

Raw ChIP-Seq Processing



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

Use this workflow sample to process raw ChIP-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;
- **Mapping:**
 - Mapping of the short reads to the specified reference sequence (the BWA-MEM tool is used in the sample);
- **Post-filtration:**
 - Filtering of the aligned short reads by SAMtools to remove reads with low mapping quality, unpaired/unaligned reads;
 - Removing of duplicated short reads.

The result of the data processing is provided in the BED format. Intermediate data files from the filtration and mapping steps are also available in the output.



How to Use This Sample

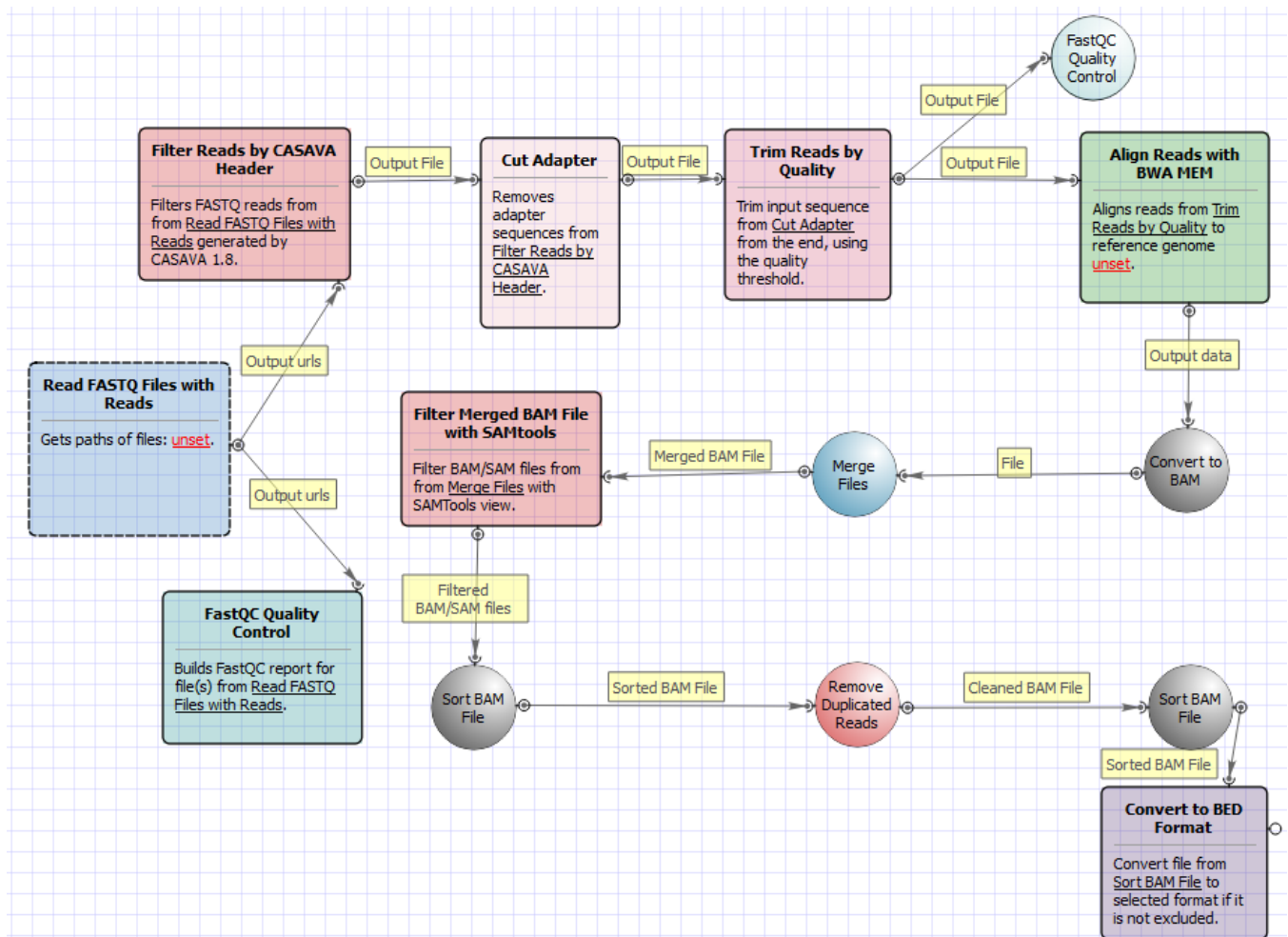
If you haven't used the workflow samples in UGENE before, look at the "[How to Use Sample Workflows](#)" section of the documentation.

