Integrated GENOMICS Cores

Navigating TracSeq

Overview

TracSeq is the user portal for entering and tracking samples submitted to the HTSF. The system provides an easy way for the HTSF staff to document sample progress and for projects to check the status of their samples. The system is currently only used for materials that will be sequenced on Illumina platforms. The HTSF continues to make upgrades to the system to provide better transparency for researchers using the HTSF. You will need an ONYEN to access this system.

TracSeq is primarily used to track the progress of samples as they make their way through processing and sequencing. Users can utilize TracSeq in many ways including submitting samples, viewing QAQC results and attachments and reviewing their sample run metrics once their samples have been sequenced.

Submissions

Verifying and Updating Your Account

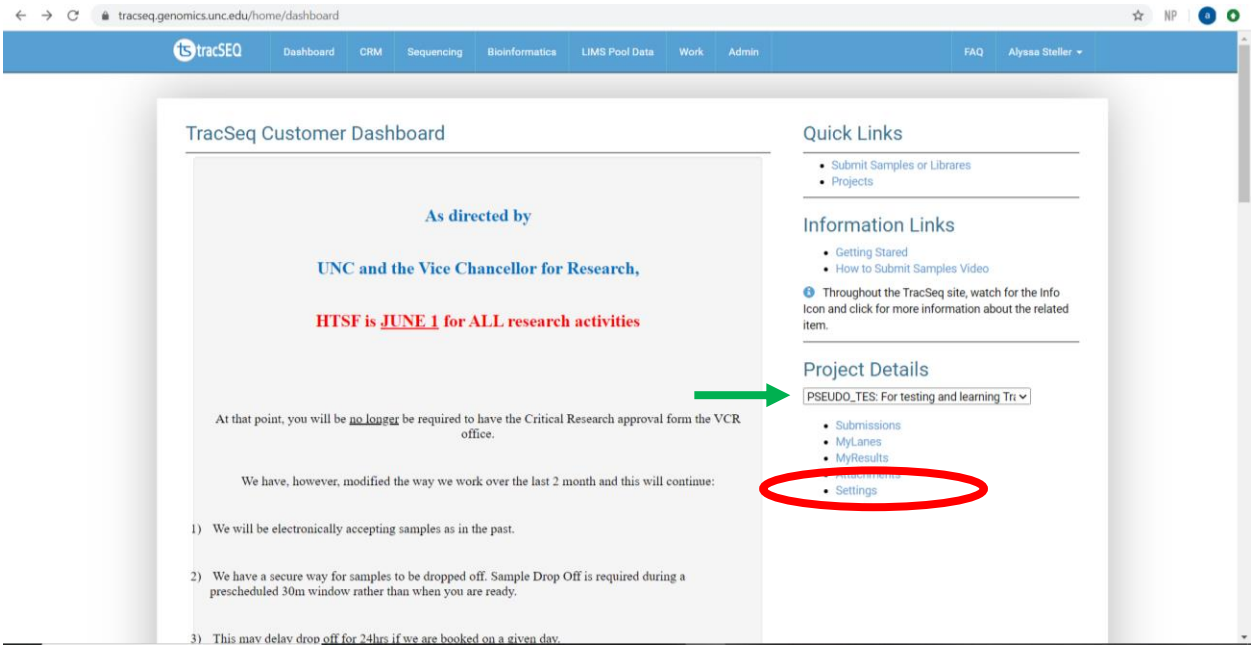
For new TracSeq users, who do not have a current account at the HTSF, please contact our Customer Service Team to set up a project. Please fill out our Account Initiation Request Form, found on our website under Forms and Guides and send it to us electronically to begin setting up a new account. For new TracSeq users, who do have a current account with the HTSF but have not yet been added to it, please send us your ONYEN and name of the account in order to be added.

For users who do not remember their account name or are a member of multiple accounts and are not sure which account to use for a submission please reach out to the Customer Service Team for assistance.

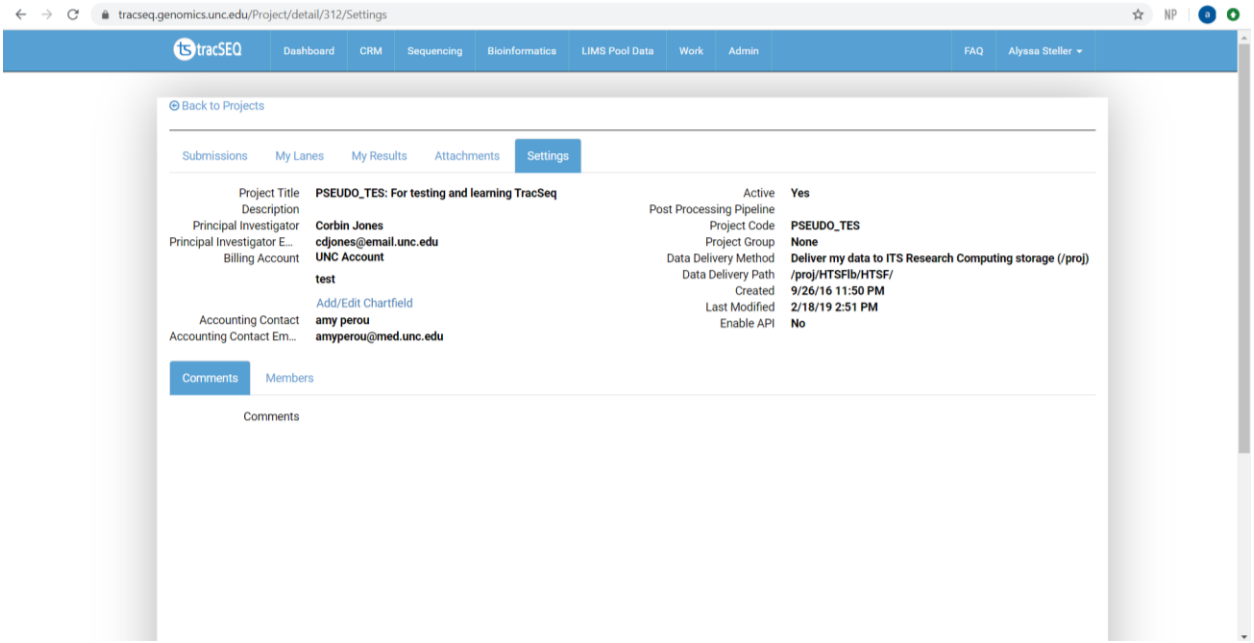
For TracSeq users who have not submitted in a significant amount of time or who would like to make updates to their project, please fill out and send the Account Update Request Form found on the Forms and Guides page on our website before submitting new material. The HTSF can then make necessary changes prior to drop-off of samples and help speed up the processing of incoming samples.

For external, non-UNC studies, please reach out to the Customer Service Team. An in-person or electronic consult may be necessary and the HTSF customer service team will submit the samples electronically on TracSeq and coordinate the shipment or drop-off of samples.

Once an account has been verified, users can begin a new submission on TracSeq. Details of a submission can be found on the Settings page from the TracSeq dashboard.



1. *Ensure the correct project is chosen from the drop down menu, then click "Settings."*

