

Importing a BED file

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A BED (Browser Extensible Data) file is a special case of a region list: it is a tab-delimited text file and the first three columns of BED files contain the chromosome, start, and stop locations. To import a bed file to be used as a data region list, follow the import instructions for region lists. A BED File might also be visualized as an annotation file containing regions in the Genome Browser.

Using a BED file as an annotation source for the genome browser

BED files do not contain individual sequences nor do the regions have names. For example, the UCSC Genome Browser has an annotation BED file for CpG islands. You might like to view this information in the context of a methylation microarray data set. Before you can visualize a BED file in the chromosome viewer, you must create a Partek annotation file from the BED file.

- Select **Tools** from the main toolbar
- Select **Annotation Manager...** (Figure 1)

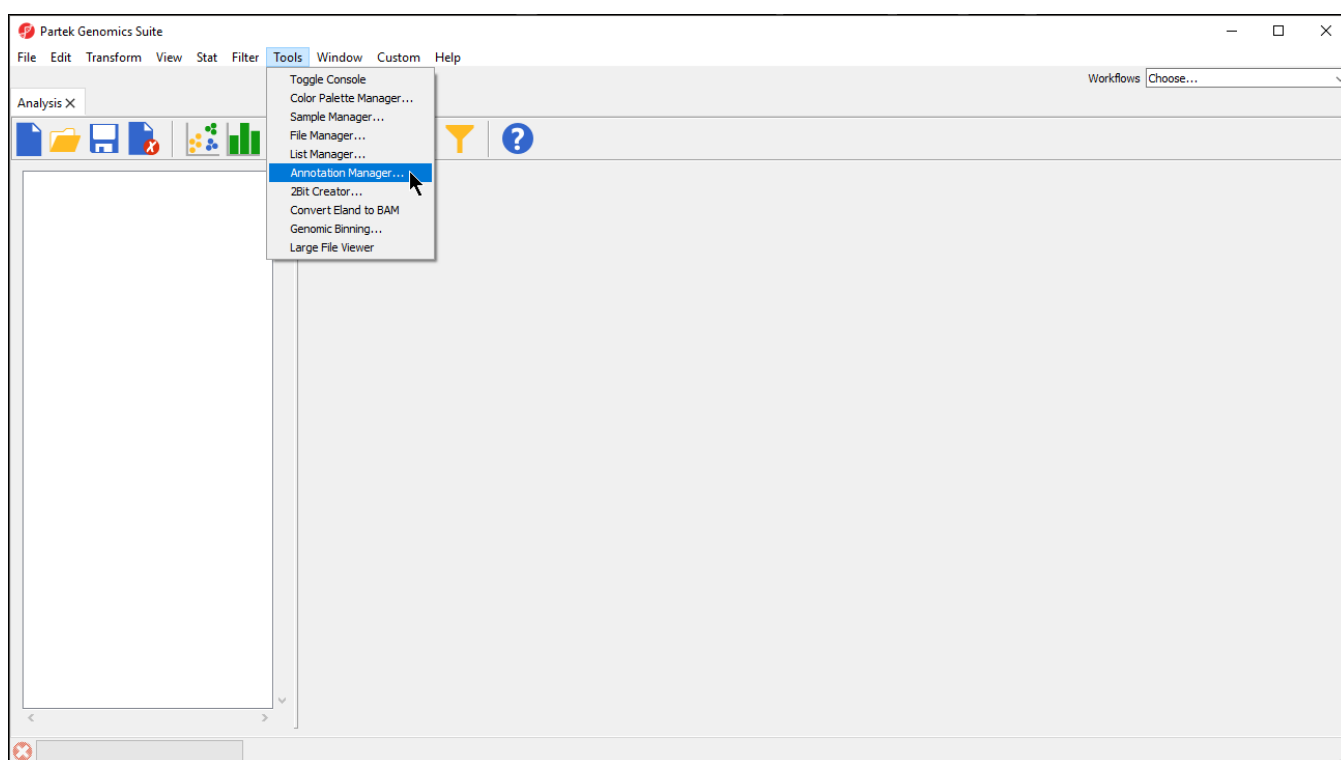


Figure 10. Selecting Annotation Manager

- Select **Create Annotation** from the *My Annotations* tab of the *Annotation Manager* dialog (Figure 2)

