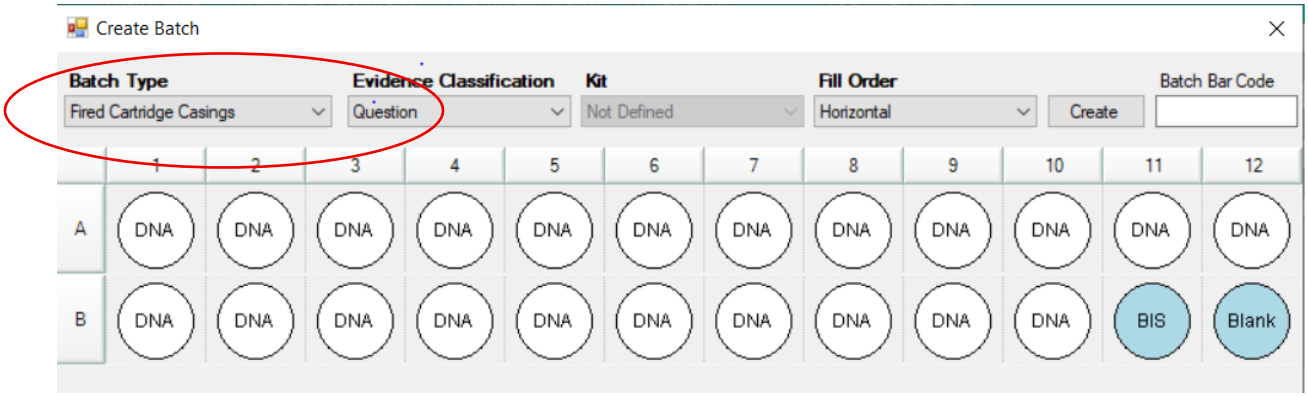
DNA Evidence Processing

I. Batch Setup – Fired Cartridge Casings

1. Forensic Biology will import FCC swabbings in STACS (see STACS SOP-2 Forensic Biology).
2. Create a lysis worksheet: Open **Processing → DNA Processing → Batch Setup.** Click **Create.**
3. Select the appropriate extraction under **Batch Type** (Fired Cartridge Casings), the corresponding **Evidence Classification** (Question), and the **Fill Order** (Horizontal).



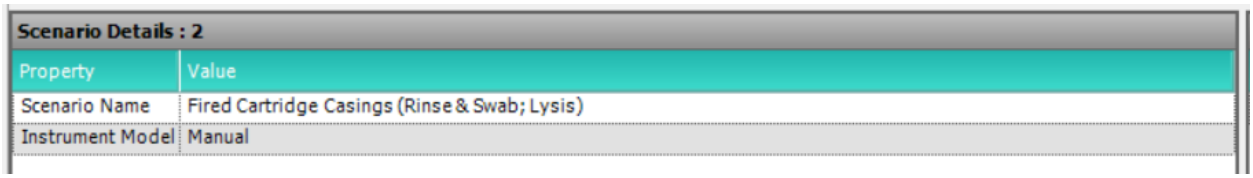
4. Click **Create**. A unique barcode associated with the extraction will be generated and printed. Moving forward, this barcode may be used to transfer the samples as a whole set.
5. Scan the extraction barcode to begin sample allocation. Or double click the batch in the upper window.
6. Select samples to be extracted from the available samples window on the left.
7. To add the BIS to the worksheet, select the designated BIS well and scan the barcode label on the EP1 tube.
8. If more samples need to be added, click Save.
9. If no changes/additions are needed, click **Complete** in the **Batch Setup** window.
10. By completing the batch, a **Blank** sample will automatically be generated. In the pop-up window, click Save. The barcode will automatically print. FCC case number, initials and date can be used for blank lot.