Workflow Sample Location

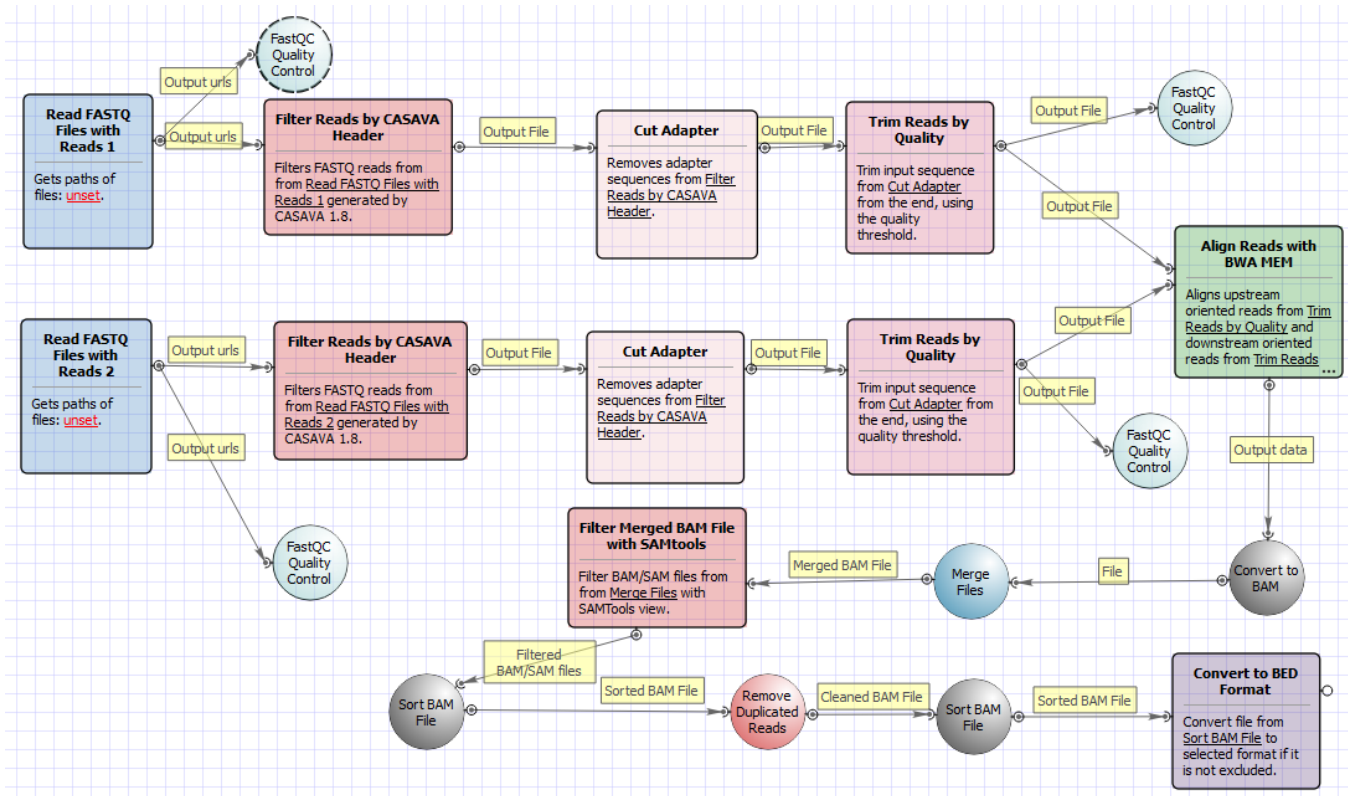
The workflow sample "Raw ChIP-Seq processing" can be found in the "NGS" section of the Workflow Designer samples.

