

Importing the tutorial data set

The tutorial data set includes 9 samples equally divided into 3 treatment groups. Sequencing was performed by an Illumina HiSeq (paired-end reads), but the workflow can be easily adapted for data generated by other sequencers. Each sample has 2 fastq files for a total of 18 fastq files.

You can obtain the tutorial data set through Partek Flow.

- Click your **avatar**
- Click **Settings** in the drop-down menu (Figure 1)

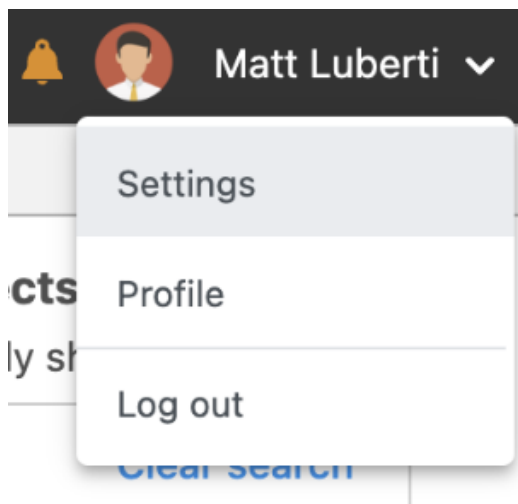


Figure 7. Location of the Settings link on the main page of Partek Flow

At the top of the *System information* page, there is a section labeled *Download tutorial data* (Figure 2).

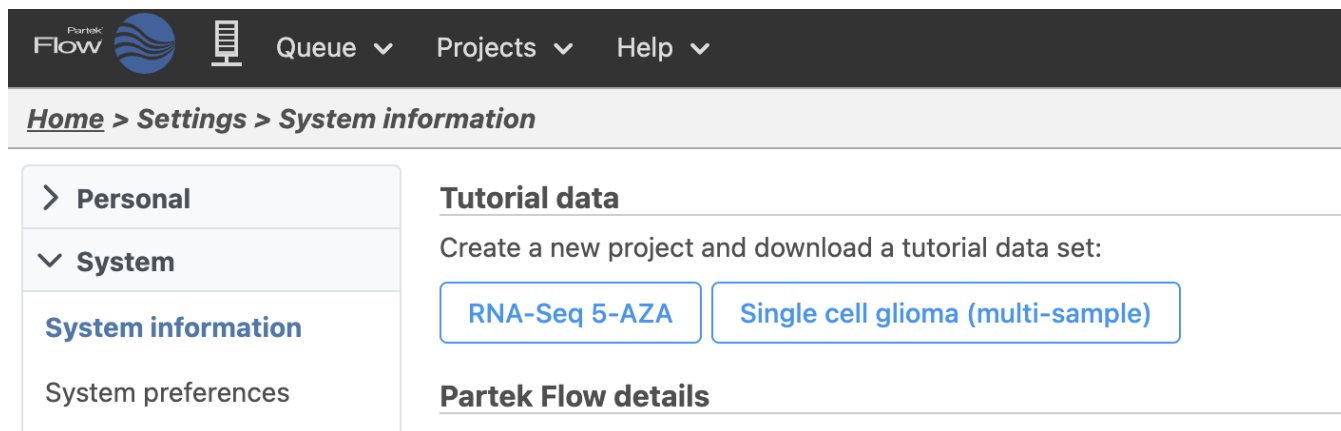
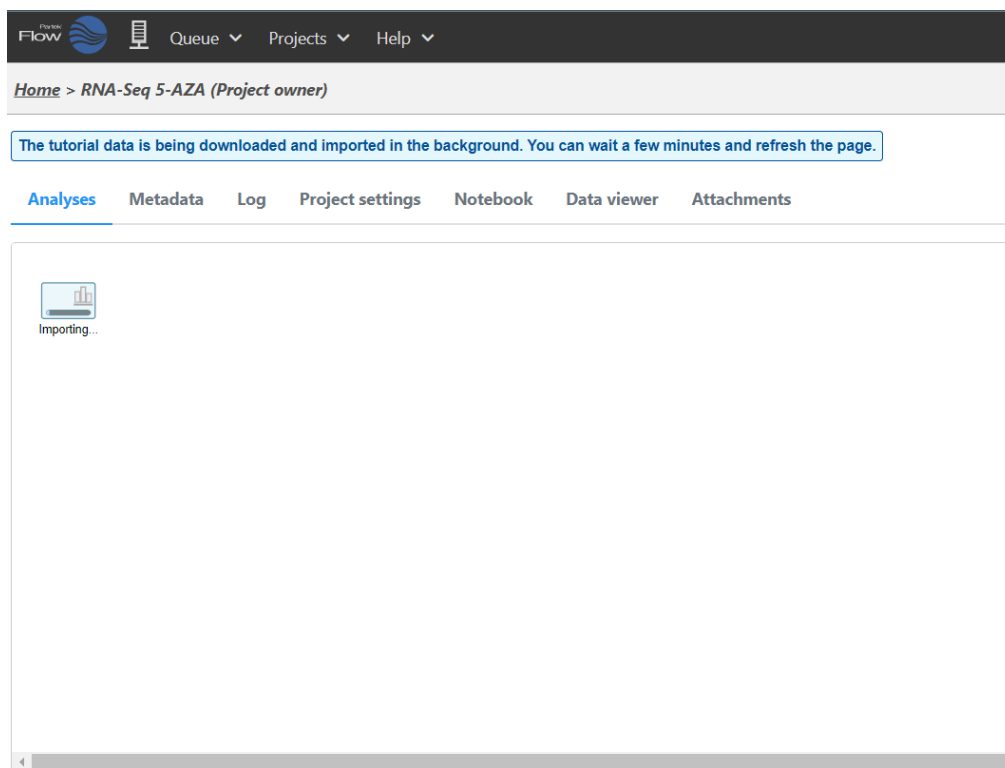


