read length of 90 consecutive bases of single-stranded data is necessary for any strand to be used to build a contig. Only under special circumstances (see 2 below) can data be reported for a read length of less than 90 bases.
- 2. Special circumstances will arise (eg., length heteroplasmy) when data from only one DNA strand can be obtained or read lengths of greater than 90 bases are not possible.
  - a. For samples with HVI or HVII length heteroplasmy, additional primers should be used in order to obtain as much complementary data as possible.
  - b. For sequence where no data is available for one of the complementary strands, this can still be reported given that the sequencing reaction that yielded the one strand of sequence data is repeated (confirmed) for this sample with the same or different primer in the same direction. All of the data from this region (eg., results from two cycle sequencing reactions) must be concordant between the two sequencing runs. Note: This type of rerun will satisfy conditions where a difference from rCRS or sequence heteroplasmy is being reported.

### **INTERPRETATION GUIDELINES**

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- c. Situations will arise which result in severe length heteroplasmy (e.g. in HVII, 310 C resulting in a homopolymeric stretch of 13 C residues). Under these conditions, it will be not be possible to sequence through this region in either the forward or reverse direction. This could result in the trimming of a strand (e.g., C1) and/or will yield runs with sequences generated from the complementary strand (e.g., D1) primer that are less than 90 bases. In these cases, the data will be acceptable at less than 90 bases. The guidelines described in b. above for run confirmations will also apply to the confirmation runs necessary in this scenario.
- 3. In situations when un-editable "N" base calls are made at a given sequence position for both DNA strands, then this base will be reported as "N". Samples with 3 or more un-editable "N" calls within a 10 base pair region of the consensus sequence in either HVI or HVII are inconclusive.

### C. Criteria for Mixture Recognition

- 1. More than two heteroplastic positions in a sample are suggestive of a DNA mixture. If possible, the sample should be re-extracted or other samples in the same case should be tested.
- 2. Samples that contain two heteroplasmic positions might warrant further testing of additional samples depending on the circumstances of the case. This is to make sure that the sample type in question is not due to a mixture.

### D. Sequence Comparisons

- 1. The positive control run with that sample must type correctly in order to report the sequence for that sample.
- 2. If either extraction or amplification negative controls contain readable sequences, the associated case sample(s) must be compared to this data before any further sequence comparisons are made. The readable extraction or amplification negative controls must differ from all case samples by at least two bases for these case samples to be interpreted and reported (see Control Tables, section A3).
- 3. When comparing sequences obtained from samples, only the regions in common will be considered.

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- 4. A specimen that yields a mixture of DNA sequences is reported as inconclusive. No comparisons and no statistical evaluation will be performed using this sample.
- The number of C nucleotides at the HVI polycytosine C-stretch will not be 5. considered for interpretation purposes if length heteroplasmy is present. Likewise, the number of C residues exhibited in samples with HVII length heteroplasmy is highly variable and care must be taken when making comparisons. In order for sequence concordance to be declared, a common length variant must be observed in both samples being compared.

# Differences between samples due to the absence of an HVII common length variant are treated as one difference.

Match Criteria for Sequencing data 6.

Concordance	When two mtDNA sequences from separate samples (e.g. from two pieces of evidence or from evidence and a maternal family reference, ource) we consistent with each other in the overlapping regions, the two samples cannot be excluded as originating from the same person or from having a maternal relationship, respectively.	
Inconclusive	The resulting comparison will be considered inconclusive when two mtDNA sequences from separate samples differ by one difference. In these cases other reference sources and/or further testing in	
$\circ$	order to obtain more sequence data may be helpful.	
Exclusion	The resulting comparison will be considered an exclusion when two mtDNA sequences from separate samples differ by two or more differences.	

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### 7. Treatment of sequence heteroplasmy

Two identical heteroplasmic bases are present at the same position in both samples.	This is not a difference (eg., C/T vs. C/T).
One heteroplasmic base is present in one sample; a common base is present at the same position in the other sample.	This is not a difference (eg., C/T vs. C; also C/T vs. T).
One heteroplasmic base is present in one sample; a different base is present at the same position in the other sample.	This is a difference (eg., C/T vs. G).
Document Control Coordinator	

### Revision History:

July 24, 2010 – Initial version of procedure.

