

# BATCH LINKING SPECIMEN BARCODES TO LAB BARCODES

Specimen barcode is the barcode that was on the sample tube that arrives to the lab. In most instances this is the "PRIMARY TUBE" field that is being entered in the Samples Google Sheet, but can differ in dry swab scenarios. In that instance, please use the barcode found on the dry swab. Cobas barcode is the tube that is going into the Roche instrument. It is always the "Secondary Tube" column in the Samples Google Sheet.

## Creating the csv file to upload to Retool

1. Copy and paste two columns, the specimen barcode and the lab barcode, into the sheet labeled "BATCH UPLOAD to retool". (See above highlight for definitions). Ensure that the column headers for A and B are labeled specimen and lab

specimen	cobas
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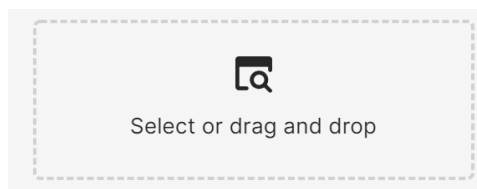
2. It should look something like this:

specimen	cobas
0000031821	CH10122079
0000031885	CH10122089
0000029816	CH10122110
0000031898	CH10122095
0000031846	CH10122093
0000031852	CH10122065
0000003954	CH10122074
0000003937	CH10122105
0000003980	CH10122122
0000031808	CH10122132
0000031817	CH10122117
0000031803	CH10122111
0000031829	CH10122130
0000031834	CH10122134
0000031824	CH10122104

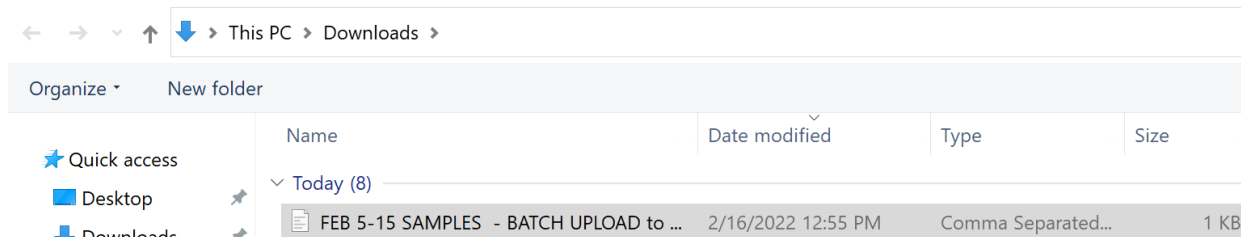
3. The next step is to create the csv file. Please go to the top left corner of the google sheet and click on: File > Download > Comma Separated Values (.csv)
4. This should download a file labeled something similar to: " FEB 5-15 SAMPLES - BATCH UPLOAD to Retool.csv"

## Uploading CSV to Retool

1. Visit Retool Link: <https://retool2.cityhealth.com/apps/Lab Tools - Barcode Batch Linking Tool>
2. Click the upload box, and find the file on your computer



Open



- Once you select the file, the retool should separate the file into rows in the Barcode Table

**Barcode Table**

specimen	cobas
0000031821	CH10122079
0000031885	CH10122089
CS99999999	CH99999999

Showing 1-3 of 3 [Clear selection](#)

1 of 1

[Validate](#) [Link Barcodes](#)

- Click the blue Validate button at the bottom to check the database for if the specimen barcodes are in our database. The results should be separated like this:

Barcode Table		Missing Specimen Barcode		Barcode Already Linked		
Specimen Barcode	Lab Barcode To Link	None		Specimen Barc...	Cobas Barcode	Reason
CS99999999	CH99999999			0000031821	CH10122079	Already Linked
				0000031885	CH10122089	Already Linked

Showing 1-1 of 1 [Clear selection](#) [Link Barcodes](#)

Showing 0 results [Link Barcodes](#)

Showing 1-2 of 2 [Link Barcodes](#)

- How to interpret the tables:

- Barcode Table - what is remaining in the barcode table are the specimen barcodes found in our database, and are ready to be linked to the lab barcode
- Missing Specimen Barcodes - these were *not* found in our database, so needs to be investigated or followed up with ops in order to link the two codes.

1. See instructions on how to resolve missing specimen barcodes [here](#)
3. Barcode Already Linked - these have been already linked in our database, so it won't be linked again.
2. Hit the blue Link Barcodes button to link the remaining barcodes. This will only be blue if there are results to link.
3. After this is done, try uploading the same csv file and validating, to ensure all the barcodes are either are linked or in the missing specimen column.

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