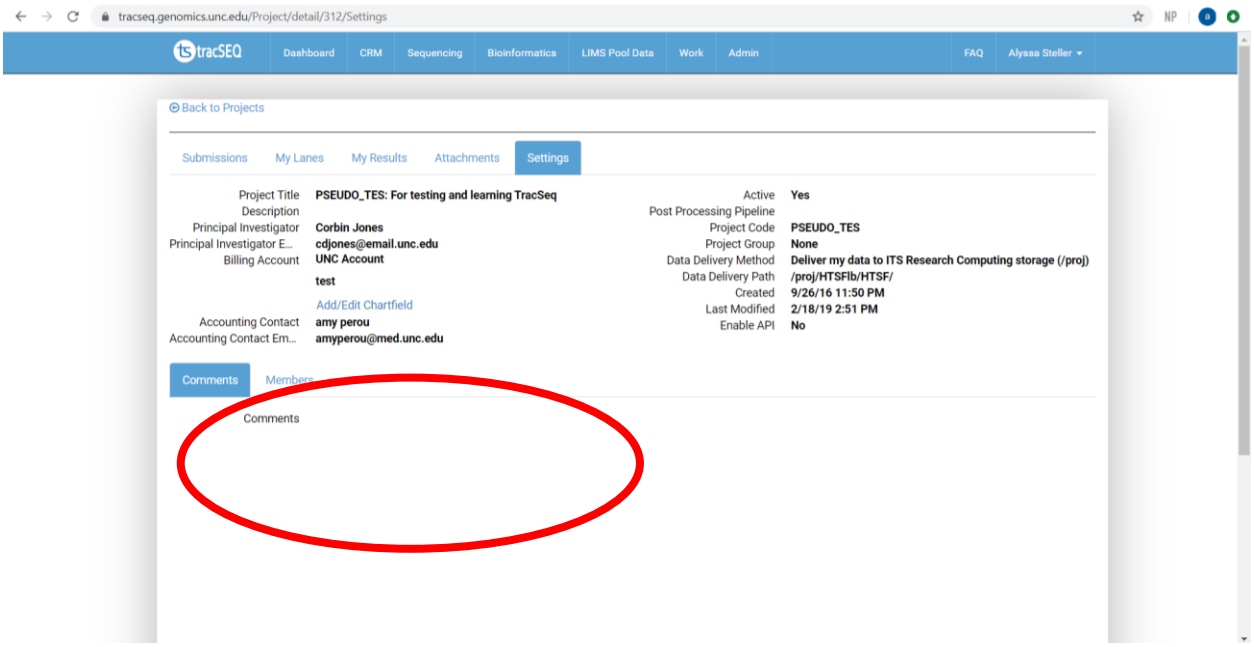


2. *Details of the project will be found on this page.*

How to Find Consultation Notes

Users can find notes from CONSULT MEETINGS with the HTSF on TracSeq. To reference these notes follow the instructions listed below:

1. Log on to TracSeq.
2. Select the correct project from the Project Details drop down tab on the right side of the landing page on TracSeq.
3. Click submissions below the selected project. Users will be directed to the Project: "XXXX" page.
4. Click on the settings tab at the top of the page. Users will then be able to view all notes and comments for the project.



All comments will be listed here for a specific project.

For users wanting to find NOTES FOR A SPECIFIC SUBMISSION, follow the steps below:

1. Log on to TracSeq.
2. Select the correct project from the Project Details drop down tab on the right side of the landing page on TracSeq.
3. Click submissions below the selected project. Users will be directed to the Project: "XXXX" page.
4. Use the search bar to search for the correct batch number or scroll down the page until finding the correct submission.

5. Select the View Details link on the submission. Users will then be navigated to the submission details page in which they can find notes and comments for the submission.

Submitting Material

UNC-affiliated users are able to log-on to TracSeq using their ONYEN and password. To begin a new submission, click on Submitting Samples or Libraries, which can be found under Quick Links. This will direct the user to the HTSF Material Submission tab. Begin by following and filling out the numbered steps, including selecting the project, material type, if the material will need to be pooled and/or sequenced, and so forth. In step 7, a detailed manifest will need to be filled out and uploaded into the system. For any questions on how to fill out a manifest, please reference our step-by-step guide on our website.

If users have any problems during the submission process, please be sure to click the Save Work button and contact the HTSF Customer Service Team for assistance.

Dropping Off Material

Once submissions have been reviewed by the HTSF customer service team, users will receive two emails usually within one business day of the submission.

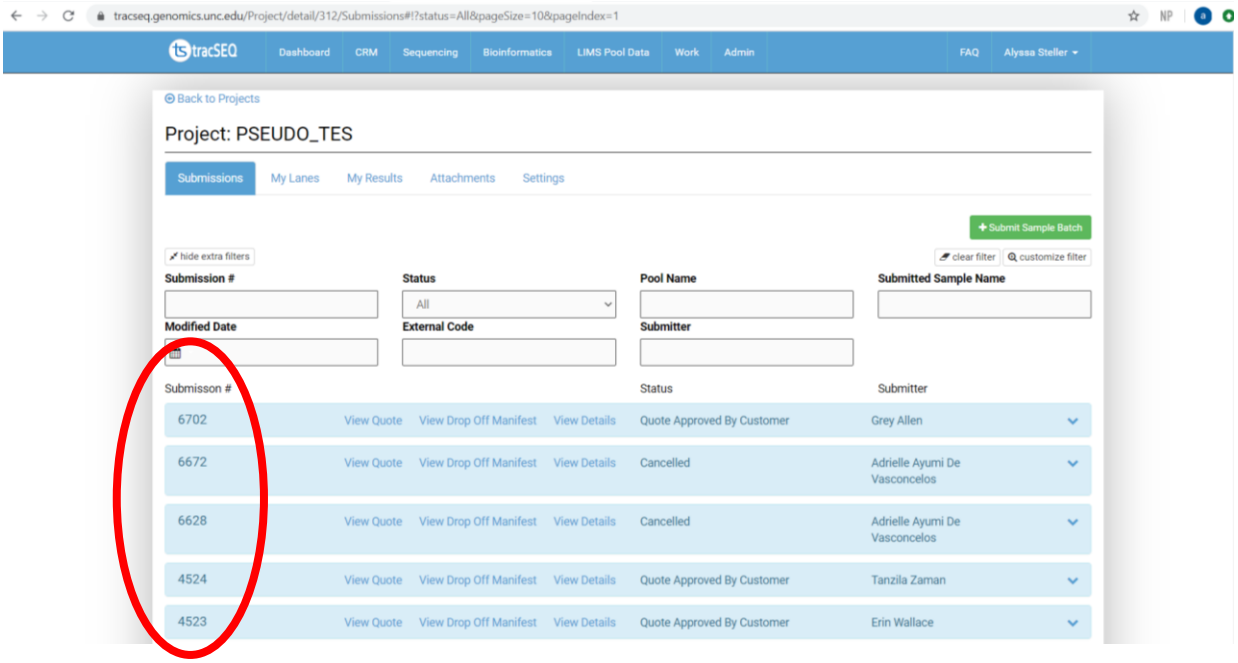
- An approval email that indicates the HTSF will be able to perform the work requested.
- A quote for the work requested on the submitted samples. Please review the quote. Keep in mind this is just an estimate. It is not uncommon that as work proceeds, modifications may be made to processing which could change the final fees billed. HTSF will always discuss this with you before changes are made.

Before dropping off samples, users must confirm the quote through the link provided in the email, select when the material will be dropped off to the lab, and print the confirmed manifest which appears in a new window. **Please bring the confirmed manifest with the samples to the lab and note your batch number**.

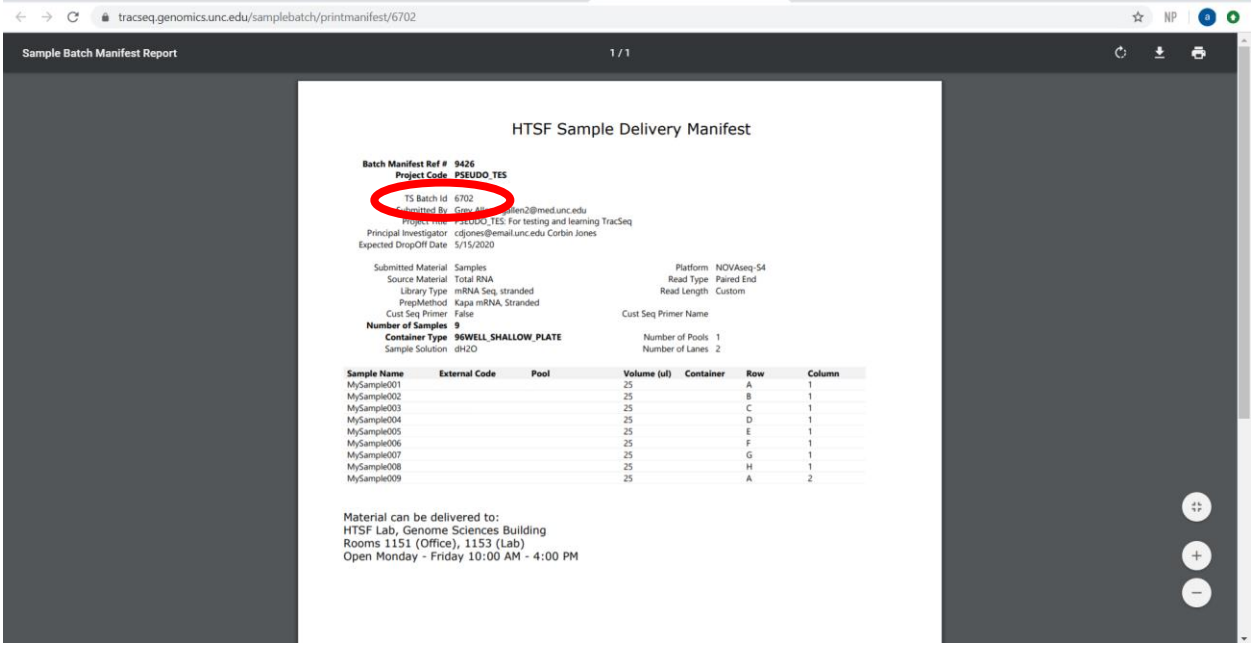
Acceptable sample containers are listed on our website along with volume and concentration requirements depending on material type.

