

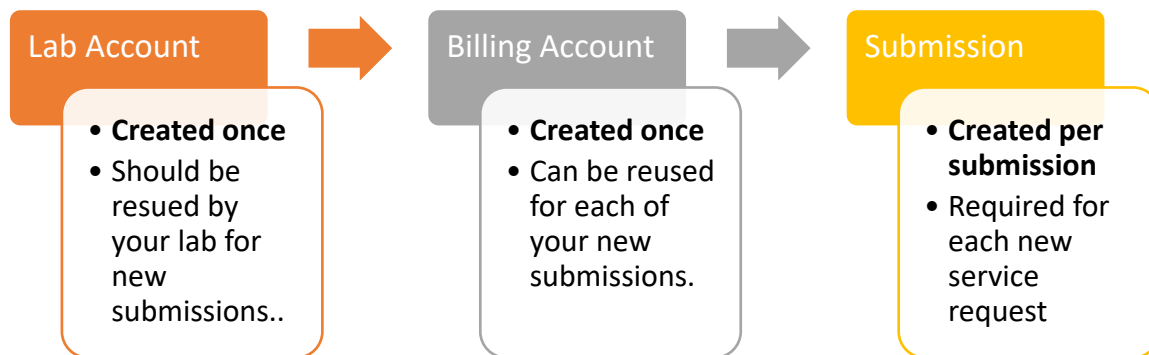
Creating a QB3 LIMS portal Genomics Submission

Access to the LIMS portal requires login information.

For Berkeley and affiliates, please email cgrrl@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).

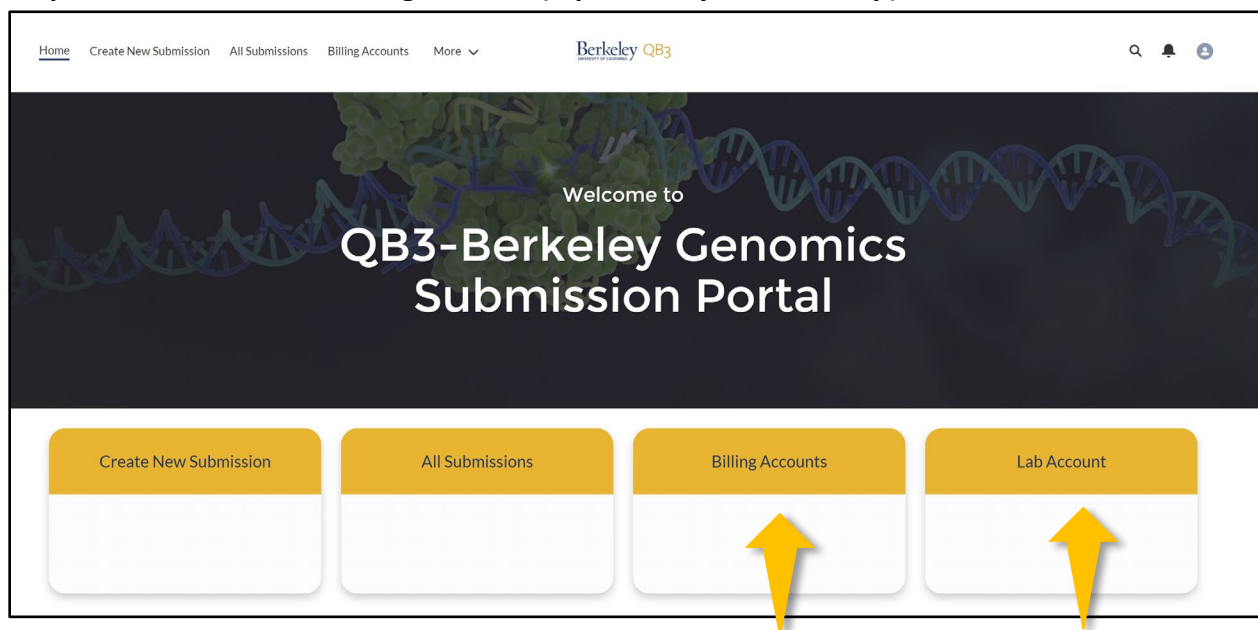
Submission Requirements:



