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 BaseSapce (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

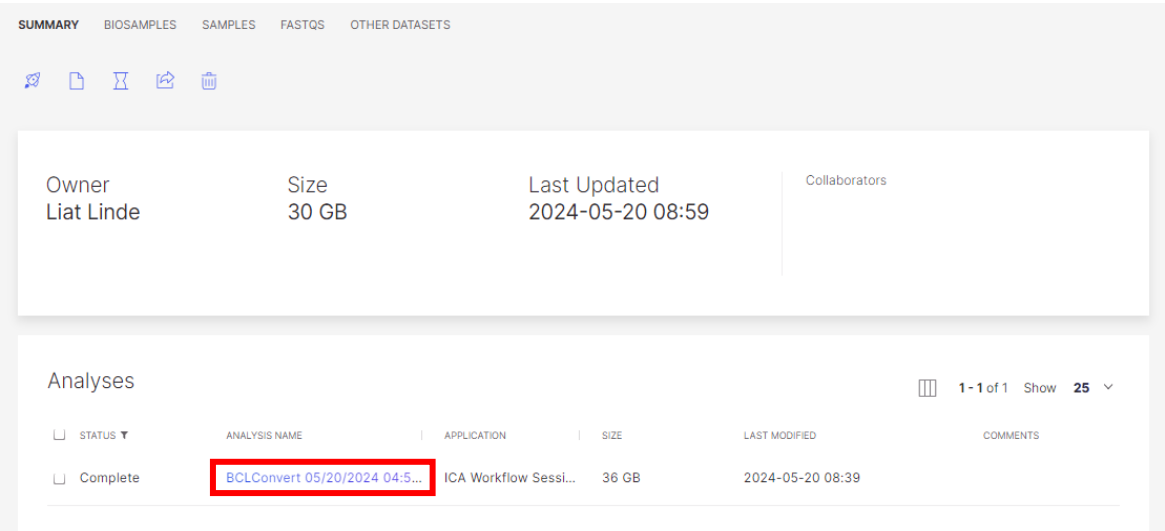
Creating a Basespace Account (free)

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.

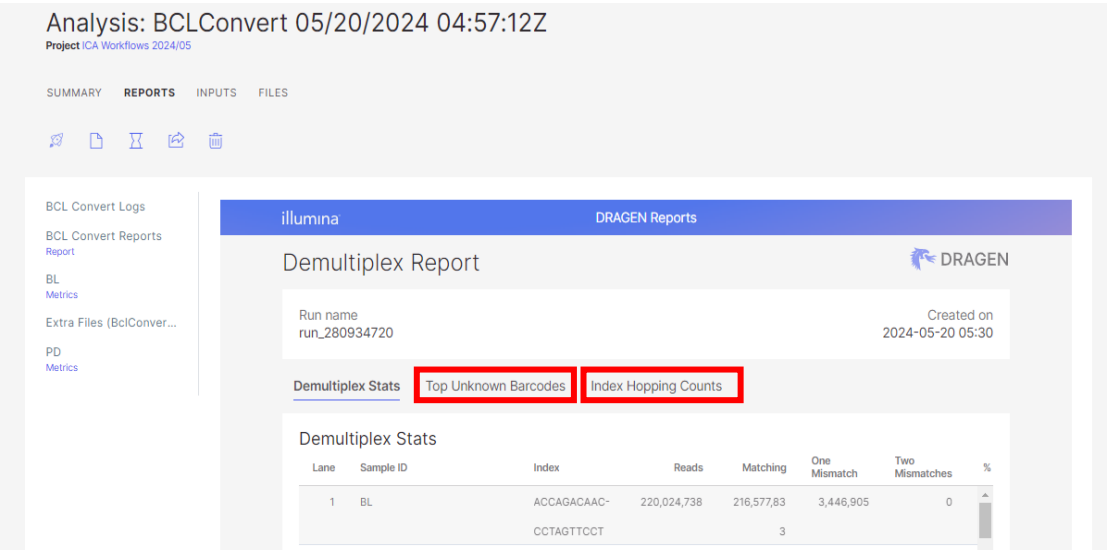


(2) The BCL Convert Reports consists of three reports: Demultiplexing Report, Top Unknown Barcodes, and Index Hopping Counts.

