

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

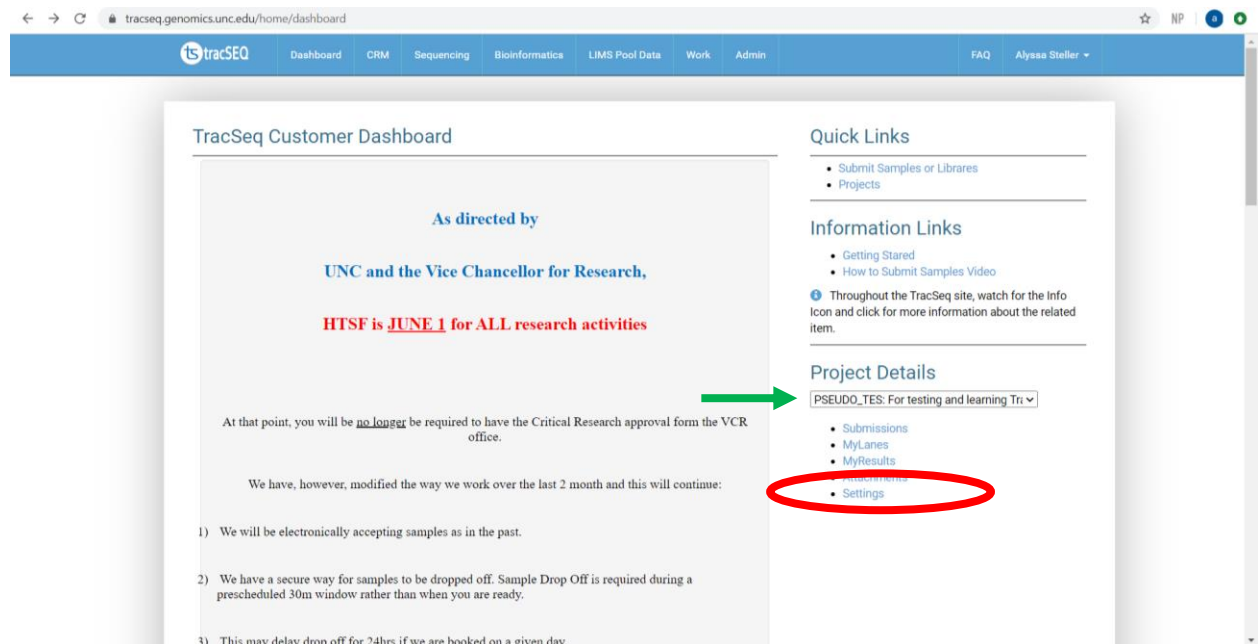
For new TracSeq users, who do not have a current account at the HTSF, please contact our Customer Service Team to set up a project. Please fill out our Account Initiation Request Form, found on our website under Forms and Guides and send it to us electronically to begin setting up a new account. For 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.

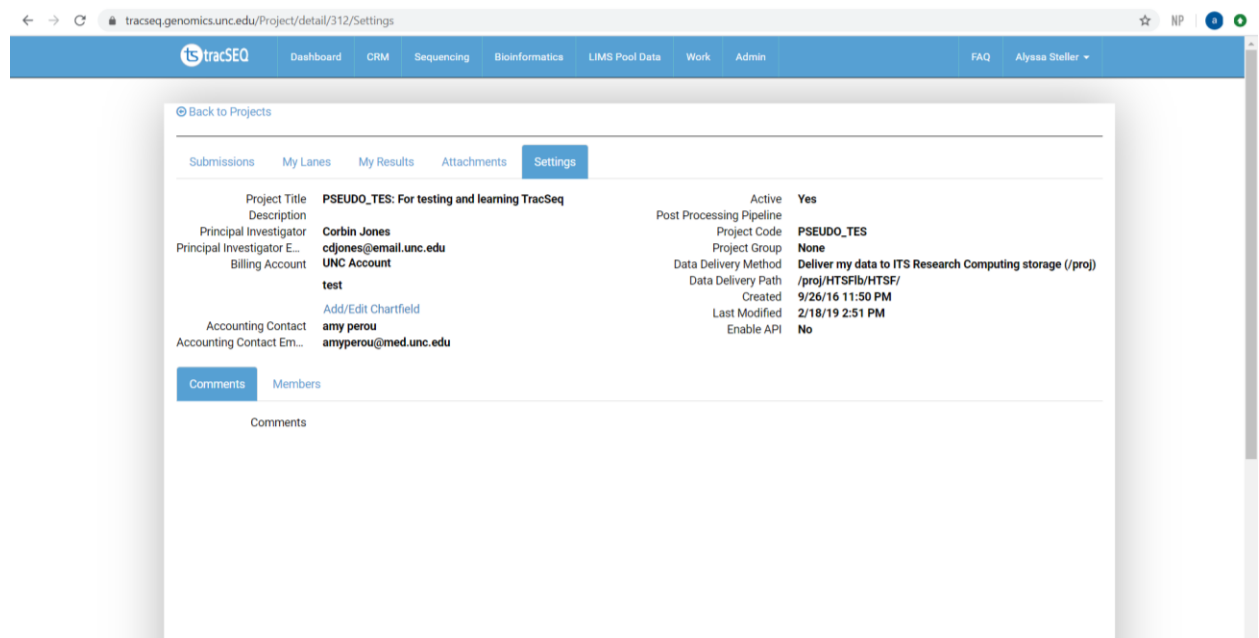
For TracSeq users who have not submitted in a significant amount of time or who would like to make updates to their project, please fill out and send the Account Update Request Form found on the Forms and Guides page on our website before submitting new material. The HTSF can then make necessary changes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