Workflow Image

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



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



Workflow Wizard

The wizard for single-end reads has 5 page.

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

Raw ChIP-seq Processing Wizard

Input data

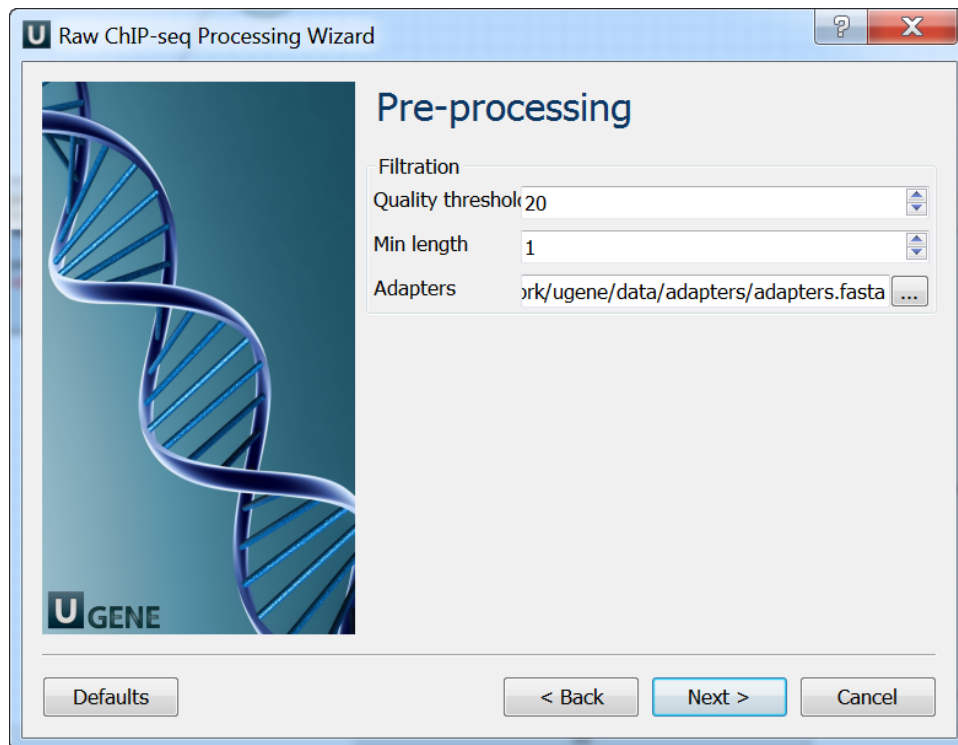
Short Reads

FASTQ files ...

