Importing ChIP-Seq data

Data for this tutorial can be downloaded from the Partek website using this link - ChIP-Seq tutorial data. To follow this tutorial, download the two .bam files and unzip them on your local computer using 7-zip, WinRAR, or a similar program.

- Store the two.bam files at C:\Partek Training Data\ChIP-Seq or to a directory of your choosing. We recommend creating a dedicated folder for the tutorial on a local drive.
- Select **ChIP-Seq** from the *Workflows* drop-down menu (Figure 1)
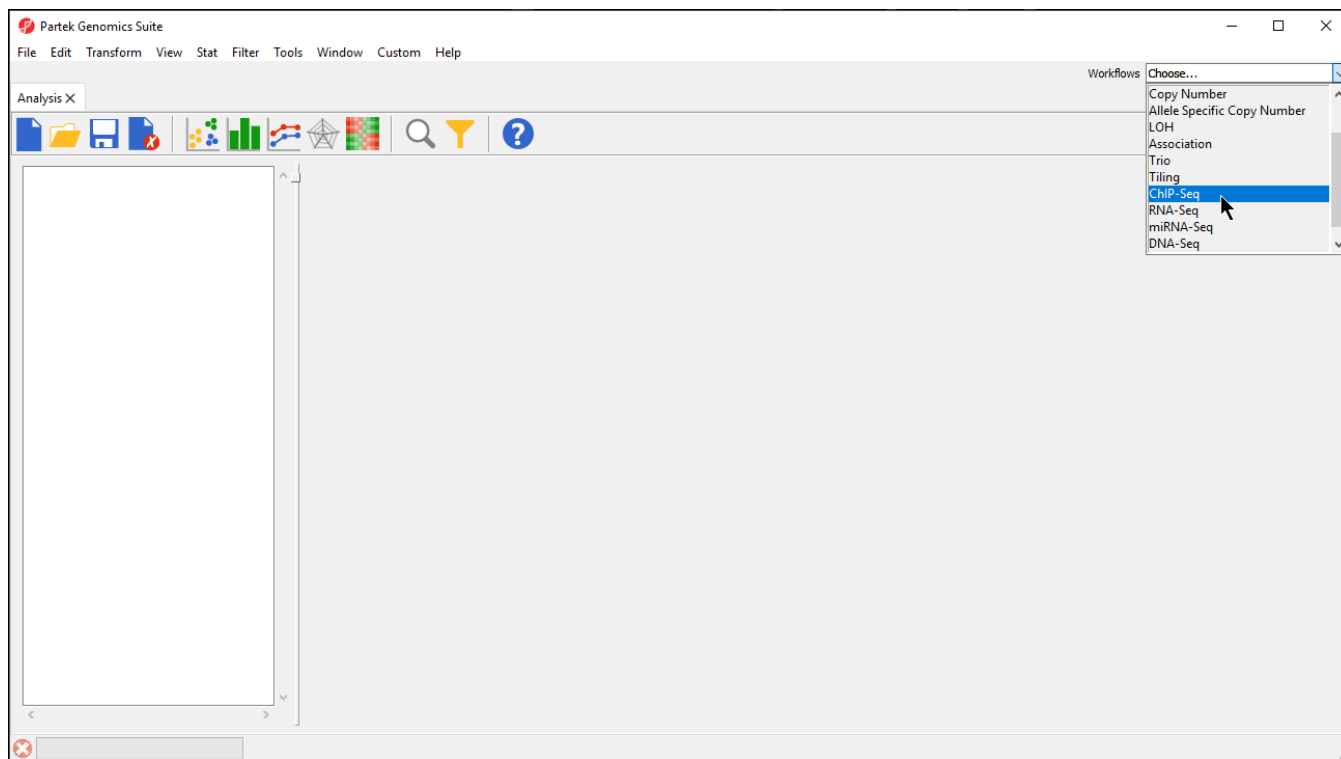

Figure 6. Selecting the ChIP-Seq workflow

- Select **Import and Manage Samples** from the *Import* section of the *ChIP-Seq* workflow
- Select **Browse...** or use the file tree to navigate to the folder where you stored the .bam files