September 3, 2010 – Revised version of procedure: sentence removed from Paragraph Bb to reflect current procedures. March 7, 2011 – General clarifications added; removed decision matrix for negative controls and added flow charts; paragraph B.1 revised to reflect "a maximum number of 3 'N' calls..."

March 17, 2012 – Changed current interpretation guideline regarding the number of "N" calls within 10 consecutive bases from 3 to 4; Minor changes and typographical corrections.

July 16, 2012 – Minor revisions in content to generalize terminology for LIMS.

### STATISTICAL ANALYSIS

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# **Statistical Analysis**

The frequency of occurrence of evidence sample types will be reported based on the type of analysis that was performed. When both Linear Array and DNA sequencing analysis are done on a given comparison, only the DNA sequencing statistical analysis will be reported. Nevertheless, the statistics for both analyses (when performed) will be included in the case file.

The extent of the sequence data that will be used for the database search and statistical analysis will be limited to the shortest range and most conservative reporting of the sequence in common between the evidence sample(s) and reference sample(s) used in the comparison (see previously discussed sequence reporting criteria). Statistical analysis will not be performed on partial Linear Array mitotypes.

Statistics may also be presented comparing evidentiary samples, in which case the statistical analysis will be limited to the shortest range and most conservative reporting of the sequence in common between the evidence samples.

A. For Linear Array types (mitotypes), the aboratory will use a database containing population sample mitotypes from Kine et al. 2005; complete database is found at: <u>http://www.cstl.nist.gov/biotech/strbase/NIST pop@a/NIST mtDNA\_LINEAR\_ARRAY\_data.xls</u>

This population database contains multiples of 666 individuals and is comprised of the following population groups: African-American (252), Caucasian (286), and Hispanic (128).

- 1. A search of this database can be done by using the LA Summary & Stats excel spreadsheet located on the Forensic Biology network. After the spreadsheet is opened, makes use the Sequence Output tab is selected. Then enter the Linear Array mitorype at the top of the worksheet in this manner, with exceptions noted on the tats spreadsheet:
  - a. When no signal is seen in the Linear Array mitotype at a given position, then a null type ("0") is used for the database comparison at that position.
  - b. When a weak signal is seen in the Linear Array mitotype, the numerical type is used for the database comparison at that position. This is a conservative search strategy.
  - c. When two signal types are seen in the Linear Array mitotype at a given position, then each type is used separately for the database search(es) and the resulting counts are combined. This is a conservative search strategy.

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- 2. Click on the **LA Stats** tab to view the calculated population statistics for your sample mitotype. The spreadsheet calculates frequency estimates for the mitotype as described below (see B.3).
- B. For sequencing data, use the database and the procedure suggested by the FBI.
  - 1. Database

The database used to obtain a frequency estimate is maintained by the FBI (Budowle et al 1999, Monson et al 2002) and is available for download at the following web address:

http://www.fbi.gov/hq/lab/fsc/backissu/april2002/milles.htm.

A copy of the database including the search window is found on mtDNA analysts' computers. The database contains HVI (16024(16365) and HVII (73-340) sequences from a variety of unrelated individuals.

2. Searching Profiles

The base pair range of the profile to be searched is limited to the shortest range of reported sequence in common for both compared samples (see previously discussed reporting criteria).

Click on the mtDNA icon on your screen. The search window will open. Several options are pre-selected as indicated below.

Mode: Database

searchforensic

Under options (in edit menu):

Listing profiles:	- not checked
Length variants:	- consider multiple insertions as one difference
Partial profiles:	- not checked
Statistics:	- display up to 2 differences
Listing haplotypes:	- check to list haplotypes that appear multiple times
Date:	- check "all profiles"
Heteroplasmic scenarios:	- not checked
Helper Apps:	- not specified

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Enter your profile ID.

Enter the searchable basepair range for HVI and click **Add**. Repeat for HVII. If your sample has the standard read length (see above) just double-click on the HVI or HVII icons. Enter all differences from the rCRS.