How do I find my batch number?

The batch number is the Submission ID listed next to each submission.



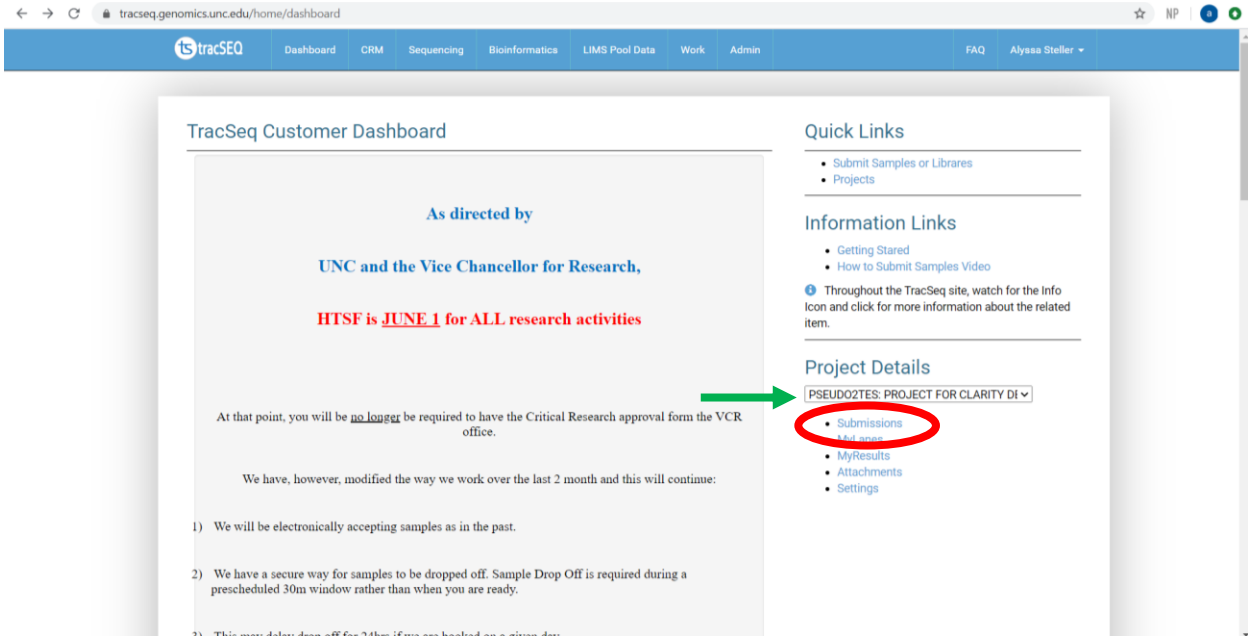
It can also be found on the confirmed manifest.



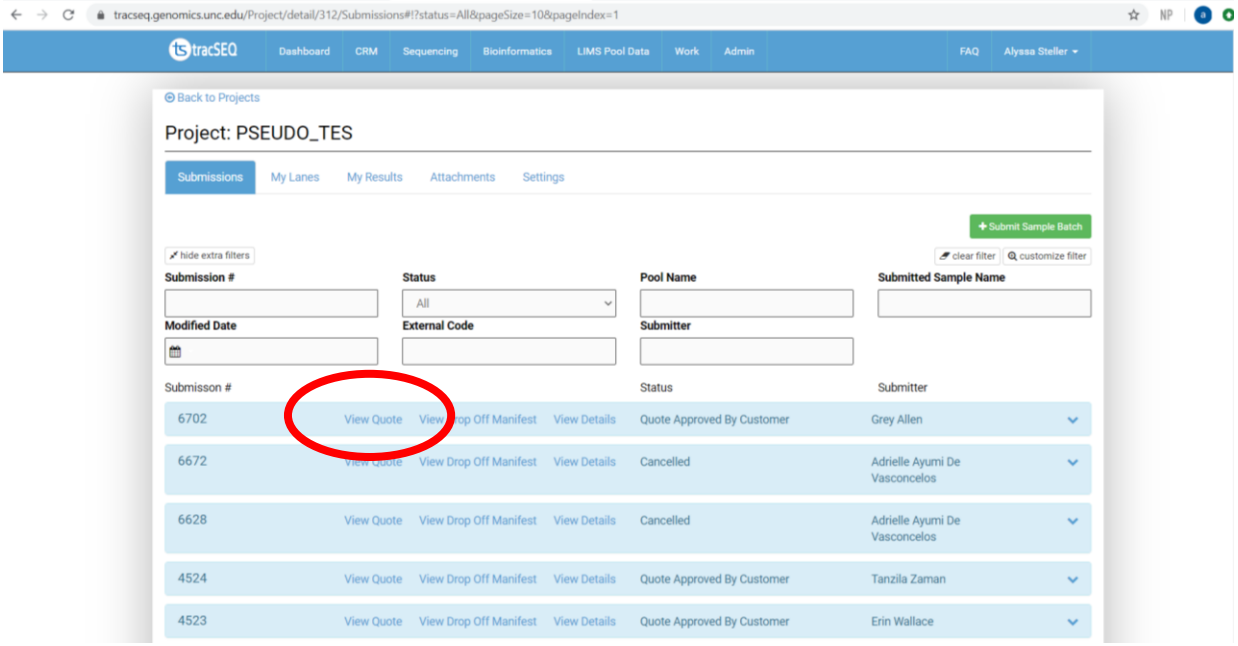
How to View Your Quote via TracSeq

For users wanting to find a quote for a specific submission, they must first select the correct project from the Project Details drop down tab on the TracSeq landing page. Once selected, users then may click the Submissions button. From there, users will be navigated to the Project: ”XXXX” window, which will populate all previous and in process

submissions. Users can use the search bar to search for the four-digit batch number or scroll to the correct submission on the page. To view the quote, select the View Quote link on the correct submission, which will take you to the quote with the cost break down of work being done on the samples.



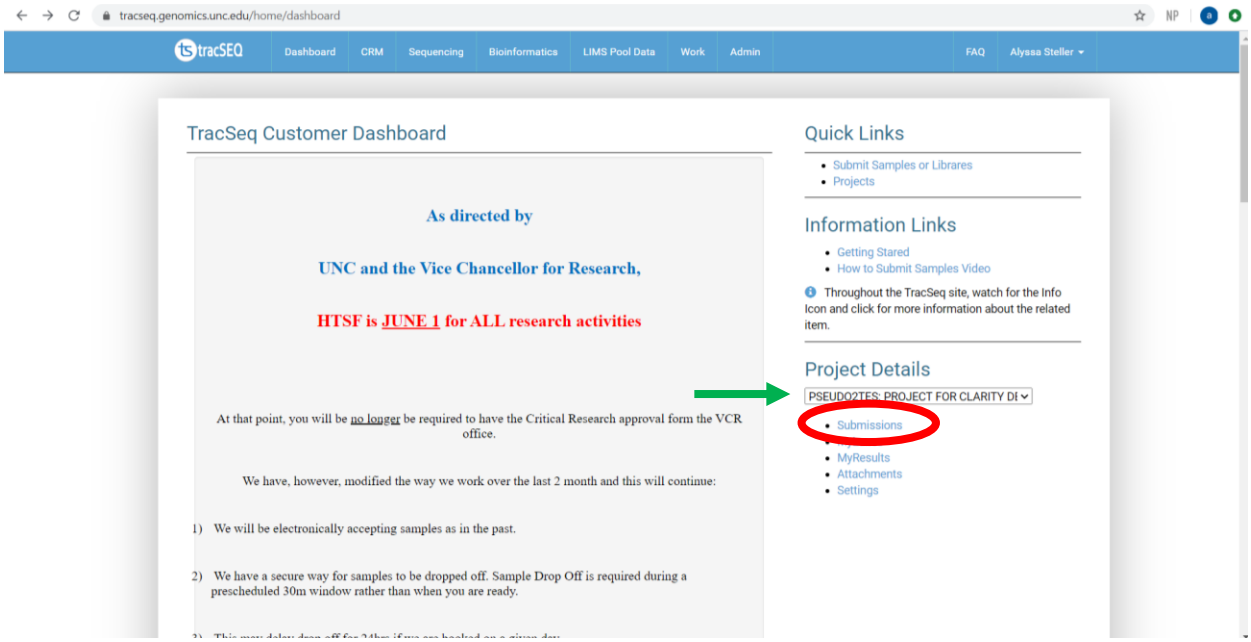
1. *Ensure the correct project is chosen from the drop down menu, then click "Submissions"*



