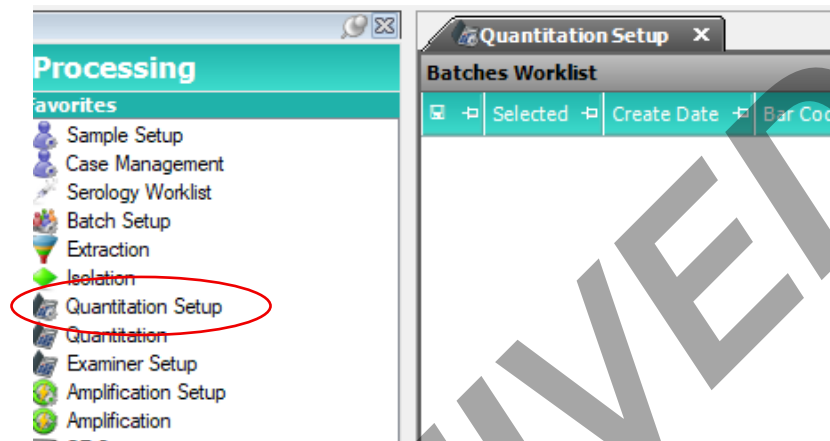


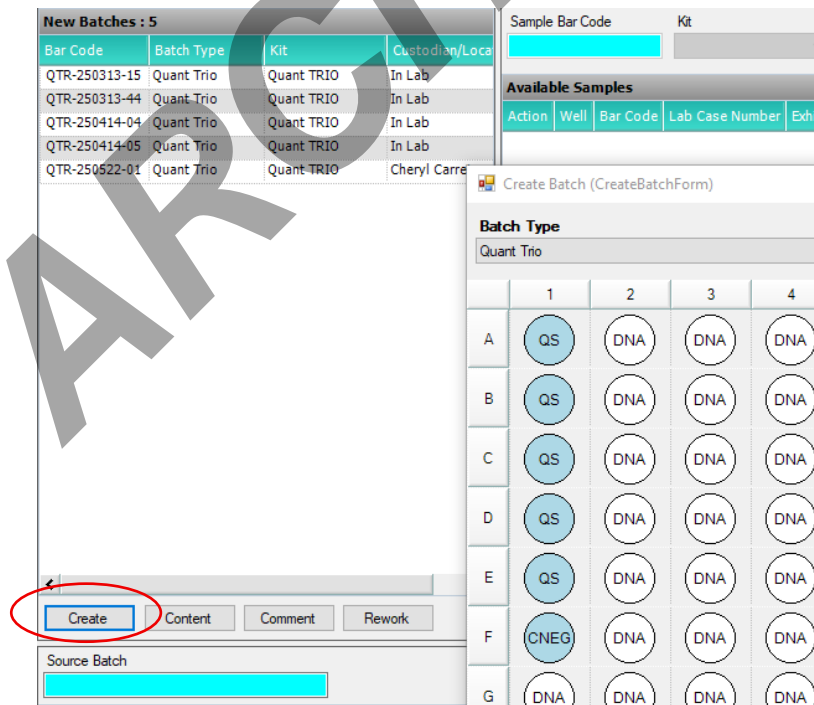
*Approved by Director: Dr. Guy Vallaro*

## I. Quantitation Setup

1. Open **Processing** → **DNA Processing** → **Quantitation Setup**.
2. Click **Create Batch**.



3. To create a new batch, click the **Create** button located under the **New Batches** worklist(upper-left corner).

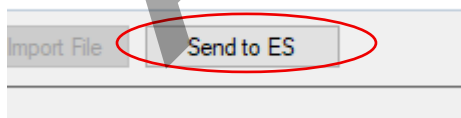


*Approved by Director: Dr. Guy Vallaro*

- a) The batch type (Quant Trio) and Kit (Quant Trio) are the default option. Select 'Vertical' sample allocation if not already selected.
  - b) Click **Create**. A unique Batch Bar Code will be generated and printed. This barcode should be affixed to the quant plate.
4. Allocate Samples to a quant batch:
- a) Scan the extraction batch bar code into the **Source** box. Individual samples barcodes may be scanned into the sample bar code box as well. This will place the samples into the 'Samples for Batch' box.
  - b) Scan the quantification plate's Batch Bar Code into the **Destination Batch**.
  - c) Click **Allocate** to allocate all qualifying samples from Samples for Batch box.



