

Filtering features

Low expression genes may be indistinguishable from noise and will decrease the sensitivity of differential expression analysis.

- Click the **Gene counts** node
- Click **Filtering** in the task menu
- Click **Filter features** (Figure 1)

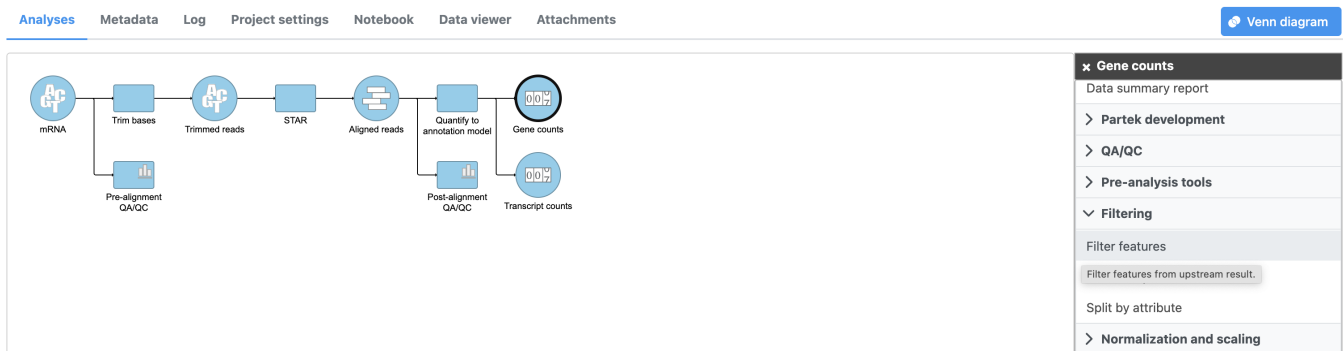


Figure 4. Selecting Filter features

- Click **Noise reduction filter**
- Set the filter to **maximum ≤ 10**
- Click **Finish** (Figure 2)

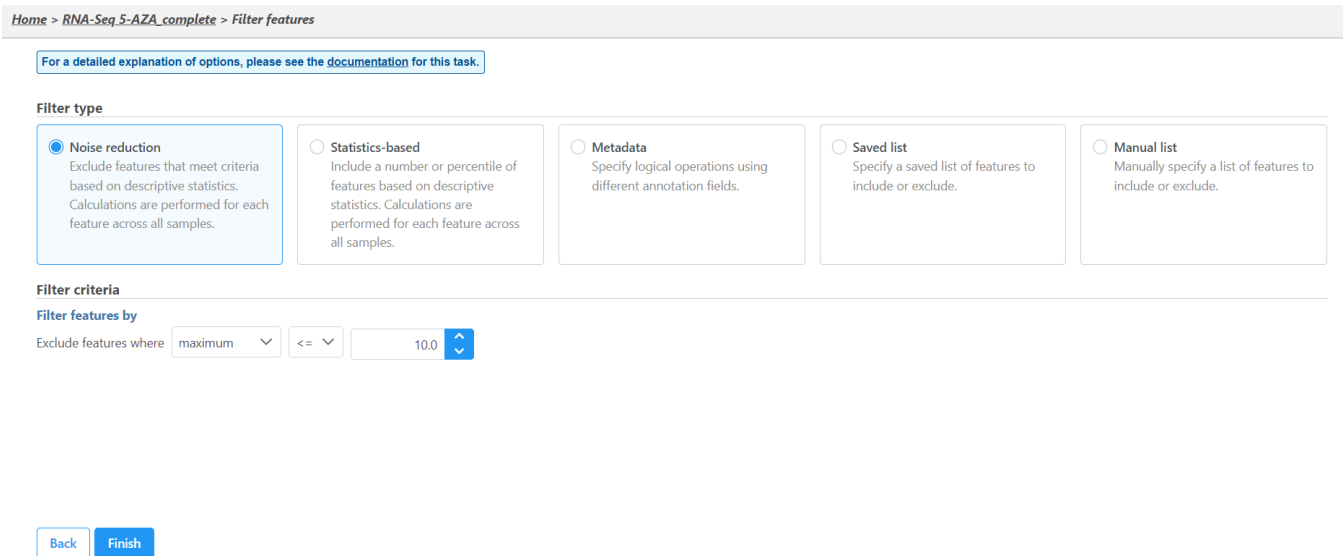


Figure 5. Filtering low expressed genes

A new *Filtered counts* node will be created (Figure 3).

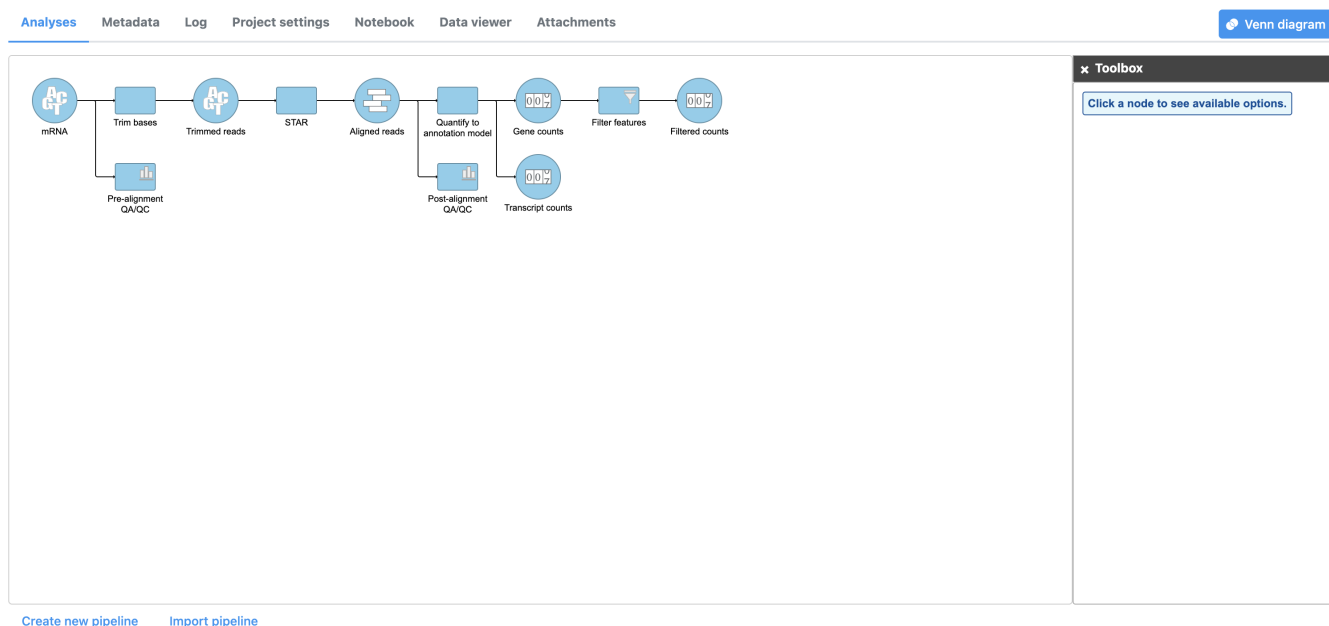


Figure 6. *Filtered counts node*

« [Quantifying to an annotation model](#) [Normalizing counts](#) »

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:



31 rates