Click search.

Select a temporary directory and name for the results file.

The search result consists of the number of samples with mismatches to the searched sample in the combined database and divided into different ethnic groups.

### ATTENTION:

When sequence heteroplasmy is present at a given position in the mtDNA sequence, the mtDNA database will be searched with an "N" at that position.

Even though mtDNA sequence HVII polycytosine length variants are entered, multiple C-stretch ength variants at the same position are considered as one difference during the database searches of concordant sequences containing this region and will not add additional rarity. In addition, the number of "C" residues in samples with HVI length heteroplasmy is not considered for comparison purposes.

- 3. Frequency estimate
  - a.

Frequency estimate when the Linear Array mitotype or mtDNA sequence is observed at least once in database.

Raw frequency estimates for the occurrence of a given mtDNA profile in the general population is based on the counting method as follows:

$$p = x/N$$
 (Eq. 1)

Where p is the frequency estimate; x is the number of times a profile has been observed in the population database, and N is the number of profiles in the population database.

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A confidence interval must be calculated from the results of the database search in order to correct the counting results for sampling errors according to the following equation

 $p \pm 1.96 [(p) (1-p)/N]^{1/2}$  (Eq. 2)

The upper 95% confidence interval value (upper bound =  $p + 1.96 [(p) (1-p)/N]^{1/2}$ ) is calculated as the maximum frequency of occurrence within each population of the same mitotype or mtDNA sequence as the searched profile.

The upper bound estimate can be calculated automatically using the Popstats spreadsheet for sequencing statistics or the LA Summary and Stats spreadsheet found on the Forensic Biology network drive.

Example #1: The Linear Array initiative or mtDNA sequence is observed 3 times in a database containing 2000 sample profiles. The frequency estimate is 3/2000 = 0.0015; the hipper bound of the confidence interval is equal to  $0.0015 + 1.961(0.006)(0.9985)/2000]^{1/2} = 0.0015 + 0.0017 = 0.0032.$ 

Meaning of example #1: With 95% confidence, the maximum true frequency of the ntDNA profile is 0.0032 or 0.32%, or 1 in 310. In other words, at least 99.68% of the population can be excluded as the source of the evidence

# b. Frequency estimate when the Linear Array mitotype or mtDNA sequence is not observed in the database.

The following equation is used:

1 - 
$$\alpha^{1/N}$$
 (Eq. 3)

 $\alpha$  is the confidence coefficient (use 0.05 for a 95% confidence interval), and N is the number of individuals in the population.
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Example #2: The Linear Array mitotype or mtDNA sequence is observed 0 times in the database containing 2000 sample profiles. The frequency estimate is  $1-0.05^{1/2000} = 1-0.999 = 0.001$ .

Meaning of example #2: For a database size of 2000 mitotypes or sequence profiles, the frequency of a mtDNA profile not observed in the database is 0.001 or 0.1%; or 1 in 1000, or, with 95% confidence, 99.9% of the population can be excluded as being the source of the evidence.

- c. Based on the FBI database, the mtDNA population database search software supplies separate results of the frequency estimates for four major populations (African-American, Hispanic, Caucasian, and Asian Origin). It is not the intent of the report to draw any inference as to the population origin of the contributor(s) of the evidence.
- d. The Linear Array mitotype population database of Kline, et.al., 2005, supplies separate results of the frequency for three major populations (African-American, Caucasian) Hispanic). It is not the intent of the report to draw any inference as to the population origin of the contributor(s) of the evidence.
- e. Reports will present the upper bound 95% confidence interval estimate for each population group, and express this as a percentage and a frequency, e.g., an upper bound 95% confidence interval estimate of 0.5% (1 in 200). Frequency estimate will be rounded down to rearest 10 or single whole number. The intent of the report is to present a conservative range of estimates of the strength of the mitochondrial DNA comparison.

#### Revision History:

July 24, 2010 – Initial version of procedure.

July 16, 2012 - Minor revisions in content to generalize terminology for LIMS.