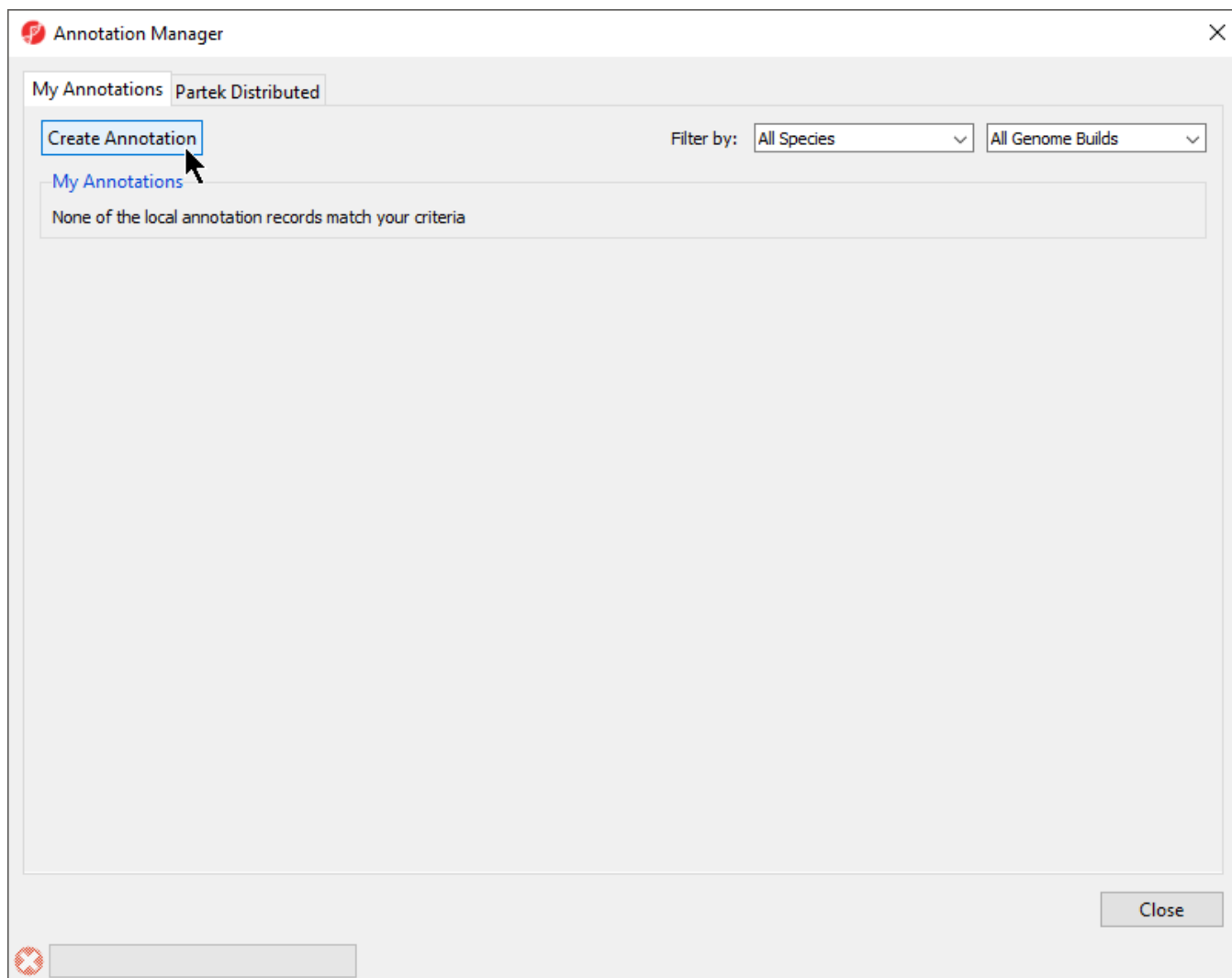


Figure 11. Creating a new annotation file

- Select **BED file (.bed)** for Annotation Type (Figure 3)