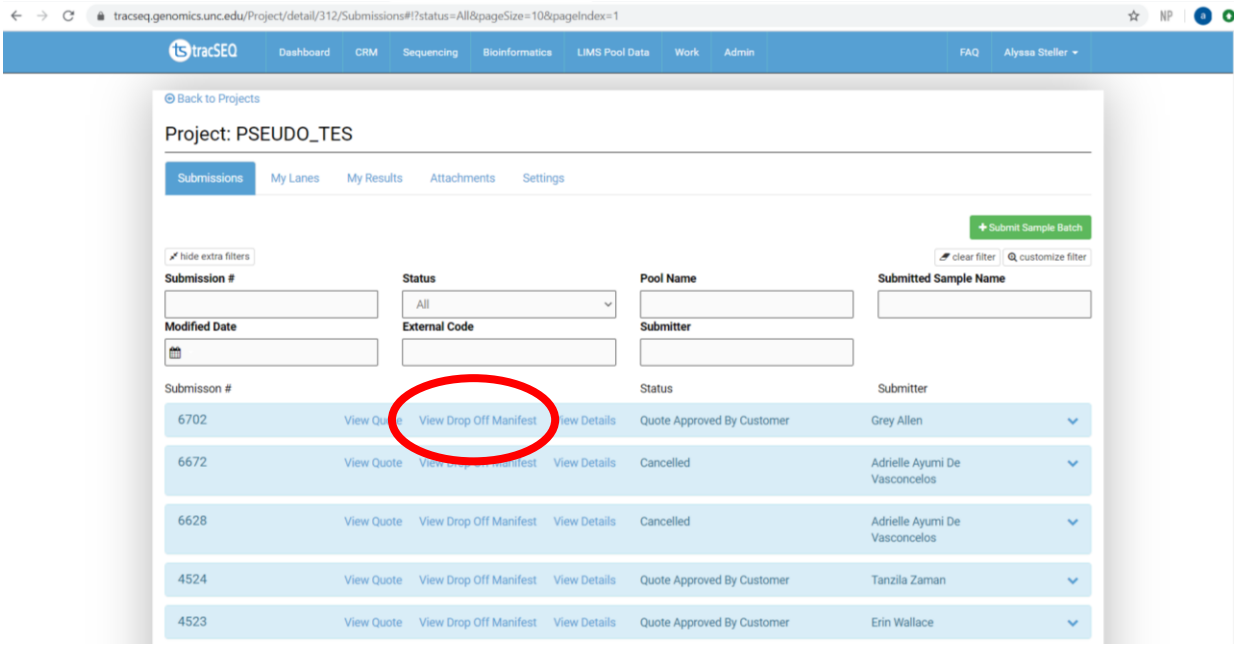
1. *Once you locate the correct batch number for the current submission, click "view quote"*

How to Print a Confirmed Manifest

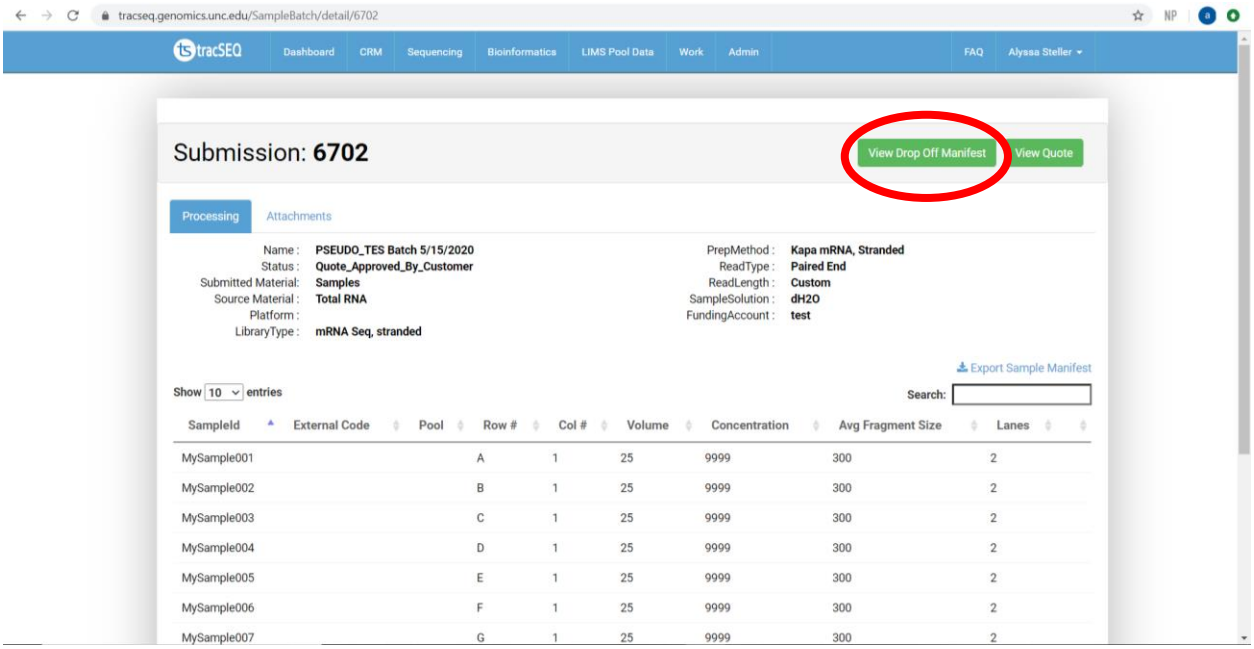
Users must print and bring a confirmed manifest when dropping off samples to the HTSF. To print a confirmed manifest, select the correct project from the Project Details drop down tab on the TracSeq landing page. Then click submissions below the selected project. Users will then be directed to the Project: “XXXX” page. Find the correct submission by either searching for the batch number in Submission # bar or scroll to the correct submission. Click the View Quote link on the submission. Once the user is navigated to the quote, find and select the green Print Confirmed Manifest button on the top righthand side of the page.