### **CREATION OF A CASEFILE CD**

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# **Creation of a Casefile CD**

When all of the sequencing analysis is completed for a case, and upon request from members of the court, a CD containing all of the data for that case may be created to fulfill the request.

- Insert a blank CD into the computer, and open the program "Roxio/Creator Home." 1. Click on the "Data," section and select "Data Disc."
- Depending on the specific request, the levels of the disc will be created according to the 2. following:

CD Main Window

- "Evidence" File
- "Exemplars" File
- Ensure that all 3130x1 downs imported from the Analyzed Archive on the network, NOT 3. the *superhero* archive

To ensure the quality of the disc, it is advisable to copy all of the necessary data to a single location on the local computer that will create the CD. Once all of the necessary files have been compiled in this file on the local hard drive, according to the tree structure above, the entire contents of the local file can be added to the CD.

- 4. For the "Volume Label" fill in the casefile number, (eg. FB05-0234).
- 5. Label the new disk with the casefile number. The disk should be delivered to the Quality Assurance Manager for transmittal.

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#### REFERENCES

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### APPENDIX A OLIGONUCLEOTIDE PRIMER SEQUENCES

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# Appendix A –Oglionucleotide Primer Sequences

Region	Primer	Nucleotide (base) Sequence	Size (no. of bases)
HVI	$A1^1$	5'- CAC CAT TAG CAC CCA AAG CT -3'	20
	A4	5'- CCC CAT GCT TAC AAG CAA GT -3'	20
	B1	5'- GAG GAT GGT GGT CAA GGG AC -3'	20
	B4	5'- TTT GAT GTG GAT TGG GTT T -3'	19
	HVIF <sup>2</sup>	5'- CTC CAC CAT TAG CAC CCA A -3'	19
	HVIR	5'- ATT TCA CGG AGG ATG GTG -3'	18
	C1	5'- CTC ACG GGA GCT CTCCAT OC -3'	20
	C2	5'- TTA TTT ATC GCA CCT ACG TTC AAT -3'	24
HVII	D1	5'- CTG TTA AAAGTG COF ACC GCC A -3'	22
	D2	5'- GGG GTT TSS TGG AAA TTT TTT G -3'	22
	HVIIF	5'- CAC CCT ATT AC CAC TCA CG -3'	20
	HVIIR	5'- CTG TTACARA GTG CAT ACC GC -3'	20

1. Nucleotide sequences for primers A1, A4, B1, B4, C1, C2, D1, and D2 are from the FBI Laboratory DNA Analysis Unit II Mitechondrial DNA Analysis Protocol (mtDNA Protocol Manual, DNA Amplification - Rev. 8, Leve Date 02/01/05 for primers A1, B1, C1, C2, D1, and D2; mtDNA Protocol Manual, Cycle Sequencing - Rev. 8, Issue Date 09/10/04 for primers A4 and B4). The primer sequences in the FBI mtDNA Protocol Manual are based on those described in the following:

Wilson MR, DiZinno JA, Polanskey D, Replogle J, Budowle, B. Validation of mitochondrial DNA sequencing for forensic casework analysis. Int J of Leg Med 1995; 108:68-74.

Wilson MR, Polanskey D, Butler J, DiZinno JA, Replogle J, Budowle B. Extraction, PCR amplification, and sequencing of mitochondrial DNA from human hair shafts, BioTechniques 1995; 18(4):662-669.

2. Nucleotide sequences for oligonucleotide primers HVIF, HVIR, HVIIF, HVIIR are from the product insert for the LINEAR ARRAY Mitochondrial DNA HVI/HVII Region-Sequence Typing Kit that is available from Roche Applied Sciences (Cat. No. 03-527-867-001; product information is available at

APPENDIX A
<b>OLIGONUCLEOTIDE PRIMER SEQUENCES</b>

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July 16, 2012 - Minor revisions in content to generalize terminology for LIMS.

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APPENDIX B MITOCHONDRIAL DNA PRIMER LOCATIONS			
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## **Appendix B – Mitochondrial DNA Primer Locations**



The above diagrams are not to scale. All primer positions are relative to the table below. All arrows indicate the directions (forward or reverse that the primer amplifies along the hypervariable region.