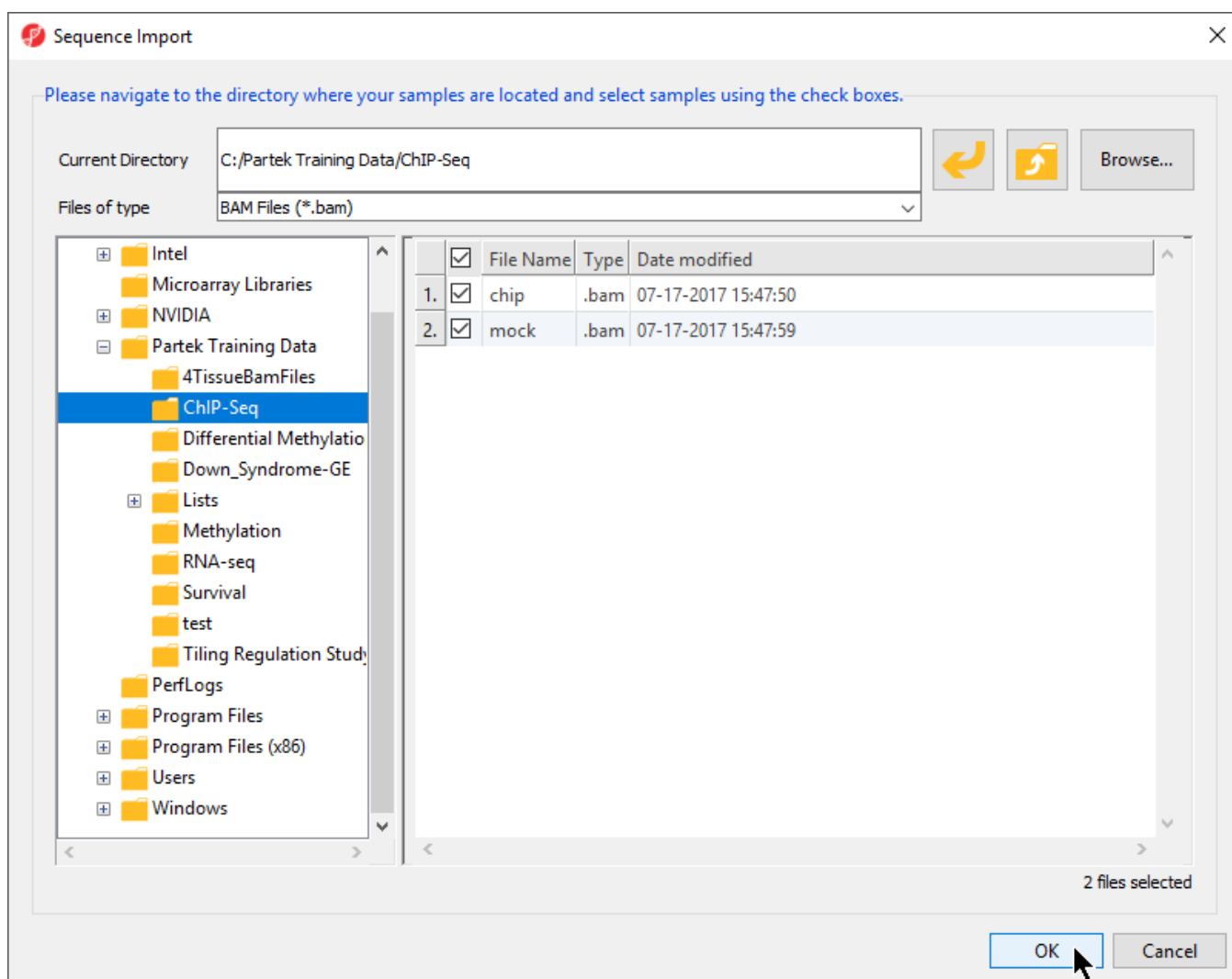All .bam files in the folder will be selected by default (Figure 2).