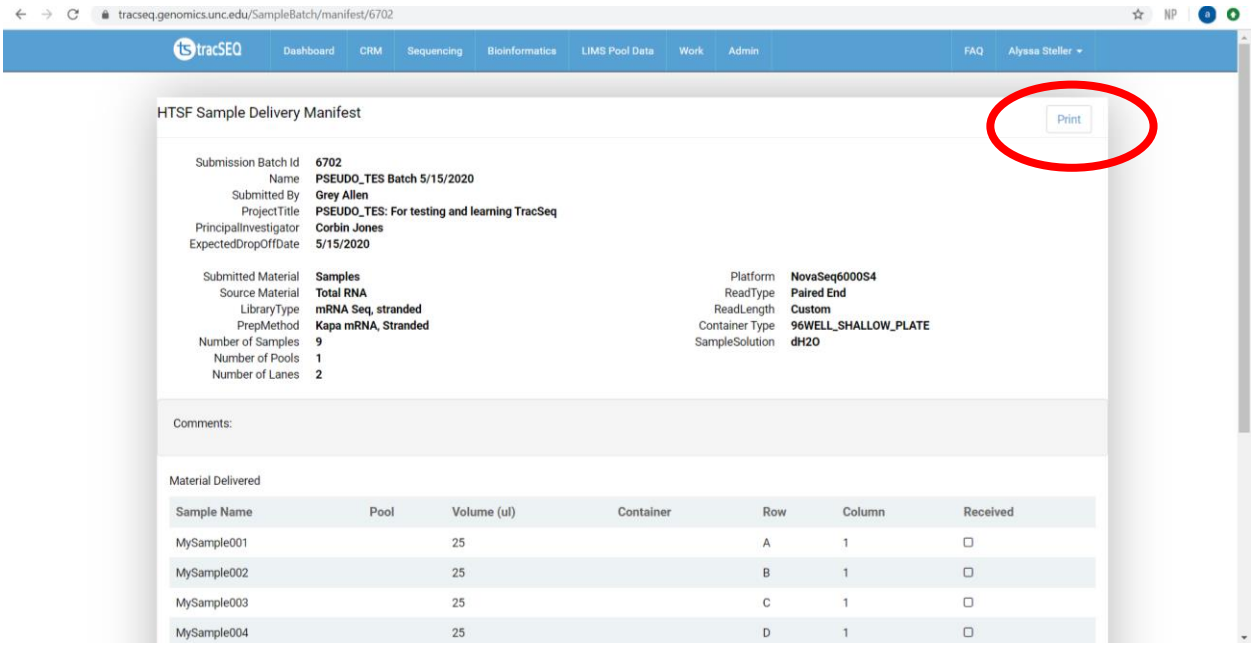
1. *Ensure the correct project is chosen from the drop down menu, then click "Submissions"*



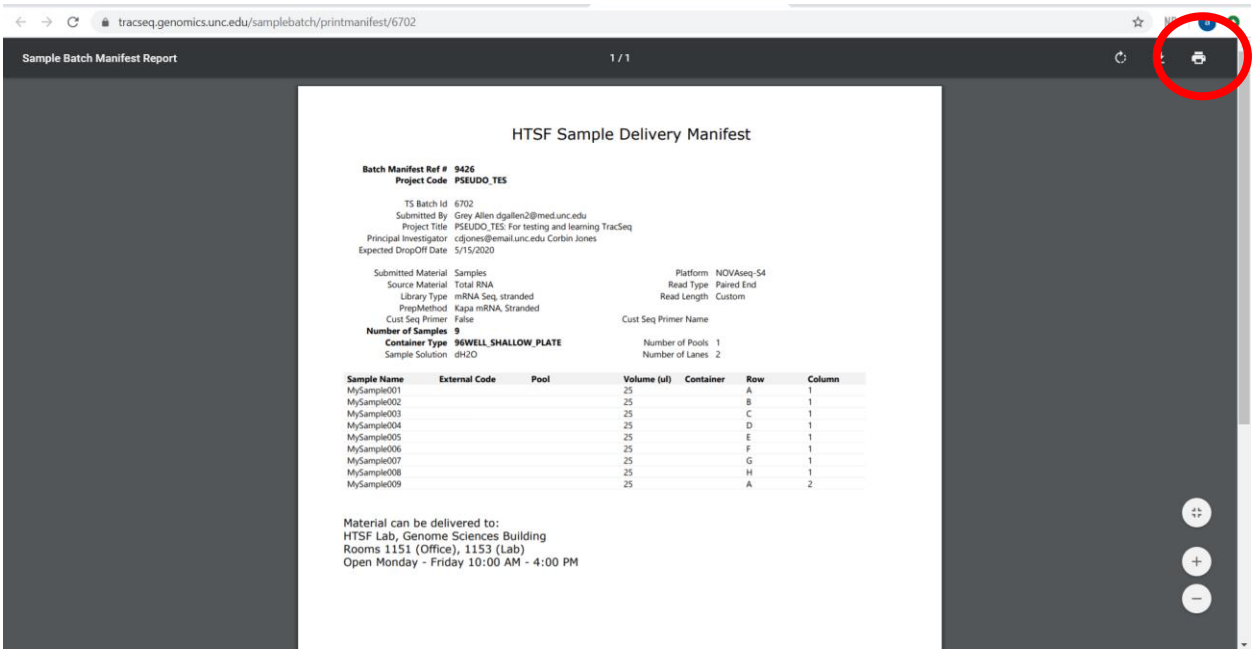
2. Once you locate the correct batch number for the current submission, click "view drop off manifest."



