## Create a marker list

To analyze differences in methylation between our experimental groups, we need to create a list of deferentially methylated loci.

- · Select Create Marker List from the Analysis section of the Illumina BeadArray Methylation workflow
- Select LCLs vs. B cells (Figure 1)

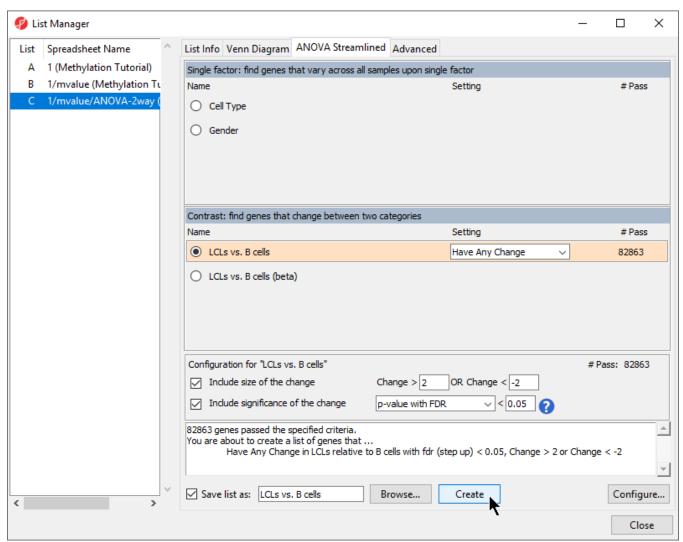


Figure 1. Creating a list of significantly differentially methylated loci

- Leave Include size of the change selected and set to Change > 2 OR Change < -2
- Leave Include significance of the change selected and set to p-value with FDR < 0.05</li>
- Select Create
- Select Close to exit the list manager

The new spreadsheet LCLs vs. B cells (LCLs vs. B cells) will open in the Analysis tab.

It is best practice to occasionally save the project you are working on. Let's take the opportunity to do this now.

- Select File from the main command toolbar
- Select Save Project...
- Specify a name for the project, we chose *Methylation Tutorial*, using the *Save File* dialog
- Select **Save** to save the project

Saving the project saves the identity and child-parent relationships of all spreadsheets displayed in the spreadsheet tree. This allows us to open all relevant spreadsheets for our analysis by selecting the project file.

« Detect differentially methylated loci Filter loci with the interactive filter »

## Additional Assistance

If you need additional assistance, please visit our support page to submit a help ticket or find phone numbers for regional support.