Note: If the reagent blank will not be quanted, select the RB(s) and click '**Send to ES**'. This will send the RB to **Examiner Setup**. This must be done after all other samples have been allocated. If doing this, you will have to allocate each sample individually by double clicking on them instead of allocating the whole batch.



5. To move samples within the allocated plate, the allocation must be saved. Samples may then be dragged to different wells to balance the plate, if necessary. Standards can't be moved from the first column. Balance the rest of the plate accordingly.

*Approved by Director: Dr. Guy Vallaro*

6. Once all samples have been allocated and no further changes are required, click **Complete** (next to Destination Batch Barcode). Close the window.

The screenshot shows a window titled "Destination Batch" with a subtitle "QTR-250613-05 (Quant TRIO)". A "Complete" button is circled in red in the top right corner. The main area is a grid with 12 columns (1-12) and 8 rows (A-H). Each cell contains a circular icon with text. Row A: Col 1 (QS), Col 2 (Blank), Col 3 (DNA), Col 4 (DNA), Col 5 (DNA), Col 6 (DNA), Col 7 (DNA), Col 8 (DNA), Col 9 (DNA), Col 10 (DNA), Col 11 (DNA), Col 12 (DNA). Row B: Col 1 (QS), Col 2 (DNA), Col 3 (DNA), Col 4 (DNA), Col 5 (DNA), Col 6 (DNA), Col 7 (DNA), Col 8 (DNA), Col 9 (DNA), Col 10 (DNA), Col 11 (DNA), Col 12 (DNA). Row C: Col 1 (QS), Col 2 (DNA), Col 3 (DNA), Col 4 (DNA), Col 5 (DNA), Col 6 (DNA), Col 7 (DNA), Col 8 (DNA), Col 9 (DNA), Col 10 (DNA), Col 11 (DNA), Col 12 (DNA). Row D: Col 1 (QS), Col 2 (DNA), Col 3 (DNA), Col 4 (DNA), Col 5 (DNA), Col 6 (DNA), Col 7 (DNA), Col 8 (DNA), Col 9 (DNA), Col 10 (DNA), Col 11 (DNA), Col 12 (DNA). Row E: Col 1 (QS), Col 2 (DNA), Col 3 (DNA), Col 4 (DNA), Col 5 (DNA), Col 6 (DNA), Col 7 (DNA), Col 8 (DNA), Col 9 (DNA), Col 10 (DNA), Col 11 (DNA), Col 12 (DNA). Row F: Col 1 (NEG), Col 2 (DNA), Col 3 (DNA), Col 4 (DNA), Col 5 (DNA), Col 6 (DNA), Col 7 (DNA), Col 8 (DNA), Col 9 (DNA), Col 10 (DNA), Col 11 (DNA), Col 12 (DNA). Row G: Col 1 (DNA), Col 2 (DNA), Col 3 (DNA), Col 4 (DNA), Col 5 (DNA), Col 6 (DNA), Col 7 (DNA), Col 8 (DNA), Col 9 (DNA), Col 10 (DNA), Col 11 (DNA), Col 12 (DNA). Row H: Col 1 (BIS), Col 2 (DNA), Col 3 (DNA), Col 4 (DNA), Col 5 (DNA), Col 6 (DNA), Col 7 (DNA), Col 8 (DNA), Col 9 (DNA), Col 10 (DNA), Col 11 (DNA), Col 12 (DNA). A large "ARCHIVED" watermark is diagonally across the grid.