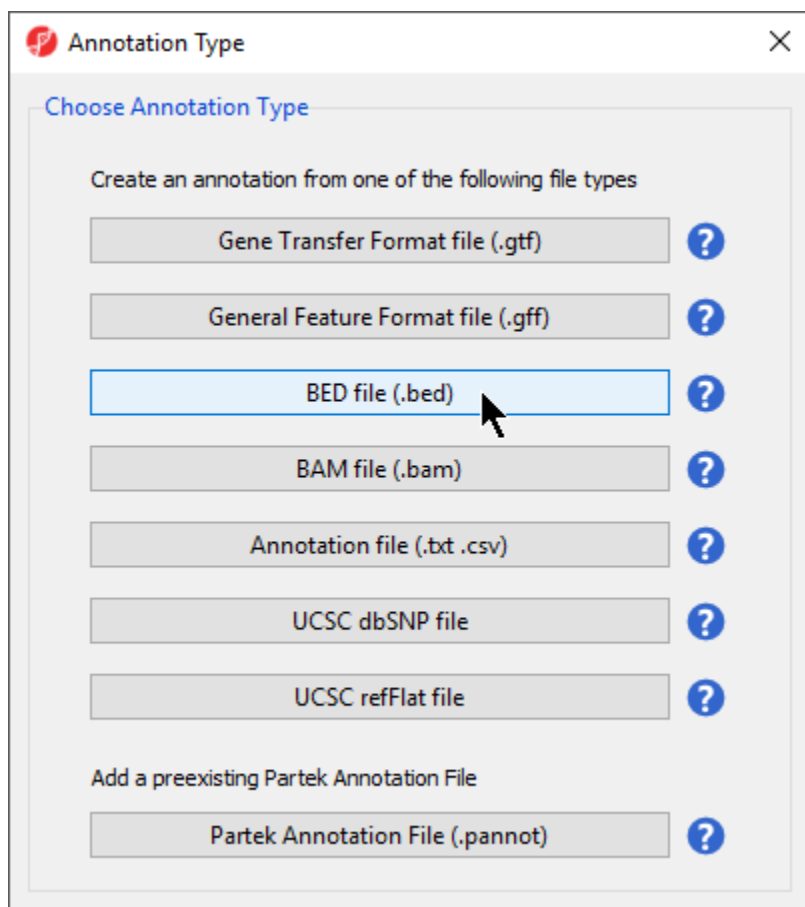


Figure 12. Selecting annotation file type

- Select **Browse...** under *Source* to specify the BED file; a default new file name and destination will populate *Result*, but this can be changed
- You can specify the name and save location of the new annotation file under *Result*, we typically choose the Microarray Libraries folder
- Specify the *Name* of the annotation database file
- Select the correct *Species* and *Genome Build* for the annotation file from the drop-down menus (Figure 4)

Create Annotation

File Locations

Source:

Result:

Annotation Details

Name: ?

Species: ▾

Genome Build: ▾

?

Description:

Created from file "C:/Partek Training Data/Lists/cpg.bed" (last modified 07/18/2017) on 07/18/2017.

Figure 13. Configuring annotation file creation

Preview Chromosome Names would be used if the original file had chromosome names that did not match the genome build that had required modification. For our example, this is unnecessary.