HVI (16024 - 16365) = 342 bp		HVII (73 - 340) = 268 bp		
Primer	Position <sup>1</sup>	Primer	Position <sup>1</sup>	
HVIF	05975	HVIIF	15	
A1	15978	C1	29	
A4 <sup>2</sup>	16190	C2	154	
B4 <sup>2</sup>	16182	D2 <sup>3</sup>	306	
B1	16410	D1	429	
HVIR	16418	HVIIR	429	

<sup>1</sup>Nucleotide position is defined as the first base at the 5' end of the primer.

<sup>2</sup> Primers A4 and B4 are used to resolve C-stretch length polymorphisms in HVI.

<sup>3</sup> Primer D2 is used when necessary to resolve the reverse strand sequence when C-stretch polymorphism is present in HVII.

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#### APPENDIX B MITOCHONDRIAL DNA PRIMER LOCATIONS

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## **Appendix C- Revised Cambridge Reference Sequence**

Hypervariable Region I (HVI)

16024	- TTCTTTCAT	G GGGAAG	CAGA '	TTTGGGTA	CC A	ACCCAAGTAT	
16064	- TGACTCACC	C ATCAACA	AACC	GCTATGTA	TT 1	FCGTACATTA	
16104	- CTGCCAGCC	CA CCATGA	ATAT '	TGTACGGT	AC (	CATAAATACT	
16144	- TGACCACCI	G TAGTACA	ATAA .	AAACCCAA	TC (	CACATCAAAA	
16184	- CCCCCTCCC	C ATGCTTA	ACAA	GCAAGTAC	AG (	CAATCAACCG	, Dx
16224	- TCAACTATO	CA CACATCA	AACT	GCAACTCC	AA A	AGCCACCC	
16264	- CACCCACTA	AG GATACCA	AACA .	AACCTACC	CA (	CCCTTAACAG	
16304	- TACATAGTA	AC ATAAAGO	CCAT '	TTACCGTA	CA 1	FAGCACIXITA	
16344	- CAGTCAAAT	C CCTTCTC	CGTC	CC - <b>1636</b>	5 ( er	nd)	
Hyper	variable Region	II (HVII)		$\sim$		<u>s</u>	
υI	0	~ /			X	<b>)</b>	
73-	ATGCACGCGA	TAGCATTGO	CG AG	ACCOTGGA	GC	CGGAGCAC	
113-	CCTATGTCGC	AGTATCTG	C TT	TAATTCCT	GCC	CTCATCCT	
153-	ATTATTTATC	GCACCTAC	эт тС	AATATTAC	AGC	GCGAACAT	
193-	ACTTACTAAA	GTGTGTTAA	AT TA	ATTATGC	TTC	GTAGGACA	
233-	TAATAATAAC	AATTGAATO	GT CT	CCACAGCC	ACT	FTTCCACA	
273-	CAGACATCAT	ААСААААА	AT TI	CACCAAA	CCC	CCCCCTCC	
313-	CCCGCTTCTG	GCCACAGCA	AC TT.	AAACAC-	340(	(end)	
		C	· ()`				
Human N	fitochondrial DNA	Revised Cambri	dge Refe	erence Sequen	ce,		
			•	-			
LOCUS	NC_012920	165 <b>69</b> bp	DNA	circular	PRI 3	30-APR-2010	
DEFINIT	TON Homo	sapiens mitocho	ondrion,	complete geno	ome.		
ACCESS	ION NC_0	12920	AC_000	0021			
VERSIO	N N	2920.1	GI: 251	831106			
SOURCE	E mitoch	ondrion Homo	sapiens (	(human)			

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

#### APPENDIX C REVISED CAMBRIDGE REFERENCE SEQUENCE

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#### REFERENCES

Anderson S, Bankier AT, Barrell BG, de Bruijn MH, Coulson AR, Drouin J, Eperon IC, Nierlich DP, Roe BA, Sanger F, Schreier PH, Smith AJ, Staden R, Young IG. Sequence and organization of the human mitochondrial genome Nature 1981; 290: 457-465. MEDLINE- 81173052 PUBMED-7219534

