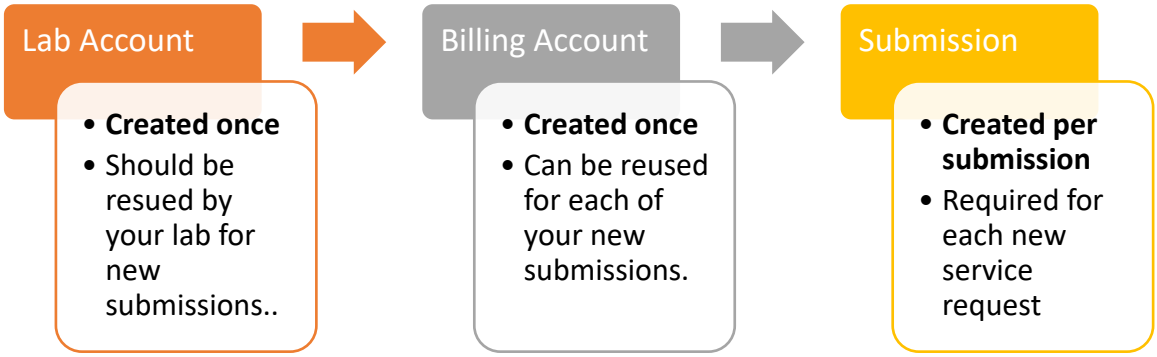
Creating a QB3 LIMS portal Genomics Submission

Access to the LIMS portal requires login information.
For Berkeley and affiliates, please email cgrl@berkeley.edu to set up an account. For external users, please use the LIMS portal to self-register. This option is only available to non-UC and non-affiliate members.

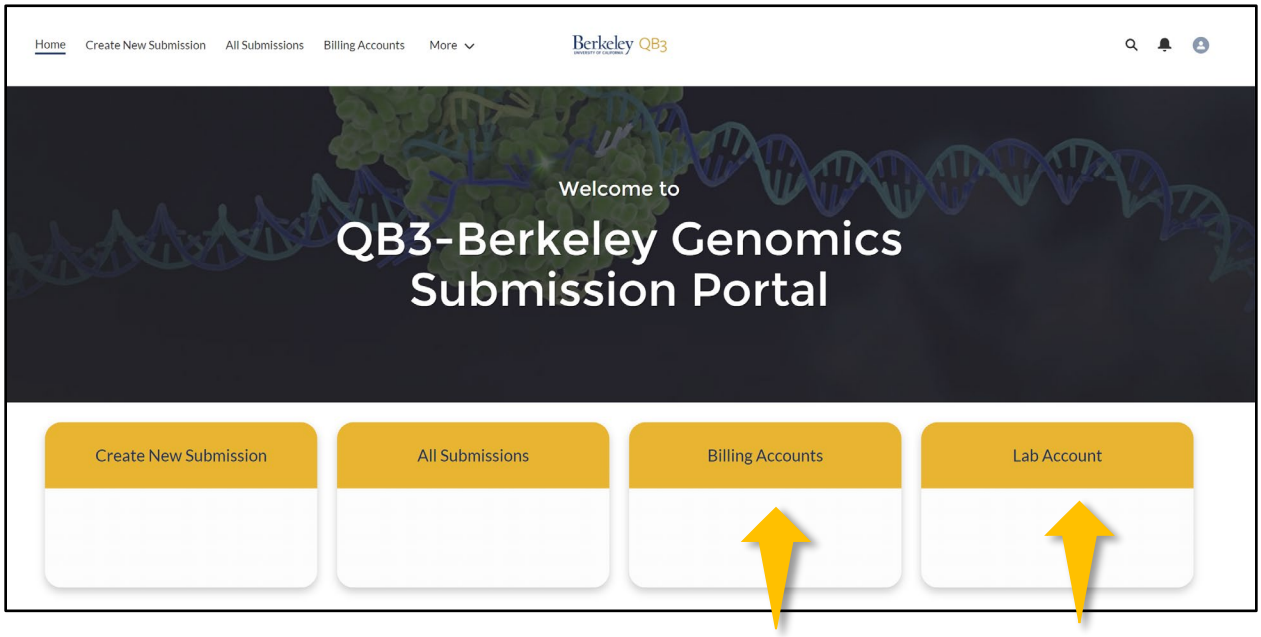
Every LIMS portal submission requires information that is either (a) entered once (typically during the first login) and can be fetched for subsequent submissions and (b) specific to each submission and requires entry for that submission (e.g., sample type, sample indexes, sequencing run type, or service needs).