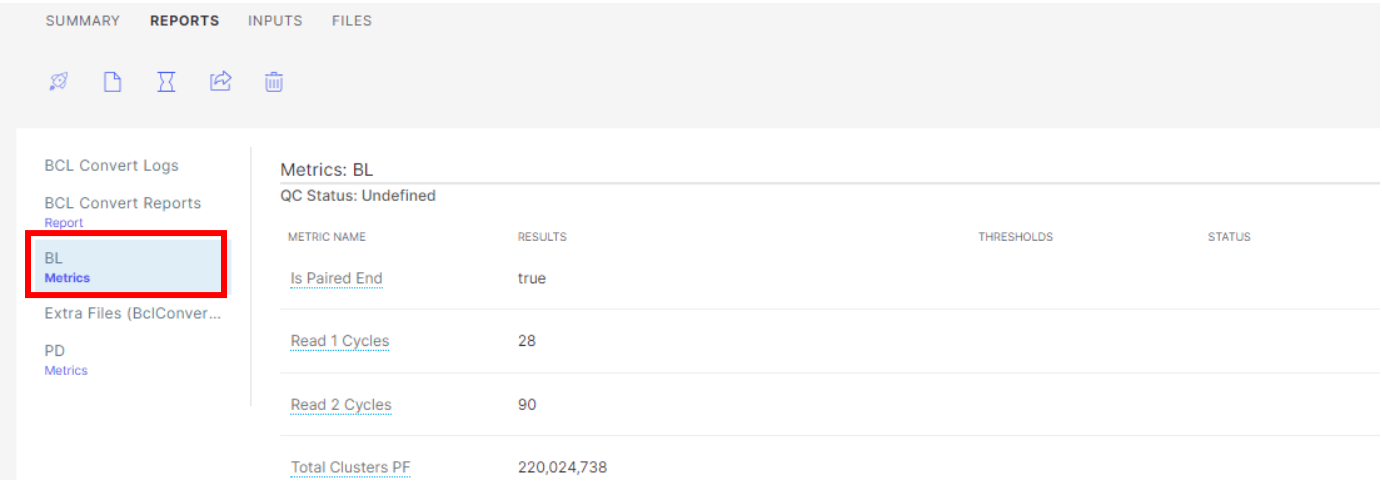
The **“Demultiplexing Report”** provides details on the number of reads assigned to each sample**.**

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.



