Running post-alignment QA/QC

After alignment has completed, we can view the quality of alignment by performing post-alignment QA/QC.

- Click the **Aligned reads** data node
- Click **QA/QC** inthe task menu
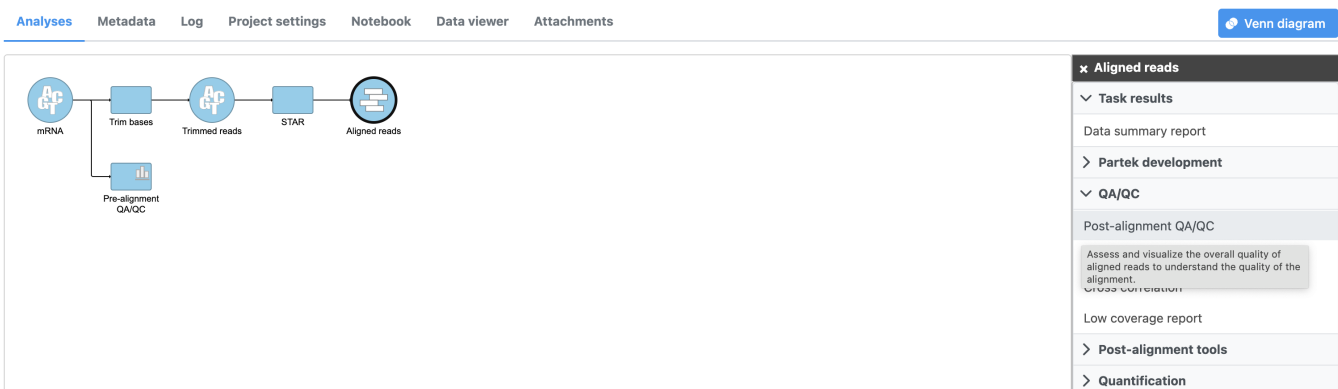- Click **Post-alignment QA/QC** from the *QA/QC* section of the task menu (Figure 1)

Figure 4. Invoking Post-alignment QA/QC

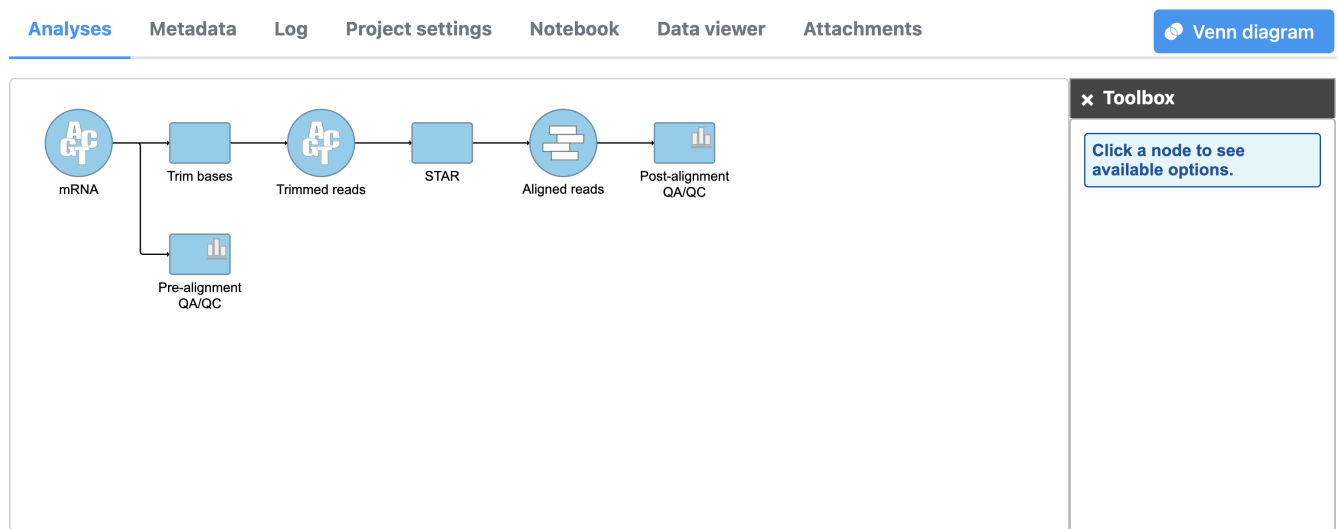A *Post-alignment QA/QC* task node will be generated (Figure 2).

Figure 5. Post-alignment QA/QC task node

- Double-click the **Post-alignment QA/QC** task node to view the task report

Similar to the *Pre-alignment QA/QC* task report, general quality information about the whole data set is displayed and sample-level reports can be opened by clicking a sample name in the table.

The top two graphs in the data set view (Figure 3) show the alignment breakdown and coverage.
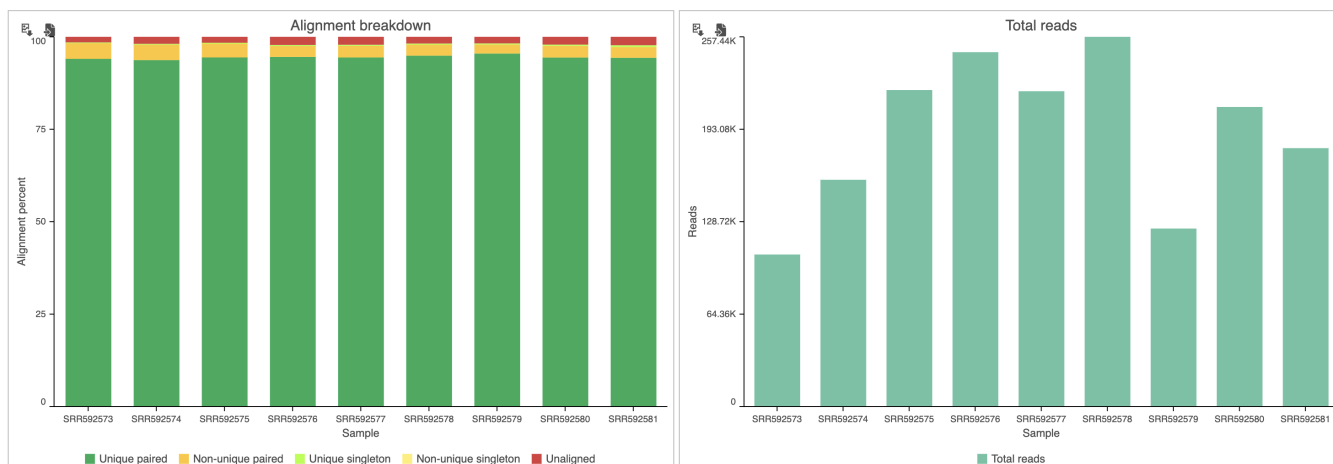
Figure 6. Alignment statistics for the data set

From these graphs, we can see that more than 95% of reads were aligned, but the total number of reads for each sample varies. Normalizing for the variability in total read counts will be addressed in a later section of the tutorial.

For more information about the graphs and information presented in the *Post-alignment QA/QC* task report, see the Post-alignment QA/QC user guide.

« Aligning to a reference genome   Quantifying to an annotation model »

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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