Submission Requirements:



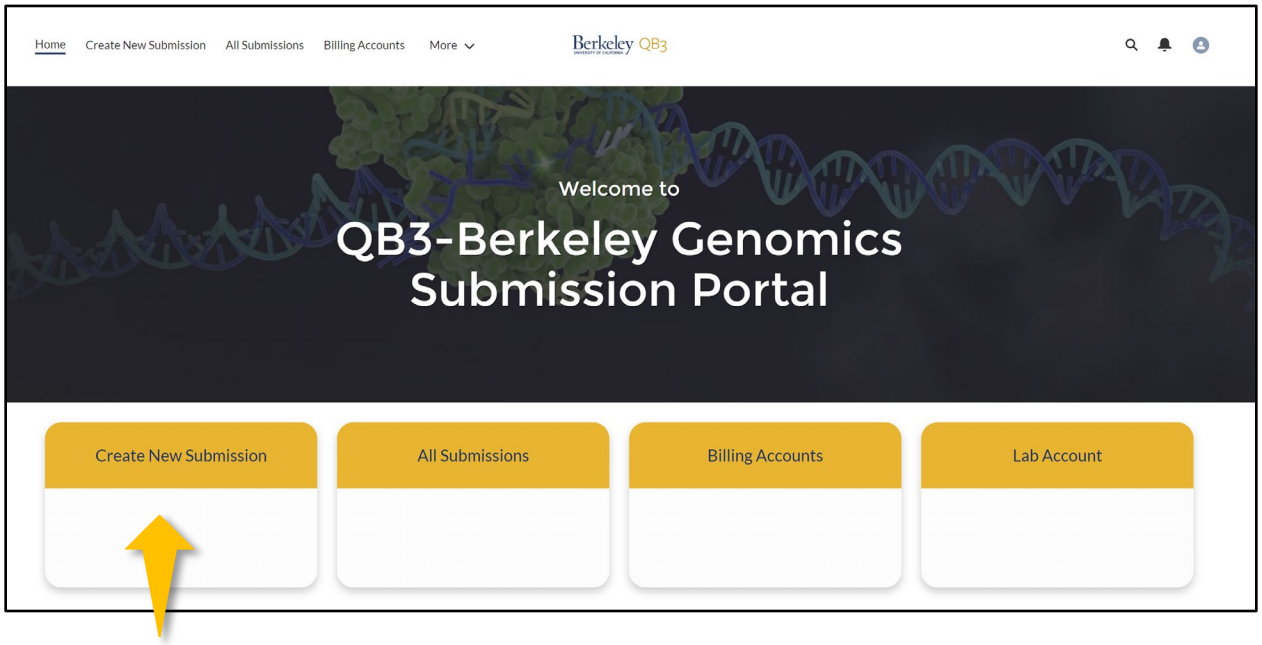
Step 1: Access the LIMS Portal
The LIMS portal can be accessed here: http://bit.ly/GSL-LIMS

Step 2: Create a Lab and Billing Account (if previously created, skip).



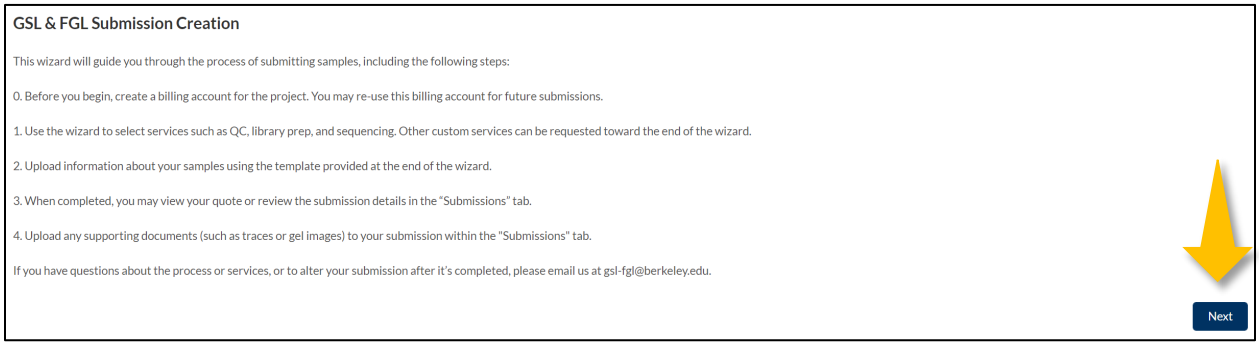
Step 3. Creating New Submission

On the main portal page, click create new submission to walk through the submission wizard. **DO NOT use your browser's back button, only the previous button on wizard if you need to go back.**



