

# Raw RNA-Seq Processing

⚠ Download and install the UGENE [FULL](#) or [NGS package](#) to use this pipeline.

Use this workflow sample to process raw RNA-seq next-generation sequencing (NGS) data from the Illumina platform. The processing includes:

- **Filtration:**
  - Filtering of the NGS short reads by the CASAVA 1.8 header;
  - Trimming of the short reads by quality;
- **[Optionally] Mapping:**
  - Mapping of the short reads to the specified reference sequence (the TopHat tool is used in the sample);

The result output of the workflow contains the filtered and merged FASTQ files. In case the TopHat mapping has been done, the result also contains the TopHat output files: the accepted hits BAM file and tracks of junctions, insertions and deletions in BED format. Other intermediate data files are also output by the workflow.

## ✔ 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.

## ✔ What's Next?

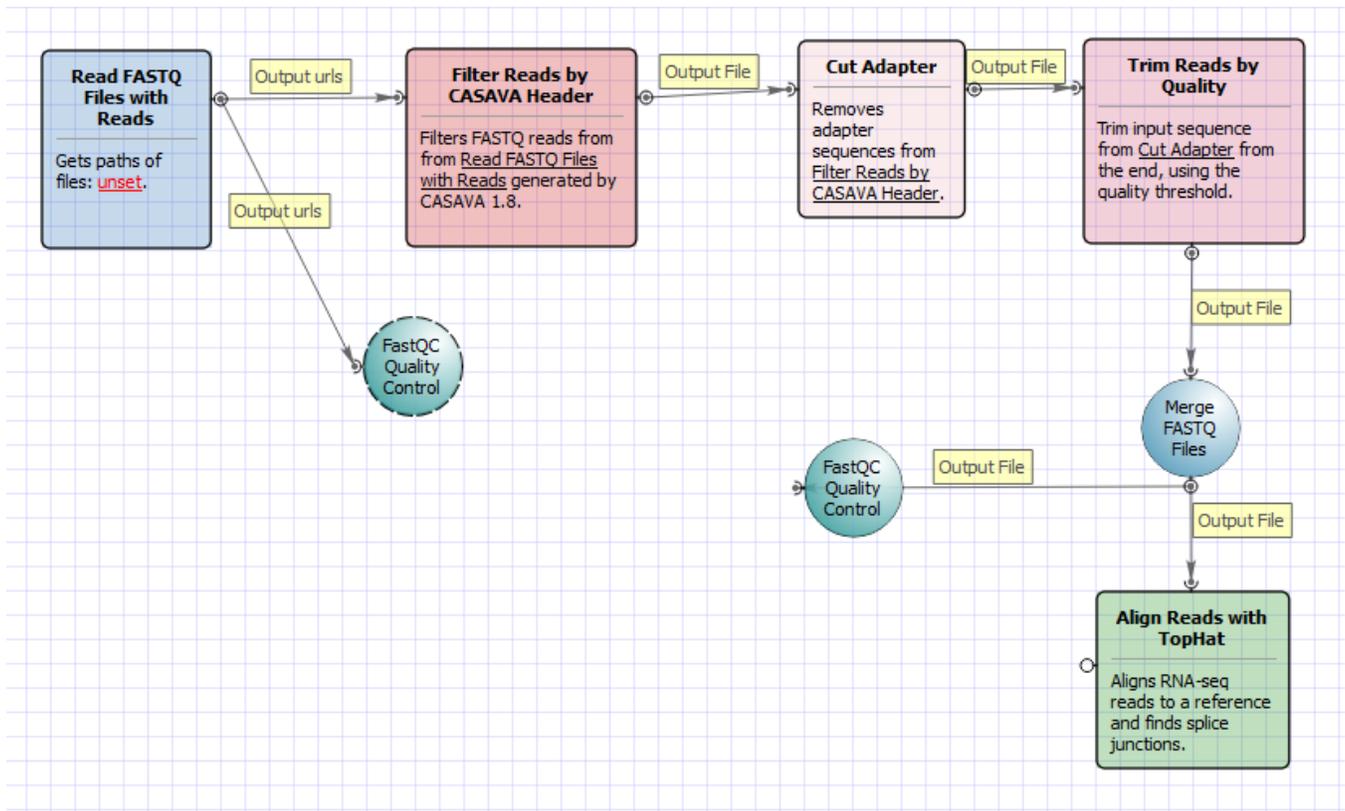
The [Tuxedo workflow](#) can be used to analyze the filtered RNA-seq data. In this case the mapping step of this workflow can be skipped, as it also present in the Tuxedo pipeline.

## Workflow Sample Location

The workflow sample "Raw DNA-Seq processing" can be found in the "NGS" section of the Workflow Designer samples.