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



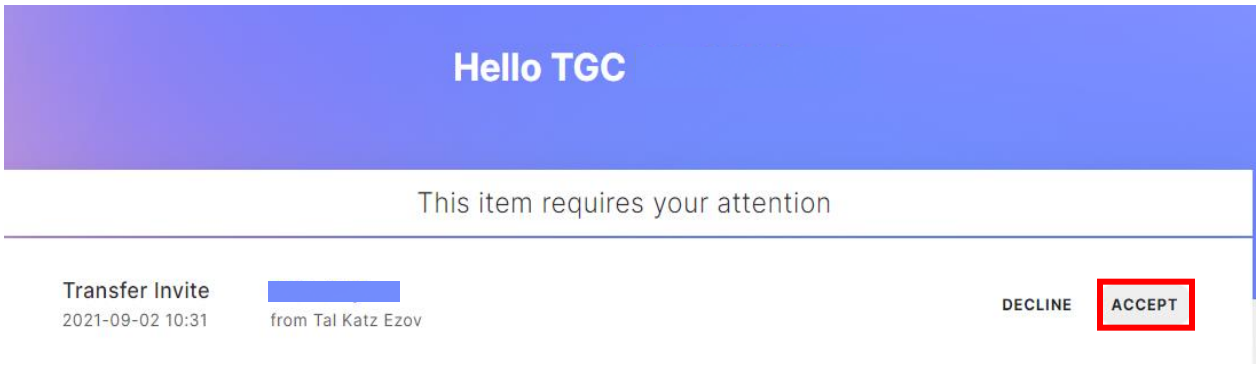
Data Demultiplexing

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

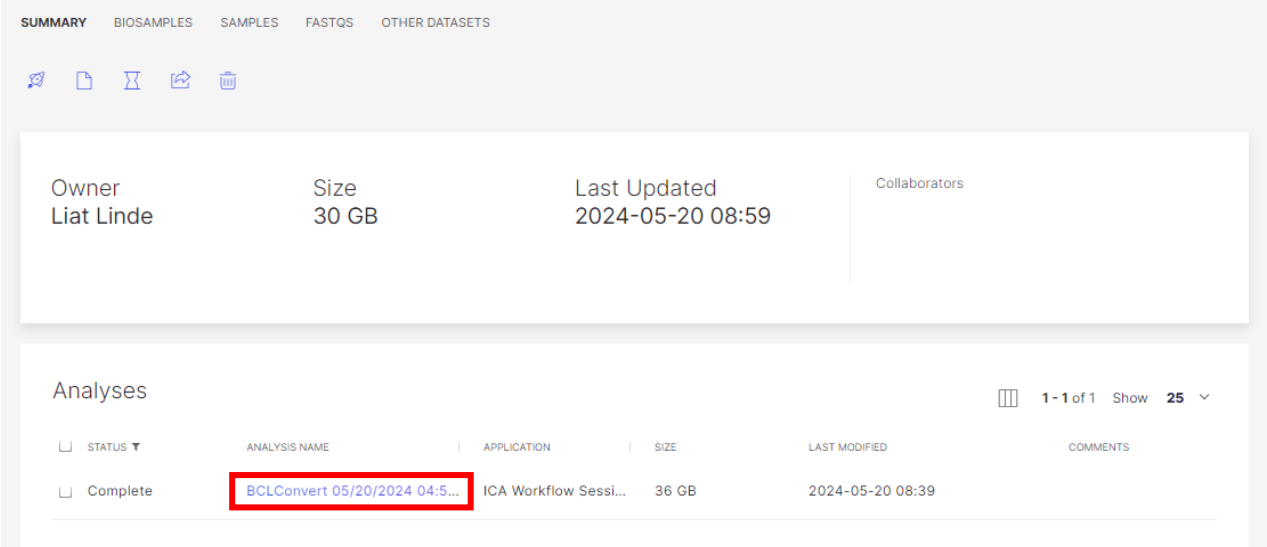
Data Download

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

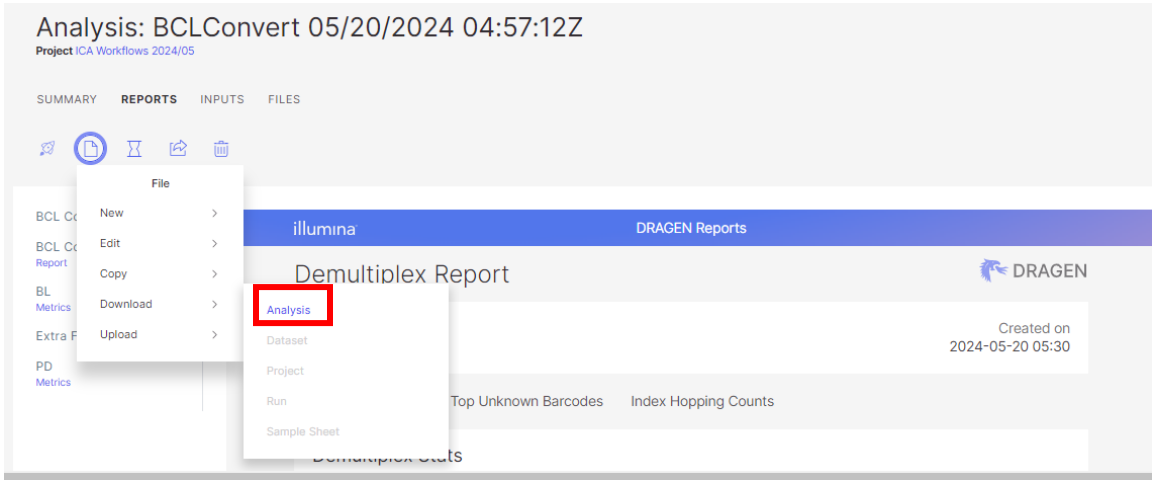


(2) Go to PROJECTS and open/choose the desired project.

(3) Choose your analysis.

