

Exploring the data set with PCA

The principal components analysis (PCA) scatter plot allows us to visualize similarities and differences between the samples in a data set.

- Click the **Normalized counts** data node
- Click **Exploratory analysis** in the task menu
- Click **PCA**
- Click **Finish** to run PCA with the default options

The *PCA* task node will be added to the pipeline (Figure 1)

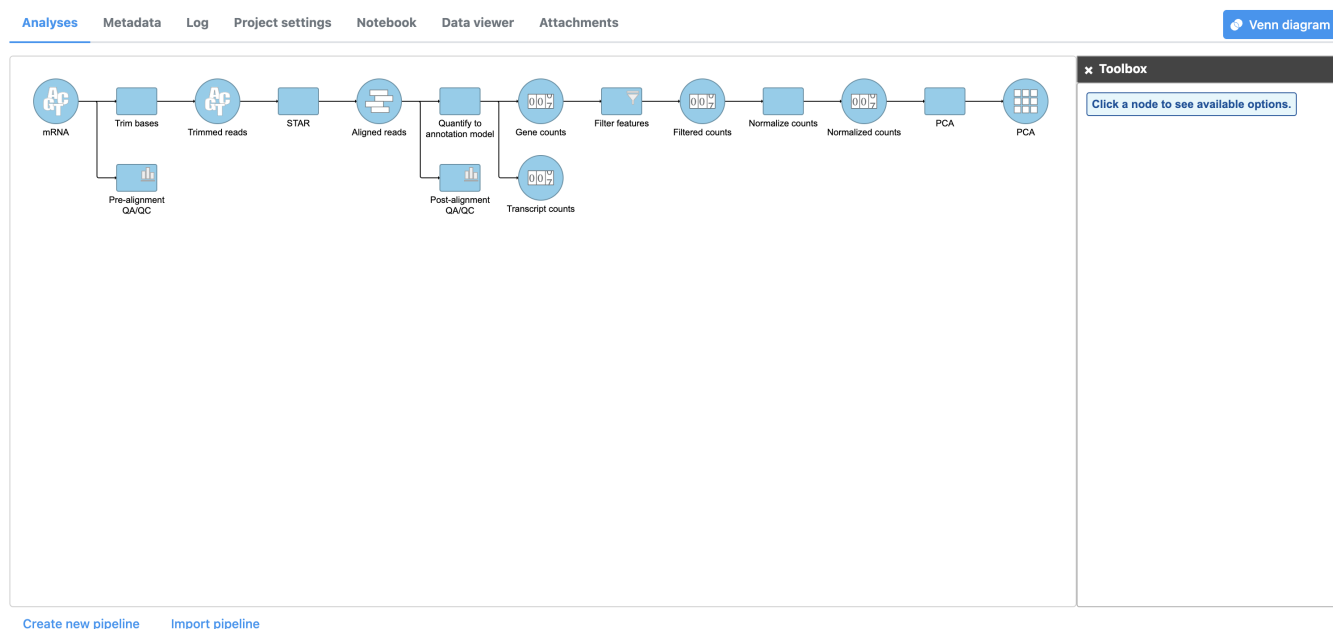


Figure 3. PCA task node

- Double click the **PCA** data node to open the PCA scatter plot (Figure 2)

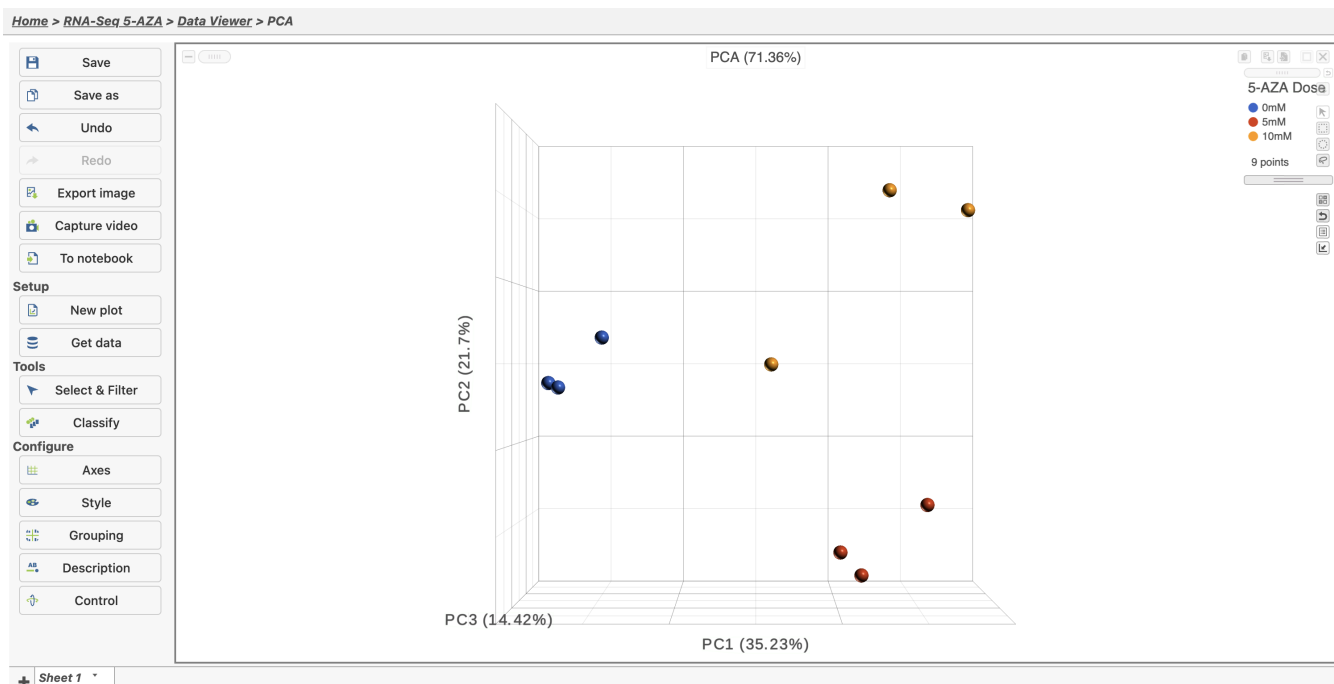


Figure 4. Viewing the PCA scatter plot

In the *Data Viewer*, click **Style** under *Configure* and set the *Color by* drop-down to **5-AZA Dose**. The scatter plot shows each sample as a sphere, colored by treatment group, in a three dimensional plot. The x, y, and z axes are the first three principal components. The percentage of total variance explained by each is listed next to the axis label. The size of each axis is determined by the variance along that axis. The plot is fully interactive; it can be rotated and points selected.

Here, we can see that samples separate based on treatment, but there is noticeable separation within treatment groups, particularly the 0M and 10M treatment groups.

For more detailed information about the PCA scatter plot, please see the [PCA](#) user guide.

« [Normalizing counts](#) [Performing differential expression analysis with DESeq2](#) »

Additional Assistance

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



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