Figure 8. Select RNA-Seq 5-AZA to download the sample data set

- Click **RNA-Seq 5-AZA** to download the tutorial data set

A new project will be created and you will be directed to the *Analyses* Tab. The data will be downloaded automatically (Figure 3) and imported into your project. Because this is a tutorial project, there is no need to click on *Add data* as it will be done automatically.



[Import pipeline](#)

Figure 9. A new project will be automatically created and populated with the tutorial data set

At first the project is empty, but the file download will start automatically in the background. You can wait a few minutes then refresh your browser or you can monitor the download progress using the *Queue*.

- Click **Queue**
- Click **View Queued Tasks** in the drop-down menu

The *Queued tasks* page will open (Figure 4).

Home > Queued tasks							
There is 1 task in the queue.							
Status	Task	Project	User	Submitted	End	Workers	Cancel
<div></div>	[Import] Sample import	RNA-Seq 5-AZA	Matt Luberti	9 Aug 2023, 04:35 AM CDT	9 Aug 2023, 04:41 AM CDT		<div></div>
<div> <div>T</div> - Waiting for upstream tasks to complete <div>R</div> - Waiting for system resources <div>A</div> - Cannot run with current system configuration </div> <p>Time estimates are being continuously updated and will become more accurate.</p>							

Figure 10. Viewing download progress in the Queued tasks page

- Click **Projects**
- Click **RNA-Seq 5-AZA** in the drop-down menu

The *Analyses* tab will open (Figure 5). If your download has completed, you will see a blue circle titled *mRNA*.

Analyses

Metadata

Log


Project settings

Notebook

Data viewer

Attachments

Venn diagram



mRNA

× Toolbox

Click a node to see available options.

∨ Import

Add data

Import pipeline

Figure 11. Analyses tab showing mRNA data node

Once the download completes, the sample table will appear in the *Metadata* tab.

- Click the **Metadata** tab

The *Metadata* tab includes the sample table with the names of each imported sample (Figure 6).



<div>▼ Import</div> <div>Add data</div> <div>▼ Sample attributes</div> <div>Manage</div> <div>Assign values from file</div> <div>Add system-wide attribute</div>	Sample name	
	1	SRR592573
	2	SRR592574
	3	SRR592575
	4	SRR592576
	5	SRR592577
	6	SRR592578
	7	SRR592579
	8	SRR592580
	9	SRR592581
<div> Show data files</div> <div> Download</div>		

Figure 12. Sample table in the Data tab after downloading the tutorial data set

In the next section of the tutorial, we will add a sample attribute that indicates the treatment group of each sample.

[« Bulk RNA-Seq](#) [Adding sample attributes](#) [»](#)

Additional Assistance

If you need additional assistance, please visit [our support page](#) to submit a help ticket or find phone numbers for regional support.



Your Rating:      Results:      30 rates