- Select **OK** to create the annotation

The *Annotation Manager* will display the new annotation in the *My Annotations* tab (Figure 5)

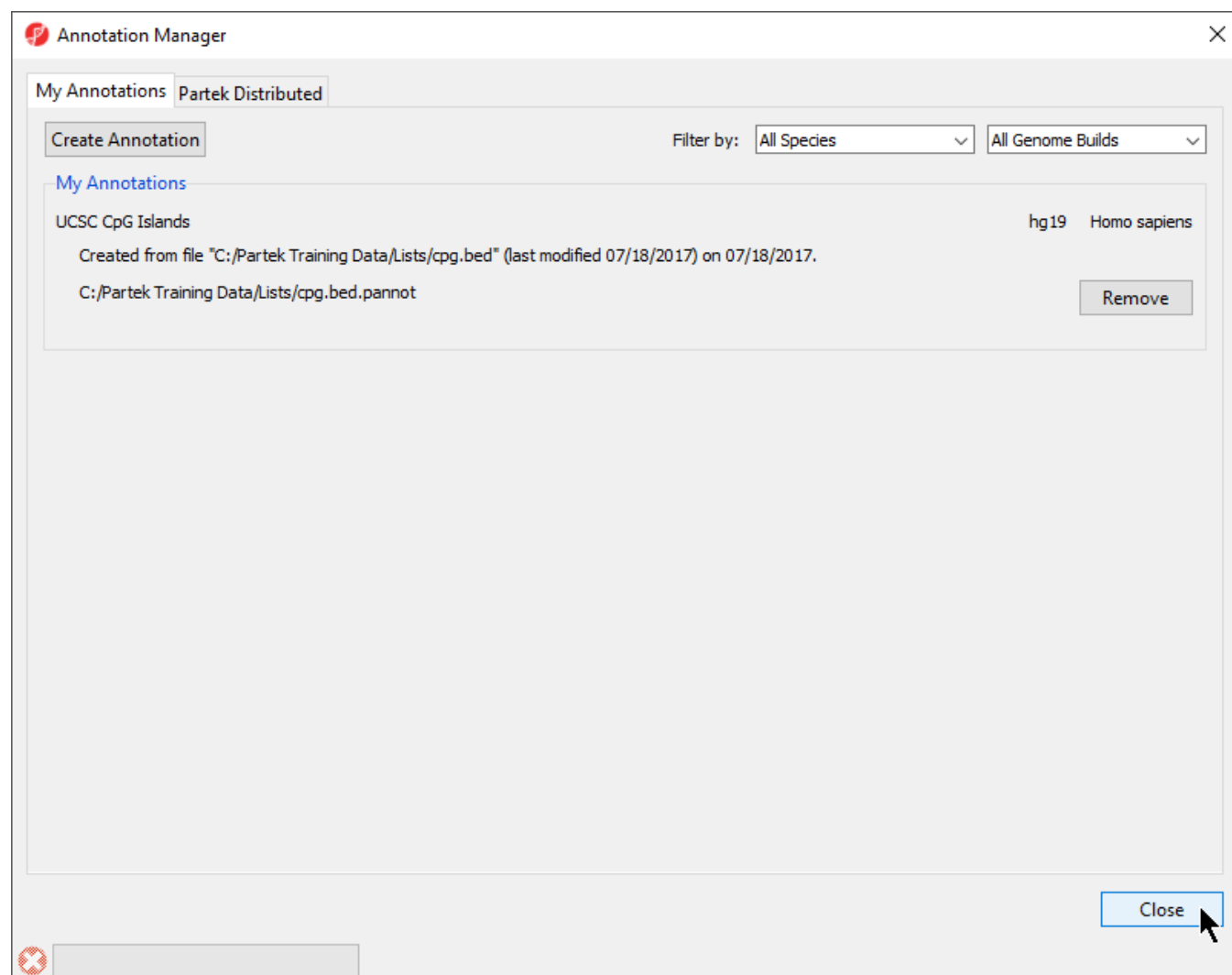


Figure 14. Viewing created annotation in *My Annotations*

Visualizing a BED file as an annotation track in the genome browser

In order to use a BED file as an Annotation track in the Genome Browser, first create the annotation file as described above, being careful to specify the correct species and genome build.