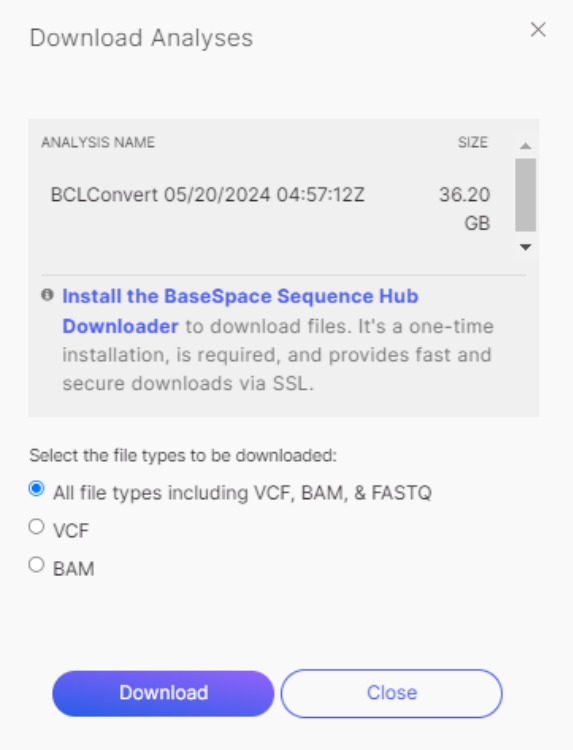


(4) Open the File menu by hovering over the page icon and then hover over 'Download', and click on 'Analysis'.



(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

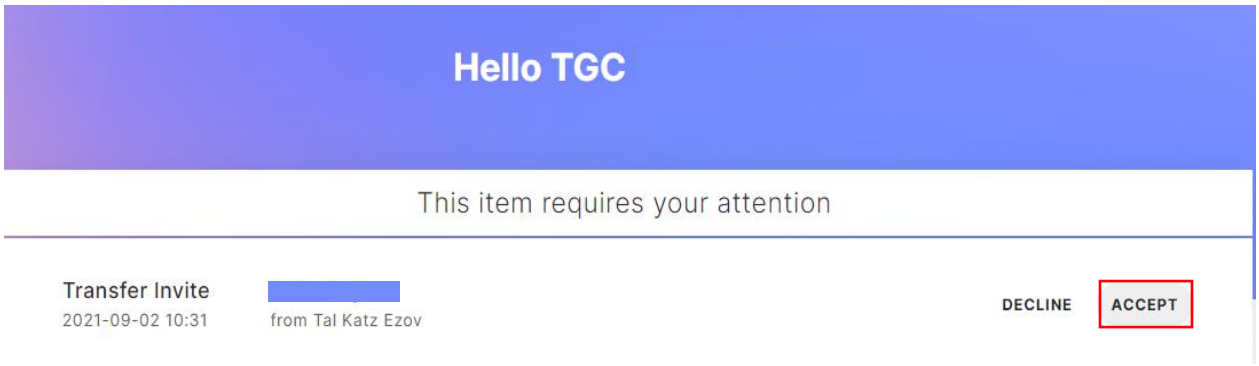
Your RUN contains the following data:

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

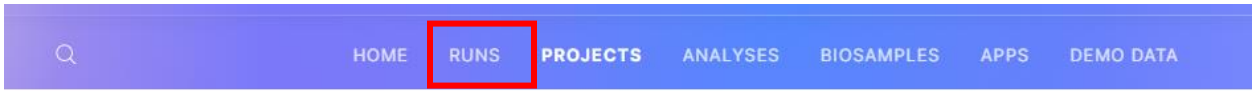
Using Windows BS downloader, it is possible to download only the metric (SAV) and data (FASTQ) files. Downloading the BCL files is only possible using the BaseSpace CLI (Command Line Interface). Please note that for most projects and applications, it is not necessary to download the BCL files. For publications,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

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

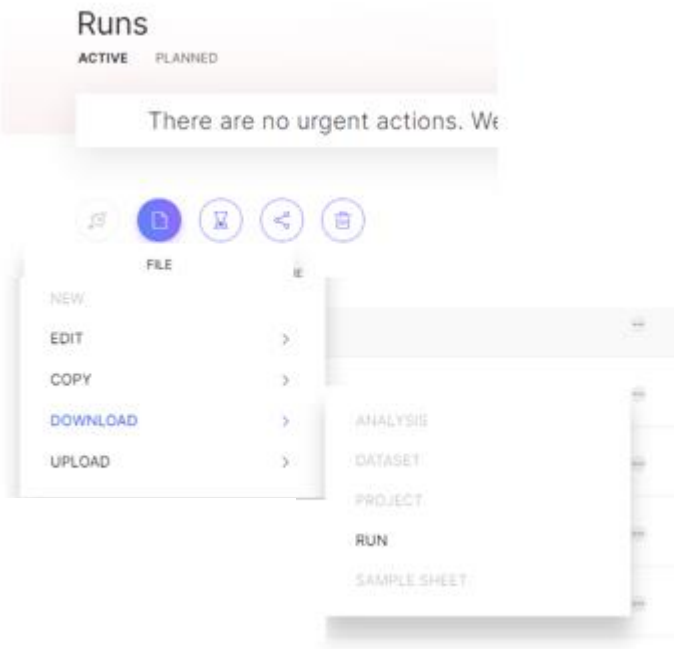
(1) In the HOME page, you will see a notification of a Transfer Invite. To transfer your sequencing run to your account, accept the invitation.