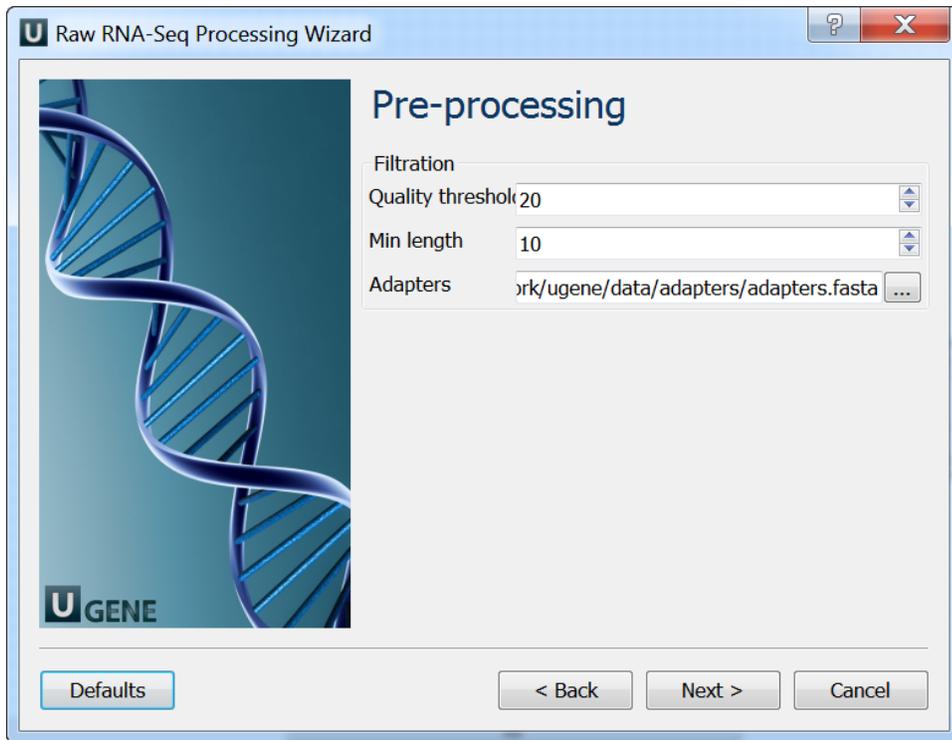
## Workflow Image

There are four versions of the workflow available. The workflow with mapping for single-end reads looks as follows:

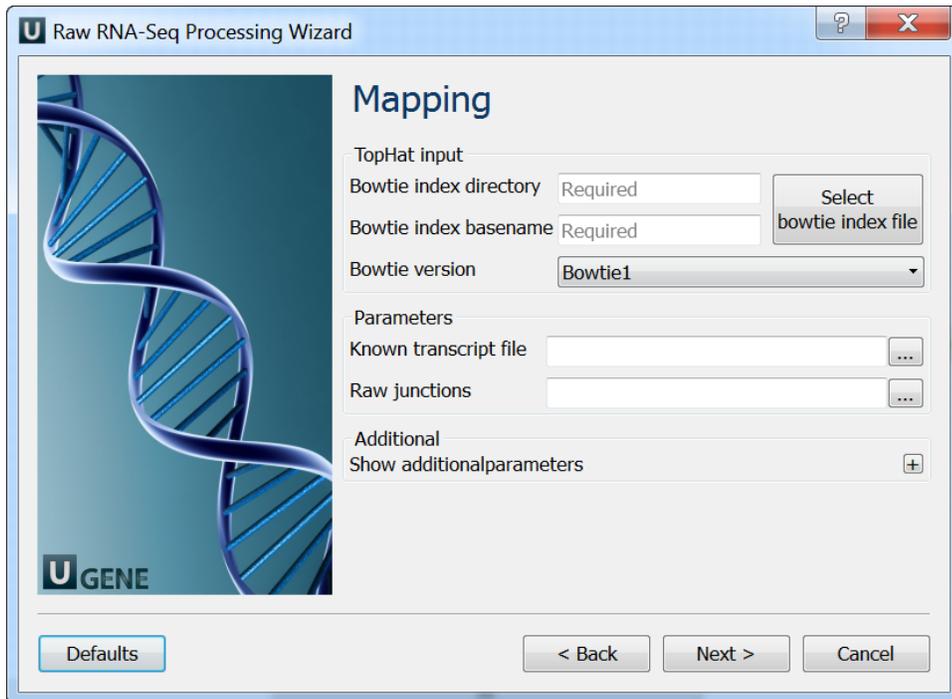


The workflow with mapping for paired-end short appearance is the following:

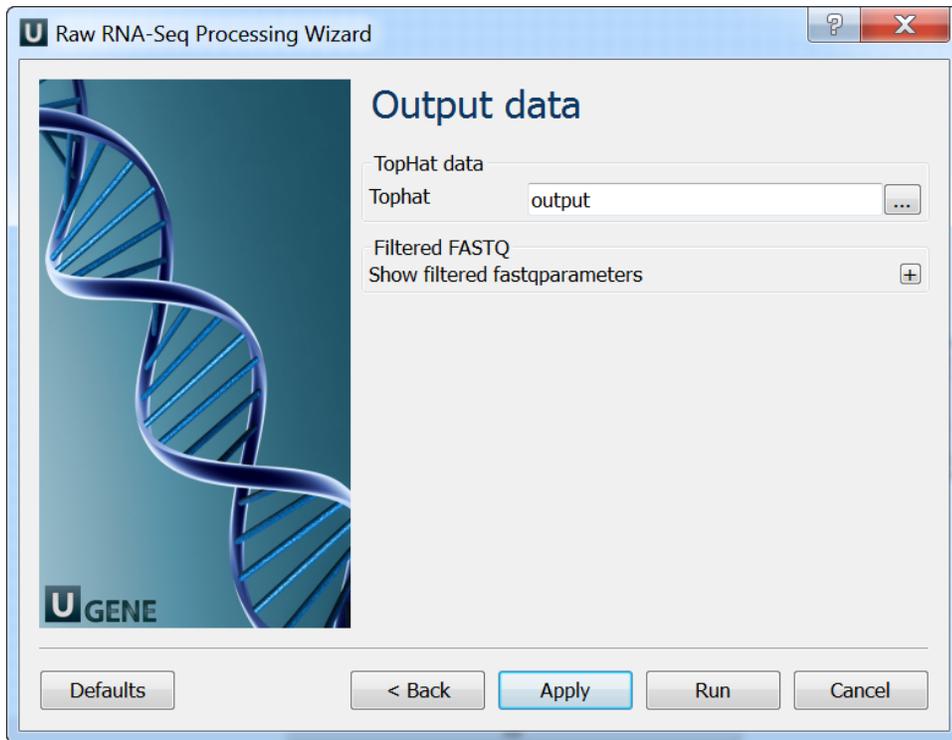




3. Mapping: On this page you must input reference and optionally modify advanced parameters.

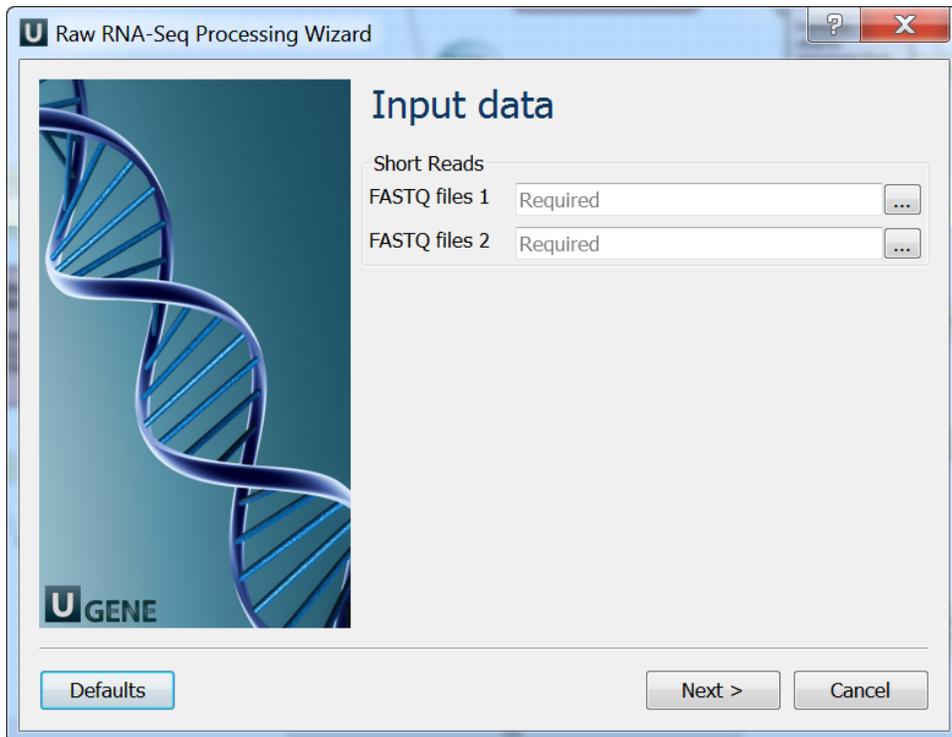


4. Output data: On this page you must input output parameters.

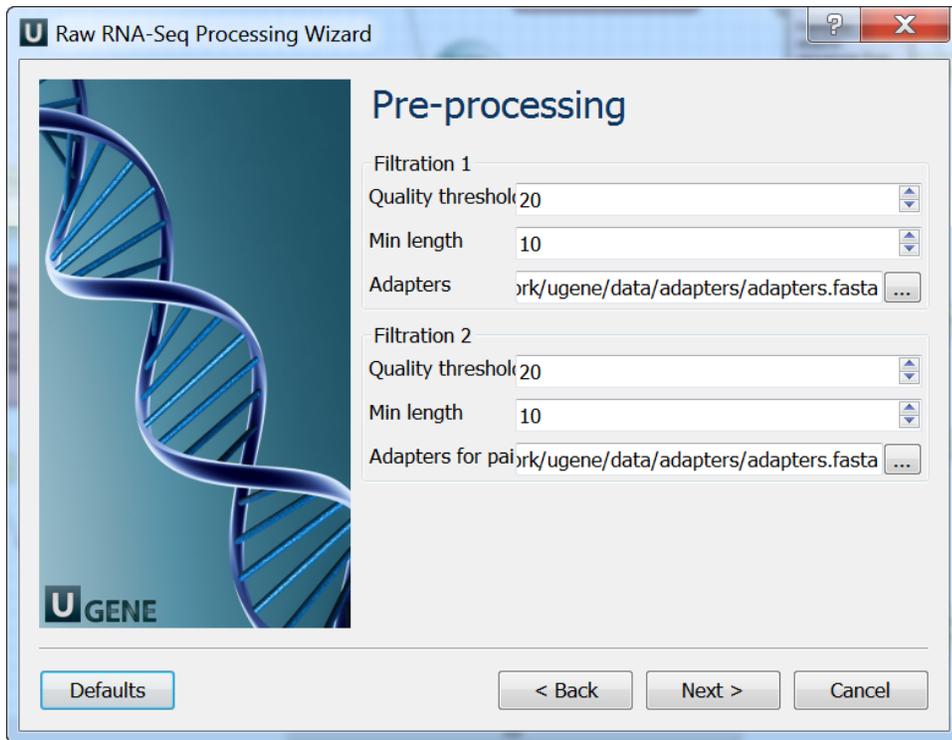


The wizard for paired-end reads has 5 page.