Step 1: Access the LIMS Portal

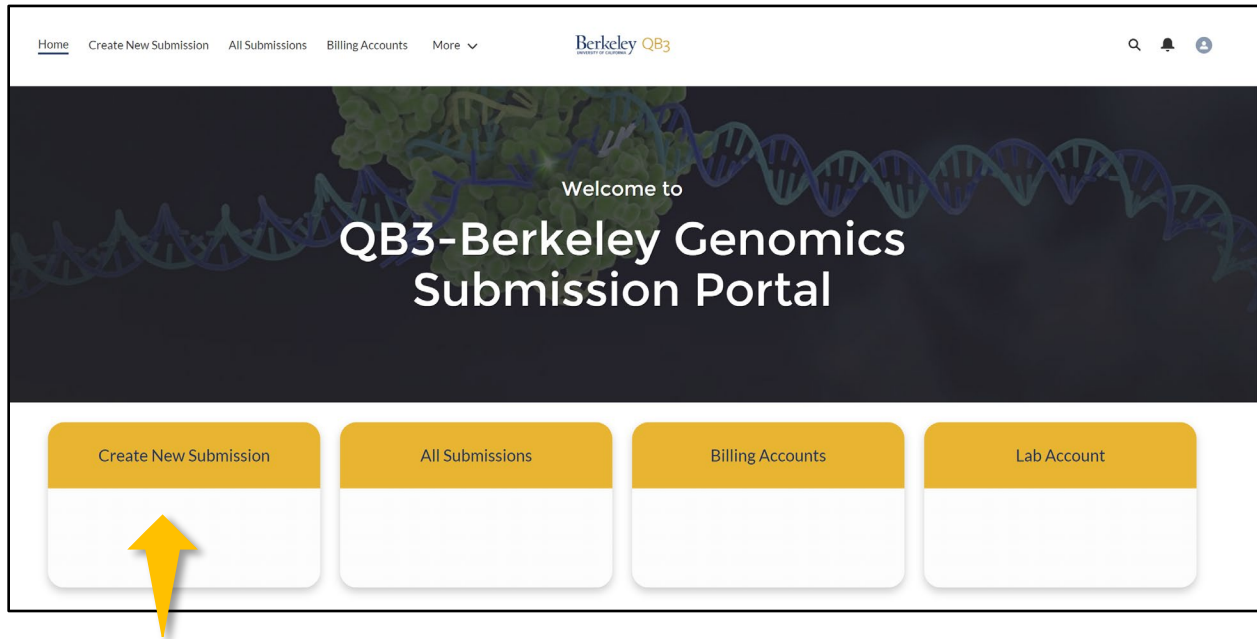
The LIMS portal can be accessed here: <http://bit.ly/GSL-LIMS>

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.

The screenshot displays the "GSL & FGL Submission Creation" introductory screen. It contains a list of steps: 0. Before you begin, create a billing account for the project. You may re-use this billing account for future submissions. 1. Use the wizard to select services such as QC, library prep, and sequencing. Other custom services can be requested toward the end of the wizard. 2. Upload information about your samples using the template provided at the end of the wizard. 3. When completed, you may view your quote or review the submission details in the "Submissions" tab. 4. Upload any supporting documents (such as traces or gel images) to your submission within the "Submissions" tab. At the bottom right, there is a blue "Next" button. A large yellow arrow points to this button.

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.

The screenshot shows the "Contact & Billing" form. It includes two search fields: "* Primary Submission Contact" with a "Search Contacts..." placeholder, and "* Billing Account" with a "Search Billing Accounts..." placeholder. Both fields have a red border and a magnifying glass icon on the right. A red line connects the two search fields. A large yellow arrow points to the "Search Contacts..." field, and another large yellow arrow points to the "Search Billing Accounts..." field. At the bottom right, there are "Previous" and "Next" buttons.

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.

General Sample Information

* Sample Type

Please make a selection

Please make a selection

Unprepped DNA

Unprepped RNA

Libraries, Pooled

Libraries, Unpooled

Tissue or Cells



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.

