

Downloading your sequencing Data from Illumina BaseSpace

Once your sequencing run is complete you will receive an invitation for ownership transfer of your run and/or project to your BaseSpace (BS) account. After accepting the transfer, the data will be available exclusively to you and will be removed from the TGC account. Please make sure to download and back up your data! It is possible to share your BS run/project with another BS collaborator or with a non-BS collaborator.

To better understand the technical aspects of your run, please visit [*Illumina Software Resources/BaseSpace™ Sequence Hub: does my sequencing run look good.*](#)

For general help with Illumina BaseSpace please visit- <https://help.basespace.illumina.com/>

Outline

1. [Open a BaseSpace account](#)
2. [Run and data statistics](#)
3. [Data download \(fastq\)](#)
4. [Run Download](#)
5. [Share Your Project with Another BS Account](#)
6. [Share Your Project with a Non-BS User](#)

Creating a BaseSpace Account (free)

To create an Illumina BaseSpace account visit the Illumina [BaseSpace login](#) page.

Please fill out your email address associated with your BS account in the appropriate place in the Sample Submission Form.

Run and Data Statistics

- (1) **To view your run and data statistics, go to your Project, and on the Summary page, click on the Analysis.**

SUMMARY BIOSAMPLES SAMPLES FASTQS OTHER DATASETS

Owner: Liat Linde | Size: 30 GB | Last Updated: 2024-05-20 08:59 | Collaborators

Analyses

STATUS	ANALYSIS NAME	APPLICATION	SIZE	LAST MODIFIED	COMMENTS
Complete	BCLConvert 05/20/2024 04:5...	ICA Workflow Sessi...	36 GB	2024-05-20 08:39	

(2) The BCL Convert Reports consists of three reports: Demultiplexing Report, Top Unknown Barcodes, and Index Hopping Counts.

The **"Demultiplexing Report"** provides details on the number of reads assigned to each sample.

The **"Top Unknown Barcodes"** report in Illumina sequencers provides information on barcodes that were observed during sequencing but could not be matched to any known barcode sequences. This report is useful when looking for samples that do not appear in your Demultiplexing Report due to barcode mistakes.

The **"Index Hopping Counts"** measure how often DNA from one sample is mistakenly assigned to the barcode of another sample during multiplexed sequencing.

Analysis: BCLConvert 05/20/2024 04:57:12Z
Project ICA Workflows 2024/05

SUMMARY REPORTS INPUTS FILES

BCL Convert Logs
BCL Convert Reports Report
BL Metrics
Extra Files (BclConver...
PD Metrics

illumina DRAGEN Reports

Demultiplex Report

Run name: run_280934720 | Created on: 2024-05-20 05:30






Demultiplex Stats | Top Unknown Barcodes | Index Hopping Counts

Demultiplex Stats

Lane	Sample ID	Index	Reads	Matching	One Mismatch	Two Mismatches	%
1	BL	ACCAGACAAC-	220,024,738	216,577,83	3,446,905	0	
		CCTAGTTCCT		3			

(3) On the left side menu, a metrics report of each sample is available.

SUMMARY **REPORTS** INPUTS FILES

BCL Convert Logs

BCL Convert Reports

Report

BL

Metrics

Extra Files (BclConver...

PD

Metrics

Metrics: BL

QC Status: Undefined

METRIC NAME	RESULTS	THRESHOLDS	STATUS
Is Paired End	true		
Read 1 Cycles	28		
Read 2 Cycles	90		
Total Clusters PF	220,024,738		

Data Demultiplexing

In the case there is a problem with data distribution across samples, it is possible to perform the data demultiplexing procedure manually on Basespace using the **Reque** option.

When there is a problem with data demultiplexing due to error in the barcode sequence in the sample sheet

Data Download

- (1) On the HOME page, you will see a notification of two transfer invites. To transfer your sequencing project to your account, accept both invitations.

Hello TGC

This item requires your attention

Transfer Invite

2021-09-02 10:31

from Tal Katz Ezov

DECLINE

ACCEPT

- (2) Go to PROJECTS and open/choose the desired project.

 HOME RUNS **PROJECTS** ANALYSES BIOSAMPLES APPS DEMO DATA

- (3) Choose your analysis.

SUMMARY BIOSAMPLES SAMPLES FASTQS OTHER DATASETS

Owner: Liat Linde | Size: 30 GB | Last Updated: 2024-05-20 08:59 | Collaborators:

Analyses 1 - 1 of 1 Show 25

STATUS	ANALYSIS NAME	APPLICATION	SIZE	LAST MODIFIED	COMMENTS
Complete	BCLConvert 05/20/2024 04:5...	ICA Workflow Sessi...	36 GB	2024-05-20 08:39	

(4) Open the File menu by hovering over the page icon and then hover over 'Download', and click on 'Analysis'.

