## Importing aligned reads

We will be using the *RNA-Seq* workflow to analyze RNA-Seq data throughout this tutorial. The commands included in the *RNA-Seq* workflow are also available form the command toolbar, but may be labeled differently.

• Select the *RNA-Seq* workflow by selecting it from the *Workflow* drop-down menu in the upper right-hand corner of the Partek Genomics Suite window (Figure 1)

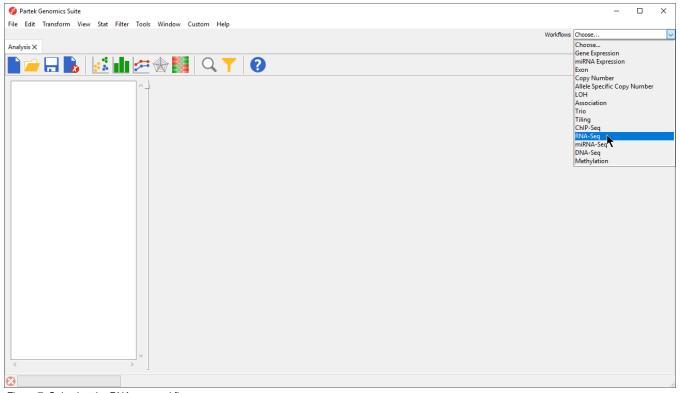


Figure 7. Selecting the RNA-seq workflow

The Partek Genomics Suite software can import next generation sequencing data that has been aligned to a reference genome. Two standard types of alignment formats can be imported: .BAM and .SAM. It is also possible to concert ELAND .txt files to .BAM files with the converter found in the *Tools* menu in the main command bar. The data used in this tutorial was aligned using the Partek<sup>®</sup> Flow<sup>®</sup> software and saved as .BAM files.

• To import the .BAM files, select **Import and Manage Samples** from the *Import* section of the *RNA-Seq* workflow. The *Sequence Import* dialog box will open (Figure 2)

Current Directory C:	/Partek Training D	)ata/F	RNA-5	eq					Browse
Files of type BA	M Files (*.bam)						\ \	•	
🗆 📻 C:\		^			File Name	Туре	Date modified		^
DRIVERS			1.	$\checkmark$	brain_fa	.bam	06-22-2017 15:38:56		
🗄 📻 Intel	Libraries		2.	$\checkmark$	heart_fa	.bam	06-22-2017 15:38:56		
E NVIDIA	Libraries		3.	$\checkmark$	liver_fa	.bam	06-22-2017 15:38:56		
🖃 🛑 Partek Trai	ining Data		4.	$\square$	muscle_fa	.bam	06-22-2017 15:38:56		
est PerfLogs Program F Program F Program F Users Users Windows									
		~	<						~
<	>		-						4 files selected

- gare er miperang izi intimee
  - Select BAM Files (\*.bam) from the Files of type drop-down menu if not set by default
  - Use the file browser panel on the left-hand side of the Sequence Dialog or select **Browse...** to navigate to the folder where you stored the tutorial . BAM files
  - Files with checked boxes next to the file name will be imported. For this tutorial, select brain\_fa, heart\_fa, liver\_fa, and muscle.fa
  - Select **OK** to confirm the file selection and open the next dialog (Figure 3)

🤣 Sequence Import			×
Output file	RNA-seq	Browse	0
Species	Homo sapiens	~	0
Genome/Transcriptome reference used to align the reads	hg 19	~	0
		OK Can	icel

Figure 9. Viewing the Sequence Import wizard; specify Output file (and directory using Browse), Species, and Genome

• Configure the dialog as shown (Figure 3)

Output file provides a name for the top-level spreadsheet. Browse can be used to change the output directory.

• Select Homo sapiens from the Species drop-down menu

This will allow us to select a human genome reference assembly alignment.

• Select hg19 for Genome/Transcriptome reference used to align the reads

This is the reference genome our tutorial data was aligned to using Partek Flow.

• Select **OK** to open the *BAM Sample Manager* dialog (Figure 4)

r (RNA-seq)				×
Bam Files		^	Samples	6
brain fa bam		_		0
		_	Remove selected samples	0
heart_fa.bam			Manage samples	0
liver_fa.bam			<b>\</b>	
muscle_fa.bam			Genomic	
		-	Manage sequence names	0
	Bam Files brain_fa.bam heart_fa.bam liver_fa.bam	Bam Files brain_fa.bam heart_fa.bam liver_fa.bam	Bam Files     ^       brain_fa.bam	Bam Files     Samples       brain_fa.bam     Add samples       heart_fa.bam     Remove selected samples       liver_fa.bam     Manage samples       musde_fa.bam     Genomic

		~ F	Chara
<	>	L	Close

Figure 10. Bam Sample Manager dialog

The *Bam Sample Manager* dialog allows additional samples to be added or removed after the initial sample import. To remove a sample, select a sample from the list and then select **Remove selected samples**. This dialog also allows us to modify samples.

• Select Manage samples to open the Assign files to samples dialog

Sample ID is by default set to the file name, which may be too long or uninformative, so the Assign files to samples dialog can be used to give informative names to samples.

• Change the samples names to Brain, Heart, Liver, and Muscle as shown (Figure 5)

The Assign files to samples dialog also allows multiple .BAM files to be merged into one sample. This is useful if reads from one sample are split into multiple .BAM files.

nassigned files			
	Sample ID: Brain	(1 files)	Remove Sample
	C:/Partek Training Data	a/RNA-seq\brain_fa.bam	<u>^</u>
	Sample ID: Heart	(1 files) a/RNA-seq\heart_fa.bam	Remove Sample
			<b>*</b>
	Sample ID: Liver C:/Partek Training Data	(1 files) a/RNA-seq\liver_fa.bam	Remove Sample
			<b>v</b>
	Sample ID: Muscle	(1 files)	Remove Sample

igure 11. Changing sample names using the Assign mes to samples that

• Select OK to close the Assign files to samples dialog

• Select Close to exit the Bam Sample Manager dialog and view the imported data (Figure 6)

Partek Genomics Suite - 1 (RNA-sec Edit Transform View Stat I		Custom Help	
			Workflows RNA-Seq
ysis X			RNA-Seq
🗀 🔒 🛃			└─ Import
			Import and Manage Samples
1 (RNA-seq)	<ul> <li>Current Selection</li> </ul>		 Add Sample Attributes
	1. Sample ID	2. Number of	Choose Sample ID Column
		Alignments 11199653	> QA/QC
	1. Heart 2. Brain	1199653	Analyze Known Genes
	3. Muscle	14486541	> Allele-Specific Analysis
	4. Liver	11583902	> Visualization
			> Biological Interpretation
>	Rows: 4 Columns	<	> V Related: Applyze a Partick Flow project
	1		Related: Analyze a Partek Flow project

Figure 12. Viewing the imported data in a spreadsheet

Additional files can be added to this spreadsheet using the *Bam Sample Manager* dialog. The *Bam Sample Manager* dialog can also be used to add imported samples to a separate spreadsheet by selecting a new option in the dialog, **Add new experiment**.

« RNA-Seq Analysis 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: ★★★★ 34 rates