Figure 7. Importing .bam files using the Sequence Import dialog

- Verify that **chip.bam** and **mock.bam** are selected
- Select **OK**

The *Sequence Import* dialog will launch (Figure 3). This allows us to choose the output file name and destination for the parent spreadsheet, as well as the species, and genome build of the imported samples. By default, the output file destination is the folder the .bam files are located.
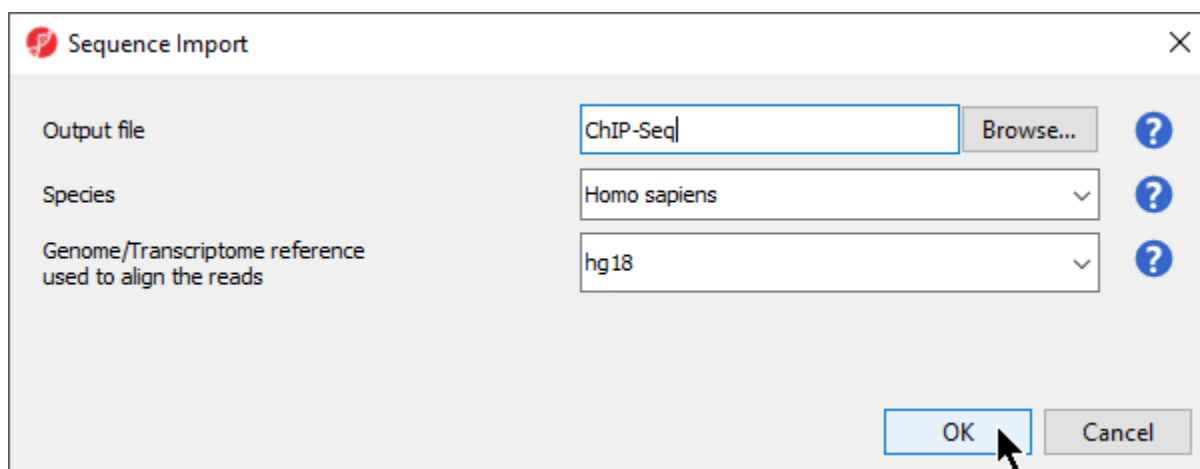
Figure 8. Setting the output file name, species, and genome build during .bam file import

- Set *Output file* to **ChIP-Seq**
- Set *Species* to **Homo sapiens** using the drop-down menu
- Set Genome build to **hg18** using the drop-down menu
- Select **OK**

The *Bam Samples Manager* dialog will open (Figure 4). This dialog can be used to add samples to the project (*Add samples*), remove samples (*Remove samples*), to associate multiple files with particular samples (*Manage samples*), and to map the chromosome names from the input files to the association files (*Manage sequence names*).

	Bam Files	
chip	chip.bam	
mock	mock.bam	

Samples

Add samples

Remove selected samples

Manage samples
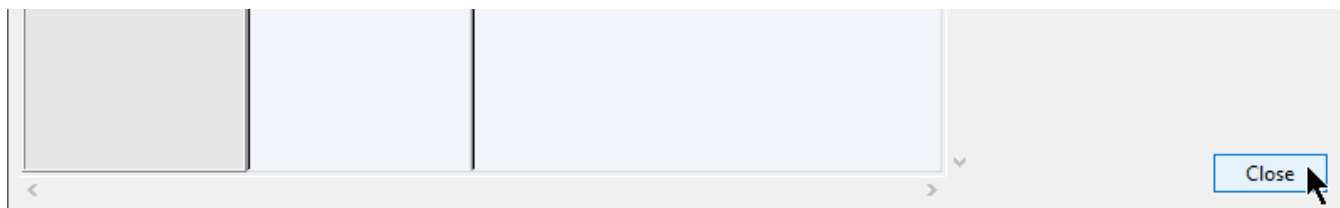
Genomic

Manage sequence names

Figure 9. The Bam Sample Manager can be used to add, remove, and manage files and samples

- Select **Close**

The *Sort bam files* dialog will open. Sorting is necessary for all imported .bam files, but you can choose to hide this hint in the future by selecting **Please don't show me this hint again**.