3. Click "view drop off manifest" in the top right corner.



4. Click "Print" in the top right corner.



5. Click the printer icon in the top right corner to print the confirmed manifest.

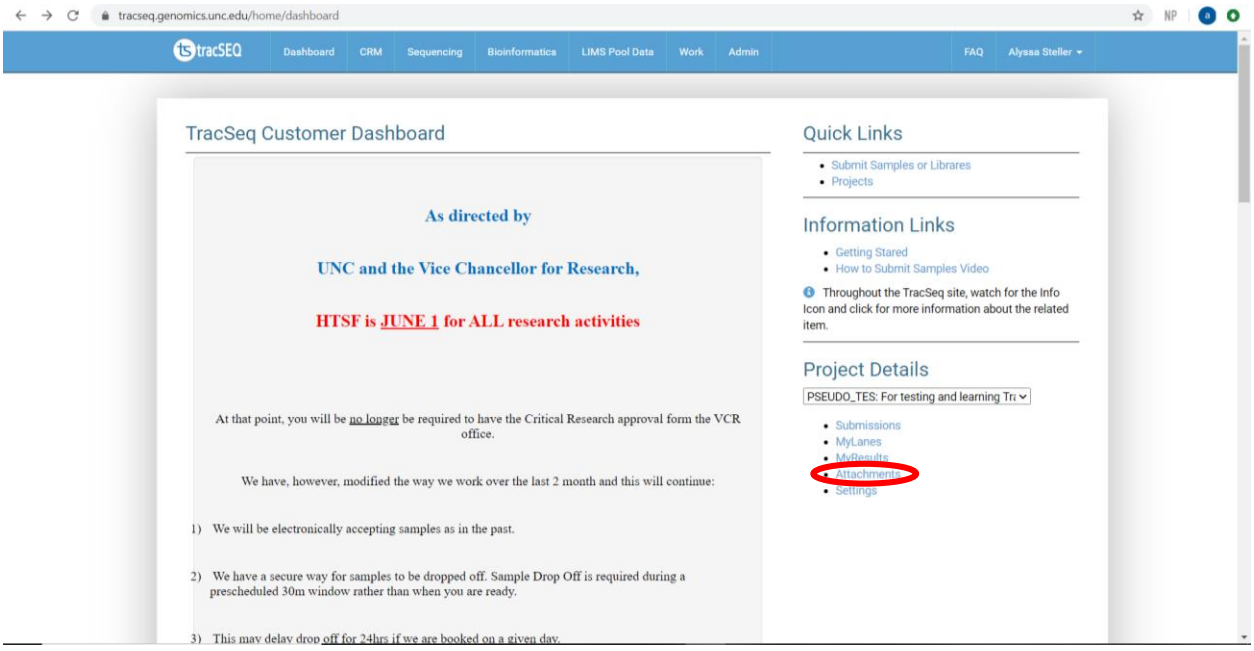
QAQC Results and Interpretation

Finding QAQC Results on TracSeq

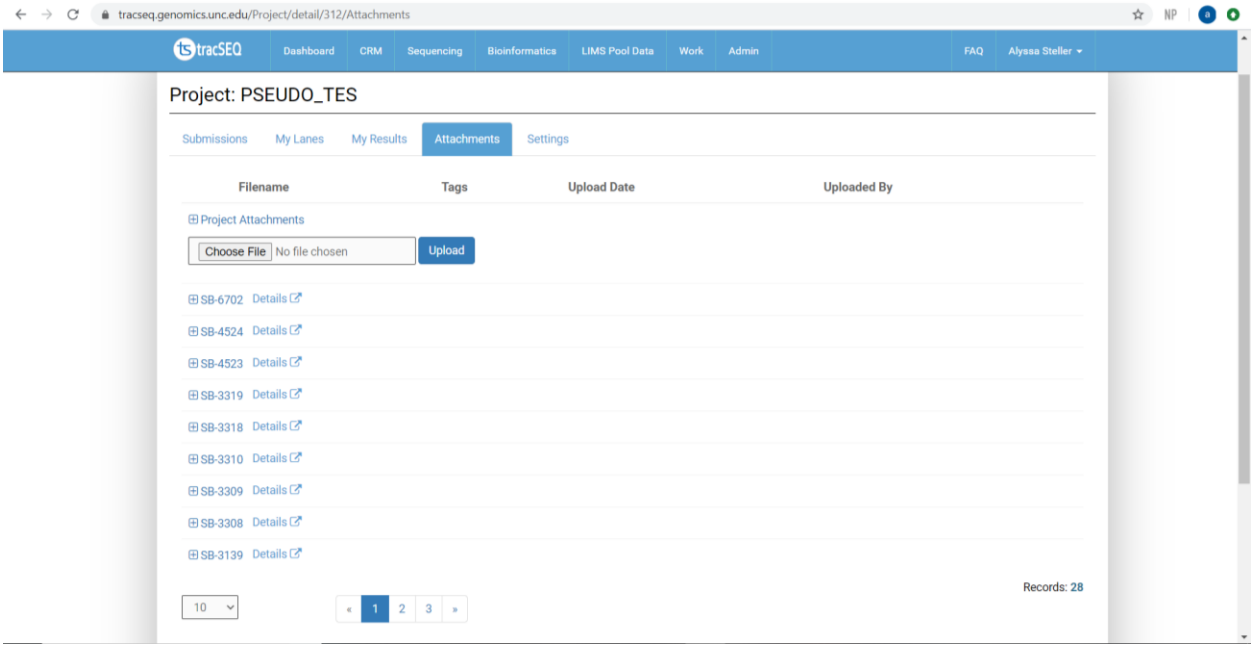
Unless otherwise specified before submitting samples, QAQC will be performed on all samples that arrive at the HTSF. This is to verify the quality of material before sequencing. QAQC results will be communicated via email by the HTSF customer service team before moving on to further processing.

To find previous QAQC results from a specific submission please refer to the following steps:

1. Log-on to TracSeq
2. If users are affiliated with more than one project, select the correct project under Quick Links → Projects OR select the correct project from the drop down tab under Project Details. Users will then be navigated to their Project: “XXXX” page.
3. Click the Attachments tab on the Project: “XXXX” page.
4. Select the correct batch number, SB-“####” from the list of prior submissions, by clicking the “+” sign to expand the submission.
5. Several attachments may be listed. QAQC documents are typically formatted as follows: “QAQC_Batch#_AbbreviatedMaterialType.” Select the correct QAQC based on the material type being referenced.



1. Ensure the correct project is chosen from the drop down menu, then click "attachments."



2. *All QAQC results will be attached to a submission and can be found here. Be sure to read the full title of the attachment to understand if it is the QAQC for the raw material, library or pool.*

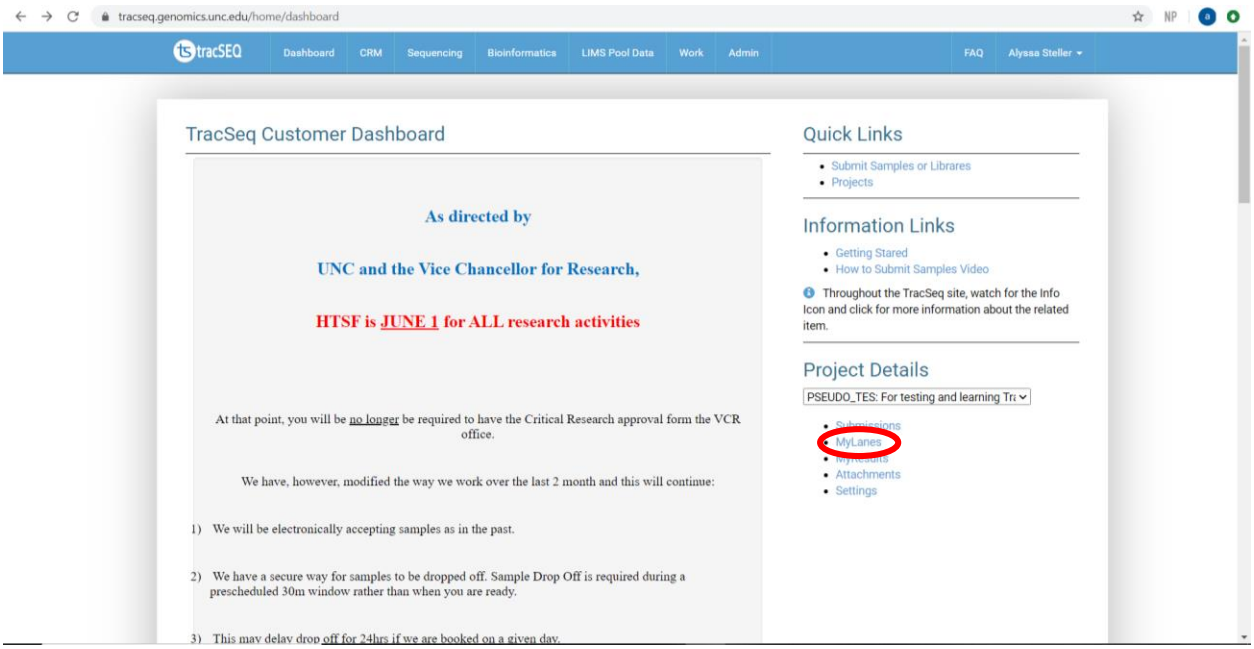
Interpreting QAQC Results

Once the correct QAQC results have been found, users may then review them. For more details on how to interpret results please refer to our QAQC tab on our website. If users have questions about their QAQC results please reach out the HTSF Customer Service Team.

Data Access and Results

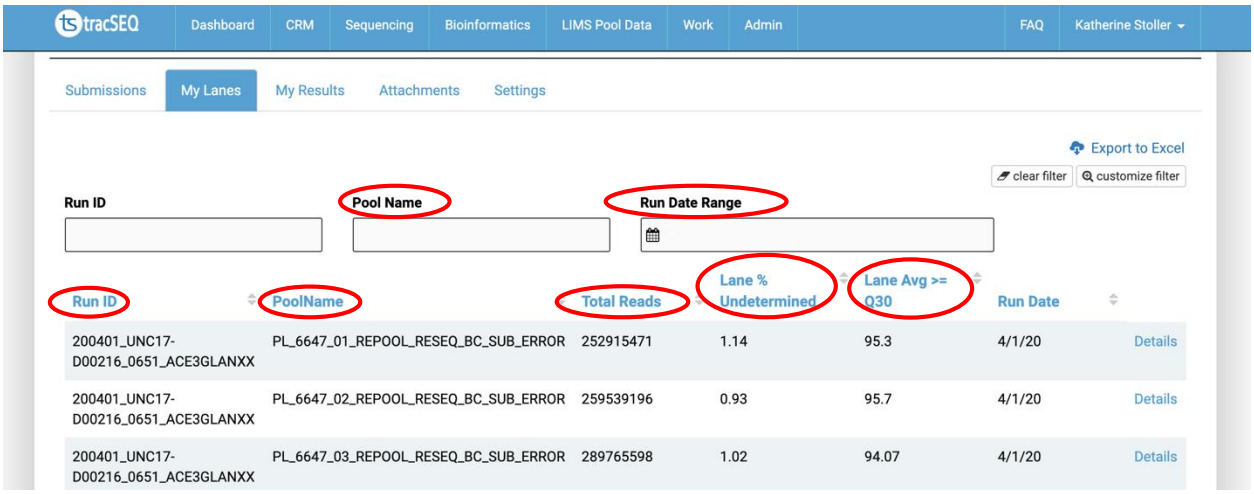
General Sequencing Run Information

To find basic information on particular sequencing runs, please first select the correct project from the project details drop down tab. Then select “My Lanes” underneath the project details drop down menu.



1. *Ensure the correct project is selected, the click "My Lanes."*

Users will be navigated to the My Lanes page where they will be able to see each pool that has been run on each lane or multiple lanes of a particular platform. Here, the user can view and find the "Run ID," pool name, total reads per run, % of the lane that is undetermined and the average Q30 for a lane. To search for a particular run, use the "pool name" or "run date range" search bar.