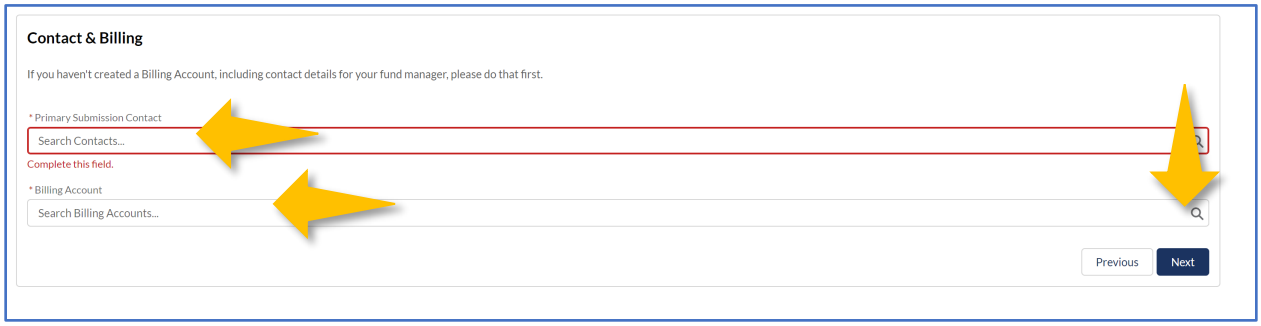
Step 4. Introductory Screen

An overview of the submission process. After reading, select next to advance.



Step 5. Choose Contact / Billing Information

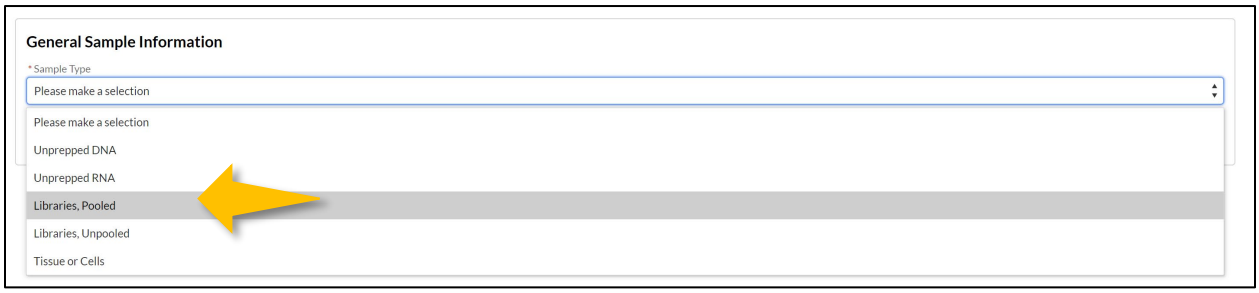
Choose the Primary Submission Contact and Billing Account details. Begin typing in the fields and a dynamic list of matching values will appear. Then select next.



Step 6. Choose General Sample Information

Example: Sequencing By-the-Lane – Single pool with 10 UDI Samples.

This overview will cover sequencing submissions of a single tube of pooled samples for by-the-lane submissions. In this example, the single tube represents a user prepared library pool of multiple human DNA amplicon samples with unique dual indexes run with a MiSeq 300PE that require post-run demultiplexing.