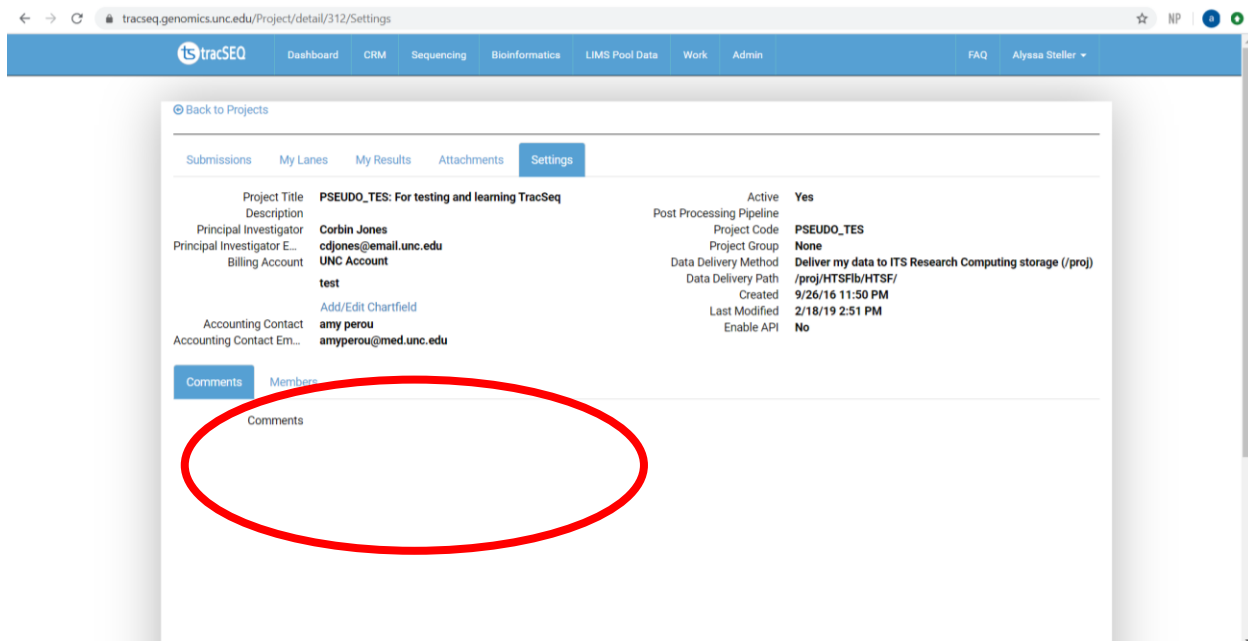


2. Details of the project will be found on this page.

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.

tracseq.genomics.unc.edu/Project/detail/312/Submissions#!?status=All&pageSize=10&pageIndex=1

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Back to Projects

Project: PSEUDO_TES

Submissions My Lanes My Results Attachments Settings

hide extra filters

Submit Sample Batch

clear filter customize filter

Submission # Status Pool Name Submitted Sample Name

Modified Date External Code Submitter

| Submission # | Status | Pool Name | Submitted Sample Name | Submitter |
|--------------|----------------------------|----------------------------|----------------------------|-------------------------------|
| 6702 | Quote Approved By Customer | Quote Approved By Customer | Quote Approved By Customer | Grey Allen |
| 6672 | Cancelled | Cancelled | Cancelled | Adrielle Ayumi De Vasconcelos |
| 6628 | Cancelled | Cancelled | Cancelled | Adrielle Ayumi De Vasconcelos |
| 4524 | Quote Approved By Customer | Quote Approved By Customer | Quote Approved By Customer | Tanzila Zaman |
| 4523 | Quote Approved By Customer | Quote Approved By Customer | Quote Approved By Customer | Erin Wallace |

It can also be found on the confirmed manifest.

tracseq.genomics.unc.edu/samplebatch/printmanifest/6702

Sample Batch Manifest Report 1 / 1

HTSF Sample Delivery Manifest

Batch Manifest Ref # 9426
Project Code PSEUDO_TES
TS Batch Id 6702
Submitted By Grey Allen gallen2@med.unc.edu
Project Name PSEUDO_TES For testing and learning TracSeq
Principal Investigator cdjones@email.unc.edu Corbin Jones
Expected Drop Off Date 5/15/2020

Submitted Material Samples Platform NOVAsq-S4
Source Material Total RNA Read Type Paired End
Library Type mRNA Seq, stranded Read Length Custom
Prep Method Kapa mRNA, Stranded
Cust Seq Primer False Cust Seq Primer Name

