Raw Chip-Seq Processing

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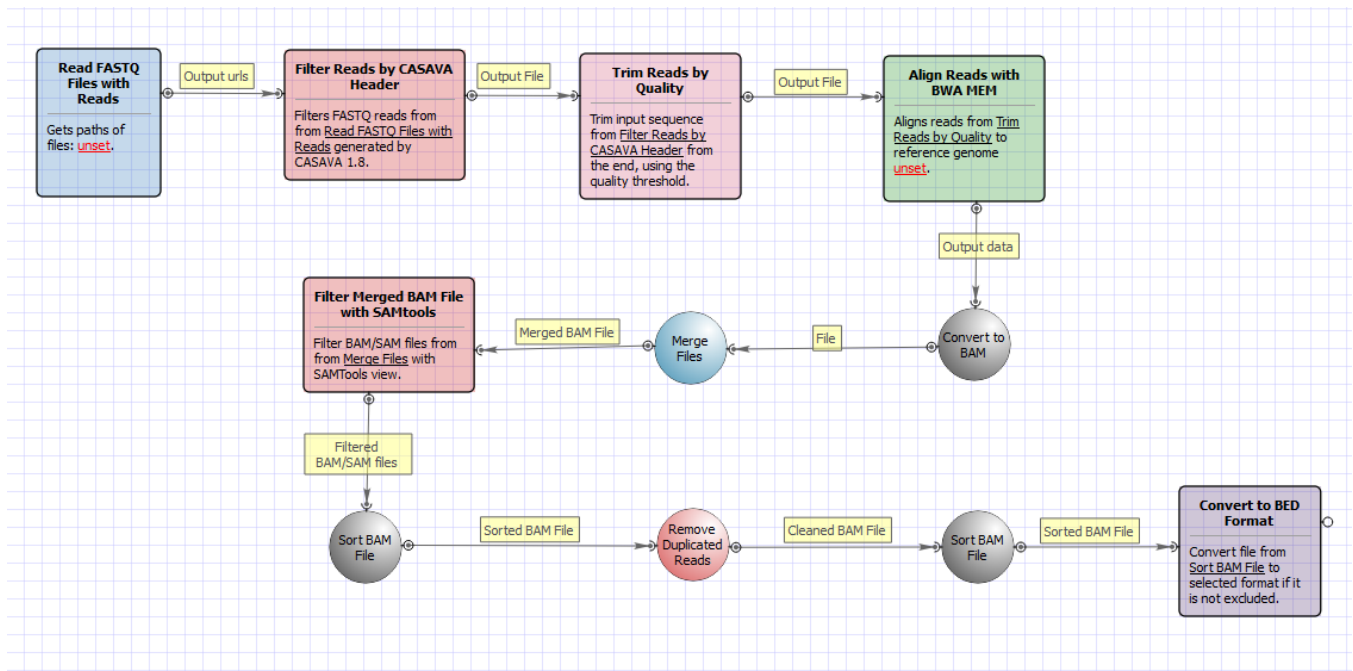
The workflow for paired-end short appearance is the following:

Read FASTQ Files with Reads 1

Gets paths of files: unset.

→ Output urls →

Filter Reads by CASAVA Header

Filters FASTQ reads from from Read FASTQ Files with Reads 1 generated by CASAVA 1.8.

→ Output File →

Trim Reads by Quality

Trim input sequence from Filter Reads by CASAVA Header from the end, using the quality threshold.

→ Output File →

Read FASTQ Files with Reads 2

Gets paths of files: unset.

→ Output urls →

Filter Reads by CASAVA Header

Filters FASTQ reads from from Read FASTQ Files with Reads 2 generated by CASAVA 1.8.

→ Output File →

Trim Reads by Quality

Trim input sequence from Filter Reads by CASAVA Header from the end, using the quality threshold.

→ Output File →

Align Reads with BWA MEM

Aligns upstream oriented reads from Trim Reads by Quality and downstream oriented reads from Trim Reads ...

→ Output data →

Convert to BAM

→ File →

Merge Files

→ Merged BAM File →

Filter Merged BAM File with SAMtools

Filter BAM/SAM files from from Merge Files with SAMTools view.

→ Filtered BAM/SAM files →

Sort BAM File

→ Sorted BAM File →

Remove Duplicated Reads

→ Cleaned BAM File →

Sort BAM File

→ Sorted BAM File →

Convert to BED Format

Convert file from Sort BAM File to selected format if it is not excluded.