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### APPENDIX D DETAILED CYCSEQ/3130XL CALCULATIONS

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# **Appendix D- Detailed CycSeq/3130xl Calculations**

Example:

Sample	Vol, Quant (µL)	Num of Linear Arrays	Vol, Linear Array (µl)	Vol, Misc (µl)	Cont, Mean HVI- HVII (ng/4 ul)	Vol, Exo- Sap (ul)	Vol, DNA (µl)	Comment	Vol, H2O (µl)
Amp. Neg	4	0	0	0	0	9.2	3.0	Control	7.8
Sample	5	1	5.4	0	56	7.9	Ę,	1/10 <sup>th</sup> dil.	6.5

### **Calculations for Amplification Negative:**

- 1. A total of  $4\mu$ L of the amplification negative was aliquotted for quantification. The quantification value was below the limit of detection (nd) for that sample, and a linear array was not run. Therefore, the analyst enters 4 into the "Vol, Quant" field and 0 each into the "Num of Linear Arrays", "Col, Linear Array", "Vol, Misc", and "Conc Mean HVI-HVII" fields.
- 2. The total remaining reaction volume is calculated to be  $46 \ \mu L \ (50 \ \mu L \ starting \ volume \ minus \ 4 \ \mu l \ used for quantification).$
- 3. The amount of ExoSAP-IT required is calculated according to the following guideline: 1  $\mu$ l of ExoSAP-IT for every 5  $\mu$ L of amplified product. Thus, the current reaction volume is divided by 5 (46/5) and 9.2 is automatically input into the "ExoSAP-IT" field.
- 4. The amount of template to add to the vele sequencing reaction is calculated. In this case, a quant value of 0 instructs the program to inter the maximum volume amount of 3  $\mu$ L into the template field. The system automatically enters "Control" into the comments field based on the nd quantification value.
- 5. Finally, the amount of weight is calculated based on the previously calculated sample volume to make the total volume quantity sufficient at 10.8  $\mu$ L. This DNA/water mixture is now ready to be added to the cycle sequencing reaction.

### **Calculations for Sample:**

- 1. In this example,  $5 \ \mu L$  of amplified sample was aliquotted for quantification. Also,  $5.4 \ \mu L$  of the sample was used for Linear Array analysis. The user also inputs 5 into the "Vol, Quant" field along with the volume of  $5.4 \ (\mu L)$  used for the Linear Array analysis into the "Vol, Linear Array" field. The user inputs 0 into the "Vol, Misc" field. Finally, the user inputs the concentration value into the "Conc, Mean HVI-HVII" field. This field is based on the amount of sample DNA in a volume of  $4 \ \mu L$ .
- 2. The total reaction volume is calculated to be 39.6  $\mu$ L, which is equal to the starting volume minus 5  $\mu$ L for the quantification volume, 5.4  $\mu$ L used for the Linear Array (50 5 5.4 = 39.6).
- 3. The amount of ExoSAP-IT required is then determined as before. The calculation indicates that the reaction requires 7.9  $\mu$ L of ExoSAP-IT (39.6/5).

### APPENDIX D **DETAILED CYCSEQ/3130XL CALCULATIONS**

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- 4. In calculating the amount of template required for the cycle sequencing reaction, the system first determines the new concentration of the DNA sample after addition of ExoSAP-IT by the dividing the original concentration [(56 ng/4  $\mu$ L)(39.6  $\mu$ L)] by the new volume (47.5 ul). The new concentration (11.67 ng/  $\mu$ L) is then used to calculate the volume of sample needed to equal 5 ng of sample DNA [(5 ng)/(11.67 ng/  $\mu$ L) = 0.428  $\mu$ L]. If the final volume is less than 1  $\mu$ L, ed. co yield a tc www.analyten and analyten anal the system will indicate that a dilution is necessary in the "Comment" filed. In this example, the calculation indicates that 4.3 ul of a 1/10 sample dilution is required.
- 5. As before, the system indicates the amount of water necessary to yield a total of 10.8 µL of sample volume for the next step of cycle sequencing.

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