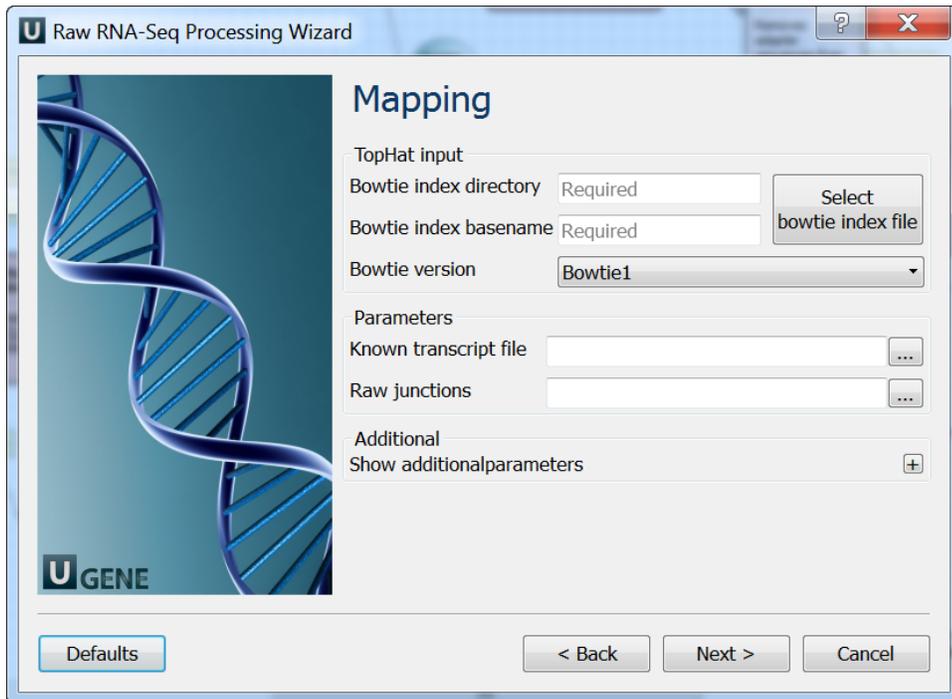
1. Input data: On this page you must input FASTQ file(s).



2. Pre-processing: On this page you can modify filtration parameters.



3. Mapping: On this page you must input reference and optionally modify advanced parameters.



4. Output data: On this page you must input output parameters.

