

Large File Viewer

Partek Flow software provides a built-in *Large File Viewer* to preview files generated by tasks within a project. The file types supported by the viewer are:

.bam	.sam	.bgx
.fastq	.	.bpm
.fastq.	csfasta	.
gz	.	probe_tab
.txt	csfastq	.qual
	.fa	.raw
	.fq	

The *Large File Viewer* is particularly useful when you would like to:

- preview large output files within a project
- preview details of a binary BAM file (including headers and summary)
- quickly preview a text file from the task details
- download specific files (if you do not want to download the whole data node)
- preview files that you have imported into a project

The preview will display up to the first 1000 lines.

This feature of Partek Flow is one of the ways the software provides access to your own data. Remember that in Partek Flow, you can also download any data node through the context-sensitive menu (select a data node and choose *Download* data from the menu). Furthermore, any table from a Task Report can be downloaded by selecting the *Download* hyperlink at the bottom right of each table.

Previewing a File from the Task Details

The way to access the viewer is through the *Task details* page. Select a rectangular task node and choose the **Task details** in the context-sensitive menu (Figure 1). You can also access the **Task details** from the bottom of any *Task report*.

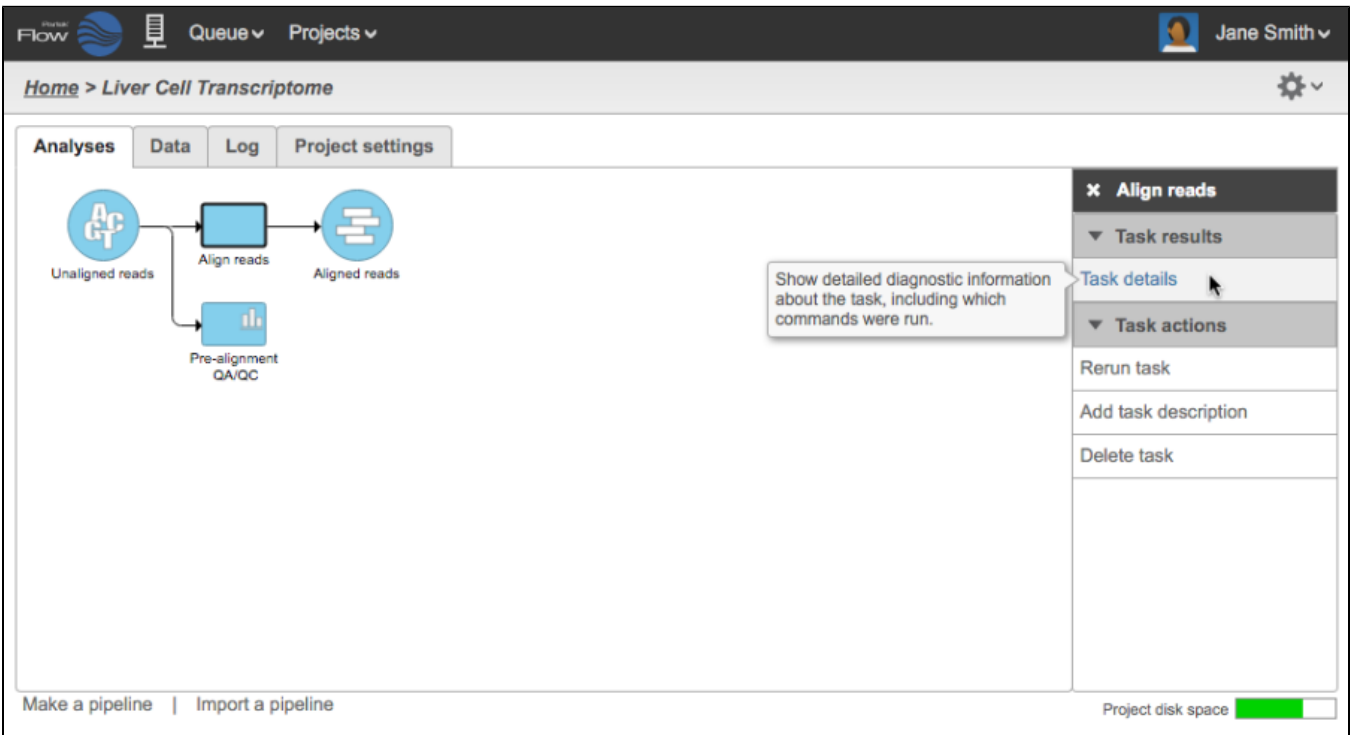


Figure 1. Opening the Task details

The *Output files* section of the *Task details* page shows the different files generated by the task (Figure 2).

