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)

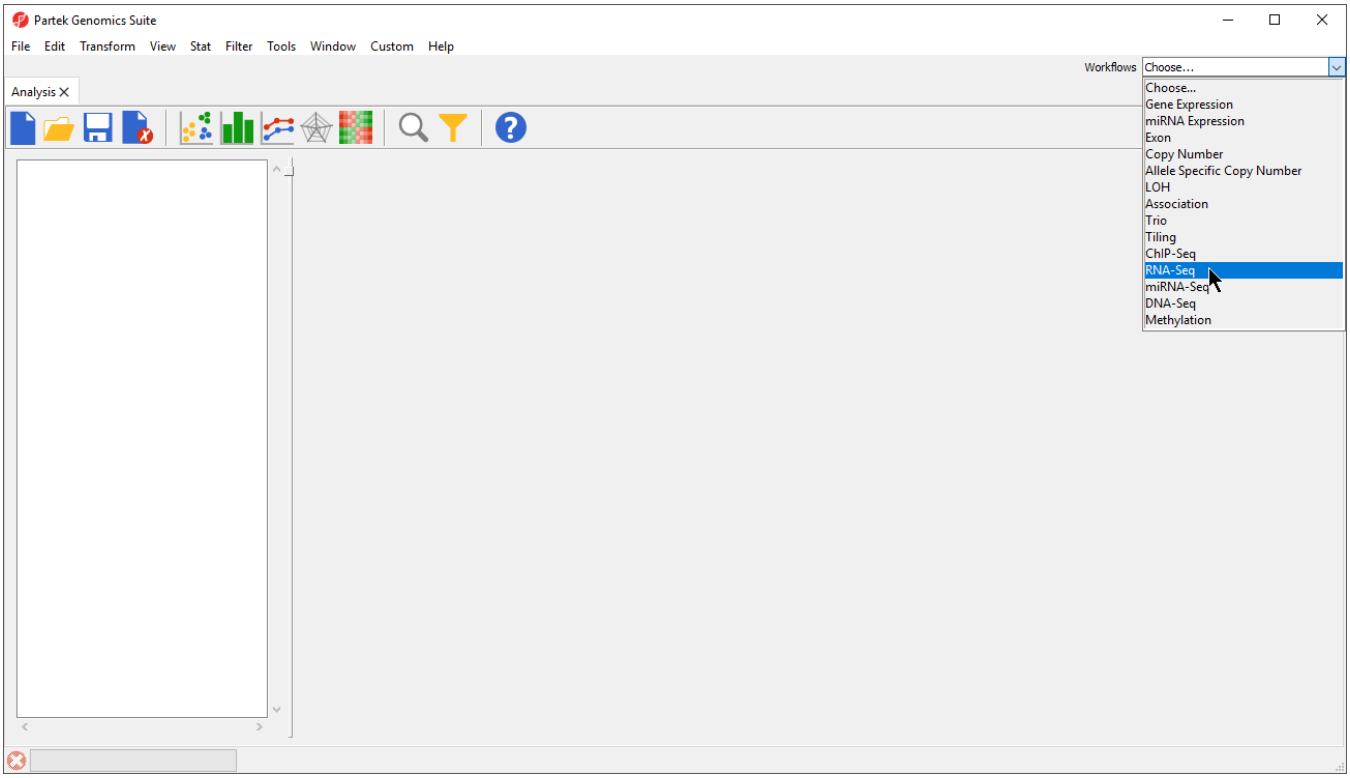

Figure 7. Selecting the RNA-seq workflow

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® Flow® 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)