Number of Samples 9
Container Type 96WELL_SHALLOW_PLATE
Sample Solution 9600

Number of Pools 1
Number of Lanes 2

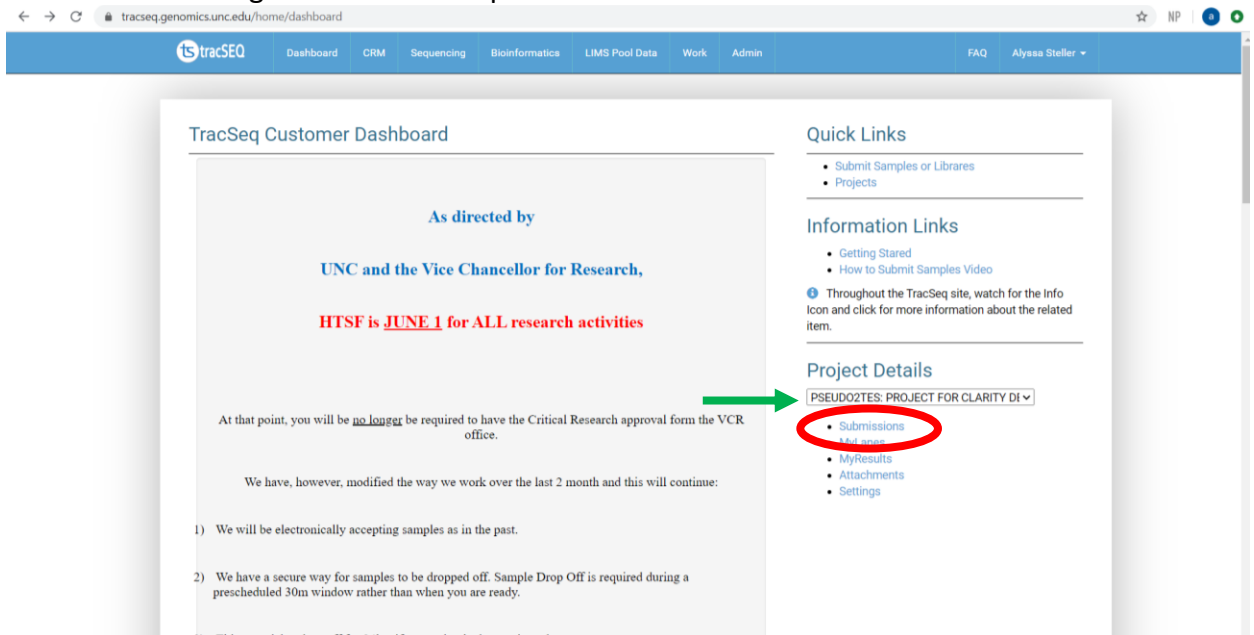
| Sample Name | External Code | Pool | Volume (ul) | Container | Row | Column |
|-------------|---------------|------|-------------|-----------|-----|--------|
| MySample001 | | | 25 | A | 1 | |
| MySample002 | | | 25 | B | 1 | |
| MySample003 | | | 25 | C | 1 | |
| MySample004 | | | 25 | D | 1 | |
| MySample005 | | | 25 | E | 1 | |
| MySample006 | | | 25 | F | 1 | |
| MySample007 | | | 25 | G | 1 | |
| MySample008 | | | 25 | H | 1 | |
| MySample009 | | | 25 | A | 2 | |

Material can be delivered to:
HTSF Lab, Genome Sciences Building
Rooms 1151 (Office), 1153 (Lab)
Open Monday - Friday 10:00 AM - 4:00 PM

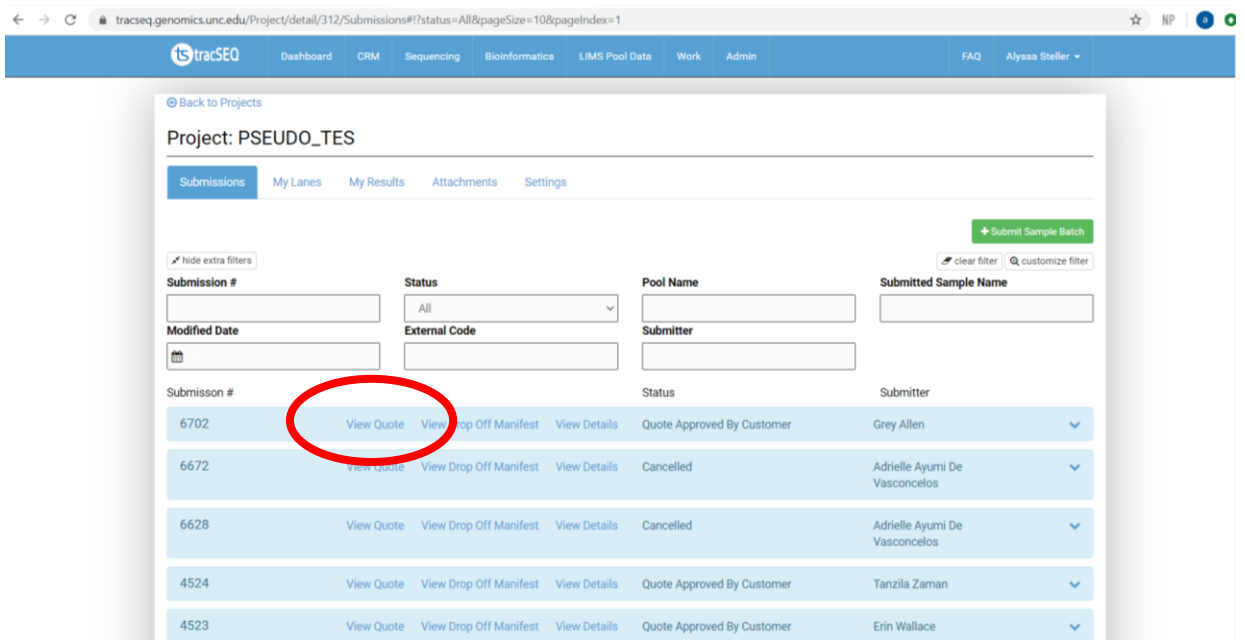
How to View Your Quote via TracSeq

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.



