

Aligning to a reference genome

With our reads trimmed, we now have high-quality reads for each sample. The next step is to align the reads to a reference genome. Alignment matches each of the short sequencing reads to a location in the reference genome.

- Click **Trimmed reads**
- Click **Aligners** in the task menu to display available aligners (Figure 1)

The screenshot shows the Partek Flow interface. At the top, there is a navigation bar with tabs: Analyses, Metadata, Log, Project settings, Notebook, Data viewer, Attachments, and a Venn diagram button. Below the navigation bar is a pipeline diagram with nodes: mRNA, Trim bases, Trimmed reads, and Pre-alignment QA/QC. On the right side, there is a panel titled 'Trimmed reads' with a 'Double click data node to view report.' button. Below this panel is a list of aligners under the 'Aligners' section: Bowtie, Bowtie 2, HISAT 2, BWA, and STAR. A tooltip for STAR is visible, stating: 'Relatively fast and accurate, but requires a lot of memory. Identifies junctions, handles gaps, detects chimeric (fusion) junctions. Can handle small RNA reads with no limit on read length.'

Figure 4. A variety of different aligners are available in Partek Flow. In this tutorial we will use STAR aligner, a popular choice for aligning RNA-Seq data.

Partek Flow offers a variety of different aligners. Mouse over any option for a short description. For this tutorial, we will use STAR, a fast and accurate aligner commonly used for RNA-Seq data. For more information about STAR and the other aligners, please consult the [Aligners](#) user guide.

- Click **STAR**

The STAR aligner options allow us to select the genome build (assembly) and index. For this tutorial, our data set contains only reads that map to chromosome 22 to minimize the time required for resource-intensive tasks, such as alignment.

- Click **Finish** to run with **hg19** selected for *Assembly* and **Whole genome** for the *Aligner index* (Figure 2)

Select STAR 2.7.8a index

Assembly

Homo sapiens (human) - hg19 ▾

Index

Whole genome (Administrator) ▾

Alignment options

Generate unaligned reads

Generate an unaligned reads node for further analysis at the expense of an increase in running time and disk space.

Advanced options

Option set

-- Default -- ▾

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Figure 5. Configuring the STAR aligner

Alignment is a resource-intensive task and may take around 20 minutes to complete, even when mapping only reads from a single chromosome. Task and data nodes that have been queued, but not completed, are shown in a lighter color than completed tasks (Figure 3).

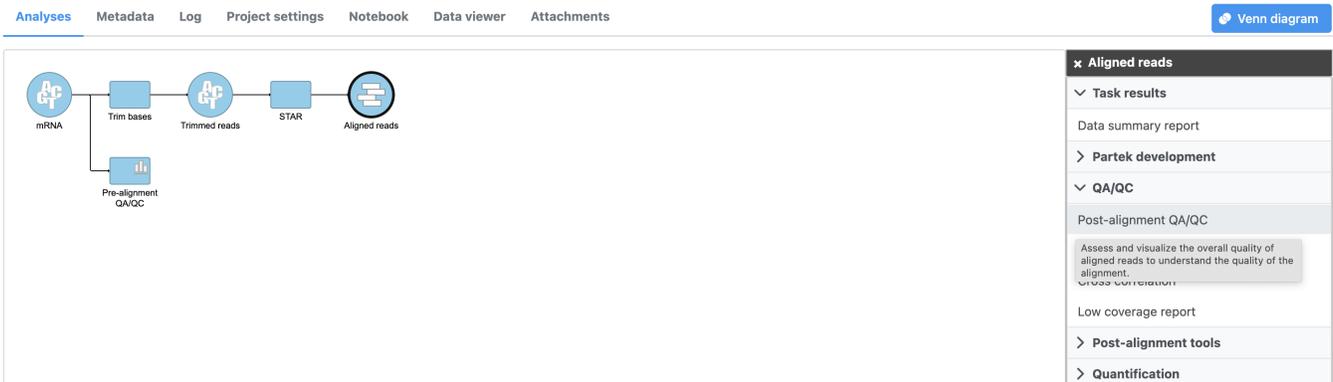


Figure 6. Queued tasks and their output data nodes are shown in a lighter color

The *Align reads* task generates an *Aligned reads* data node once complete. You can wait for the alignment task to finish or you can continue building the pipeline while the results of alignment are pending; additional tasks can be added to the pipeline and queued before the current task has completed.

[« Trimming bases and filtering reads](#) [Running post-alignment QA/QC](#) »

Additional Assistance

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