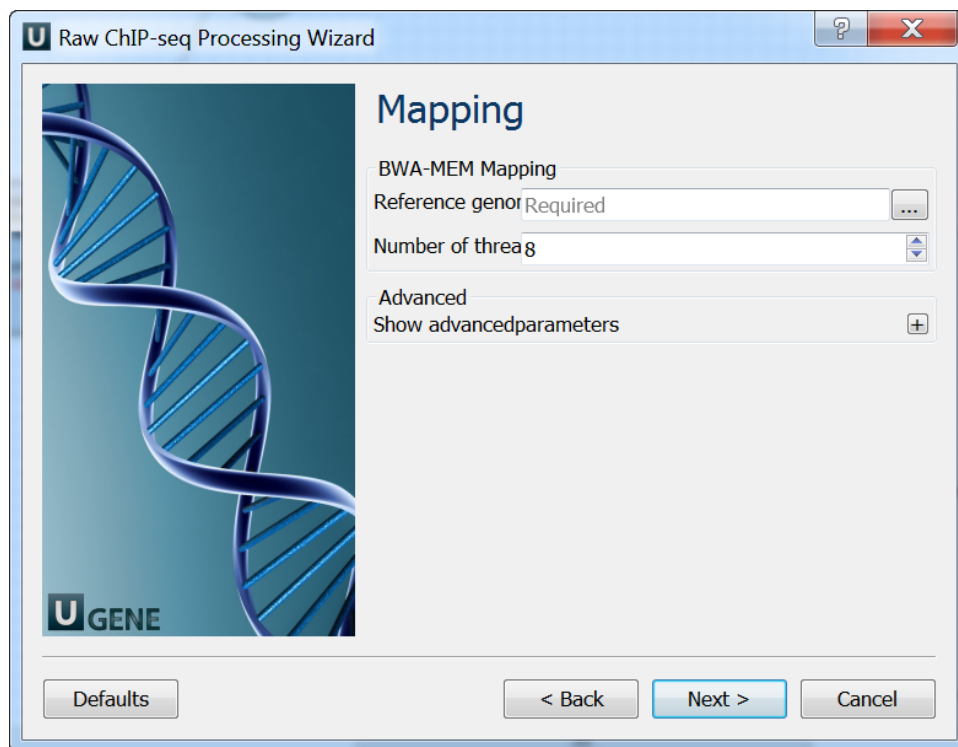
UGENE

Defaults Next > Cancel

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. Post-processing: On this page you can modify post-processing parameters.