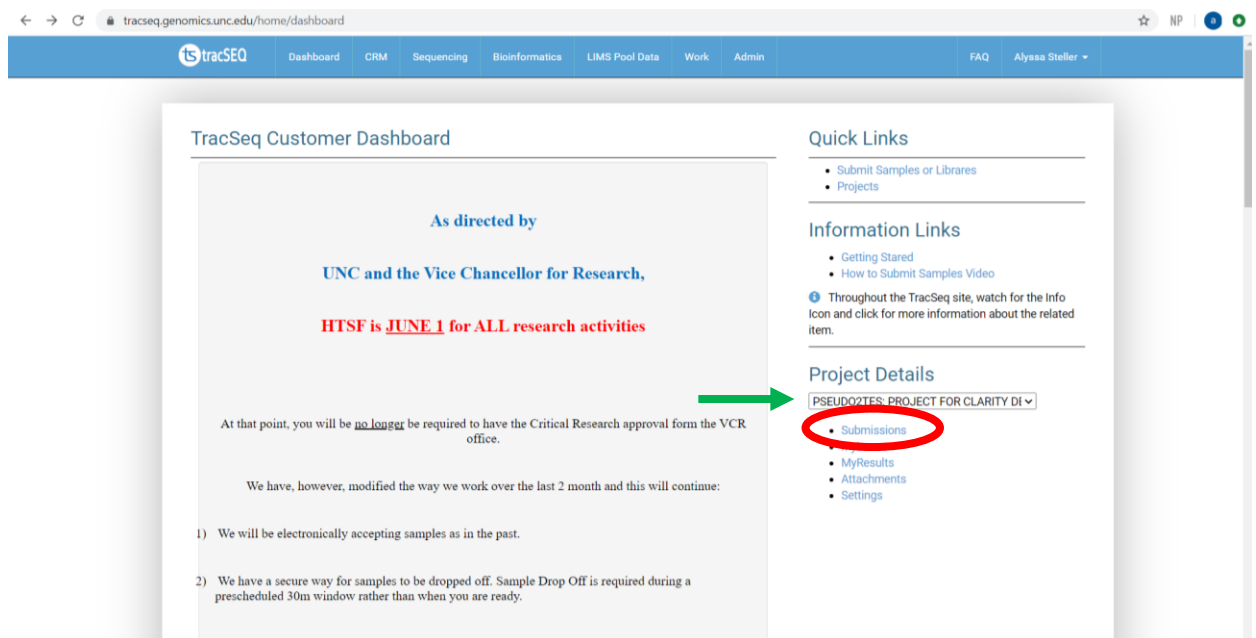
1. Ensure the correct project is chosen from the drop down menu, then click "Submissions"



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"

tracseq.genomics.unc.edu/Project/detail/312/Submissions#!?status=All&pageSize=10&pageIndex=1

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Back to Projects

Project: PSEUDO_TES

Submissions My Lanes My Results Attachments Settings

Submit Sample Batch

hide extra filters

Submission # Status Pool Name Submitted Sample Name

Modified Date External Code Submitter

Submission # Status Submitter

| | | | | | |
|------|------------|------------------------|--------------|----------------------------|-------------------------------|
| 6702 | View Quote | View Drop Off Manifest | View Details | Quote Approved By Customer | Grey Allen |
| 6672 | View Quote | View Drop Off Manifest | View Details | Cancelled | Adrielle Ayumi De Vasconcelos |
| 6628 | View Quote | View Drop Off Manifest | View Details | Cancelled | Adrielle Ayumi De Vasconcelos |
| 4524 | View Quote | View Drop Off Manifest | View Details | Quote Approved By Customer | Tanzila Zaman |
| 4523 | View Quote | View Drop Off Manifest | View Details | Quote Approved By Customer | Erin Wallace |

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

tracseq.genomics.unc.edu/SampleBatch/detail/6702

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Submission: 6702

View Drop Off Manifest View Quote

Processing Attachments

Name: PSEUDO_TES Batch 5/15/2020
Status: Quote Approved By Customer
Submitted Material: Samples
Source Material: Total RNA
Platform: mRNA Seq, stranded
LibraryType: mRNA Seq, stranded

PrepMethod: Kapa mRNA, Stranded
ReadType: Paired End
ReadLength: Custom
SampleSolution: dH2O
FundingAccount: test

Export Sample Manifest

Show 10 entries

Search:

| SampleID | External Code | Pool | Row # | Col # | Volume | Concentration | Avg Fragment Size | Lanes |
|-------------|---------------|------|-------|-------|--------|---------------|-------------------|-------|
| MySample001 | | A | 1 | 25 | 9999 | 300 | 2 | |
| MySample002 | | B | 1 | 25 | 9999 | 300 | 2 | |
| MySample003 | | C | 1 | 25 | 9999 | 300 | 2 | |
| MySample004 | | D | 1 | 25 | 9999 | 300 | 2 | |
| MySample005 | | E | 1 | 25 | 9999 | 300 | 2 | |
| MySample006 | | F | 1 | 25 | 9999 | 300 | 2 | |
| MySample007 | | G | 1 | 25 | 9999 | 300 | 2 | |

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

tracseq.genomics.unc.edu/SampleBatch/manifest/6702

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HTSF Sample Delivery Manifest

