Creating a gene list with advanced options

The basic method of creating a gene list from ANOVA results based on fold-change and p-value cut-offs is detailed in Creating gene lists from ANOVA results. Advanced options enable the creation of lists based on more complex criteria. For example, we can use the *Create Gene List* function to identify transcripts that are both significantly differentially expressed AND alternatively-spliced among the four tissue samples.

- Select **Create Gene List** from the *Analyze Known Genes* panel of the *RNA-Seq* workflow to invoke the *List Manager* dialog
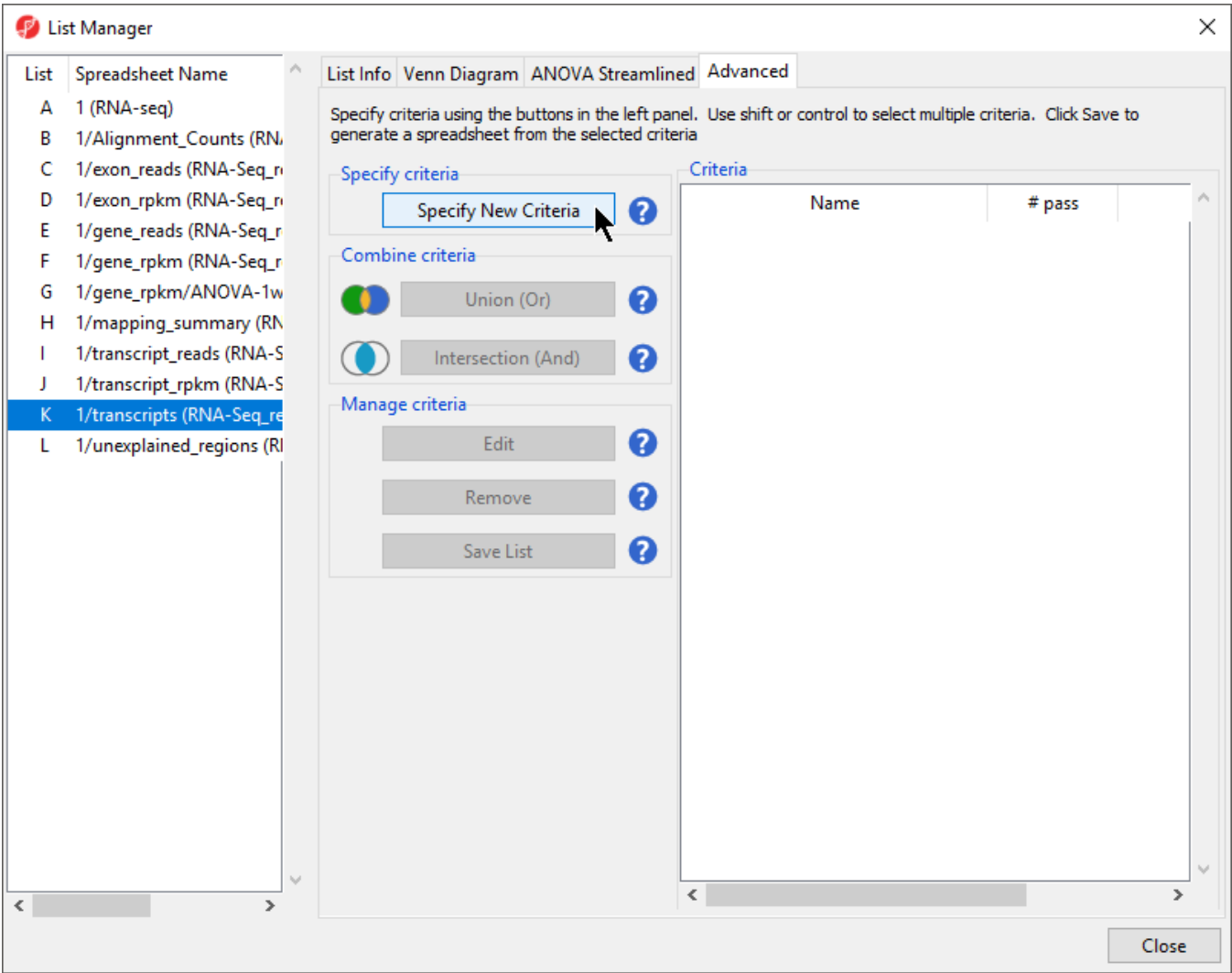- Select the *Advanced* tab (Figure 1)