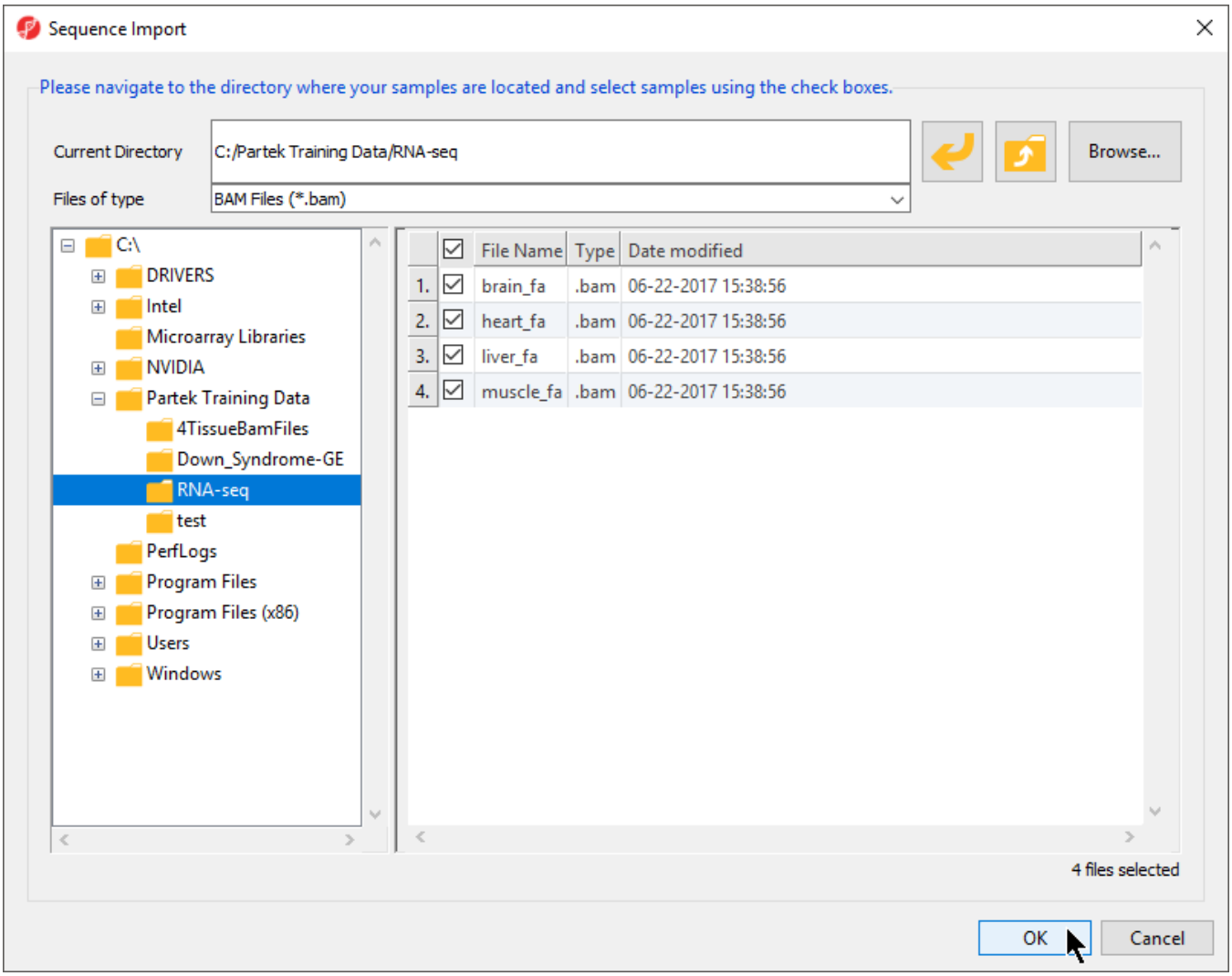

Figure 8. Importing .BAM files

- 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)