Print

Submission Batch Id: 6702
 Name: PSEUDO_TES Batch 5/15/2020
 Submitted By: Grey Allen
 Project Title: PSEUDO_TES: For testing and learning TracSeq
 Principal Investigator: Corbin Jones
 Expected DropOff Date: 5/15/2020

Submitted Material: Samples
 Source Material: Total RNA
 Library Type: mRNA Seq, stranded
 Prep Method: Kapa mRNA, Stranded
 Number of Samples: 9
 Number of Pools: 1
 Number of Lanes: 2

Platform: NovaSeq6000S4
 Read Type: Paired End
 Read Length: Custom
 Container Type: 96WELL_SHALLOW_PLATE
 Sample Solution: dh20

Comments:

Material Delivered

| Sample Name | Pool | Volume (ul) | Container | Row | Column | Received |
|-------------|------|-------------|-----------|-----|--------|--------------------------|
| MySample001 | | 25 | | A | 1 | <input type="checkbox"/> |
| MySample002 | | 25 | | B | 1 | <input type="checkbox"/> |
| MySample003 | | 25 | | C | 1 | <input type="checkbox"/> |
| MySample004 | | 25 | | D | 1 | <input type="checkbox"/> |

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

tracseq.genomics.unc.edu/samplebatch/printmanifest/6702

Sample Batch Manifest Report 1 / 1

HTSF Sample Delivery Manifest

Batch Manifest Ref #: 9426
 Project Code: PSEUDO_TES

TS Batch Id: 6702
 Submitted By: Grey Allen dgallen2@med.unc.edu
 Project Title: PSEUDO_TES: For testing and learning TracSeq
 Principal Investigator: cjjones@email.unc.edu Corbin Jones
 Expected DropOff Date: 5/15/2020

Submitted Material: Samples
 Source Material: Total RNA
 Library Type: mRNA Seq, stranded
 Prep Method: Kapa mRNA, Stranded
 Cust Seq Primer: False
 Number of Samples: 9
 Container Type: 96WELL_SHALLOW_PLATE
 Sample Solution: dh20

Platform: NOVAseq-S4
 Read Type: Paired End
 Read Length: Custom
 Cust Seq Primer Name:
 Number of Pools: 1
 Number of Lanes: 2

| Sample Name | External Code | Pool | Volume (ul) | Container | Row | Column |
|-------------|---------------|------|-------------|-----------|-----|--------|
| MySample001 | | | 25 | | A | 1 |
| MySample002 | | | 25 | | B | 1 |
| MySample003 | | | 25 | | C | 1 |
| MySample004 | | | 25 | | D | 1 |
| MySample005 | | | 25 | | E | 1 |
| MySample006 | | | 25 | | F | 1 |
| MySample007 | | | 25 | | G | 1 |
| MySample008 | | | 25 | | H | 1 |
| MySample009 | | | 25 | | A | 2 |

Material can be delivered to:
 HTSF Lab, Genome Sciences Building
 Rooms 1151 (Office), 1153 (Lab)
 Open Monday - Friday 10:00 AM - 4:00 PM

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

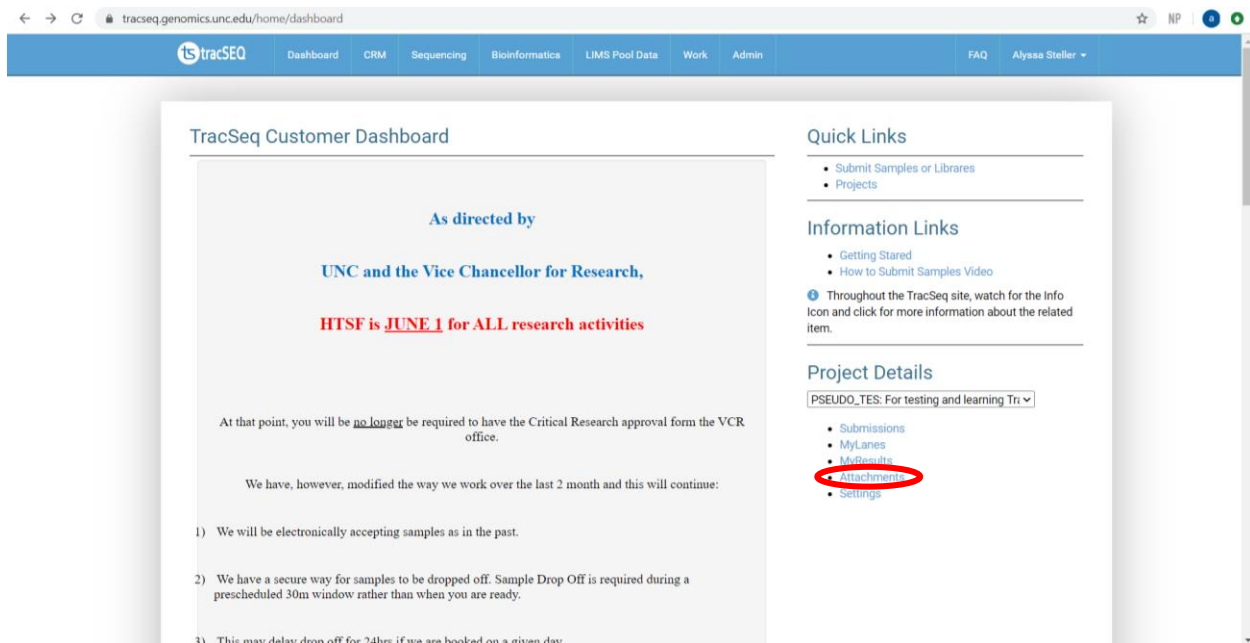
QAQC Results and Interpretation

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."