II. Extraction/Isolation – Fired Cartridge Casings

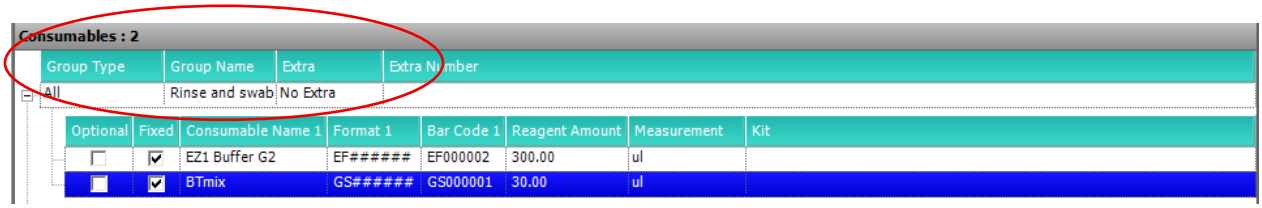
Extraction (steps #1-8) refers to sample lysis. Isolation (steps #7-21) encompasses instrument purification.

1. Open **Processing → DNA Processing → Extraction.**

2. Select the batch to be processed from the worklist and click **Select Scenario**. Fired Cartridge Casings (Rine & Swab; Lysis) will automatically be selected for FCC processing.

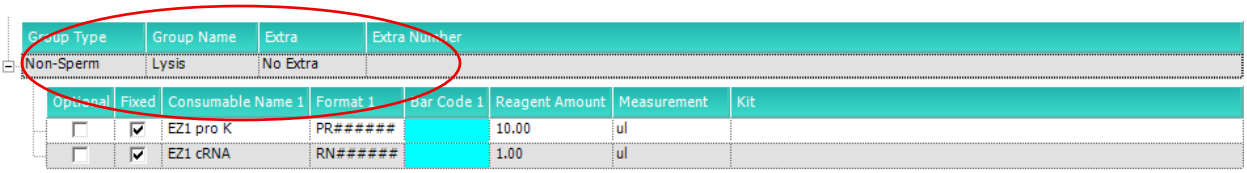


3. Scan extraction barcode.
4. FCC consumables are split into 2 groups. Highlight the **Rine and Swab** group. Scan the consumable barcodes for G2 Buffer and BTmix only. The Consumable window will display the reagent volumes required for the lysis.

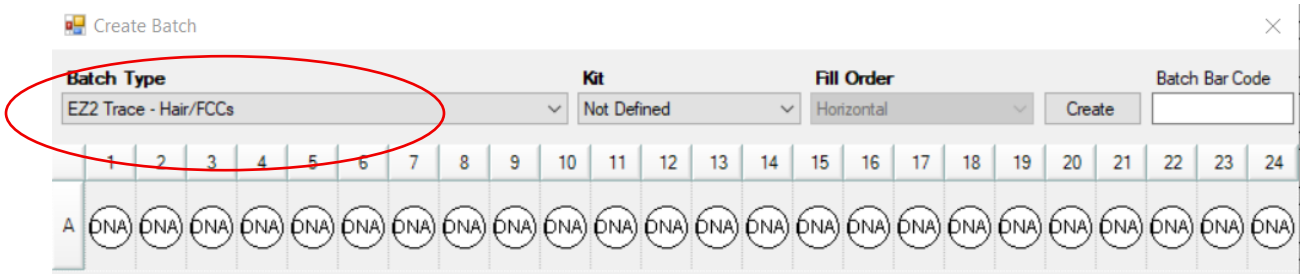


5. Click **Start Process**.
6. Complete the tube check by scanning the tube labels. Click ok.
7. Store sample tube(s), BIS and Blank in the refrigerator Pending Non-SA Rack. In **Storage Subsystem (Utilities → Storage → Storage Subsystem)**, select the **Store** tab, scan the appropriate storage unit bar code and item bar code(s). Select **Save.**
8. To discard empty bottles/tubes of G2 buffer/BTmix go to **Storage Subsystem (Utilities → Storage → Storage Subsystem)**, select the **Discard** tab, under Discard Reason select Consumed and scan the reagent bar code. Click Save.
9. **The DNA processor will then take over from this point on.**
    - In STACS, assign the appropriate samples to the processing DNA examiner. This can be done in **Processing → Receipt → Sample Setup.** Under the **Sample Status** dropdown, select **Processing**. Select the appropriate samples and choose **Assign**. The Reporting Analyst may be selected at this time, if known.
    - Take custody of the sample tube(s) to be processed. In **Storage Subsystem (Utilities → Storage → Storage Subsystem)**, select the **Retrieve** tab, scan the item bar code(s) to be put into your custody. Select **Save.**
10. Open **Processing → DNA Processing → Extraction.** Select the batch to continue processing from the worklist and click **Load Scenario**.