- Select **OK**

The imported spreadsheet will open while the .bam files are sorted. Progress in sorting will be displayed on the progress bar in the lower left-hand corner of the Partek Genomics Suite window. Once sorting has completed, there will be samples on rows with the sample names in column *1. Sample* ID and the number of reads mapped to the reference genome for each sample in column *2. Number of allignments* (Figure 5).
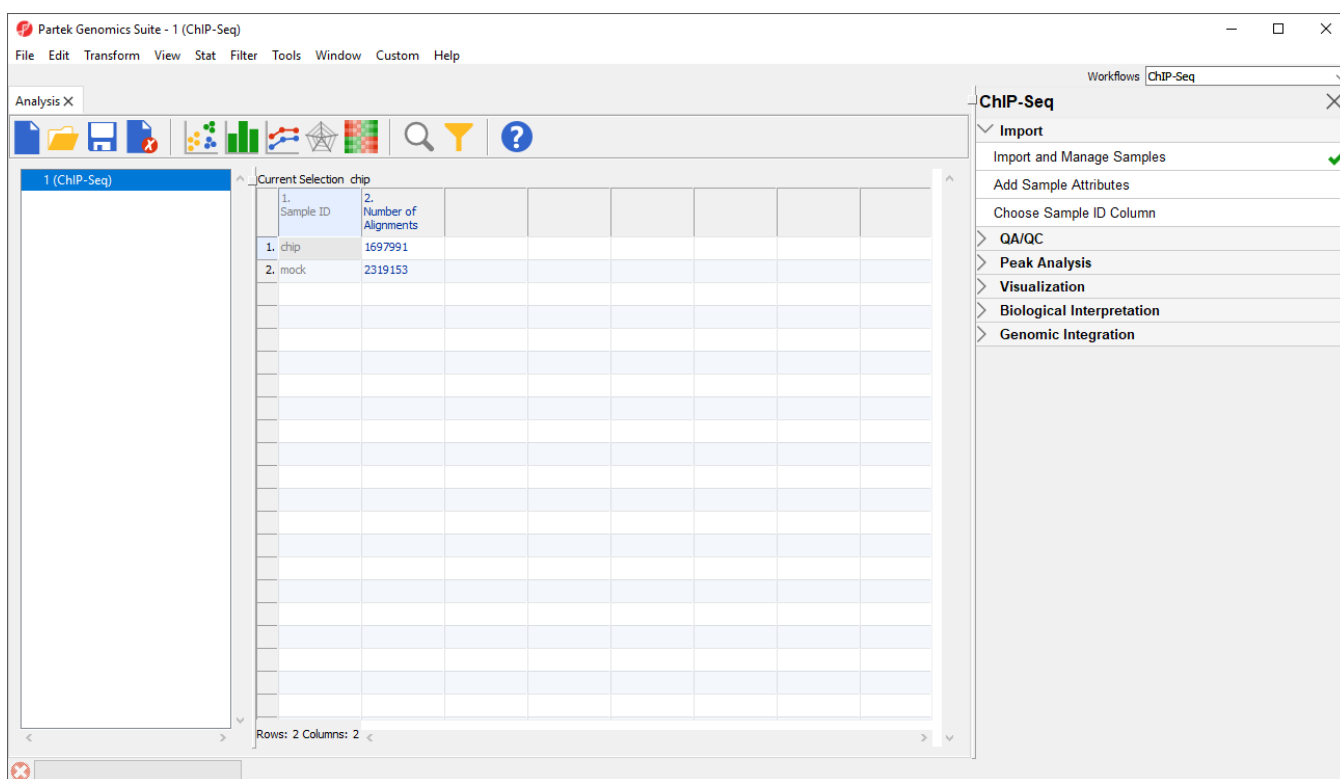

Figure 10. Imported .bam files with one sample in each row

« ChIP-Seq Analysis   Quality control for ChIP-Seq samples »

Additional Assistance

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Your Rating: ☆☆☆☆☆   Results: ★★★★⯪ 36 rates