tracseq

Dashboard CRM Sequencing Bioinformatics LIMS Pool Data Work Admin

FAQ Alyssa Steller

Project: PSEUDO_TES

Submissions My Lanes My Results **Attachments** Settings

| Filename | Tags | Upload Date | Uploaded By |
|---|---------|-------------|---------------------------------------|
| Project Attachments | | | |
| <input type="button" value="Choose File"/> No file chosen | | | <input type="button" value="Upload"/> |
| SB-6702 | Details | | |
| SB-4524 | Details | | |
| SB-4523 | Details | | |
| SB-3319 | Details | | |
| SB-3318 | Details | | |
| SB-3310 | Details | | |
| SB-3309 | Details | | |
| SB-3308 | Details | | |
| SB-3139 | Details | | |

10

1 2 3 ...

Records: 28

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.

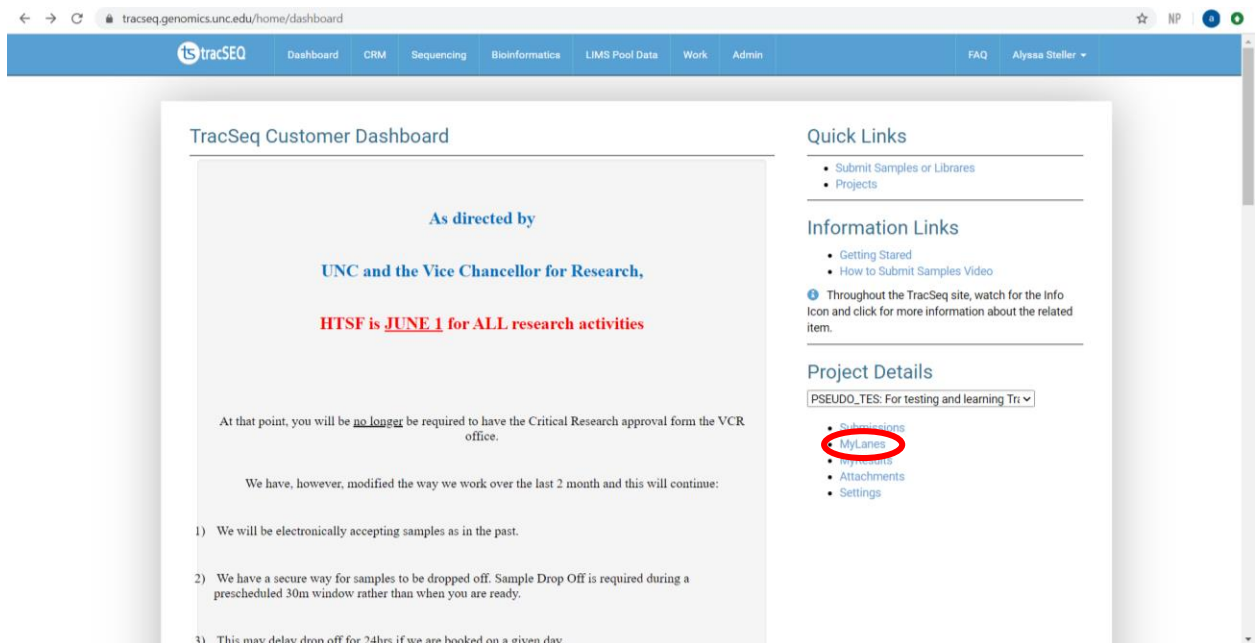
Interpreting QAQC Results

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.

| Run ID | PoolName | Total Reads | Lane % Undetermined | Lane Avg >= Q30 | Run Date |
|-------------------------------------|--------------------------------------|-------------|---------------------|-----------------|----------|
| 200401_UNC17-D00216_0651_ACE3GLANXX | PL_6647_01_REPOOL_RESEQ_BC_SUB_ERROR | 252915471 | 1.14 | 95.3 | 4/1/20 |
| 200401_UNC17-D00216_0651_ACE3GLANXX | PL_6647_02_REPOOL_RESEQ_BC_SUB_ERROR | 259539196 | 0.93 | 95.7 | 4/1/20 |
| 200401_UNC17-D00216_0651_ACE3GLANXX | PL_6647_03_REPOOL_RESEQ_BC_SUB_ERROR | 289765598 | 1.02 | 94.07 | 4/1/20 |

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.

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Submissions **My Lanes** My Results Attachments Settings

Export to Excel clear filter customize filter

Run ID Pool Name Run Date Range

| Run ID | PoolName | Total Reads | Lane % Undetermined | Lane Avg >= Q30 | Run Date | Details |
|-------------------------------------|--------------------------------------|-------------|---------------------|-----------------|----------|---------|
| 200401_UNC17-D00216_0651_ACE3GLANXX | PL_6647_01_REPOOL_RESEQ_BC_SUB_ERROR | 252915471 | 1.14 | 95.3 | 4/1/20 | Details |
| 200401_UNC17-D00216_0651_ACE3GLANXX | PL_6647_02_REPOOL_RESEQ_BC_SUB_ERROR | 259539196 | 0.93 | 95.7 | 4/1/20 | Details |
| 200401_UNC17-D00216_0651_ACE3GLANXX | PL_6647_03_REPOOL_RESEQ_BC_SUB_ERROR | 289765598 | 1.02 | 94.07 | 4/1/20 | Details |

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.