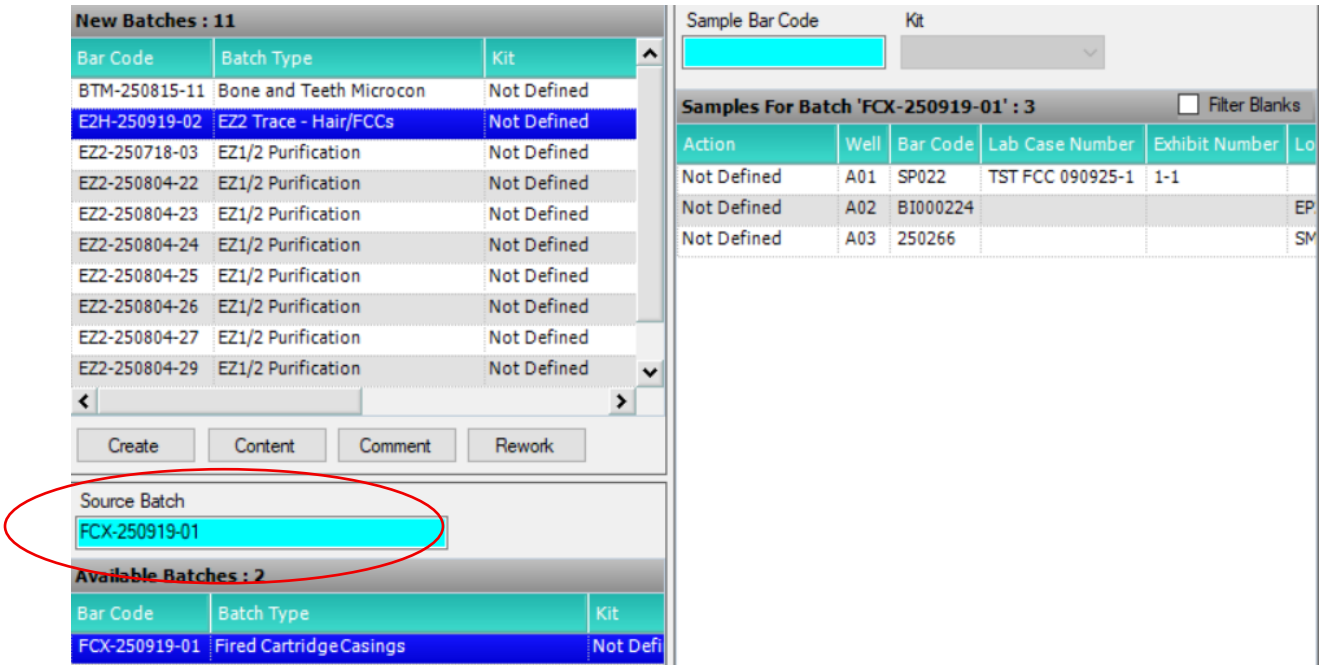
11. Highlight the **Lysis** group. Scan the consumable barcodes for EZ1 Pro K and EZ1 cRNA only. The Consumable window will display the reagent volumes required for the lysis.