7. On the Quantitation Setup tab select/scan the batch to be processed from the worklist and click **Select Scenario**.
8. Scan the hood/workstation barcode and consumable barcodes to enter the lot numbers. The volumes needed to make the mastermix are shown in the reagent amount column. Either water or Dilution Buffer can be scanned to be used for the Neg Control.

**STACS SOP-5 Quantification**

Document ID: 50100

Revision: 1

Effective Date: 09/18/2025

Status: Published

Page 4 of 8

*Approved by Director: Dr. Guy Vallaro*

Consumables : 1										
Group Type	Group Name	Extra	Extra Number							
All		# Extra Reactions	3							
Optional	Fixed	Consumable Name 1	Format 1	Bar Code 1	Consumable Name 2	Format 2	Bar Code 2	Reagent Amount	Measurement	Kit
<input type="checkbox"/>	<input checked="" type="checkbox"/>	Quant Trio	DU#####							Quant TRIO
<input type="checkbox"/>	<input type="checkbox"/>	Quant Trio Reaction Mix	TM#####					170.00	ul	Quant TRIO
<input type="checkbox"/>	<input type="checkbox"/>	Quant Trio Primers	TP#####					136.00	ul	Quant TRIO
<input type="checkbox"/>	<input checked="" type="checkbox"/>	dH2O	WA#####		Quant Trio Dilution Buffer	TD#####		2.00	ul	

9. Click **Start Process**.
10. Complete the tube check by scanning the sample tube labels.
11. For ease of processing in the hood, the quant worksheet may be printed or viewed from the **Content** button.
12. When the plate has been aliquoted, click **Complete Process**. Choosing **Process Successful** will generate the 7500-import file. Save the file to **U:\STACS share\Quantitation\7500 import files**. If not already generated click **Generate** to generate the 7500 Import File. You can then import this file into the instrument.

## STACS SOP-5 Quantification

*Approved by Director: Dr. Guy Vallaro*

Document ID: 50100

Revision: 1

Effective Date: 09/18/2025

Status: Published

Page 5 of 8

Select Scenario

Load Scenario

Print Scenario

Consumable List

Robot Bar Code

Manual

Start Process

Complete Process

Close

Complete Batch Activity (CompleteBatchActivityForm)

☒ Process Successful ☐ Process Aborted ☐ Process Failed

**Batches : 1**

Bar Code	Process	Status	New Status	Batch Comment
QTR-250523-09	Success	Quantitation Batch Create	Quantitation Setup Complete	

**Samples : 8**

Batch Bar Code	Sample	Kit	Lab Case Number	Exhibit Number	Transferred (uL)	Source Sample R
QTR-250523-09	CC022.A	Quant TRIO	CLC-250522-1417	12	2.0	28.0
QTR-250523-09	BI000193.A	Quant TRIO			2.0	28.0
QTR-250523-09	240018.A	Quant TRIO			2.0	28.0
QTR-250523-09	240019.A	Quant TRIO			2.0	28.0
QTR-250523-09	CC023.A	Quant TRIO	CLC-250522-1417	13	2.0	28.0
QTR-250523-09	BI000193.A	Quant TRIO			2.0	28.0
QTR-250523-09	250086.A	Quant TRIO			2.0	28.0
QTR-250523-09	250087.A	Quant TRIO			2.0	28.0