Queue

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Home > Liver Cell Transcriptome > Task details

Task

BowtieTwo - 2.2.5

Submitted

25 Mar 2016, 06:17 PM CDT

User

Jane Smith

Status

Done

Started

25 Mar 2016, 06:17 PM CDT

Duration

00:01:37

Ended

25 Mar 2016, 06:19 PM CDT

Task-specific disk usage

0.3 GB

System disk usage

34973/52049 GB (67.2%)

Output files

File name	Result	Created	Size
SRR1020608.fastq.bam	Aligned reads	25 Mar 2016, 06:19 PM CDT	307.87 MB
SRR1020608.fastq.bam.bai	Aligned reads	25 Mar 2016, 06:19 PM CDT	4.10 MB
SRR1020608.fastq.bam.partek.index	Aligned reads	25 Mar 2016, 06:19 PM CDT	2.59 MB

Figure 2. Selecting an output file to preview from the Task details

Note that since some filenames created by Partek Flow are generated by appending the filename of an input file, files may contain several file name extensions. The last extension is the actual file format for the file. In the example in Figure 2, the file in the first row (SRR1020608.fastq.bam) is a BAM file generated from a FASTQ file.

To open the *Large File Viewer*, click the name of the output file and select from the viewing options (Figure 3), which depends on the data type selected.

Note that only files listed in the first section of this document are compatible with the viewer. If you select a file from the table that is not compatible (such as a zip file), the file will not be not previewed, but would be downloaded to your local drive.

Once you have made your selection from the radio buttons (Figure 3), click **View Data**. You also have the option to **Download** the selected file instead of previewing it.

View data

File name

SRR1020608.fastq.bam

☒ View raw data
 ☐ View BAM header
 ☐ View simple stats

Download

View data

Cancel

Figure 3. Choices when viewing a BAM file

For raw data, the *Large File Viewer* will display an *Output file preview* in a scrollable window showing up to 1000 lines (Figure 4). The filename, filesize, and the name of the task that generated the file are also displayed.

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Home > Liver Cell Transcriptome > Task details > Output file preview

Output file preview

File generated by BowtieTwo

SRR1020608.fastq.bam (307.87 MB) - showing up to 1000 lines

1	SRR1020608.937866	0	chr10	82563	1	45M	*	0	0	CTTAAAGGAGCTGATGGAGCTGAAACCAAGGCTCGAGAACTACG	DA.88,7.6?ABCEGAEIEEF88:
2	SRR1020608.3273722	16	chr10	89386	31	16M	*	0	0	AGTCTGGTAGTATTTC	1122;8:377BB<BBB AS:i:0 XS:i:-3 XN:i:0 XM:i:0
3	SRR1020608.1616912	16	chr10	92834	0	82M2I9M1I25M	*	0	0	TTGATAAGACACTTTATTAGTCAAACCGCATACTATAAAAAATGCTTTAAACGCAGCA	
4	SRR1020608.4369835	16	chr10	92867	1	100M	*	0	0	CTATAAAAAATGCTTTAAACGCAGCAGGAGATGTGAAGACACAAATTAACAAGCGTATAGTGACACA	
5	SRR1020608.3769506	16	chr10	93026	1	91M	*	0	0	CATCCTCCTCCTCCTCGGCCGTGGCATCCTGATATTGCTGATATTCAGACACCAGGTCGTTTCATGTTGCTC	
6	SRR1020608.1960446	16	chr10	93108	1	34M	*	0	0	GAATTCATCTCATCCATGCCCTCGCCCGTGAC	1*5-?<@ADDDAD=D@?77?@<>>;?768BB@9
7	SRR1020608.4889765	16	chr10	93146	1	31M1D15M	*	0	0	GGAGGAAGGCCCTTGCGCCTGAACATTGCTGTAAGTCTGCTGAGACA	=772627-@8<:>==:
8	SRR1020608.1628894	16	chr10	93172	18	144M	*	0	0	GCTGTAAGTCTGCTGAGACGCGCTTGAAGAGTTCCTGGATGGCCGTATTATCCCAATGAAGTGG	
9	SRR1020608.3338634	16	chr10	93458	6	87M	*	0	0	GCTGGGTAAGCTCAGCCACAGTCAAGGCCCGGTACTGCTGGCTGCCCGGCTGGTCAGTGGGGCAAAGCCG	
10	SRR1020608.358689	16	chr10	93549	1	80M	*	0	0	GGGAAACGGGACCATGTTACGGCCAGCTTCCGCAGGTCAGCATTGCTGGCCCGGGAAGCGCAGGCACG	

Figure 4. Output file preview for viewing raw data

For BAM files, additional options are to display the headers that were generated by the aligners (Figure 5) and the SAMtools flagstat summary statistics (Figure 6).

