Pre-alignment tools

Partek® Flow® provides *Pre-alignment tools* that allow the user to process next-generation sequencing data before proceeding to alignment. These tools are not only useful for controlling the quality of data, but can also be used for subsampling prior to analyzing the full dataset. There are three functions available in *Pre-alignment tools*:

- Trim bases
- Trim adapters
- Filter reads
- Trim tags

User is expected to have preliminary understanding of:

- File formats for next generation sequencing data
- Phred-quality score

Showing Pre-alignment tools

In order to show the *Pre-alignment tools*, select an **Unaligned reads** or **Trimmed reads** data node. They will appear on the context-sensitive menu on the right of the screen (Figure 1).
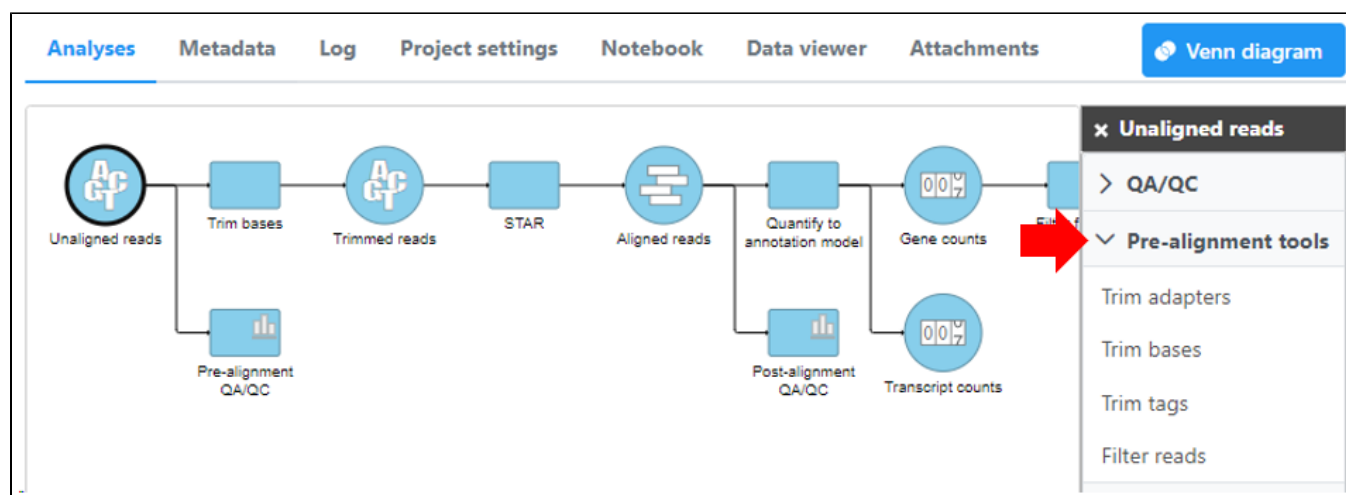

Figure 1. Showing Pre-alignment Tools from an unaligned reads node

Different *Pre-alignment tools* are available for different formats of unaligned reads. For example: if the reads are in FASTQ format, then all four tools are available. On the other hand, if the unaligned reads are in FASTA or SFF format, then the *Filter reads* option is not available.

Additional Assistance

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