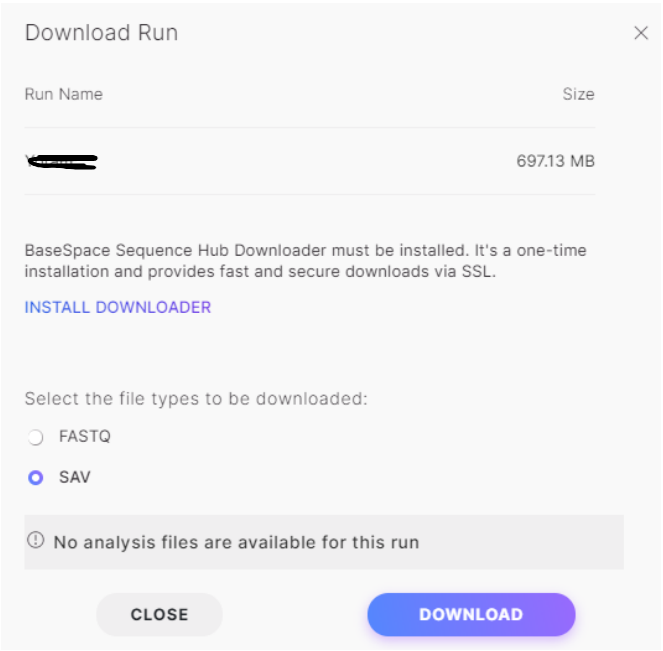
(2) Go to RUNS and open/choose the desired run.



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



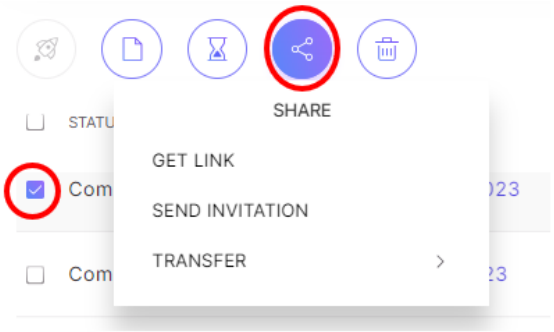
(4) Select the file type you want to download.



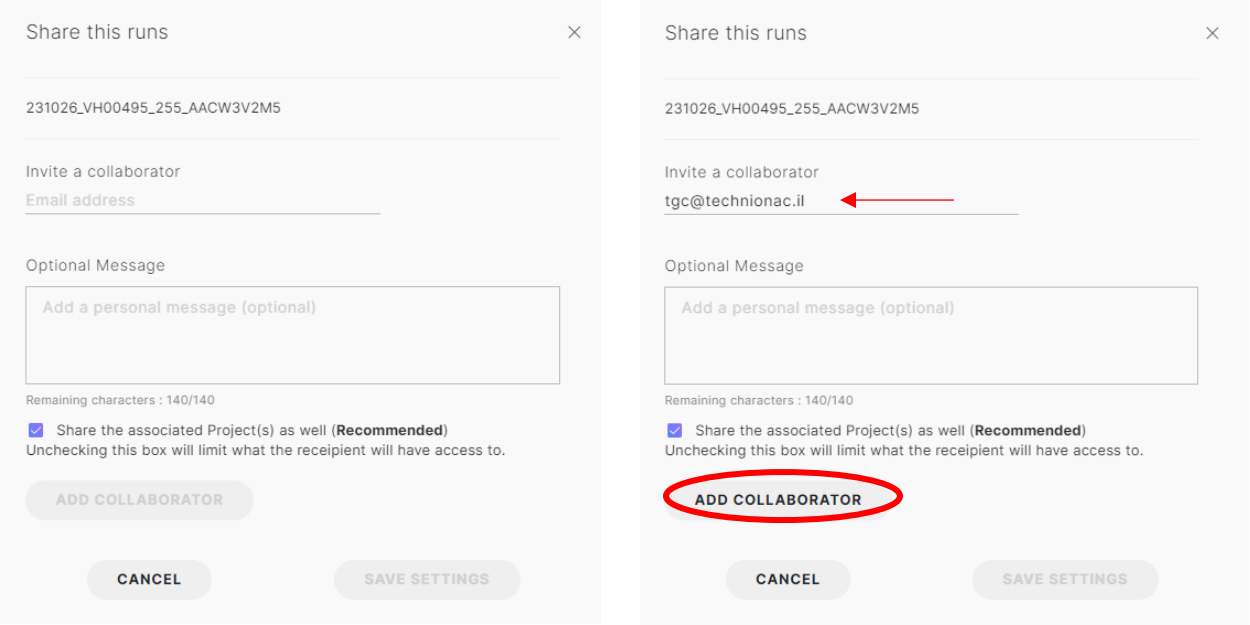
If you do not have the FASTQ option available, see [Data Download].