Raw ChIP-seq Processing Wizard

Post-processing

Filtration

MAPQ threshold 1

Skip flag Read is the first in a pair;The read is unmapped

Region

Remove Duplicates

For single-end reads True

Defaults < Back Next > Cancel

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

Raw ChIP-seq Processing Wizard

Output data

Aligned data

Output file name out.sam

Output directory output

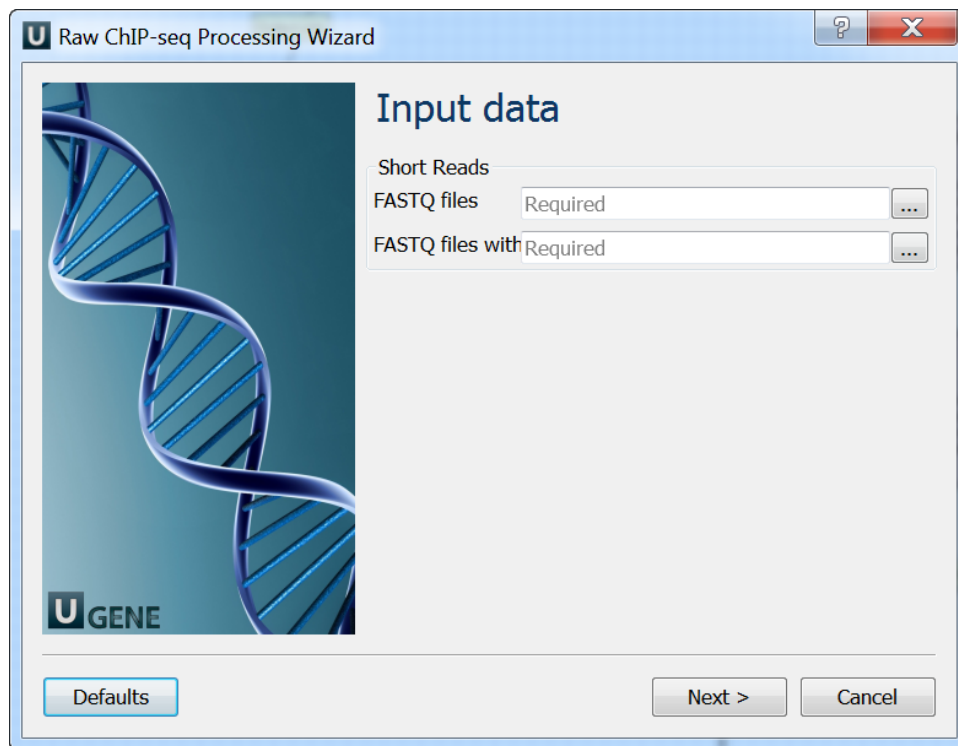
Filtered FASTQ

Show filtered fastqparameters

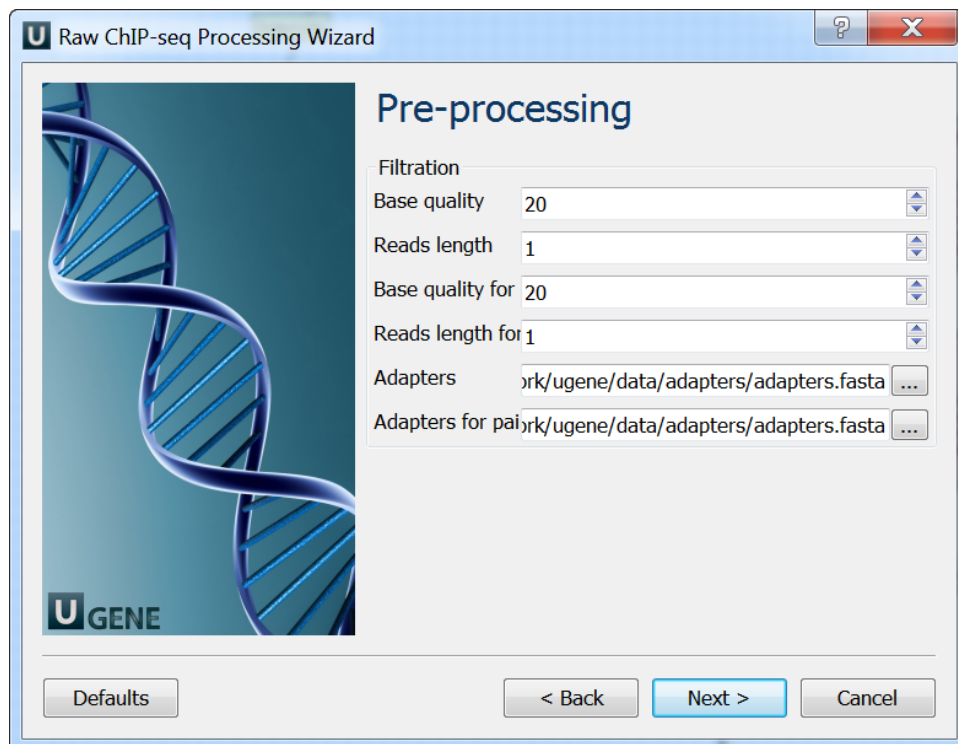
Defaults < Back Apply Run Cancel

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.

U Raw ChIP-seq Processing Wizard

Mapping

BWA-MEM Mapping

Reference genome ...

Number of threads

Advanced
Show advanced parameters

U GENE

Defaults < Back Next > Cancel

4. Post-processing: On this page you can modify post-processing parameters.

U Raw ChIP-seq Processing Wizard

Post-processing

Filtration

MAPQ threshold

Skip flag

Region

Remove Duplicates
For single-end reads

U GENE

Defaults < Back Next > Cancel


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

U

Raw ChIP-seq Processing Wizard

?

X



U GENE

Output data

Aligned data

Output file name

Output directory ...

Filtered FASTQ

Show filtered fastqparameters +

Defaults

< Back

Apply

Run

Cancel