- Right-click a row on any spreadsheet that has genomic features on rows (gene lists, ANOVA results, SNP detection)
- Select either **Browse to Row** or **Browse to Location** to invoke the *Genome Browser* tab
- Select **New Track** from the *Tracks* panel of the *Genome Browser* (Figure 6)



Figure 15. Adding a new track to the Genome Viewer

- Select **Add an annotation track with genomic features from a selected annotation source** from the *Track Wizard* dialog (Figure 7)

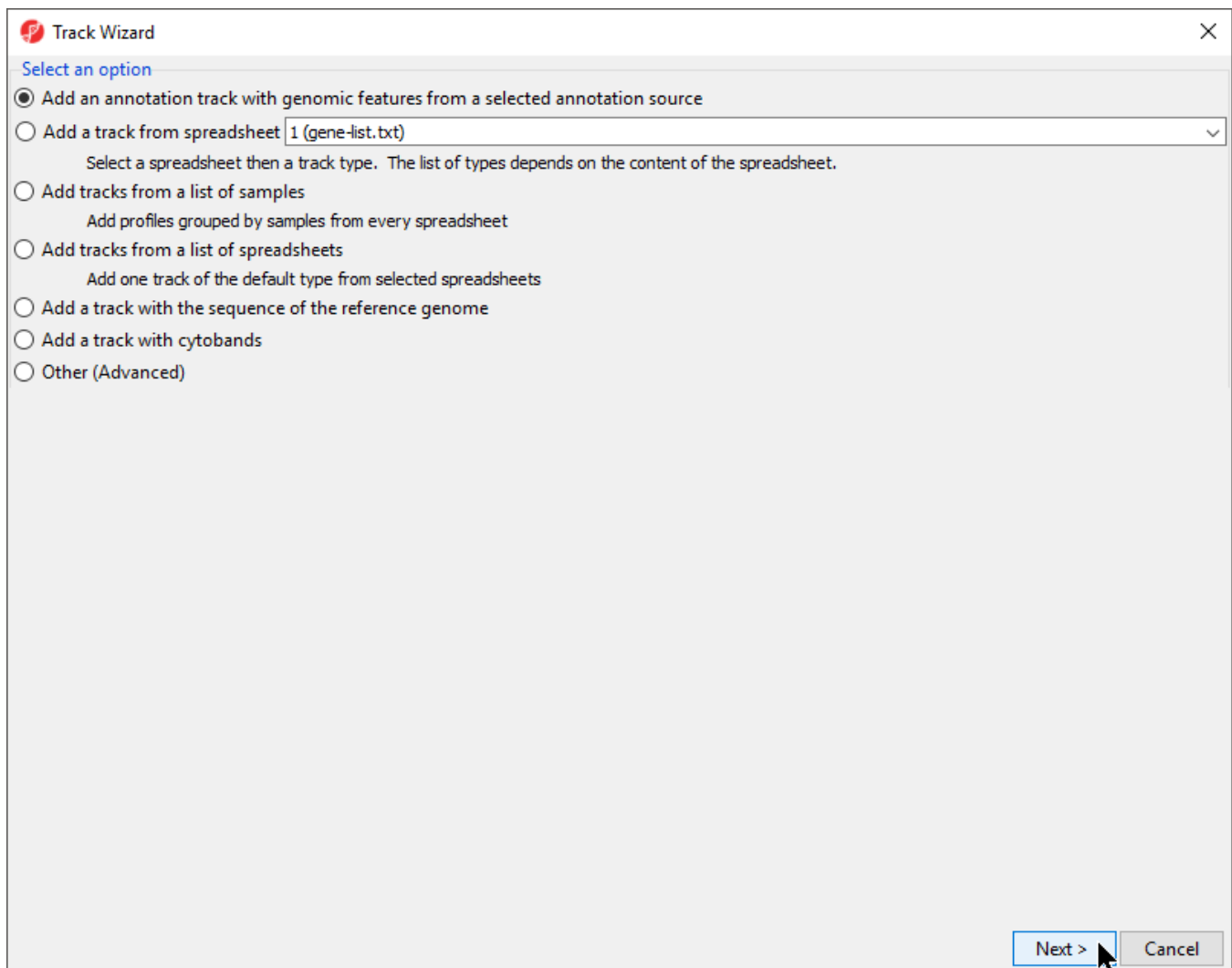


Figure 16. Track Wizard dialog

- Select **Next >**
- Choose the annotation file you created; here we have selected **UCSC CpG Islands** (Figure 8)
- If your annotation file does not contain strand information for each region, deselect **Separate Strands**; here we have deselected it