General Sample Information

* Sample Type

Libraries, Pooled

Your sequencing application is used to determine PhiX ratio (if applicable) and interpret quality metrics. You can select multiple types by CTRL/CMD clicking all that apply.

* Sequencing Application(s)

WGS

RNA-Seq (mRNA, cDNA, or other)

Whole Exome

Amplicon Sequencing

ATAC-Seq

* Sample Buffer/s (Please list all used)

water

* Organism or Sample Provenance

Human

* Number of tubes you are submitting

1


☐ Return Samples?

☐ Samples are a possible biohazard

General submission comments


Previous

Next



Step 8: Choose Sequencing Services

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

Sequencing Services
<input checked="" type="checkbox"/> Sequencing By the Lane 

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

* Sequencing by the Lane: Sequence Type
MiSeq v3 300PE
* Total Number of Sequencing Lanes
1
* Index_Type
Dual
* Index Length (e.g., AATTCC=6)
8

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.

QC Services
Quantification and fragment analysis can be ordered as stand-alone services, as well as for QC prior to prep or sequencing.

Step 10: Choose Molecular Biology Services

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

Molecular Biology Services
Please select any other molecular biology services you require. After QC, if it looks like your samples require additional treatment,

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.

Sample Details

You have successfully created a new draft submission!

Please using the following template for sample details. You may upload multiple files (e.g. one file per plate).

[Import Sequencing Libraries Template](#)

When you are ready to upload libraries using the correct CSV template, please click on the following link:

[Import Sequencing Libraries](#)

A new pop-up window will appear when you click on the upload link. When you are done uploading sample data, close that browser window and return to this browser window to continue.

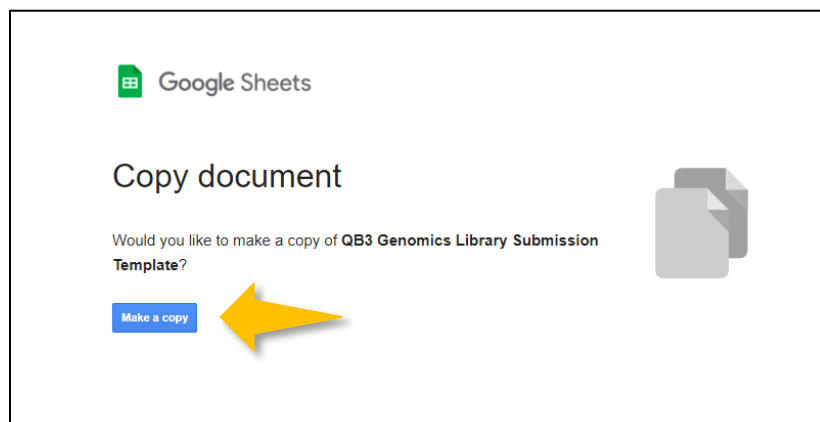
When you are finished uploading your samples/libraries, press "Next" to prepare the submission for creating a quote.

Next

See detailed steps below ...

14.1 Download and fill in empty sequencing library template CSV file

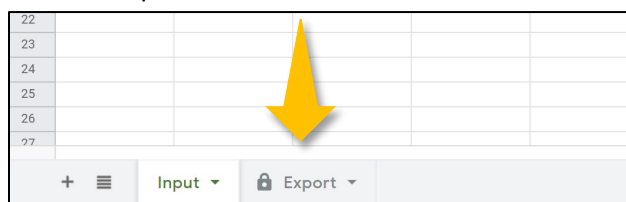
Click “Import Sequencing Libraries Template” and then Select “Make a Copy” to open your own instance of the template