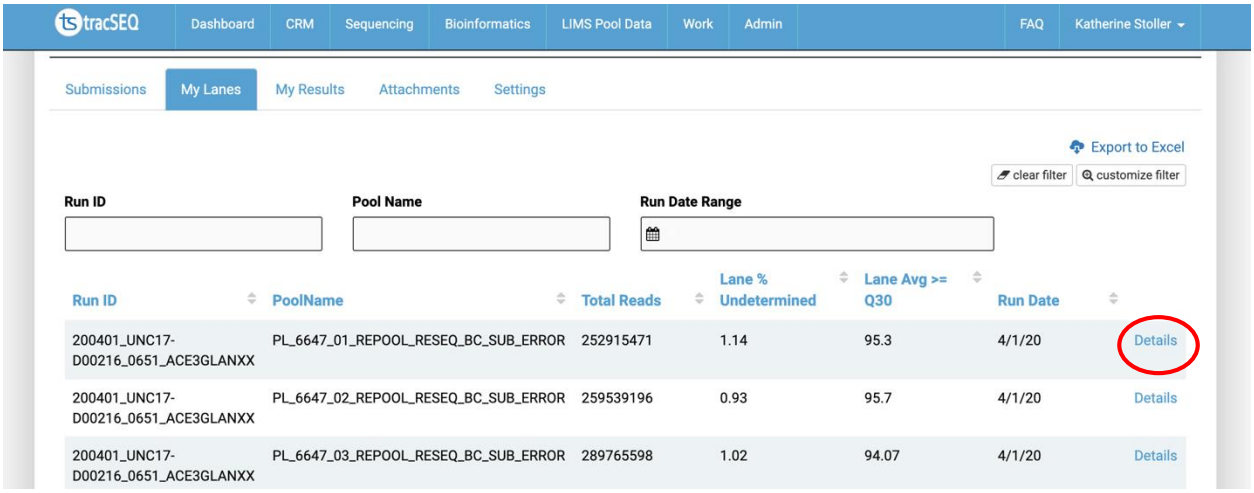


2. *Basic information on each sequencing run.*
3.

Sequencing Run Set Up Information

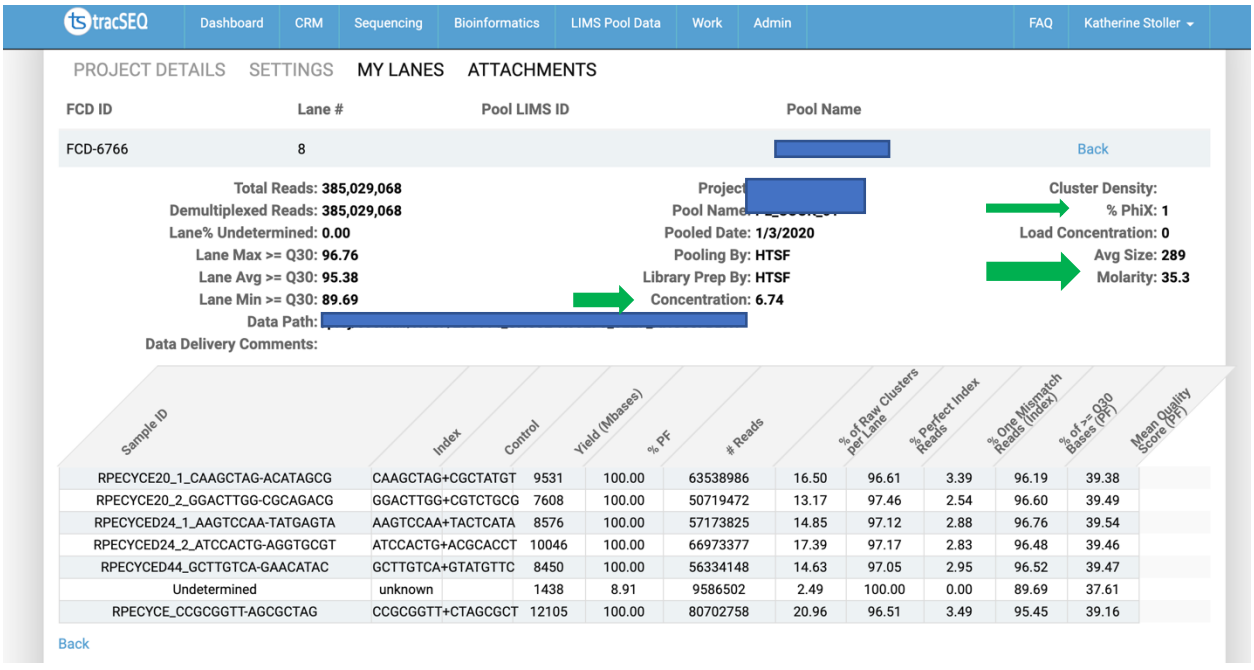
To find sequencing run set up information on particular sequencing runs, please first select the correct project from the project details drop down tab. Then select “My Lanes” underneath the project details drop down menu.

Once users determine the run they would like to view by navigating to the “My Lanes” page, users can then click the “Details” button at the right side of the screen for more set up information on a particular run.



4. *Click “Details” button for run of interest.*

Here, users can find sequencing run set up information such as % PhiX loaded on the sequencer, average fragment size of the pool, concentration of the pool and molarity of the pool.

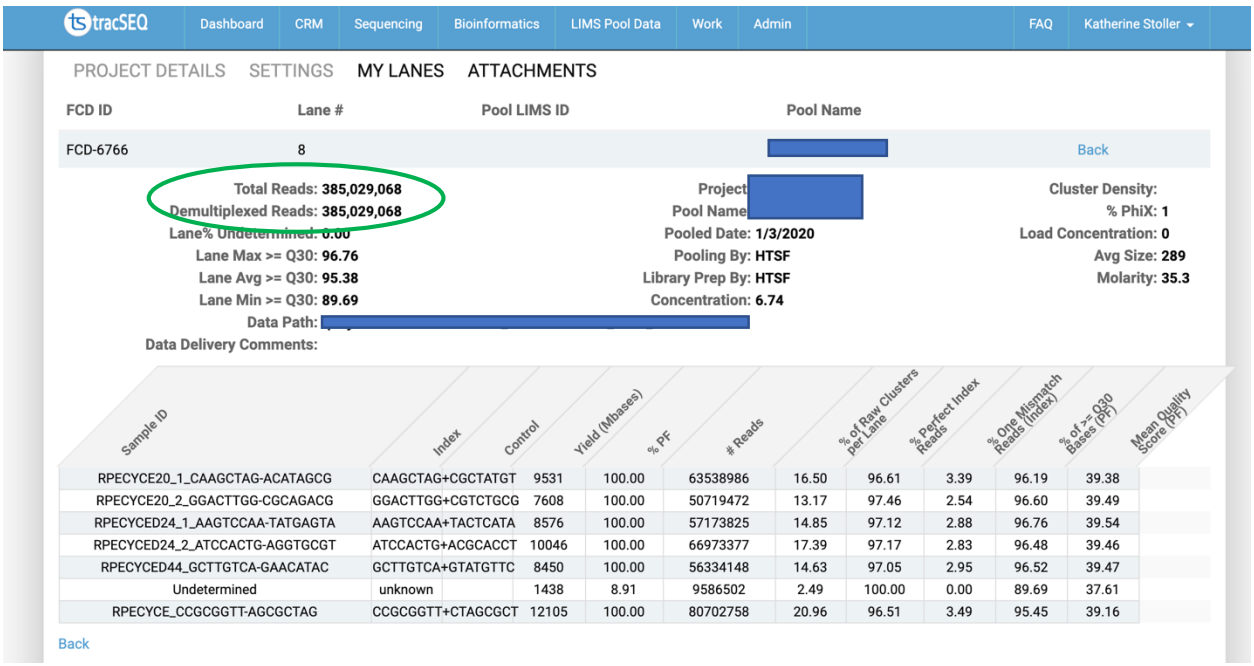


5. *Sequencing run set up information highlighted above.*

Sequencing Run Total Reads and Demultiplexed Reads

To find sequencing run total reads and demultiplexed reads information on particular sequencing runs, please first select the correct project from the project details drop down tab. Then select “My Lanes” underneath the project details drop down menu.

Once users determine the run they would like to view by navigating to the “My Lanes” page, users can then click the “Details” button at the right side of the screen for more read information on a particular run.