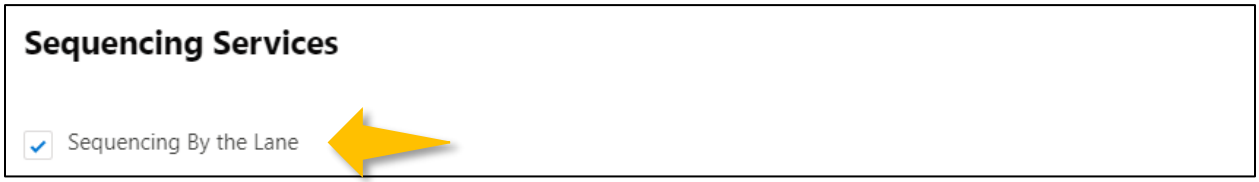


Step 7: Enter General Sample Information

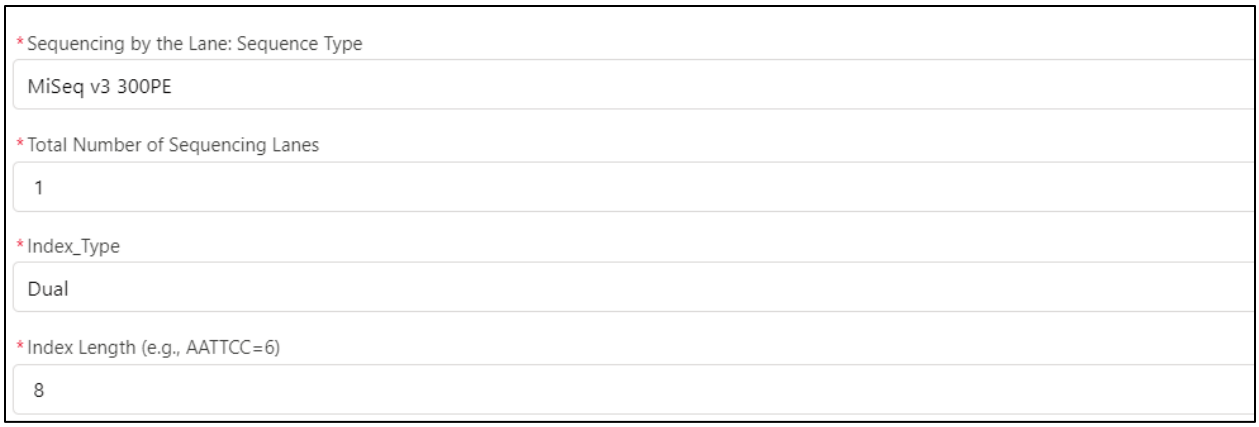
Enter information relevant to your submitted sample. Required fields are highlighted by a red asterisk. When complete, select next.

Step 8: Choose Sequencing Services

For this example, choose sequencing by the lane for receive a full lane of sequencing.

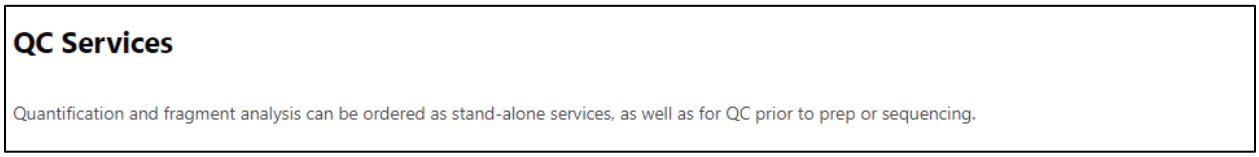


Then select the sequencing required. For this example, MiSeq v3 300PE, 1 Tube, Dual Index, 8bp length. GSL determines PhiX concentration.



Step 9: Choose Quality Control Services

Indicate if you will require or be supplying either quantification information and/or fragment analysis. You must either provide or allow GSL to run. Select next when done.



Step 10: Choose Molecular Biology Services

Indicate if you will require any molecular biology services. Select next when done.

Step 11: Choose Data Analysis Options

Indicate if you prefer demultiplexing and/or lane merging (when ordering multiple lanes - default). Select next when done.

Data Analysis

Please select which complimentary data analysis services you would like (most users prefer all options).

Step 12: Choose Custom Services

Indicate if you have any custom needs pre- or post-sequencing. Charged at $100/hr. We will email you with an estimate of the custom service charge. Select next when done.

Custom Services

Please check the box and describe any custom services you are interested in. We will get back to you with an estimate.

Step 13: Review of Services

Submission services summarized for review. Select next when done.

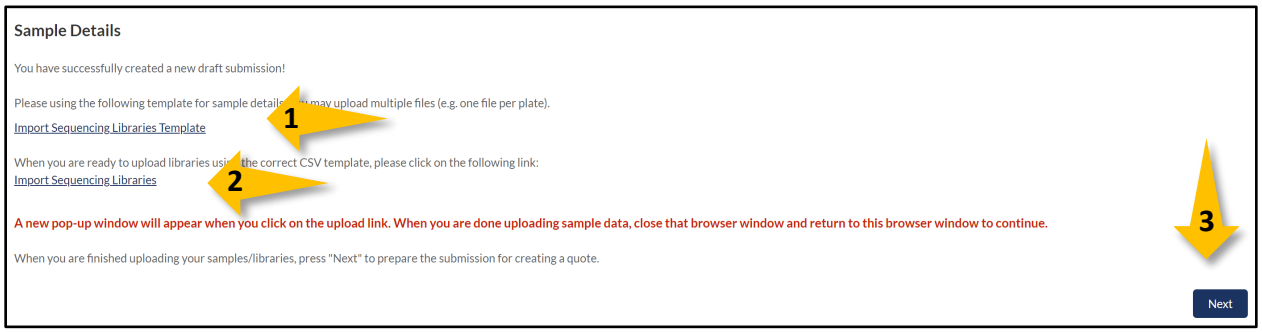
Review of Services

Step 14: Sample Details

At this point the submission process requires you enter in sample details for the sample library pool.