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Home > Liver Cell Transcriptome > Task details > BAM header preview

BAM header preview

File generated by BowtieTwo

SRR1020608.fastq.bam (307.87 MB) - showing up to 1000 lines

1	@HD VN:1.0 SO:coordinate
2	@SQ SN:chr10 LN:135534747
3	@SQ SN:chr11 LN:135006516
4	@SQ SN:chr12 LN:133851895
5	@SQ SN:chr13 LN:115169878
6	@SQ SN:chr14 LN:107349540
7	@SQ SN:chr15 LN:102531392
8	@SQ SN:chr16 LN:90354753
9	@SQ SN:chr17 LN:81195210
10	@SQ SN:chr18 LN:78077248

Figure 5. BAM header preview

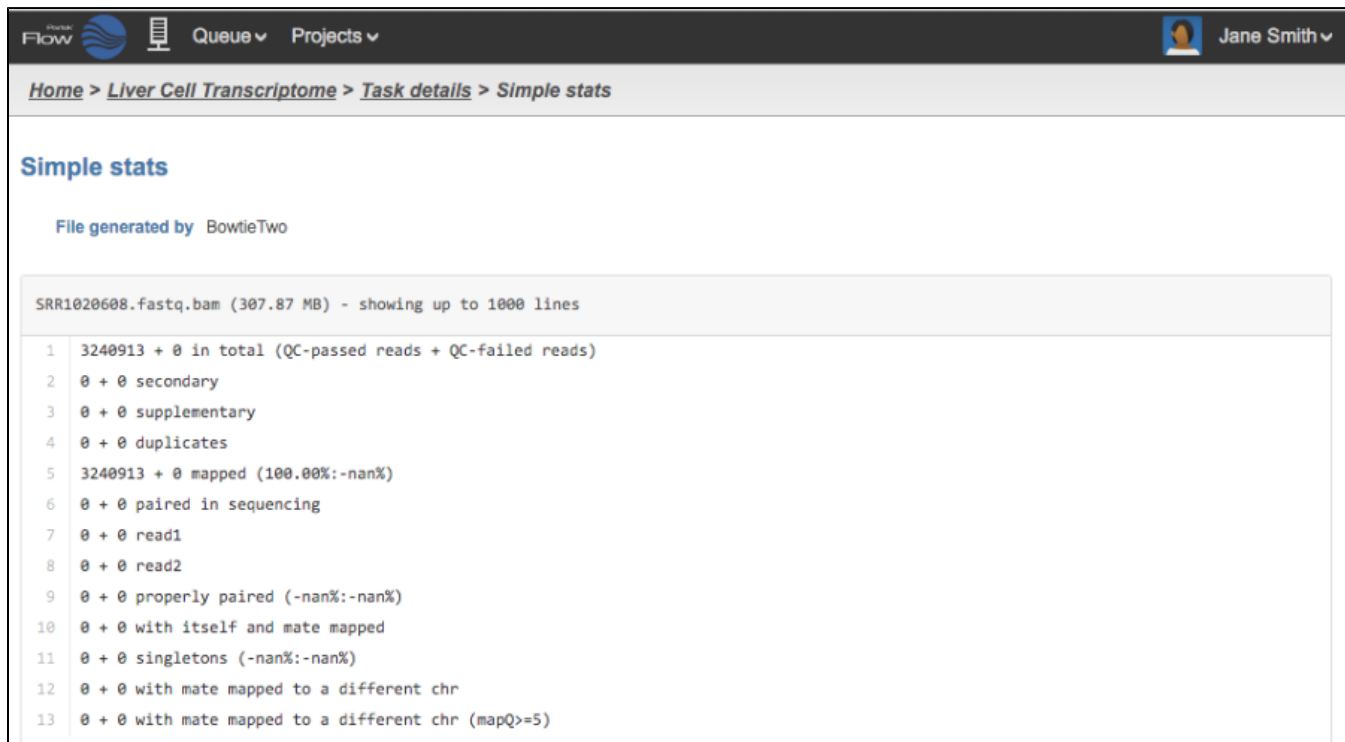


Figure 6. Simple stats (samtools flagstat) for a BAM file

Previewing an Imported File

There may be situations when you wish to preview files that were originally imported into a project. However the first data node in project (known as the origin data node) does not have any task details associated with it in the context-sensitive menu (Figure 7).