Analysis: BCLConvert 05/20/2024 04:57:12Z
Project ICA Workflows 2024/05

SUMMARY **REPORTS** INPUTS FILES

File

- New
- Edit
- Copy
- Download
- Upload

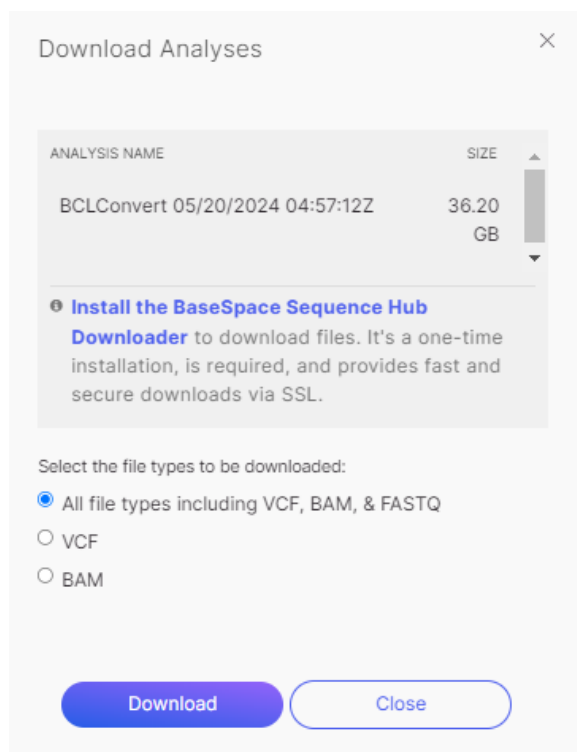
DRAGEN Reports

Demultiplex Report

Created on 2024-05-20 05:30

(5) Select 'All file types' and 'Download'.

If this is your first time downloading data from Illumina BS you will be prompted to download Basespace Sequence Hub Downloader.



(6) Choose where you want to save your files and press 'start downloading'.

(7) After the downloading has finished, you will have two folders in your run folder. One with your sequencing data (FASTQ) files and one with your projects' statistics files.

Run Download

Your RUN contains the following data:

- Raw sequencing imaging (Base Call or BCL) files
- Sequencing data (FASTQ) files
- Metrics input files (SAV) to view using the [Illumina Sequencing Analysis Viewer](#).

Using Windows BS downloader, it is possible to download only the metric (SAV) and data (FASTQ) files. Downloading the BCL files is only possible using the [BaseSpace CLI \(Command Line Interface\)](#). Please note that for most projects and applications, it is not necessary to download the BCL files. For publications, FASTQ is considered 'raw data'.

To download your SAV or FASTQ files use the following steps:

(1) In the HOME page, you will see a notification of a Transfer Invite. To transfer your sequencing run to your account, accept the invitation.

Hello TGC

This item requires your attention

Transfer Invite

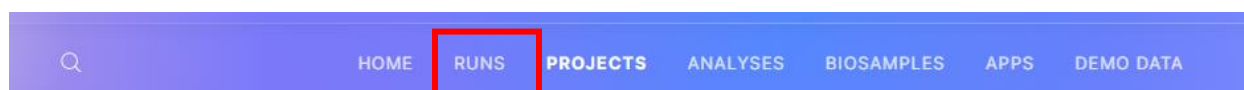
2021-09-02 10:31

from Tal Katz Ezov

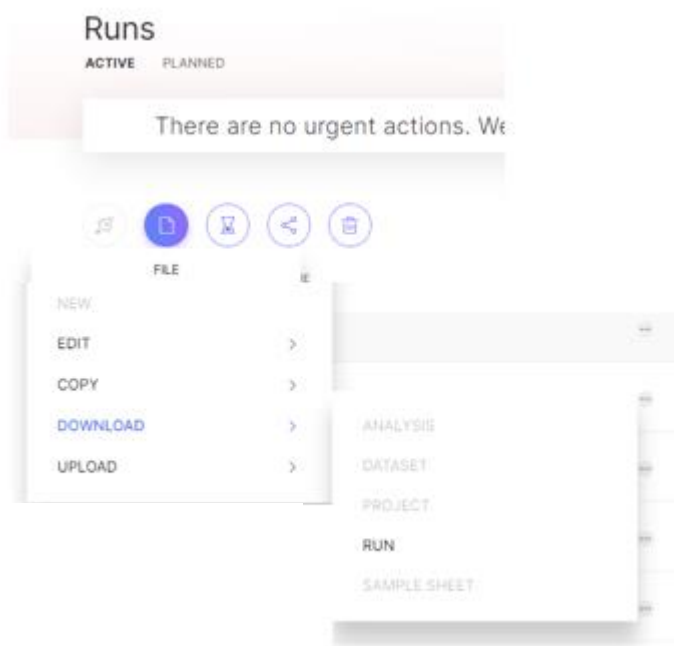
DECLINE

ACCEPT

(2) Go to RUNS and open/choose the desired run.