Sample Pool Detail Overview:

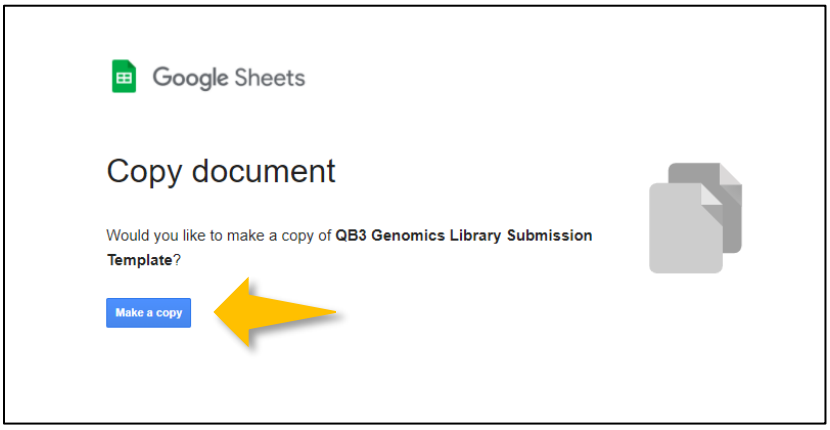
- 14.1 Download and fill in empty sequencing library template CSV file
- 14.2 Import filled in CSV template
- 14.3 Select next when done.



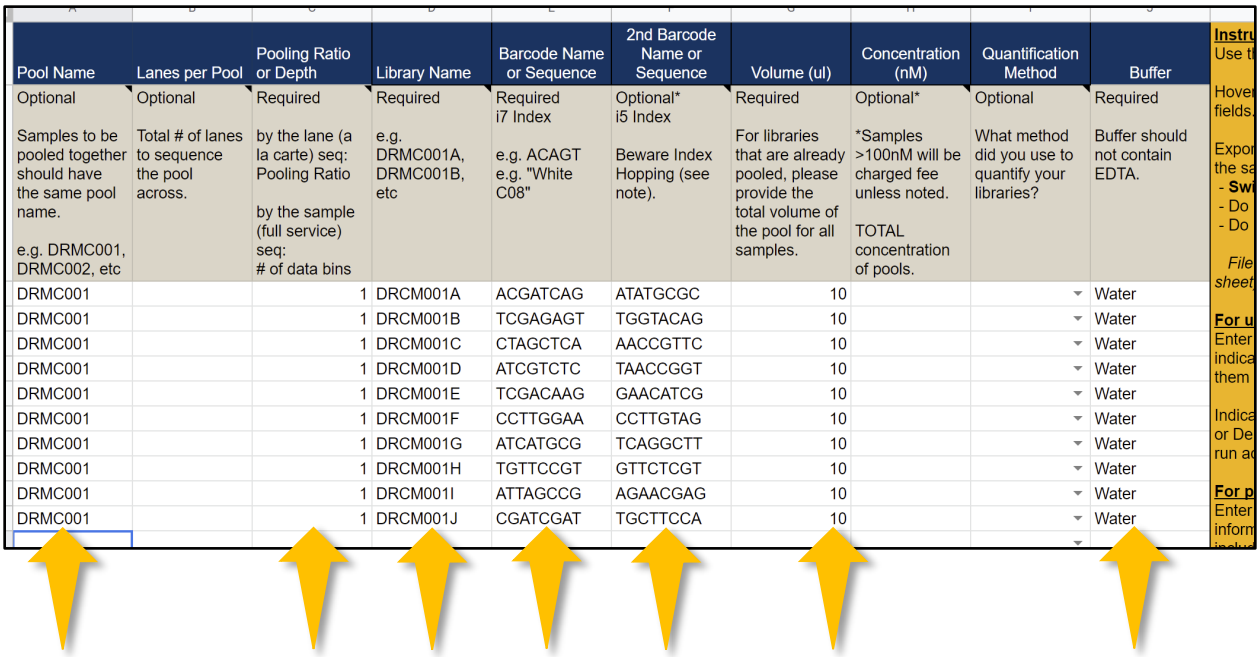
See detailed steps below …

14.1 Download and fill in empty sequencing library template CSV file

Click “Import Sequencing Libraries Template” and the Select “Make a Copy” to open your own instance of the template

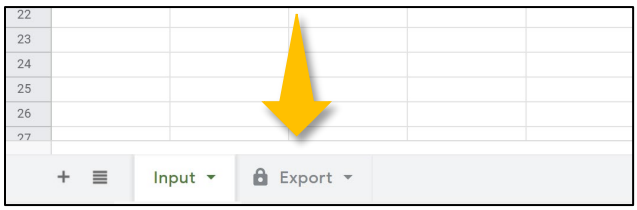


Fill in required information (arrows below) for your samples within the pool. You may elect to fill in optional information. Please refer to either the instructions in the yellow highlighted section or the column comments for further detail.