Figure 8. Creating a gene list using advanced options

- Select **Specify New Criteria** to invoke the *Configure Criteria* dialog (Figure 2)

Figure 9. Configuring criteria for transcripts with a p-value < 0.05

- In the *Configure Criteria* dialog box (Figure 2), provide a name for the list (**Diff Exp**)
- Select **1/transcripts (RNA-Seq_results.transcripts)** from the *Spreadsheet* drop-down menu
- Select **8. p-value(DiffExp)** from the *Column* drop-down menu
- Set *Include p-values* to **significant with FDR** with a value of **0.05**

A list of 38,285 transcripts that pass this criteria will be generated according to the *# pass* score on the right-hand side of the dialog. If the settings are changed, this number will automatically update.

- Select **OK**
- Repeat the same steps to create a list of transcripts that are likely alternatively spliced, named *Alt Splice,* using the same p-value cutoff and *Column* set to **10. p-value (AltSplice)** (Figure 3)

Figure 10. Configuring criteria for a list of alternatively spliced genes

- Select **OK** to generate *Alt Splice*
- Select both lists in the right-hand panel under the *Criteria* panel while holding the **Ctrl** key on your keyboard
- Select **Intersection** from the left-hand panel of the *List Manager* dialog (Figure 4)
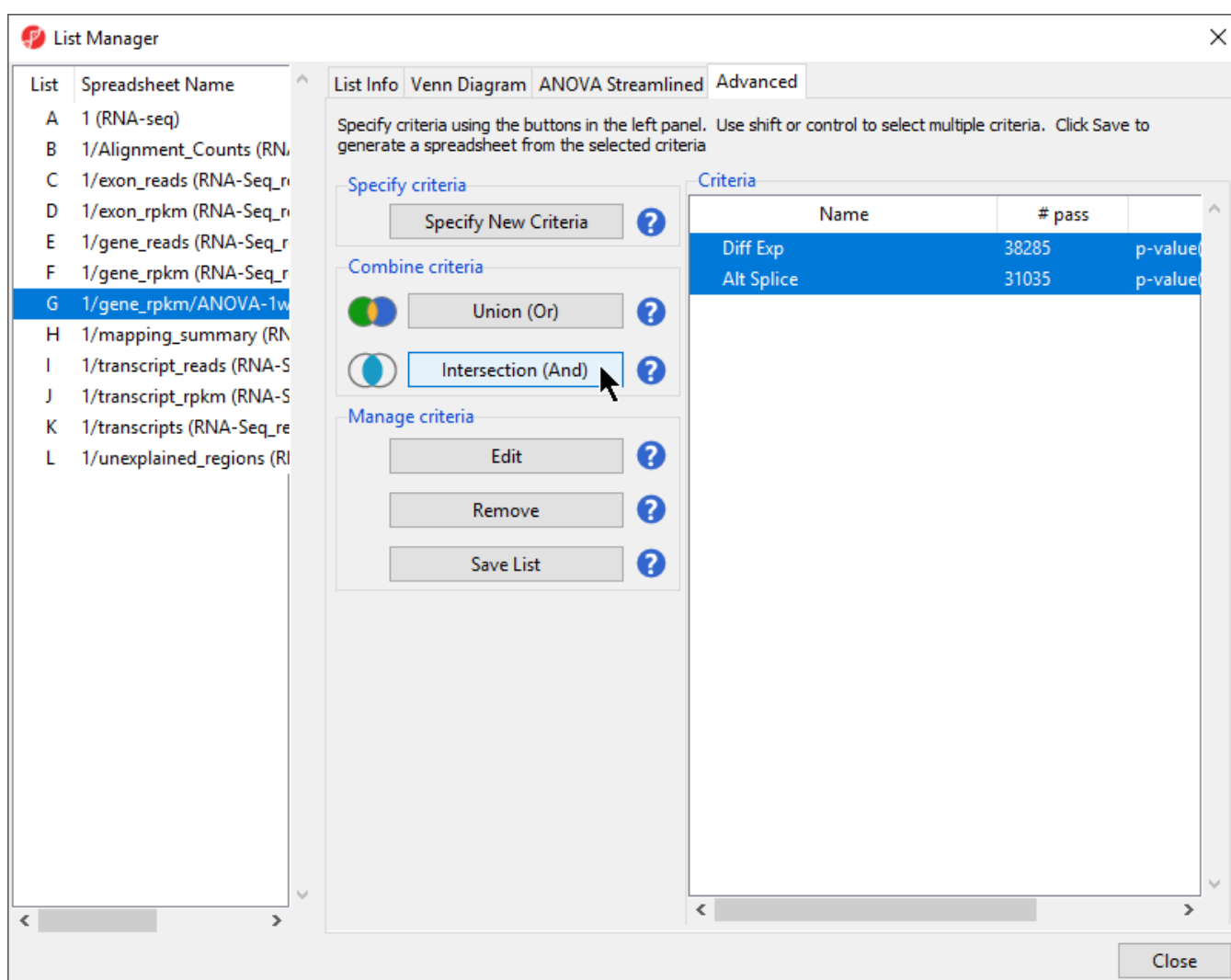
Figure 11. Creating a gene list at the intersection of two criteria