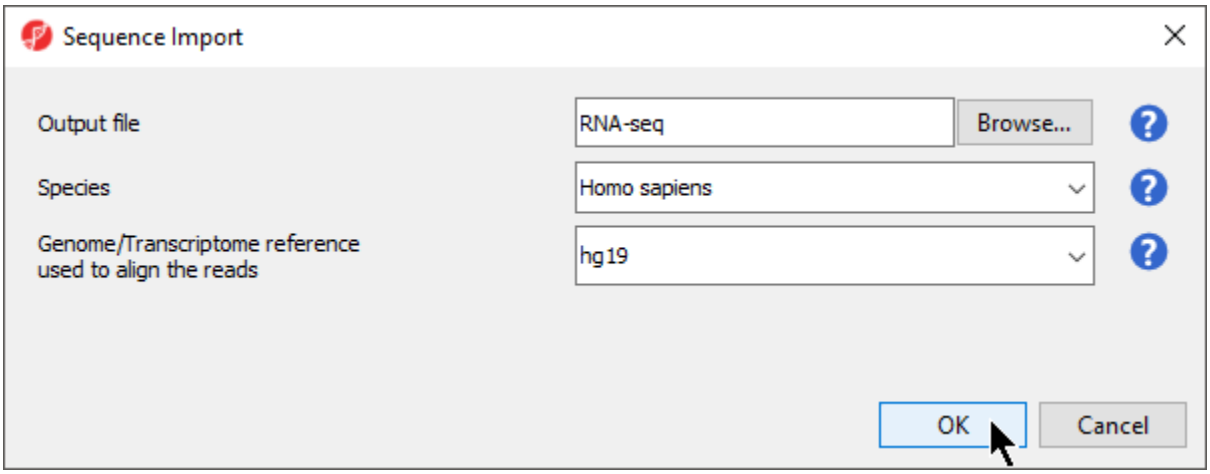

Figure 9. Viewing the Sequence Import wizard; specify Output file (and directory using Browse), Species, and Genome

- 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)

