

# 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)

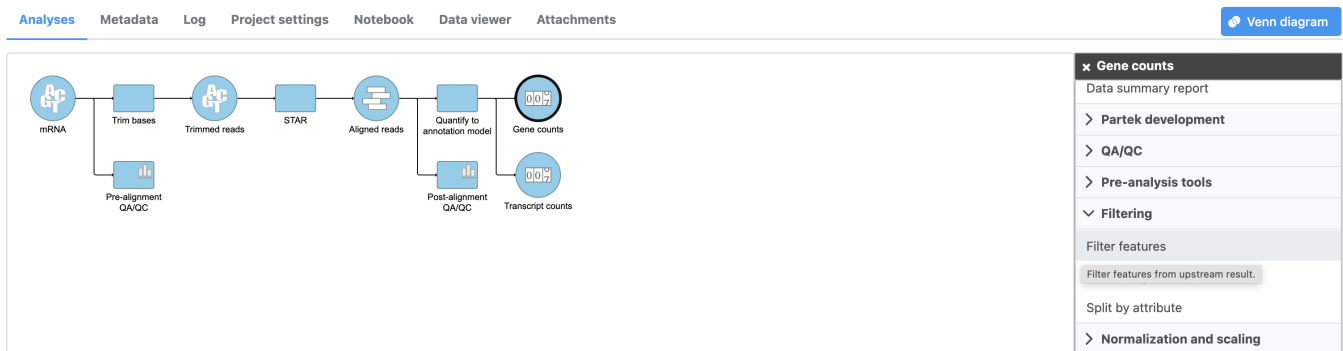


Figure 4. Selecting Filter features

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

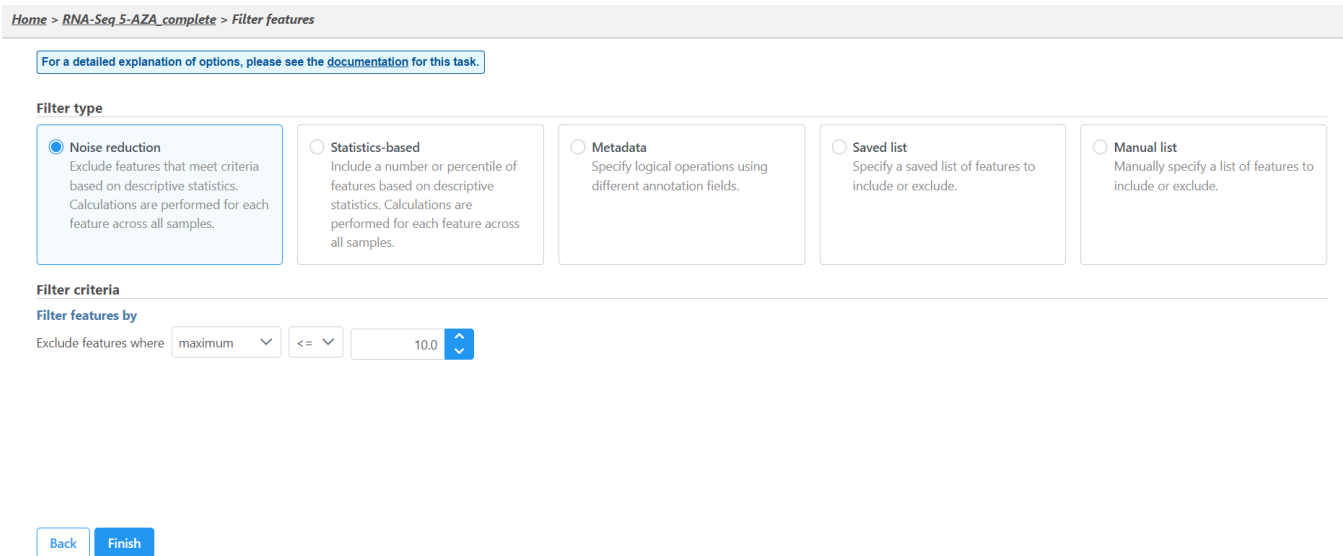


Figure 5. Filtering low expressed genes

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

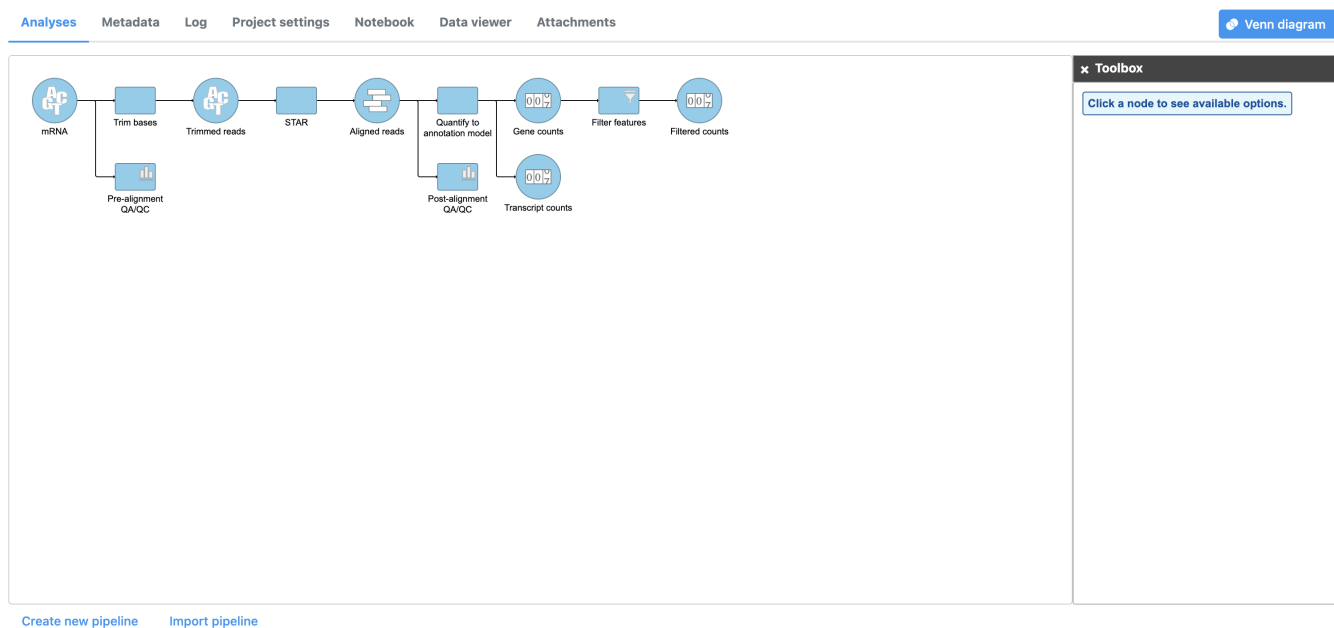


Figure 6. Filtered counts node

« Quantifying to an annotation model Normalizing counts »

## Additional Assistance

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