- Enter a name for the criteria (*Diff Exp and Alt Splice*)
- Select **OK** to close the naming dialog and **OK** again to close the list creation hint dialog
- Select **Save List** from the *Manage criteria* section of the *List Manager* dialog (Figure 5)
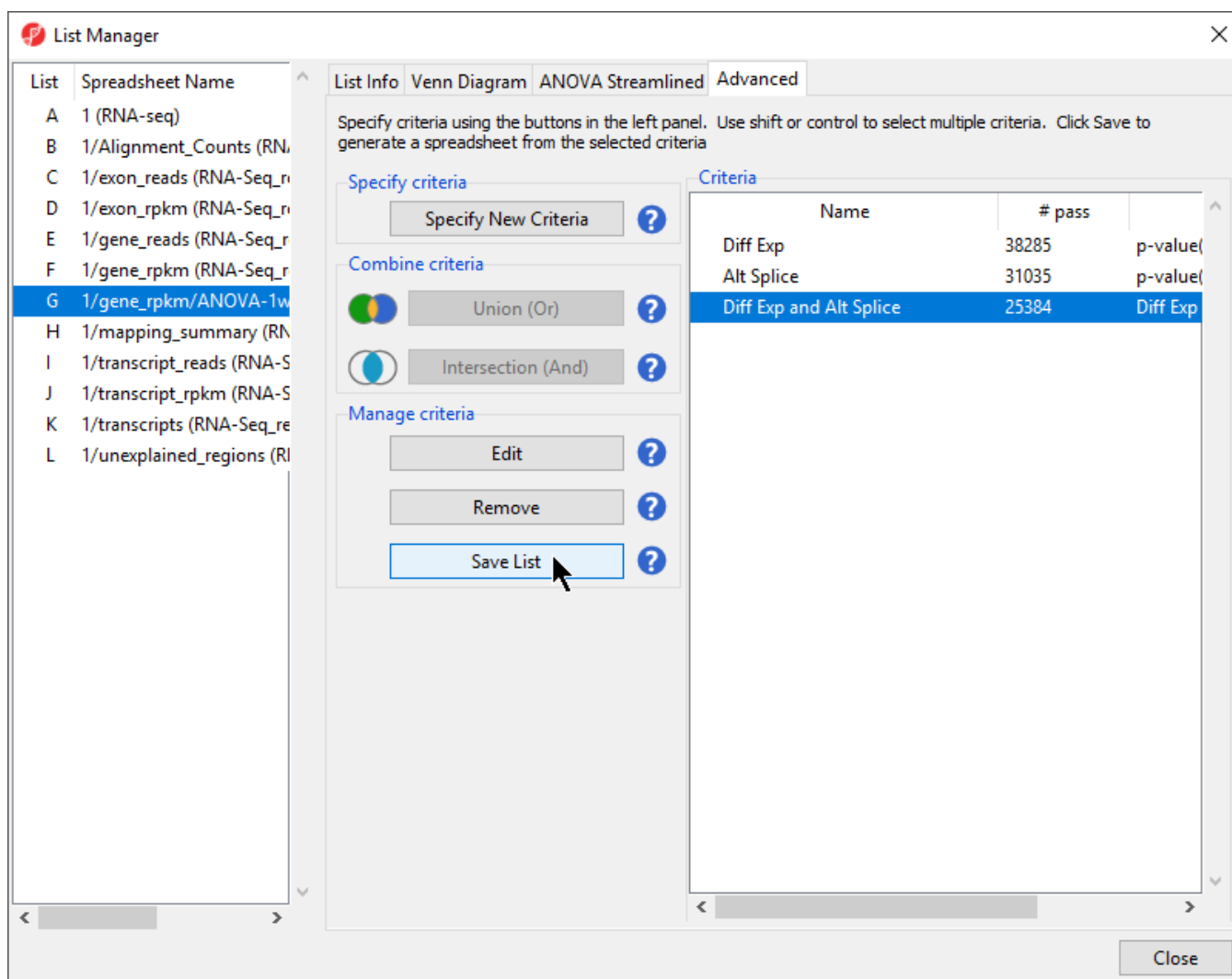
Figure 12. Saving a created list criteria