Share Your Project with Another BS Account

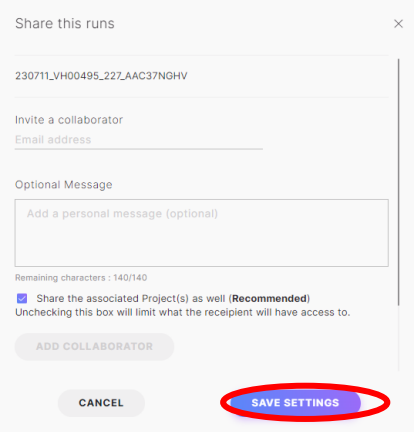
(1) Check the box of the project you want to share and then, using the 'Share' button, send a sharing invitation to your collaborator (Send Invitation).



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

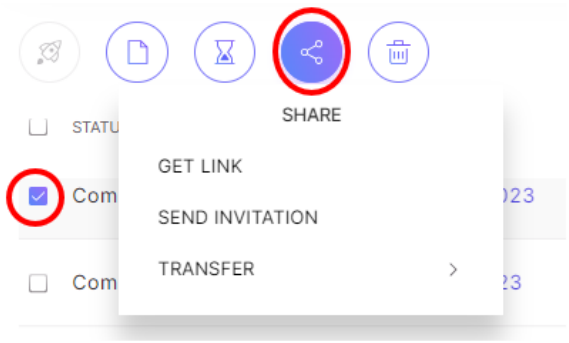


(3) Save the settings.

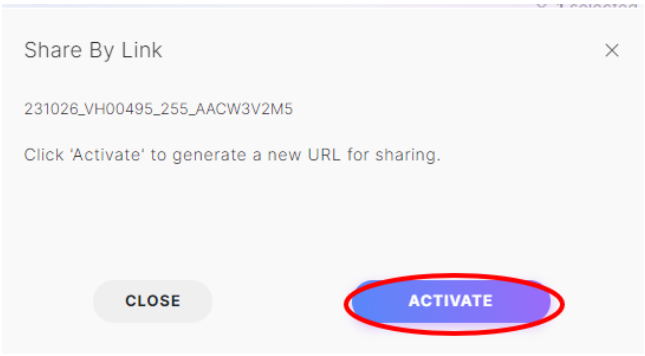


Share Your Project with a Non-BS User

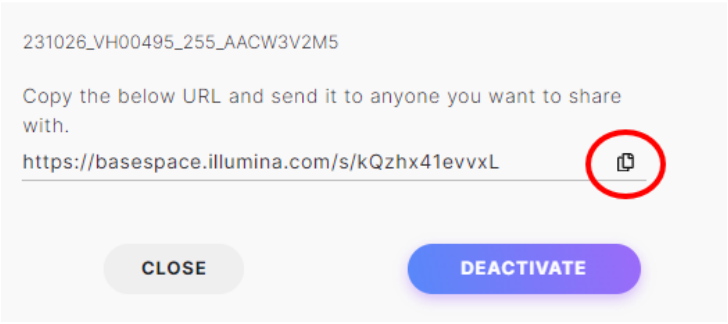
(4) Check the box of the project you want to share and then, using the 'Share' button, create a link (Get Link).



(5) Activate the link.



(6) Copy the link.



If you encounter problems, contact the [TGC team](mailto:tgc@technion.ac.il).