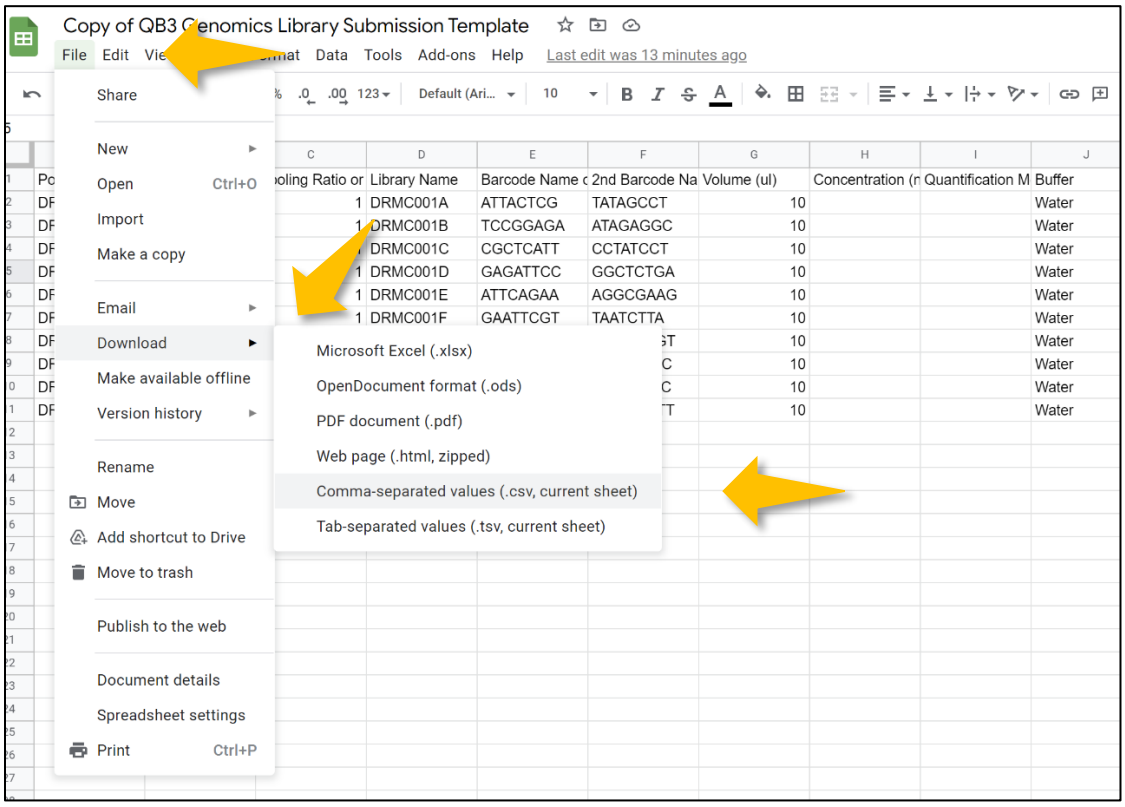


Pool Name	Lanes per Pool	Pooling Ratio or Depth	Library Name	Barcode Name or Sequence	2nd Barcode Name or Sequence	Volume (ul)	Concentration (nM)	Quantification Method	Buffer
Optional Samples to be pooled together should have the same pool name. e.g. DRMC001, DRMC002, etc	Optional Total # of lanes to sequence the pool across.	Required by the lane (a la carte) seq: Pooling Ratio by the sample (full service) seq: # of data bins	Required e.g. DRMC001A, DRMC001B, etc	Required i7 Index e.g. ACAGT e.g. "White C08"	Optional* i5 Index Beware Index Hopping (see note).	Required For libraries that are already pooled, please provide the total volume of the pool for all samples.	Optional* *Samples >100nM will be charged fee unless noted. TOTAL concentration of pools.	Optional What method did you use to quantify your libraries?	Required Buffer should not contain EDTA.
DRMC001		1	DRCM001A	ACGATCAG	ATATGCGC	10			Water
DRMC001		1	DRCM001B	TCGAGAGT	TGGTACAG	10			Water
DRMC001		1	DRCM001C	CTAGCTCA	AACCGTTC	10			Water
DRMC001		1	DRCM001D	ATCGTCTC	TAACCGGT	10			Water
DRMC001		1	DRCM001E	TCGACAAG	GAACATCG	10			Water
DRMC001		1	DRCM001F	CCTTGGAA	CCTTGTAG	10			Water
DRMC001		1	DRCM001G	ATCATGCG	TCAGGCTT	10			Water
DRMC001		1	DRCM001H	TGTTCCGT	GTTCTCGT	10			Water
DRMC001		1	DRCM001I	ATTAGCCG	AGAACGAG	10			Water
DRMC001		1	DRCM001J	CGATCGAT	TGCTTCCA	10			Water

Switch to Export Tab to export the sample information.