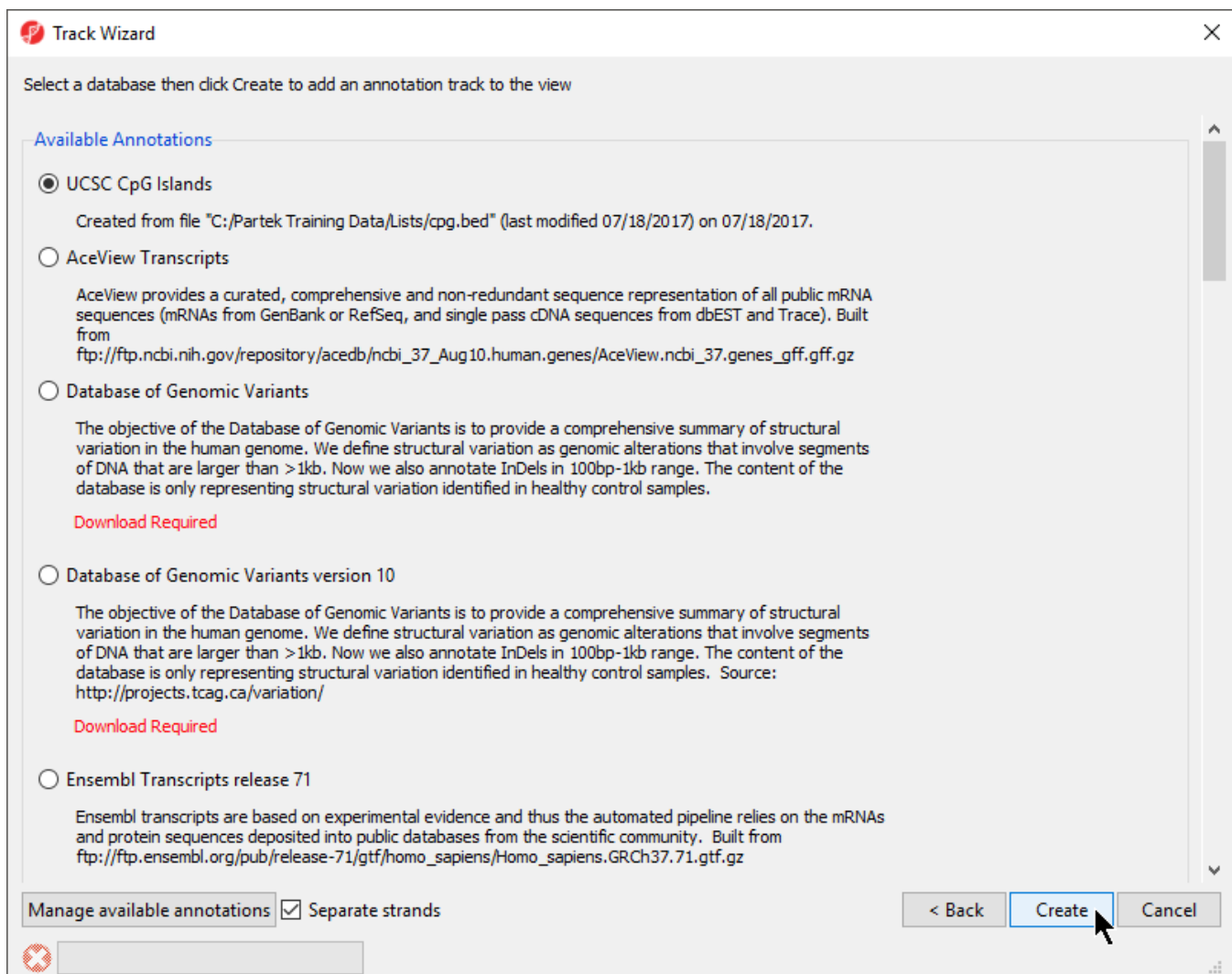


Figure 17. Choosing the annotation file

- Select **Create**

A new track will be created from the annotation file (Figure 9). If *Separate Strands* had been selected, there would be two tracks, one for each strand, like we see for the *RefSeq Transcripts - 2014-01-03 (+) and (-)* tracks (Figure 8).