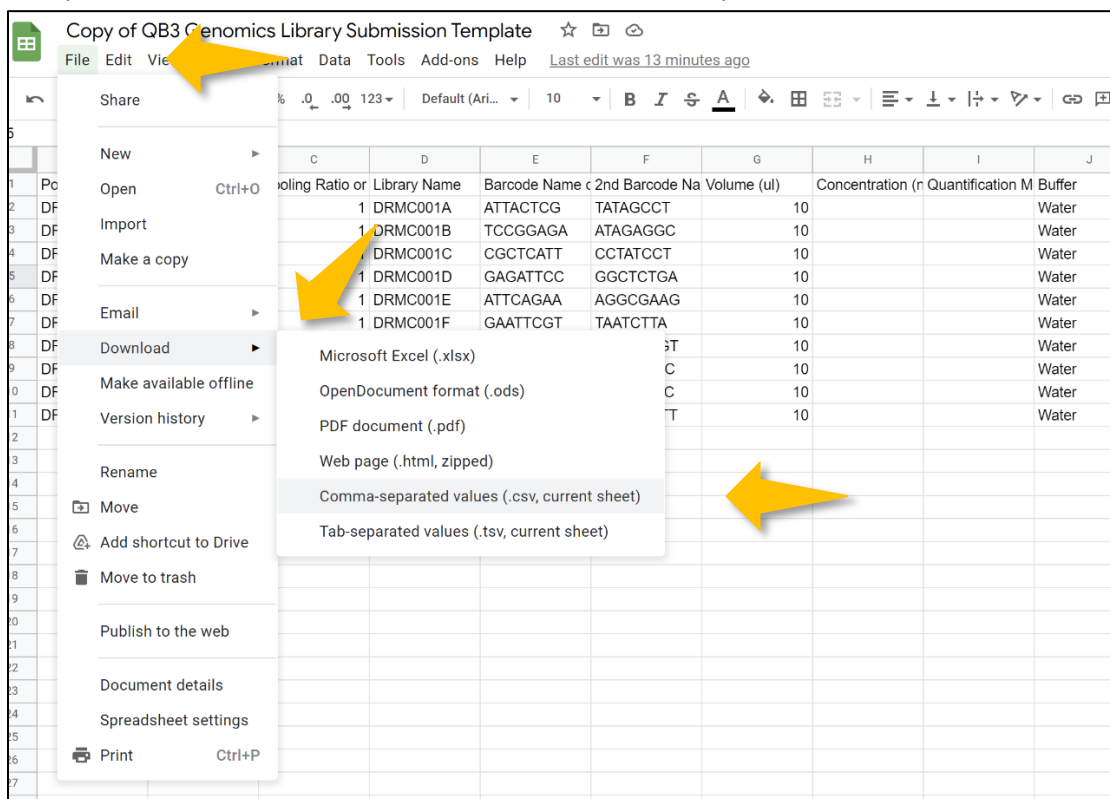
Fill in required information (arrows below) for your samples within the pool. You may elect to fill in optional information. Please refer to either the instructions in the yellow highlighted section or the column comments for further detail.

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	Instru Use t
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. ACGAGT 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.	Hover fields. Export the sa - Sw - Do - Do File sheet
DRMC001			1 DRMC001A	ACGATCAG	ATATGCGC	10			Water	For u
DRMC001			1 DRMC001B	TCGAGAGT	TGGTACAG	10			Water	Enter indica them
DRMC001			1 DRMC001C	CTAGCTCA	AACCGTTC	10			Water	Indica or De run ad
DRMC001			1 DRMC001D	ATCGTCTC	TAACCGGT	10			Water	For p
DRMC001			1 DRMC001E	TCGACAAG	GAACATCG	10			Water	Enter inform
DRMC001			1 DRMC001F	CCTTGGAA	CCTTGTAG	10			Water	
DRMC001			1 DRMC001G	ATCATGCG	TCAGGCTT	10			Water	
DRMC001			1 DRMC001H	TGTTCCGT	GTTCTCGT	10			Water	
DRMC001			1 DRMC001I	ATTAGCCG	AGAACGAG	10			Water	
DRMC001			1 DRMC001J	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.

Upload your CSV file here After uploading samples, go back to the previous window to complete your submission.