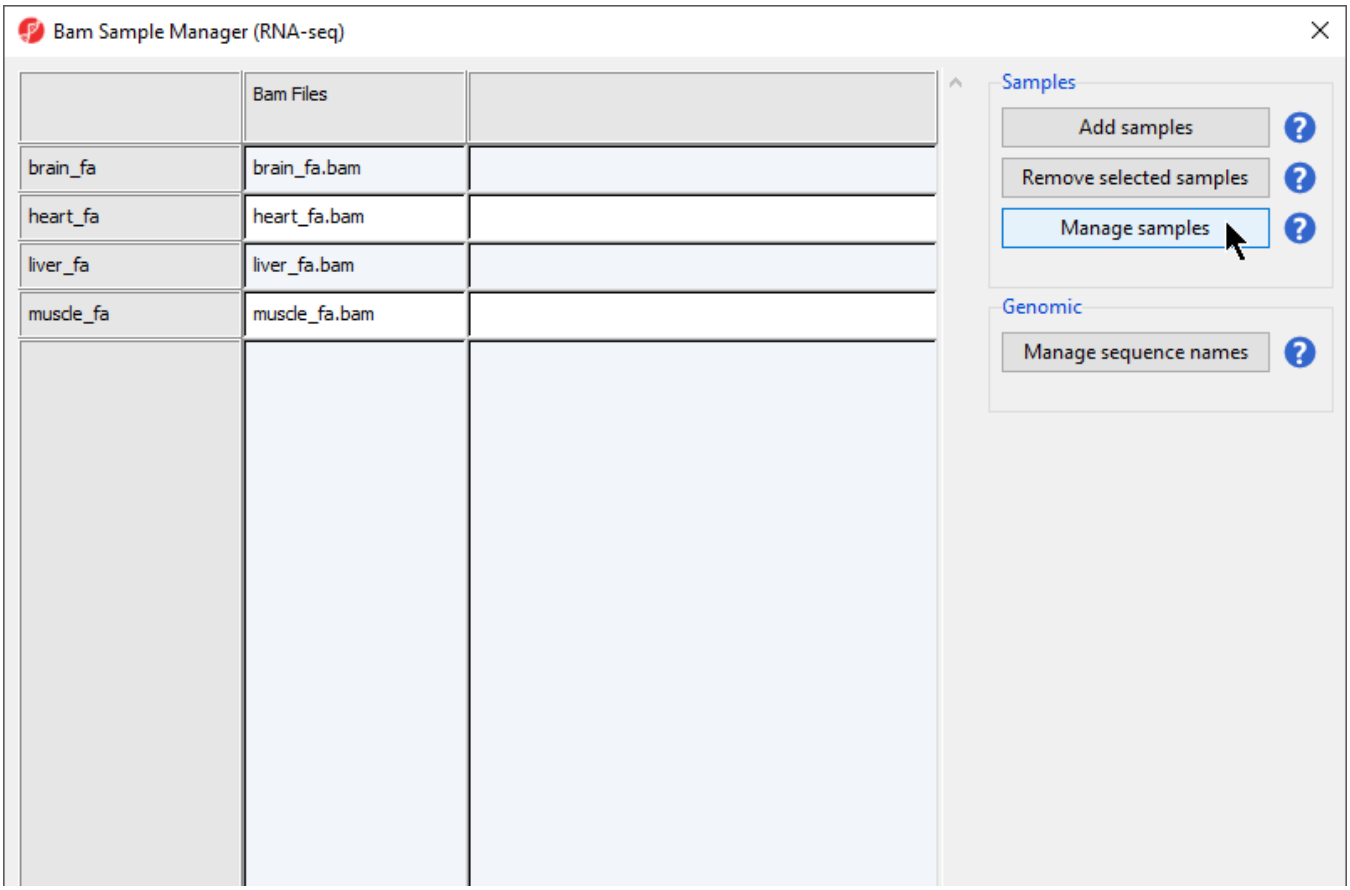

Figure 10. Bam Sample Manager dialog

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.

