

# Trim and Align Sanger Reads

The workflow does the following things:

- 1) Reads a set of Sanger sequencing reads from ABI files.
- 2) Trims ends of the reads by the quality value.
- 3) Filter the short trimmed reads.
- 4) Aligns the filtered trimmed reads to a reference sequence.

You can change the workflow parameters:

- 1) Quality threshold for the trimming.
- 2) Minimum read length. If length of a trimmed read is less than the minimum value then the read is filtered.

The output data are:

- 1) Multiple sequence alignment file. The first sequence of the alignment is the reference and other ones are the reads.
- 2) Annotated reference sequence file. The annotations are the aligned reads.



## How to Use This Sample

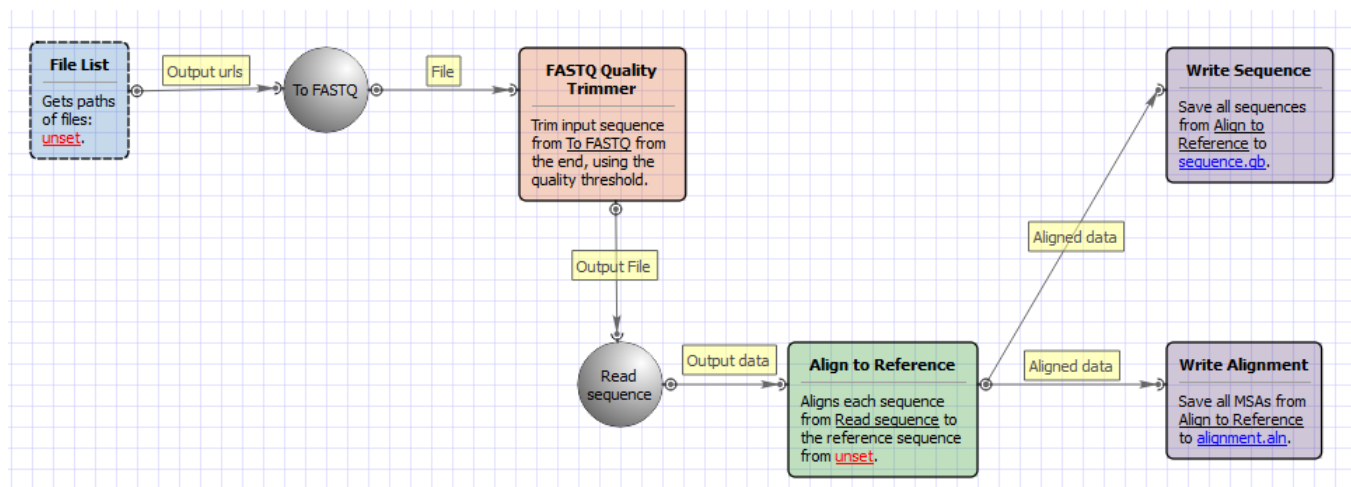
If you haven't used the workflow samples in UGENE before, look at the "[How to Use Sample Workflows](#)" section of the documentation.

## Workflow Sample Location

The workflow sample "Trim and Align Sanger Reads" can be found in the "Sanger Sequencing" section of the Workflow Designer samples.

## Workflow Image

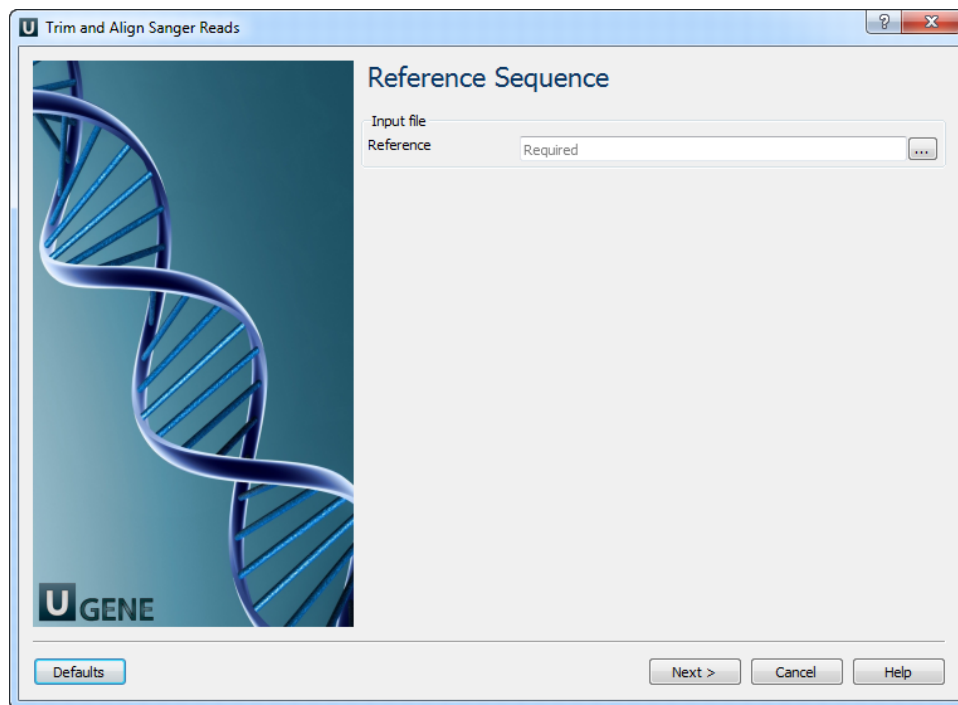
The opened workflow looks as follows:



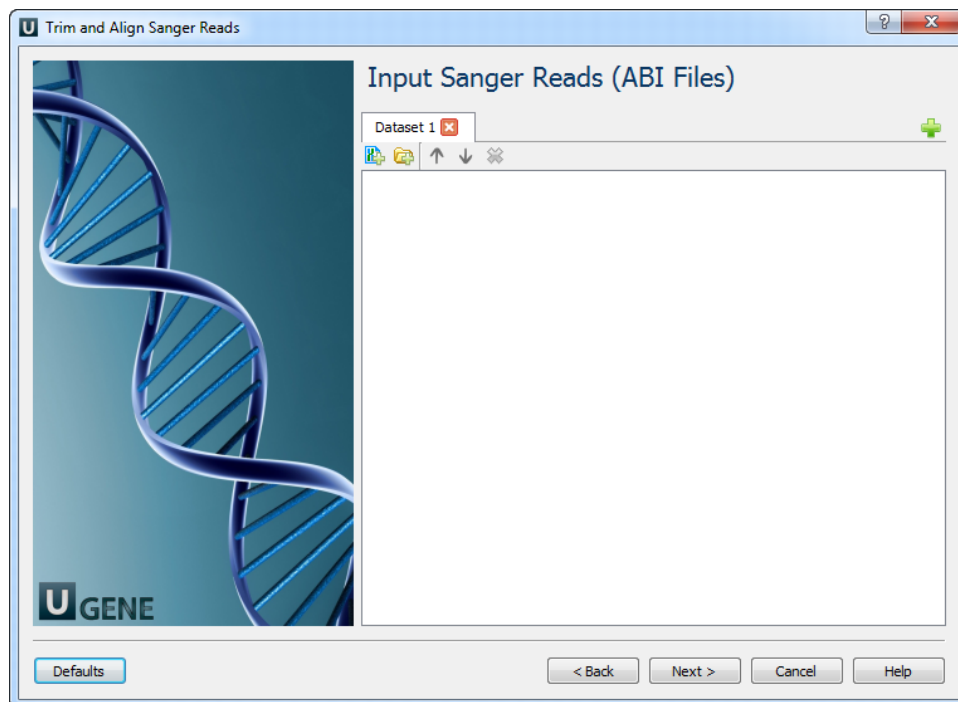
## Workflow Wizard

The wizard has 4 pages.

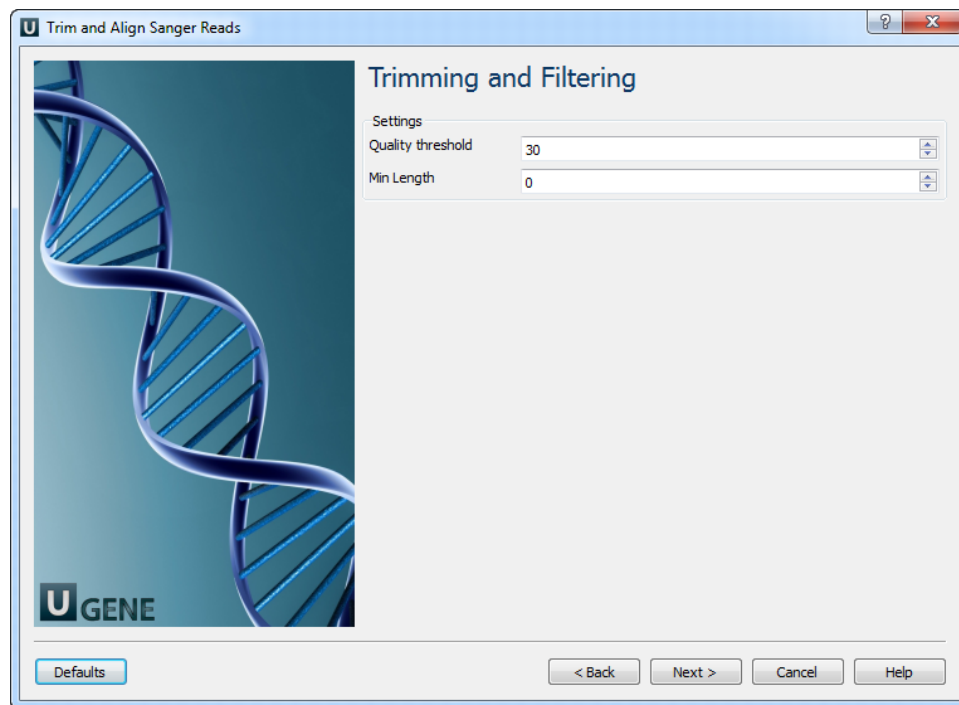
1. Reference Sequence: On this page you must input reference sequence.



2. Input Sanger Reads (ABI Files): On this page you must input ABI file(s).



3. Trimming and Filtering: On this page you can modify trimming and filtering settings.



The following parameters are available:

|                   |                                              |
|-------------------|----------------------------------------------|
| Quality threshold | Quality threshold for trimming.              |
| Min Length        | Too short reads are discarded by the filter. |

4. Results: On this page you can modify output files settings.