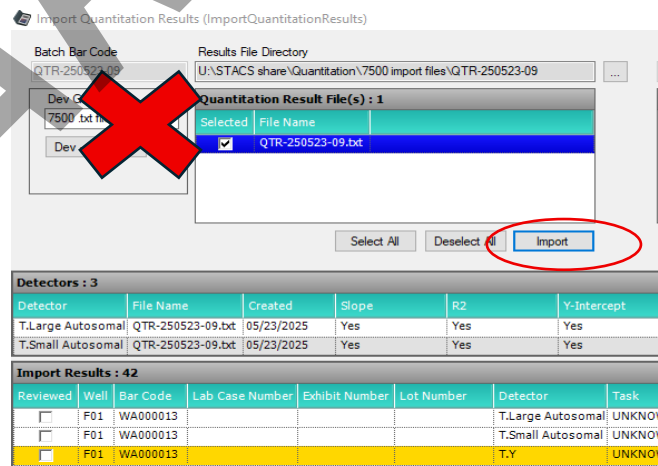
*Approved by Director: Dr. Guy Vallaro*

**II. Quantitation** – This section pertains to the documentation related to the instrument run. STACS steps should be completed in the post-amp lab.

1. Open **Processing → DNA Processing → Quantitation**
2. Scan the Batch Bar Code from the Batches Worklist.
3. Scan the barcode for the 7500 instrument to be used.
4. Click **Start Process**.
5. Once the runs is complete, completing batch activity in STACS
  - a) Scan the bath from the Batches Worklist.
  - b) Click **Complete Process** and select the appropriate option, this step should be done by the person analyzing the quant and making the amp sheet.

**III. Post-Quantitation**

1. Export the quantitation results from instrument. Click **Import** and select the appropriate file.
  - a) Run the 7500 per normal process.
  - b) Export from the instrument and upload the file into the Trio Software.
  - c) “Analyze” the data and save the .xls file in the STACS 7500 results folder **U:\STACS share\Quantitation\7500 Results**.
  - d) In STACS import the .xls file



*Approved by Director: Dr. Guy Vallaro*

2. The **Action** column will auto-populate with suggested actions based on system configurations (highlighting the sample).
3. Adjust the actions for each detector for each sample. **No Amp** is for sample/detector that will not be used for amp. **Use As Is** is for sample/detector whose quant value will be used. **Dilute** is for sample/detector that will be diluted prior to amplification. **Concentrate** is for sample/detector that will require concentration prior to amplification (if choosing this option, be sure to do the same for the blank control associated with the sample). For samples going to YFP amplification, be sure to choose the Y detector to move forward. For samples with high degradation index, be sure to choose the Large Autosomal detector to move forward.

Note: Samples with no detected values in any detector category will be flagged in red and 'No Amp' will automatically be assigned. These samples will not be available for amplification in the Examiner Setup module unless manually changed.

4. Review standards, curve thresholds and controls. If TL signoff is needed, add a batch comment and notify the TL with the batch name. Save the quant without reviewing. Once TL has reviewed, continue with steps below.
5. Mark samples as reviewed by selecting all samples and click **Save**.

Detectors : 3			
Detector		File Name	
T.Large Autosomal		QTR-250523-0	
T.Small Autosomal		QTR-250523-0	

Results : 42			
Reviewed	Well	Bar Code	Lab
<input checked="" type="checkbox"/>	F01	WA000013	
<input checked="" type="checkbox"/>	F01	WA000013	
<input checked="" type="checkbox"/>	F01	WA000013	
<input checked="" type="checkbox"/>	A02	240018.A	
<input checked="" type="checkbox"/>	A02	240018.A	
<input checked="" type="checkbox"/>	A02	240018.A	
<input checked="" type="checkbox"/>	B02	240019.A	
<input checked="" type="checkbox"/>	B02	240019.A	
<input checked="" type="checkbox"/>	B02	240019.A	
<input checked="" type="checkbox"/>	E02	250086.A	
<input checked="" type="checkbox"/>	E02	250086.A	
<input checked="" type="checkbox"/>	E02	250086.A	
<input checked="" type="checkbox"/>	F02	250087.A	
<input checked="" type="checkbox"/>	F02	250087.A	

*Approved by Director: Dr. Guy Vallaro*

6. Fill out the **Complete Batch Activity** window.
7. See SOP-6 for next step which is: **Examiner Setup**.

ARCHIVED