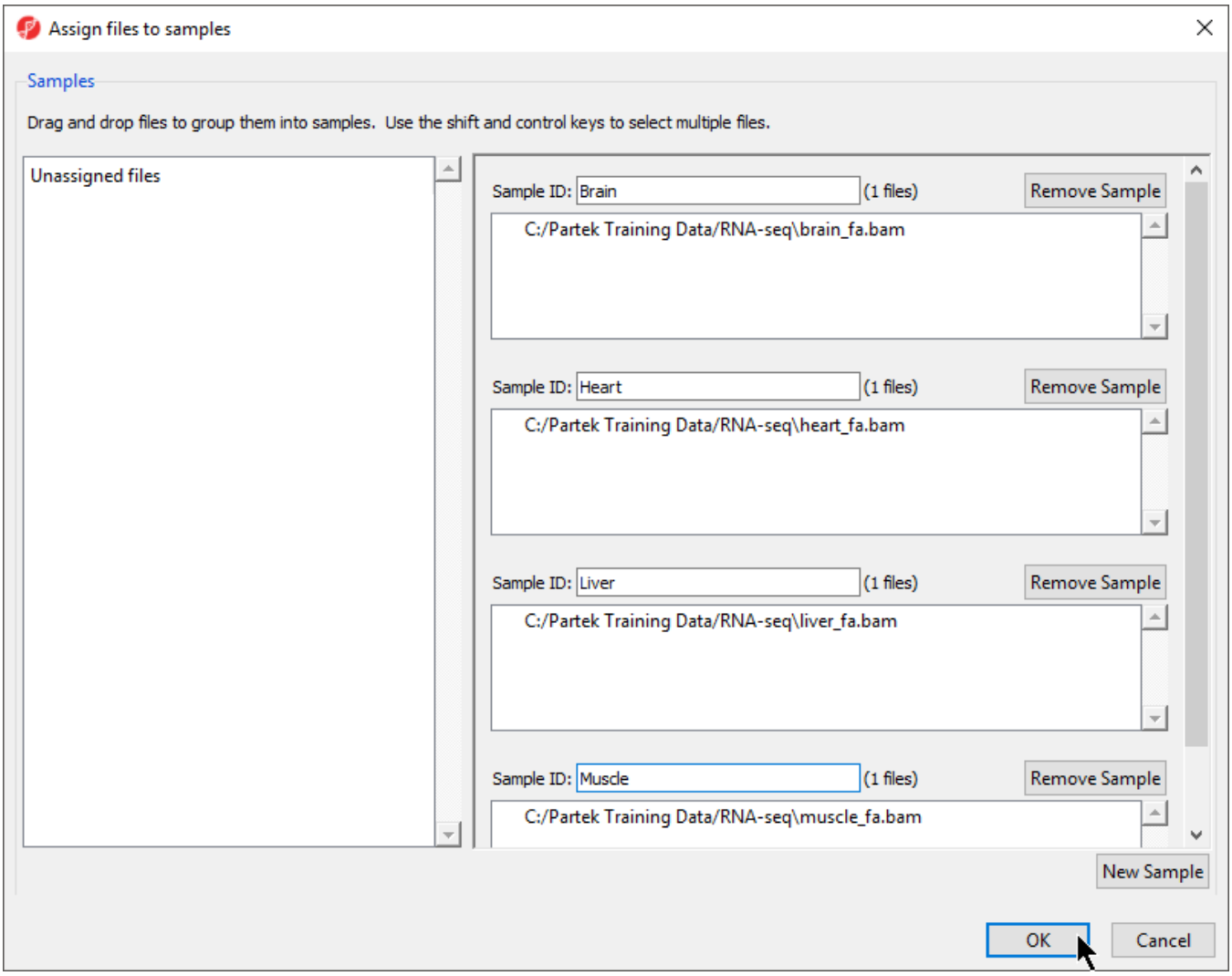

Figure 11. Changing sample names using the Assign files to samples dialog

- 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)

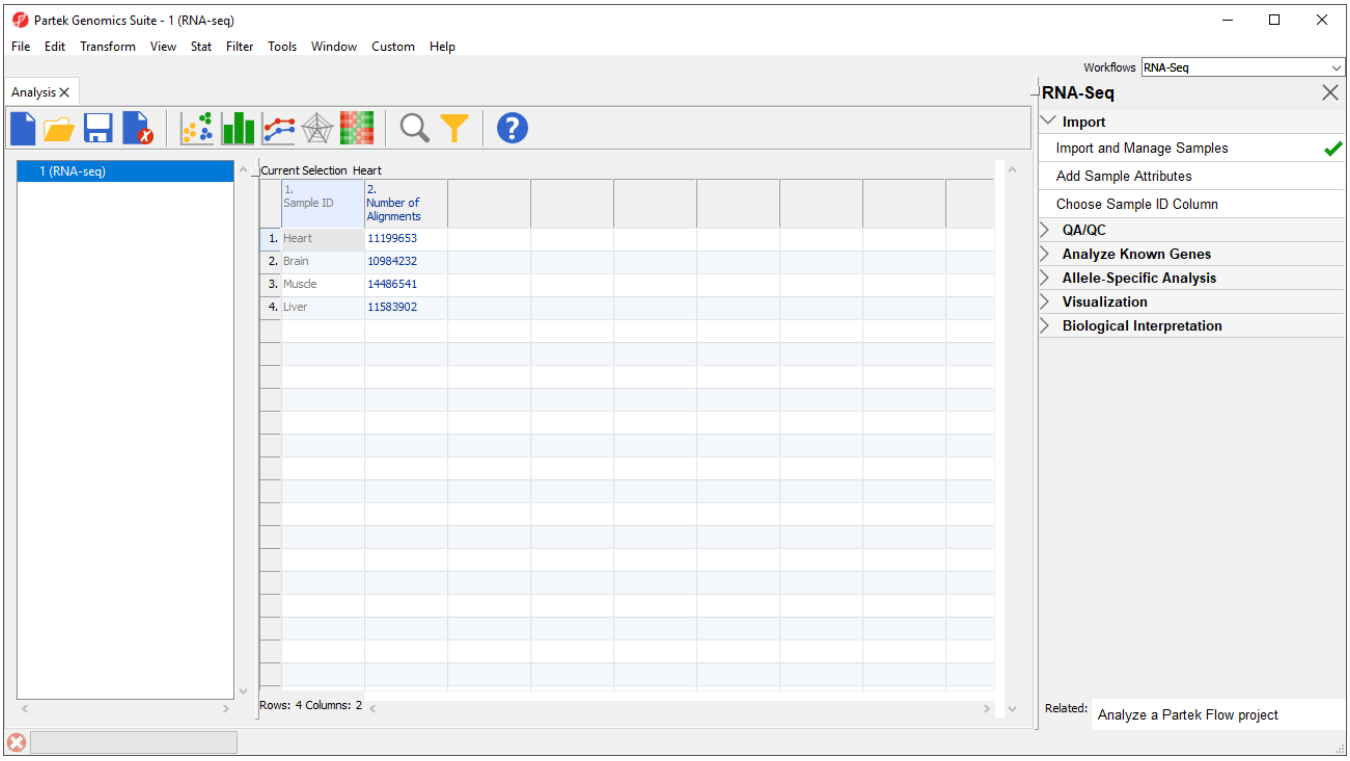

Figure 12. Viewing the imported data in a spreadsheet

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