Copy of QB...port (1).csv

Pool Name ⇒ Pool Name	Lanes per Pool ⇒ Lanes per Pool	Pooling Ratio or Depth ⇒ Pooling Ratio/Depth	Library Name ⇒ Sample Name	Barcode Name or Sequence ⇒ Barcode Name/Sequence	2nd Barcode Name or Sequence ⇒ 2nd Barcode Name/Sequence	Volume (ul) ⇒ Volume, Library (μL)	Concentration (nM) ⇒ Concentration, Library (nM)	Quantification Method ⇒ Quantification Method (Library)	Buffer ⇒ Sample Buffer
DRMC001	1	1	DRMC001A	ACGATCAG	ATATGCGC	10			Water
DRMC001	1	1	DRMC001B	TCGAGAGT	TGGTACAG	10			Water
DRMC001	1	1	DRMC001C	CTAGTCTA	AACCGTTC	10			Water
DRMC001	1	1	DRMC001D	ATGCTCTC	TAACCGGT	10			Water
DRMC001	1	1	DRMC001E	TCGACAAG	GAACATCG	10			Water
DRMC001	1	1	DRMC001F	CCTTGAA	CCTTGATAG	10			Water
DRMC001	1	1	DRMC001G	ATCATGCG	TCAGGCTT	10			Water
DRMC001	1	1	DRMC001H	TGTTCCGT	GTTCCTGT	10			Water
DRMC001	1	1	DRMC001I	ATTAGCCG	AGAACGAG	10			Water
DRMC001	1	1	DRMC001J	CGATCGAT	TGCTTCCA	10			Water

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

Upload your CSV file here

Choose File

Copy of QB... - Export.csv

Success!
10 records were inserted

Data Preview

Looks good, import!

Pool Name ⇒ Pool Name	Lanes per Pool ⇒ Lanes per Pool	Pooling Ratio or Depth ⇒ Pooling Ratio/Depth
DRMC001		1
DRMC001		1

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.

Sample Data

You have selected to perform fragment analysis of your own samples, which requires you to upload the data for review. Please use the upload section below to upload any file(s).

When you are finished, closed the new window and return to this window and click "Next" to continue.

Upload Fragment Analysis Data

Upload Files

Or drop files

Next

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.

Quote Creation

Your submission has 10 samples associated with it and is now ready for a quote.

Press "Next" to generate a quote.

Next

Step 16: Quote Creation

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

Quote Creation

Click on the following link to download a copy of the quote:
[Quote Download](#)

If the download of the quote is problematic, you can try to press "Previous" (takes you to previous screen) then "Next" (takes you back to this screen), and then try to download the quote again. If that is unsuccessful, the quote can also be accessed on the submission record page, in the "Files" list (on the right side of the page). Click on the following link to take you to this page: [Submission Record](#)

If the quote is accurate, press "Next" to submit your submission.

If the quote is inaccurate you can begin the process again by simply refreshing your browser screen. Alternately, you can also choose to re-upload your samples if there is an error (see toggle below to allow you to re-upload your samples).

Toggle ☐ Submission is okay to submit

[Previous](#) [Next](#)

Step 17: Sample Manifest Create

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

Sample Manifest Creation

Please wait just a few seconds so the system can generate the sample manifest and then click "Next" to take you to a screen where you can download a copy of the manifest.

[Next](#)

Sample Manifest

Click on the following link to download a copy of the sample manifest:
[Manifest Download](#)

Print a copy of this sample manifest and include it with your samples. (This form replaces the previous paper submission forms).

If the download of the manifest is problematic, you can try to press "Previous" (takes you to previous screen) then "Next" (takes you back to this screen), and then try to download the manifest again. If that is unsuccessful, the manifest can also be accessed on the submission record page, in the "Files" list (on the right side of the page). Click on the following link to take you to this page: [Submission Record](#)

If the sample manifest is accurate, press "Next" to complete the submission process.

[Previous](#) [Next](#)

Step 18: Your Submission is Complete.

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

Submission Complete!

If you have further questions, please contact the appropriate core staff.

General Inquiries and Submissions	Illumina library prep & QC fgl-qb3@berkeley.edu Illumina sequencing, and all PacBio/ONT services gsl-fgl@berkeley.edu
Billing	gsl_billing@berkeley.edu
Christopher Hann-Soden Director of Informatics and QB3 Genomics	Consulting, experimental design, quotes, contracts, and other inquiries channsoden@berkeley.edu
Computational Genomics Resource Laboratory	Savio accounts, bioinformatics software, and data analysis consulting cgri@berkeley.edu

[Finish](#)