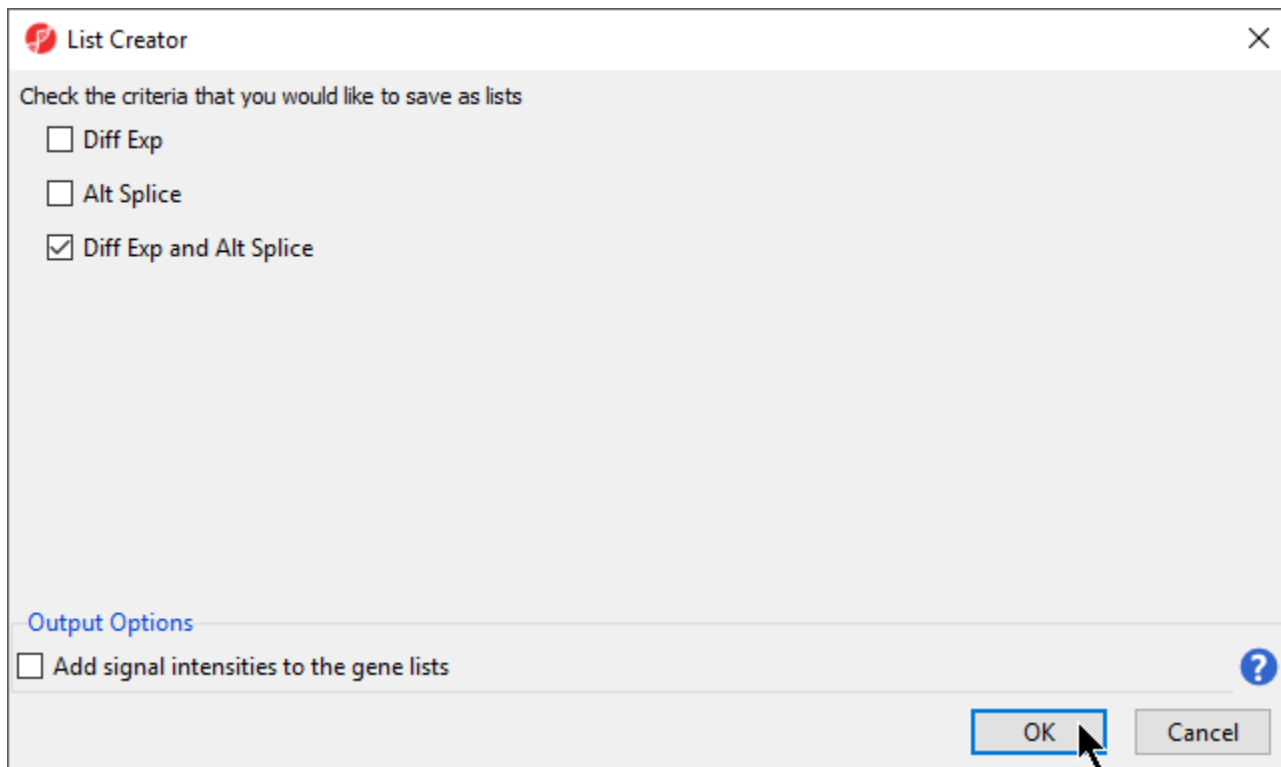- Select **Diff Exp and Alt Splice** in the *List Creator* dialog (Figure 6)