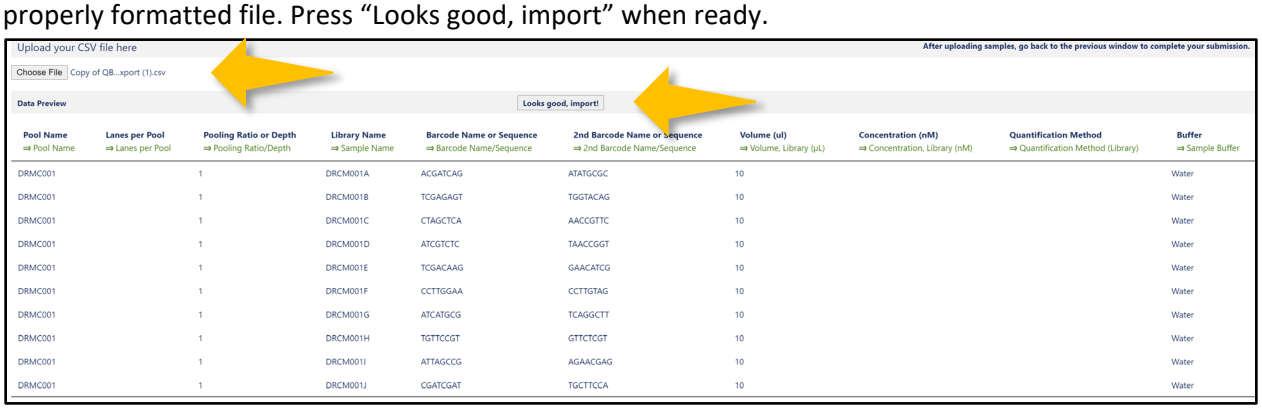
Export only from this sheet as a csv: File > Download > Comma-separated values



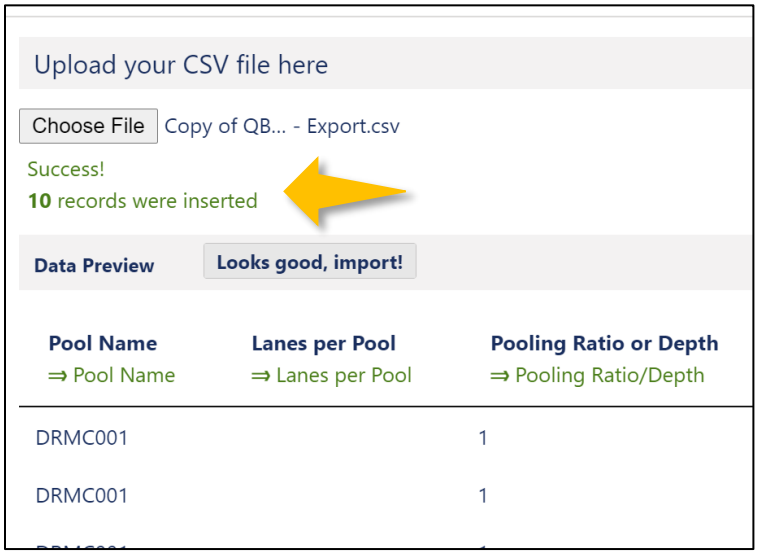
14.2 Import filled in CSV template

Return to LIMS to import sample information

Choose the sample *.csv from prior step and import into the LIMS. Values should populate indicating a properly formatted file. Press “Looks good, import” when ready.



You will receive a message upon successful import and values will populate.