(3) Select File, point to Download, and then select Run.



(4) Select the file type you want to download.

Download Run
×

Run Name	Size
	697.13 MB

BaseSpace Sequence Hub Downloader must be installed. It's a one-time installation and provides fast and secure downloads via SSL.

[INSTALL DOWNLOADER](#)

Select the file types to be downloaded:

☐ FASTQ
☒ SAV

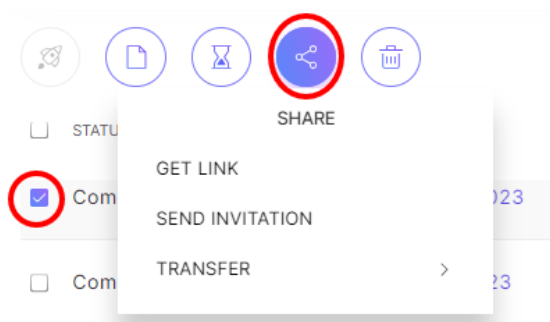
ⓘ No analysis files are available for this run

CLOSE
DOWNLOAD

If you do not have the FASTQ option available, see [Data Download](#).

Share Your Project with Another BS Account

(1) Check the box of the project you want to share and then, using the 'Share' button, send a sharing invitation to your collaborator (Send Invitation).



(2) Fill in your collaborator Basespace user account email and then press the 'Add Collaborator' button.

Share this runs

231026_VH00495_255_AACW3V2M5

Invite a collaborator
Email address

Optional Message
Add a personal message (optional)

Remaining characters : 140/140

☒ Share the associated Project(s) as well (**Recommended**)
Unchecking this box will limit what the recipient will have access to.

ADD COLLABORATOR

CANCEL SAVE SETTINGS

(3) Save the settings.

Share this runs

230711_VH00495_227_AAC37NGHV

Invite a collaborator
Email address

Optional Message
Add a personal message (optional)

Remaining characters : 140/140

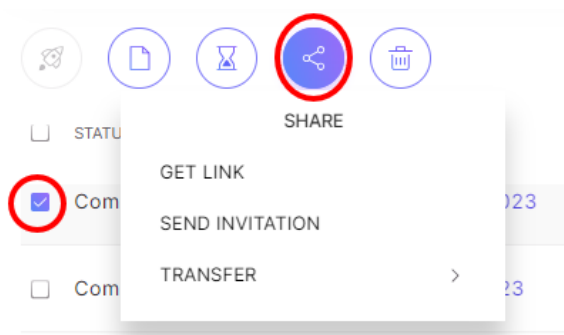
☒ Share the associated Project(s) as well (**Recommended**)
Unchecking this box will limit what the recipient will have access to.

ADD COLLABORATOR

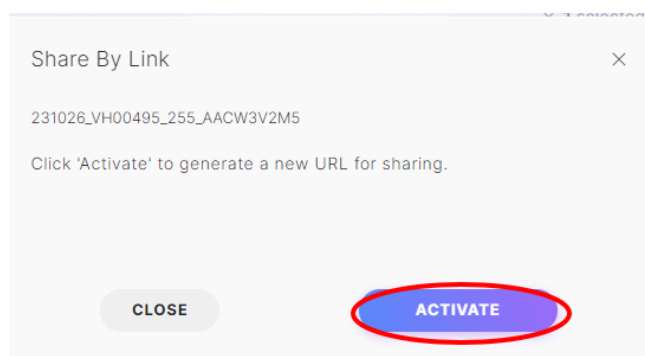
CANCEL SAVE SETTINGS

Share Your Project with a Non-BS User

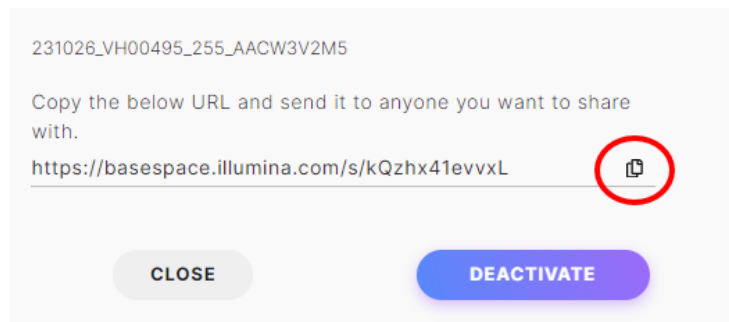
(4) Check the box of the project you want to share and then, using the 'Share' button, create a link (Get Link).



(5) Activate the link.



(6) Copy the link.



If you encounter problems, contact the [TGC team](#).