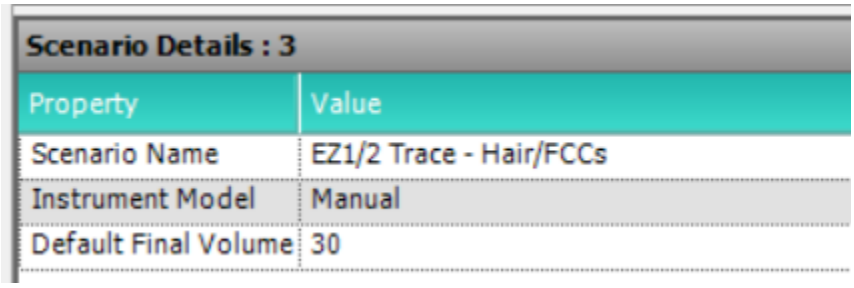
12. While incubating, elution tube barcode labels can be printed from the **Print Labels** button.
13. When lysis is complete, click **Complete Process** and record the results using the Complete Batch Activity screen.
    - **Process Successful**: the batch advances to the next processing step.
    - **Process Aborted:** the batch remains on the Extraction Batches worklist. A **Batch Comment** is required with this option.
    - **Process Failed:** the batch is abandoned and all samples return to Batch Setup. A batch comment is required with this option.
14. Click **Save**.
15. Create an Isolation (purification)worksheet: Open **Processing → DNA Processing → Isolation.**
16. Click **Create Batch.**
17. Click the **Create** button under the New Batches worklist.
18. Select a **Batch Type (EZ2 Trace – Hair/FCCs)** and click **Create** to create the unique barcode associated with the isolation.



19. Scan the newly created barcode into the **Destination Batch** section.
20. Scan the extraction barcode into the **Source Batch** section. Click **Allocate** to add the lysed samples to the isolation worksheet. If sample(s) need to be moved, this can be done after the allocation is saved, followed by dragging the sample(s) as needed.



21. Once finished, click **Complete** (at the top of the screen next to Destination Batch).
22. Under **Isolation**, in the Batches Worklist window, select the appropriate batch and click **Select Scenario** (EZ1/2 Trace – Hair/FCCs).



23. Scan the batch barcode and all necessary consumables and instrumentation.
24. Click **Start Process**.
25. Complete the tube check by scanning the lysis tube barcode labels followed by elution tube labels.
26. Once the isolation is complete, click **Complete Process** and select the appropriate option. Adjust the elution volumes if needed.
    - **Process Successful:** the batch advances to the next processing step.

- **Process Aborted**: the batch remains on the Isolation worklist. A **Batch Comment** is required with this option.
- **Process Failed:** the batch is assigned a **Status** of '**Abandoned**' and its samples are returned to Isolation Batch Create to be allocated to a new batch. A **Batch Comment** is required with this option. Only use if machine crashes or something that affects all samples.

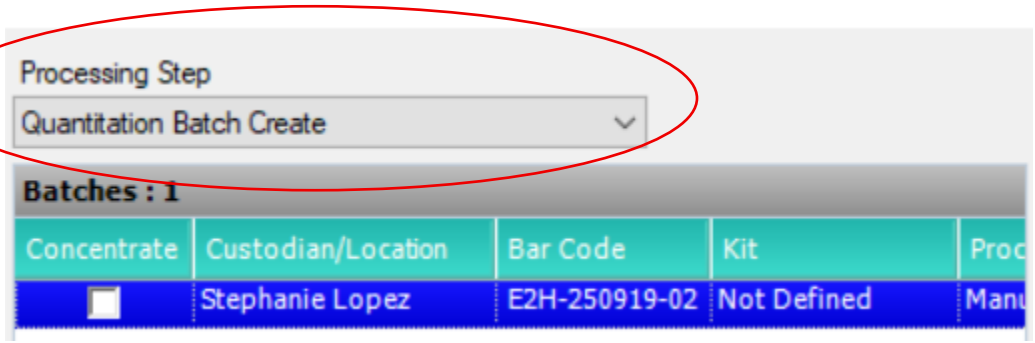
27. If an elution volume discrepancy results in a manual volume check, this will be captured in the **Complete Process** window. Enter each sample's elution volume as measured off the instrument and select **Process Successful**. See comment in Diff section.

    Proceed to the **Batch Management** module to document subsequent adjustments. Scan the extraction batch or locate using the **Quantitation Batch Create** option in the **Processing Step** dropdown.