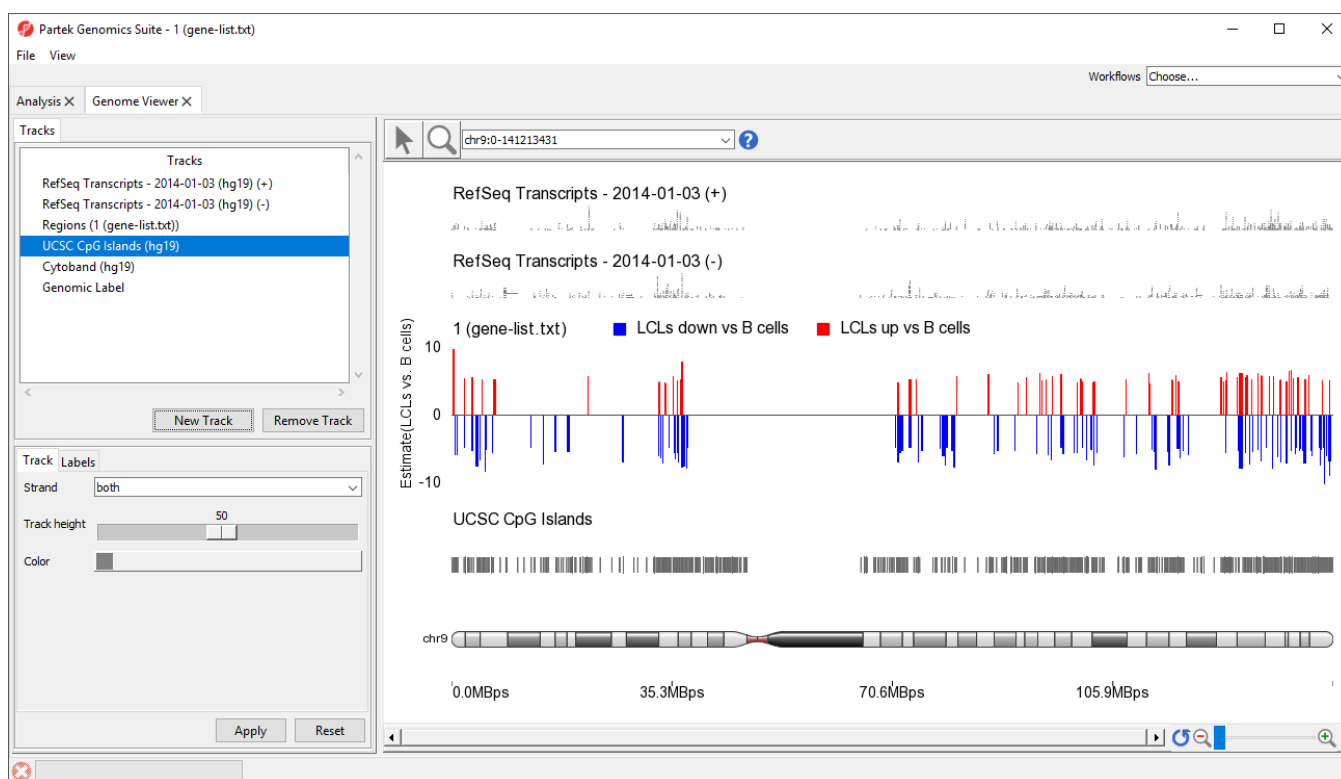


Figure 18. Viewing the added annotation file as a track in the genome viewer

« Starting with a list of SNPs Additional options for lists »

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