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PROJECT DETAILS SETTINGS **MY LANES** ATTACHMENTS

FCD ID Lane # Pool LIMS ID Pool Name

FCD-6766 8 [Redacted] Back

Total Reads: 385,029,068
Demultiplexed Reads: 385,029,068
Lane% Undetermined: 0.00
Lane Max >= Q30: 96.76
Lane Avg >= Q30: 95.38
Lane Min >= Q30: 89.69
Data Path: [Redacted]
Data Delivery Comments:

Project [Redacted]
Pool Name [Redacted]
Pooled Date: 1/3/2020
Pooling By: HTSF
Library Prep By: HTSF
Concentration: 6.74

Cluster Density: [Redacted]
% PhiX: 1
Load Concentration: 0
Avg Size: 289
Molarity: 35.3

| Sample ID | Index | Control | Yield (Mbases) | % PF | # Reads | % of Raw Clusters per Lane | % Perfect Index | % One Mismatch Reads (Index) | % of >= Q30 Bases (PF) | Mean Quality Score (PF) |
|--------------------------------|-------------------|---------|----------------|----------|---------|----------------------------|-----------------|------------------------------|------------------------|-------------------------|
| RPECYCE20_1_CAAGCTAG-ACATAGCG | CAAGCTAG+CGCTATGT | 9531 | 100.00 | 63538986 | 16.50 | 96.61 | 3.39 | 96.19 | 39.38 | |
| RPECYCE20_2_GGACTTGG-CGACAGCG | GGACTTGG+CGTCTGCG | 7608 | 100.00 | 50719472 | 13.17 | 97.46 | 2.54 | 96.60 | 39.49 | |
| RPECYCED24_1_AAGTCCAA-TATGAGTA | AAGTCCAA+TACTCATA | 8576 | 100.00 | 57173825 | 14.85 | 97.12 | 2.88 | 96.76 | 39.54 | |
| RPECYCED24_2_ATCCACTG-AGGTGCGT | ATCCACTG+ACGCACCT | 10046 | 100.00 | 66973377 | 17.39 | 97.17 | 2.83 | 96.48 | 39.46 | |
| RPECYCED44_GCTTGTCA-GAACATAC | GCTTGTCA+GTATGTTC | 8450 | 100.00 | 56334148 | 14.63 | 97.05 | 2.95 | 96.52 | 39.47 | |
| Undetermined | unknown | 1438 | 8.91 | 9586502 | 2.49 | 100.00 | 0.00 | 89.69 | 37.61 | |
| RPECYCE_CCGCGGTT+AGCGCTAG | CCGCGGTT+CTAGCGCT | 12105 | 100.00 | 80702758 | 20.96 | 96.51 | 3.49 | 95.45 | 39.16 | |

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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.

PROJECT DETAILS SETTINGS MY LANES ATTACHMENTS

FCD ID: FCD-6766 Lane #: 8 Pool LIMS ID: Pool Name: [Back](#)

Total Reads: 385,029,068
Demultiplexed Reads: 385,029,068
 Lane% Undetermined: 0.00
 Lane Max >= Q30: 96.76
 Lane Avg >= Q30: 95.38
 Lane Min >= Q30: 89.69

Project: Pool Name: Pooled Date: 1/3/2020
 Pooling By: HTSF Library Prep By: HTSF Concentration: 6.74

Cluster Density: % PhiX: 1
 Load Concentration: 0
 Avg Size: 289
 Molarity: 35.3

Data Path: Data Delivery Comments:

| Sample ID | Index | Control | Yield (Mbases) | % PF | # Reads | % of Raw Clusters per Lane | % Perfect Index Reads | % One Mismatch Reads (Index) | % of >= Q30 Bases (PF) | Mean Quality Score (PF) |
|--------------------------------|--------------------|---------|----------------|----------|---------|----------------------------|-----------------------|------------------------------|------------------------|-------------------------|
| RPECYCE20_1_CAAAGCTAG-ACATAGCG | CAAGCTAG+CGCTATGT | 9531 | 100.00 | 63538986 | 16.50 | 96.61 | 3.39 | 96.19 | 39.38 | |
| RPECYCE20_2_GGACTTGG-CGCAGACG | GGACTTGG+CGTCTGCG | 7608 | 100.00 | 50719472 | 13.17 | 97.46 | 2.54 | 96.60 | 39.49 | |
| RPECYCED24_1_AAGTCCAA-TATGAGTA | AAGTCCAA+TACTCATA | 8576 | 100.00 | 57173825 | 14.85 | 97.12 | 2.88 | 96.76 | 39.54 | |
| RPECYCED24_2_ATCCACTG-AGGTGCGT | ATCCACTG+ACGCACCT | 10046 | 100.00 | 66973377 | 17.39 | 97.17 | 2.83 | 96.48 | 39.46 | |
| RPECYCED44_GCTTGTCGA-GAACATAC | GCTTGTCGA+GTATGTTC | 8450 | 100.00 | 56334148 | 14.63 | 97.05 | 2.95 | 96.52 | 39.47 | |
| Undetermined | unknown | 1438 | 8.91 | 9586502 | 2.49 | 100.00 | 0.00 | 89.69 | 37.61 | |
| RPECYCE_CCGCGGTT-AGCGCTAG | CCGCGGTT+CTAGCGCT | 12105 | 100.00 | 80702758 | 20.96 | 96.51 | 3.49 | 95.45 | 39.16 | |

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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.