Figure 13. Selecting list to save in List Creator dialog

- Select **OK** to save the list
- Select **Close** to exit the *List Manager* dialog and view the *Diff_Exp_and_Alt_Splice* spreadsheet (Figure 7)
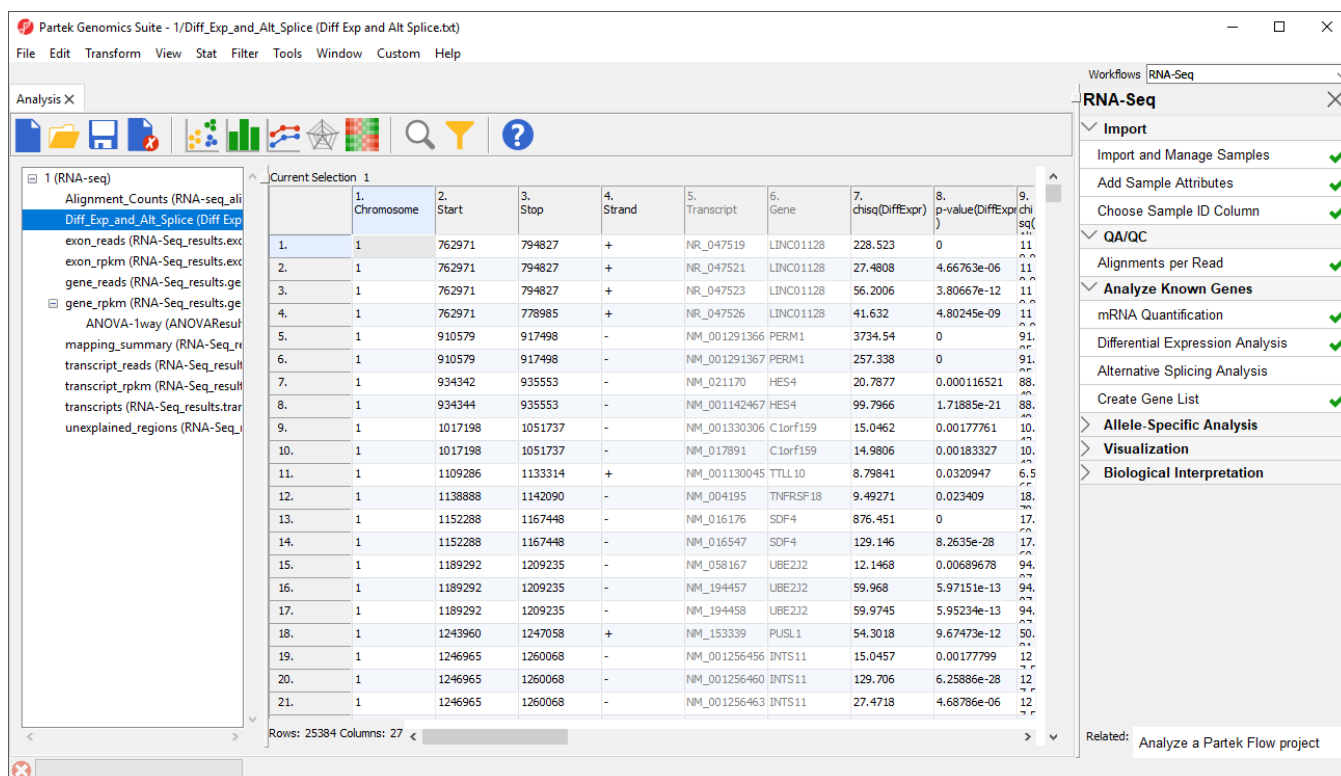
Figure 14. A list of the differentially expressed and alternatively spliced genes is now available for downstream analysis

This list of differentially expressed and alternatively spliced transcripts will be used later in the tutorial.

« Detecting differential expression in RNA-Seq data   Visualizing mapped reads with Chromosome View »

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