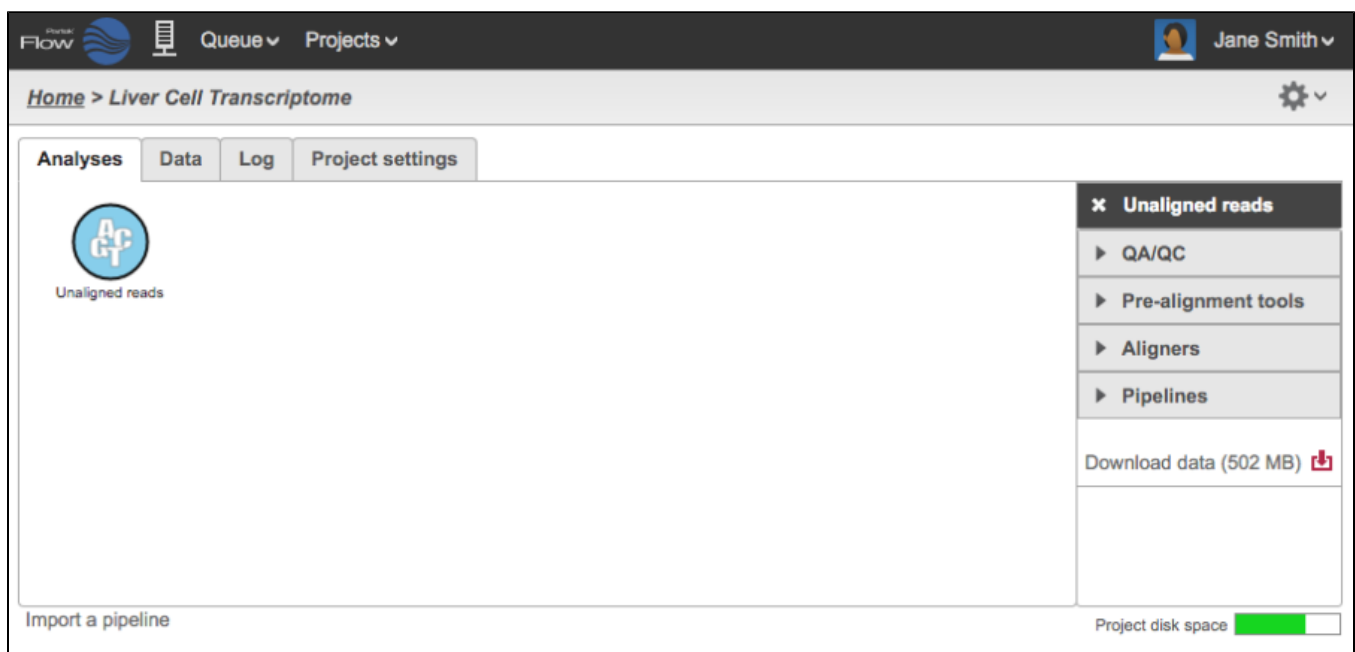


Figure 7. The origin data node does not have task details in the context-sensitive menu

To access the task details in an import task, go to the **Log** tab of the project and select the **Import** task in the table (Figure 8). Select the top level task **Import** (and not the *Import unaligned reads*).

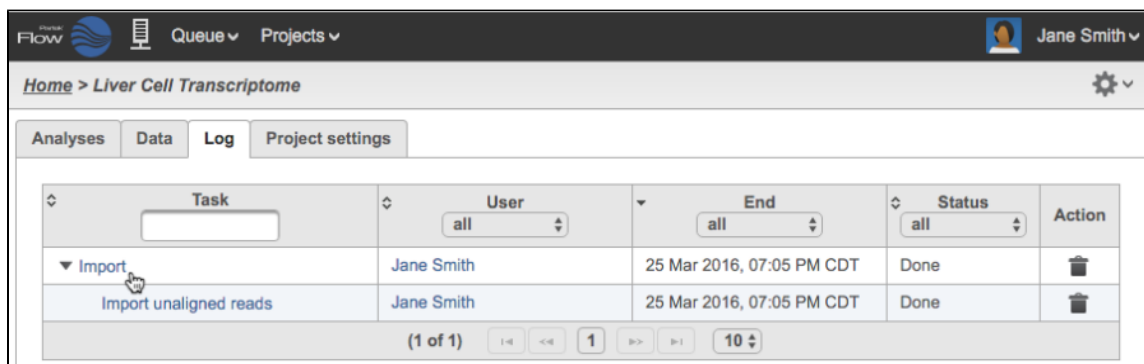





Figure 8. The log tab showing the Import task

Selecting the **Import** from the *Log* table reveals the *Task details* and the file that was successfully imported (Figure 9). Note that even though the file has just been imported, it is placed under the *Output files* section because it has already gone through the import process of file validation and other file checks.

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 Jane Smith ▾

Home > Liver Cell Transcriptome > Task details

Task

Import

Submitted

25 Mar 2016, 07:04 PM CDT

User

Jane Smith

Status

Done

Started

25 Mar 2016, 07:04 PM CDT

Duration

00:00:24

Ended

25 Mar 2016, 07:05 PM CDT

Output files

File name	Result	Created	Size
SRR1020608.fastq.gz	Unaligned reads	24 Mar 2016, 11:04 PM CDT	502.26 MB

Figure 9. Task details of an Import task


To open the *Large File Viewer*, simply select the filename of the file you wish to preview as explained in the previous section.


Additional Assistance


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




















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