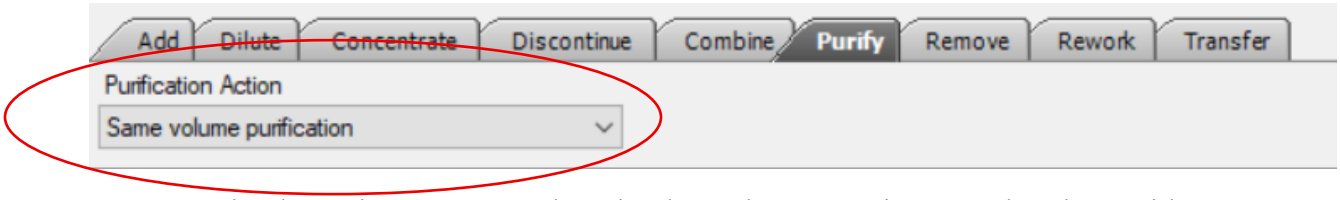
    - If an elution volume is significantly increased (>40µL), select the sample(s) and control(s) and proceed to the **Concentrate** tab.
    - If an elution volume is significantly reduced (0-20µL), select the sample(s) and control(s) and click on the **Rework** tab. Select **Isolation Batch Create** in the **Rework Entry Point** dropdown and document the **Rework Reason**. Click **Save**. The sample(s)/control(s) can now be added to a new isolation batch.
    - If an eluate needs a volume adjustment, this can be done through the **Dilute** tab.

III. Purification

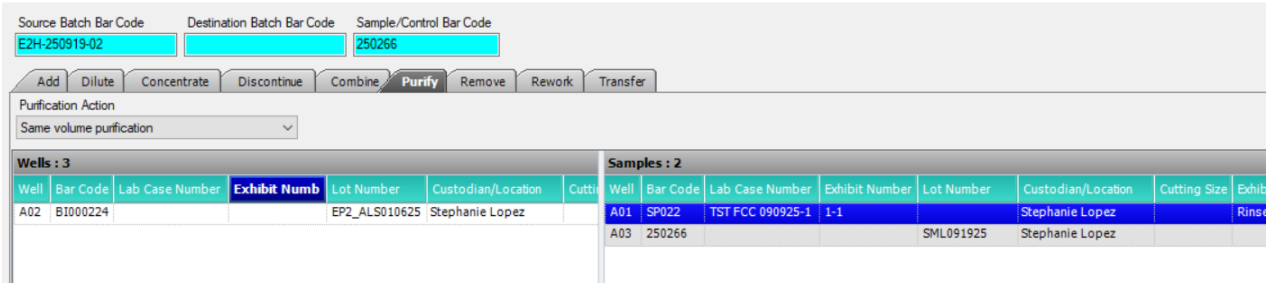
1. The post-EZ2 purification required for FCCs will be completed in the Batch Management module.
2. In Batch Management, under the Processing Step drop down, select 'Quantitation Batch Create'.



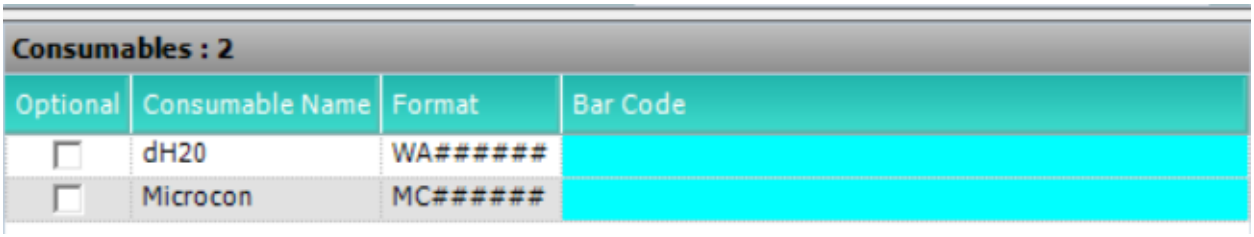
3. Select the Purify tab. Under Purification Action, select Same volume purification.



4. Select/scan the Source Batch. Select/scan the appropriate samples along with reagent blank(s). Once selected/scanned, the samples will move from the left hand side of the screen to the right hand side of the screen.



5. Scan the required consumables. Click save.



6. Once purification is complete, the samples can proceed with **Quantitation Setup**.