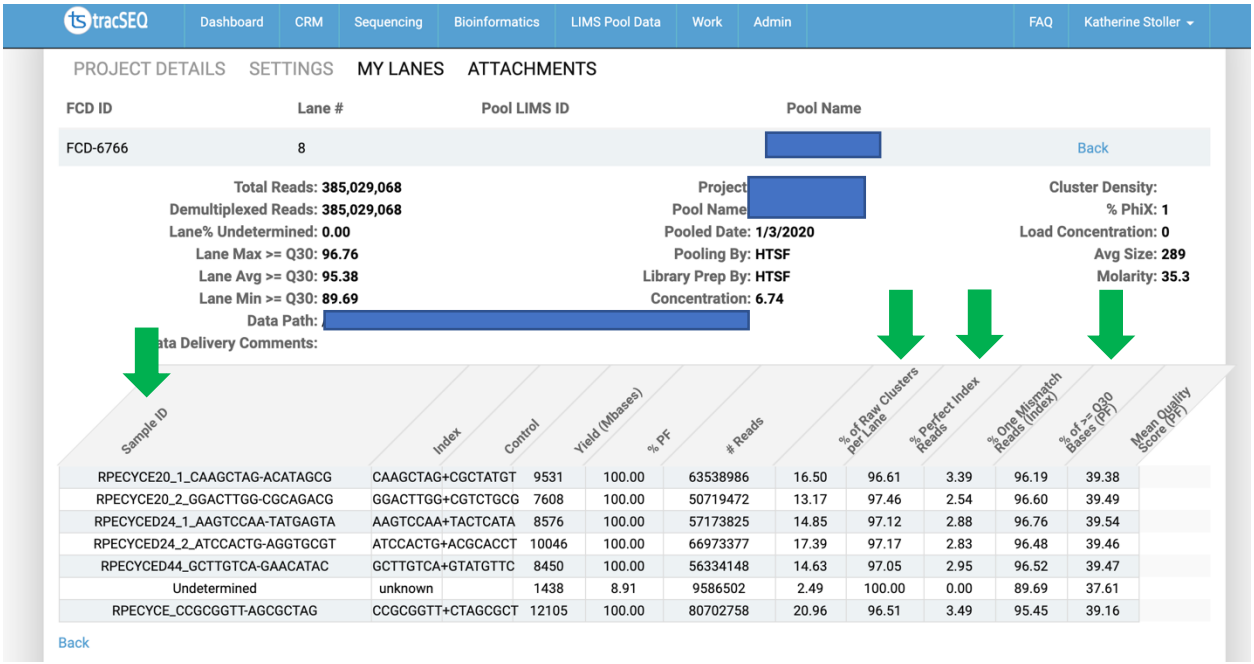
6. *Total read and demultiplexed information indicated above.*

Sequencing Run Metrics for Each Library in a Pool

To find sequencing metrics for each library in a pool on particular sequencing runs, please first select the correct project from the project details drop down tab. Then select “My Lanes” underneath the project details drop down menu.

Once users determine the run they would like to view by navigating to the “My Lanes” page, users can then click the “Details” button at the right side of the screen for sequencing run metrics.

Each sample in the pool is listed on the bottom half of the page. Here users can find % of clusters, % perfect index reads and Q30.



7. *Sequencing run metrics for each library indicated above.*

How to Translate the RUN NAME

Each run on the Illumina machine is assigned a unique RUN NAME. This name appears in TracSeq is several place once the data has been delivered (ie: MY LANES feature). It is part of the data file name for each sample so you always have the run information linked to your sample data.

These run IDs are also important to us when we need to communicate with Illumina about a failed run due to reagent or equipment failures. It is how we can trace down consistent issue with machines or bad lots of reagents.

An example of a run name is below and what each section indicates.

200428_UNC31-K00269_0276_BHH5TMBBXY

- Date the run was started:
  - **200428**_UNC31-K00269_0276_BHH5TMBBXY
  - 200428 = date it ran in year, month , day format
  - For this example : April 4, 2020

- Machine it ran on
  - 200428_**UNC31**-K00269_0276_BHH5TMBBXY
  - Each machine has an HTSF ID name. This also indicated what platform type.
    - MiSeq Platform = UNC21, UNC22, UNC23, UNC24

        - HS2500 Platform = UNC17, UNC18
        - HS4000 Platform = UNC31, UNC32
        - Novaseq6000 – UNC41
    - If a machine is retired, the name is also retired
    - For this example = this was a HS4000 run

- The Illumina serial number of the machine
    - 200428_UNC31-**K00269**_0276_BHH5TMBBXY
    - For this example, the HS4000 serial number is K000269

- The run number since the machine was installed at the HTSF
    - 200428_UNC31-K00269_**0276**_BHH5TMBBXY
    - For this example it was the 276th run on this specific HS4000

- The side of the machine it ran on
    - 200428_UNC31-K00269_0276_**B**HH5TMBBXY
    - There are 2 side to a machine so 2 separate flowcells can be run at the same time. Side A and Side B
    - For this example, the flowcell ran on side B

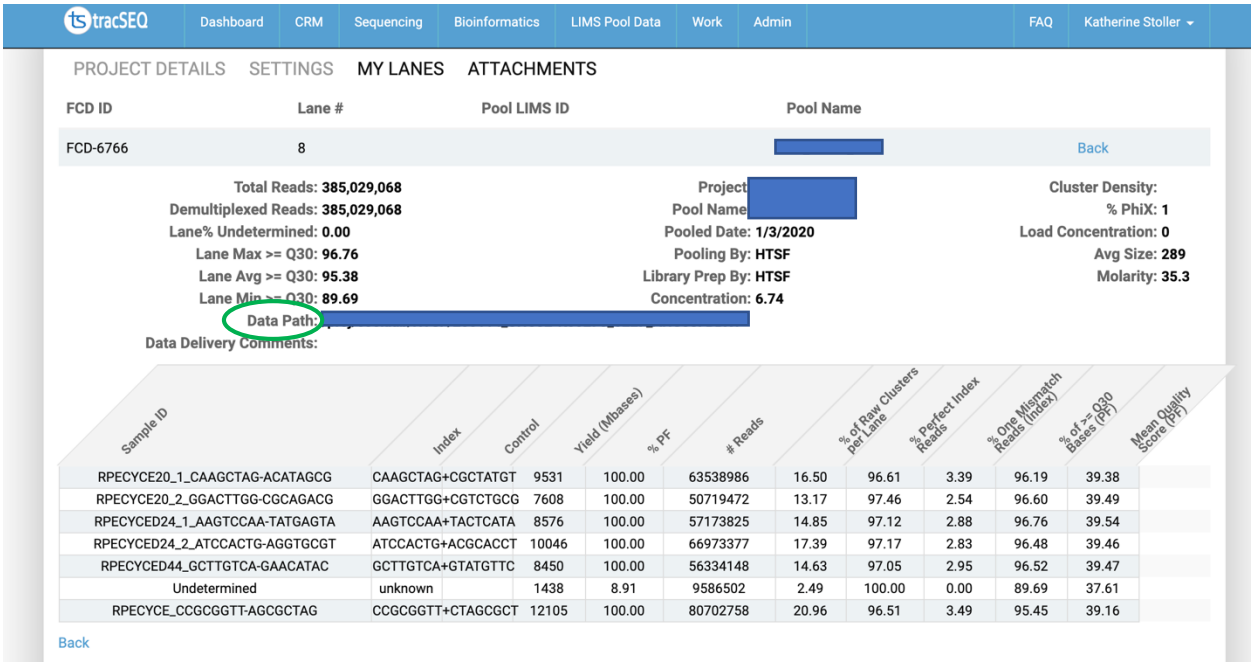
- The flowcell kit ID number
    - 200428_UNC31-K00269_0276_B**HH5TMBBXY**
    - For this example, the unique flowcell reagent kit # is HH5TMBBXY

How to Find Link to Data Folder

To the link to a data folder for a particular sequencing run, please first select the correct project from the project details drop down tab. Then select “My Lanes” underneath the project details drop down menu.

Once users determine the run they would like to view by navigating to the “My Lanes” page, users can then click the “Details” button at the right side of the screen.

The link to the data delivery folder is located in the center of the page. The data path shows your data folder name and the flowcell run name



8. *Link to specific data delivery folder is indicated above.*