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PROJECT DETAILS SETTINGS MY LANES ATTACHMENTS

FCD ID Lane # Pool LIMS ID Pool Name

FCD-6766 8 [Redacted] [Back](#)

Total Reads: 385,029,068
 Demultiplexed Reads: 385,029,068
 Lane% Undetermined: 0.00
 Lane Max >= Q30: 96.76
 Lane Avg >= Q30: 95.38
 Lane Min >= Q30: 89.69
 Data Path: [Redacted]
 Data Delivery Comments:

Project [Redacted]
 Pool Name [Redacted]
 Pooled Date: 1/3/2020
 Pooling By: HTSF
 Library Prep By: HTSF
 Concentration: 6.74

Cluster Density:
 % PhiX: 1
 Load Concentration: 0
 Avg Size: 289
 Molarity: 35.3

| Sample ID | Index | Control | Yield (Mbases) | % PF | # Reads | % of Raw Clusters per Lane | % Perfect Index Reads | % One Mismatch Reads (Index) | % of >= Q30 Bases (PF) | Mean Quality Score (PF) |
|--------------------------------|-------------------|---------|----------------|----------|---------|----------------------------|-----------------------|------------------------------|------------------------|-------------------------|
| RPECYCE20_1_CAAGCTAG-ACATAGCG | CAAGCTAG+CGCTATGT | 9531 | 100.00 | 63538986 | 16.50 | 96.61 | 3.39 | 96.19 | 39.38 | |
| RPECYCE20_2_GGACTTGG-CGCAGACG | GGACTTGG+CGTCTGCG | 7608 | 100.00 | 50719472 | 13.17 | 97.46 | 2.54 | 96.60 | 39.49 | |
| RPECYCED24_1_AAGTCCAA-TATGAGTA | AAGTCCAA+TACTCATA | 8576 | 100.00 | 57173825 | 14.85 | 97.12 | 2.88 | 96.76 | 39.54 | |
| RPECYCED24_2_ATCCACTG-AGGTGCGT | ATCCACTG+ACGCACCT | 10046 | 100.00 | 66973377 | 17.39 | 97.17 | 2.83 | 96.48 | 39.46 | |
| RPECYCED44_GCTTGTCA-GAACATAC | GCTTGTCA+GTATGTTC | 8450 | 100.00 | 56334148 | 14.63 | 97.05 | 2.95 | 96.52 | 39.47 | |
| Undetermined | unknown | 1438 | 8.91 | 9586502 | 2.49 | 100.00 | 0.00 | 89.69 | 37.61 | |
| RPECYCE_CCGCGGTT-AGCGCTAG | CCGCGGTT+CTAGCGCT | 12105 | 100.00 | 80702758 | 20.96 | 96.51 | 3.49 | 95.45 | 39.16 | |

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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 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**BHH5TMBBXY
 - 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

Dashboard
CRM
Sequencing
Bioinformatics
LIMS Pool Data
Work
Admin
FAQ
Katherine Stoller

PROJECT DETAILS
SETTINGS
MY LANES
ATTACHMENTS

FCD ID
Lane #
Pool LIMS ID
Pool Name

FCD-6766
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Total Reads: **385,029,068**
Demultiplexed Reads: **385,029,068**
Lane% Undetermined: **0.00**
Lane Max >= Q30: **96.76**
Lane Avg >= Q30: **95.38**
Lane Min >= Q30: **89.69**

Project
Pool Name
Pooled Date: **1/3/2020**
Pooling By: **HTSF**
Library Prep By: **HTSF**
Concentration: **6.74**

Cluster Density:
% PhiX: **1**
Load Concentration: **0**
Avg Size: **289**
Molarity: **35.3**

Data Path:
Data Delivery Comments:

| Sample ID | Index | Control | Yield (Mbases) | % PF | # Reads | % of Raw Clusters per Lane | % Perfect Index Reads | % One Mismatch Reads (Index) | % of >= Q30 Bases (PF) | Mean Quality Score (PF) |
|--------------------------------|-------------------|---------|----------------|----------|---------|----------------------------|-----------------------|------------------------------|------------------------|-------------------------|
| RPECYCE20_1_CAAGCTAG-ACATAGCG | CAAGCTAG+CGCTATGT | 9531 | 100.00 | 63538986 | 16.50 | 96.61 | 3.39 | 96.19 | 39.38 | |
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| RPECYCED24_2_ATCCACTG-AGGTGCGT | ATCCACTG+ACGCACCT | 10046 | 100.00 | 66973377 | 17.39 | 97.17 | 2.83 | 96.48 | 39.46 | |
| RPECYCED44_GCTTGTCA-GAACATAC | GCTTGTCA+GTATGTTC | 8450 | 100.00 | 56334148 | 14.63 | 97.05 | 2.95 | 96.52 | 39.47 | |
| Undetermined | unknown | 1438 | 8.91 | 9586502 | 2.49 | 100.00 | 0.00 | 89.69 | 37.61 | |
| RPECYCE_CCGCGGTT-AGCGCTAG | CCGCGGTT+CTAGCGCT | 12105 | 100.00 | 80702758 | 20.96 | 96.51 | 3.49 | 95.45 | 39.16 | |

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