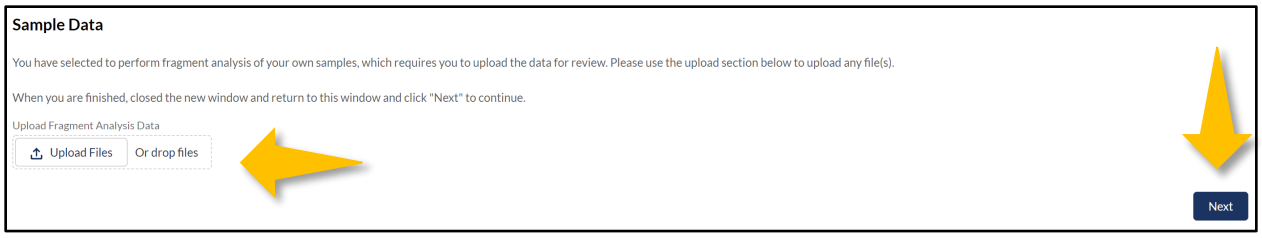


14.3 Select next when done.

Go back to the LIMS portal to finalize your submission.

Step 14: Sample Data

If you elected to run your own QC, please upload any relevant documents (e.g., fragment analysis traces) to continue. Use the upload button or drag and drop into the sample data box. Select next to continue.

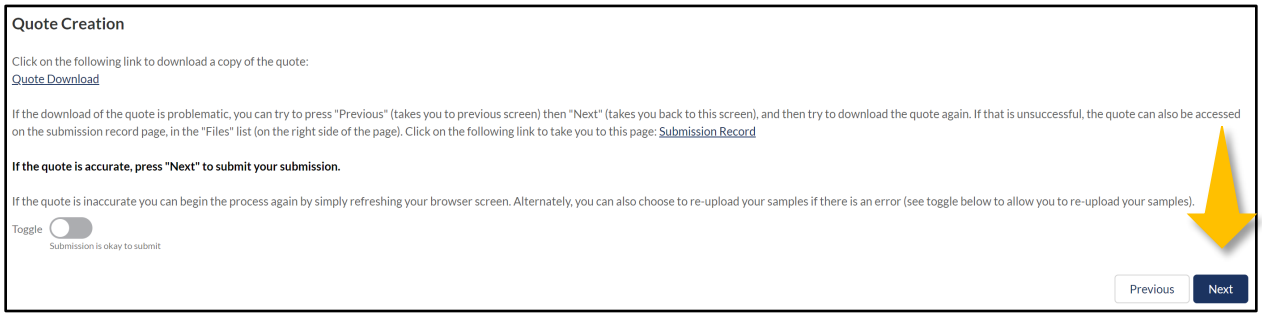


Step 15: Quote Creation

A quote is generated for you. Click next to download. It may take several seconds to generate quote. Hit next to continue retrying.

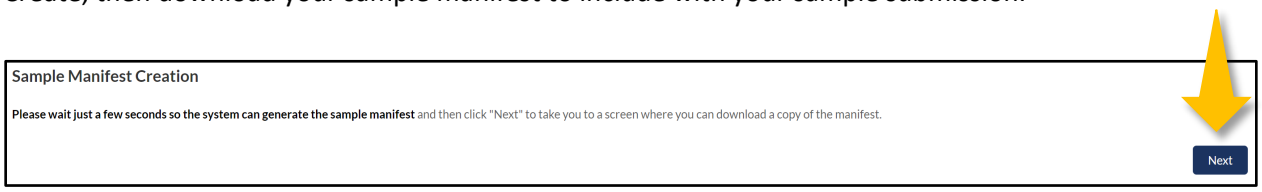
Step 16: Quote Creation

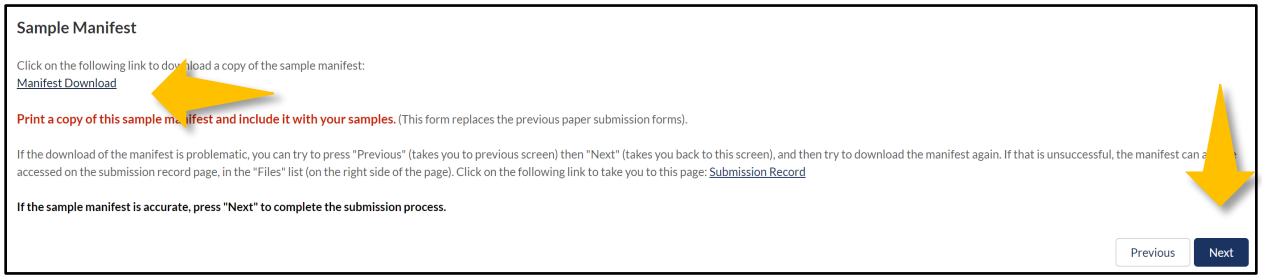
Download quote to review. If quote seems accurate select next to continue.



Step 17: Sample Manifest Create

Create, then download your sample manifest to include with your sample submission.





Step 18: Your Submission if Complete.

Select finish. Your submission has been successfully entered into our system.