

# FASTQ Quality Trimmer Element

The workflow scans each input sequence from the end to find the first position where the quality is greater or equal to the minimum quality threshold. Then it trims the sequence to that position. If a the whole sequence has quality less than the threshold or the length of the output sequence less than the minimum length threshold then the sequence is skipped.

**Element type:** QualityTrim

## Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
<b>Output directory</b>	Select an output directory. Custom - specify the output directory in the 'Custom directory' parameter. Workflow - internal workflow directory. Input file - the directory of the input file.	Input file	<b>out-mode</b>	<i>numeric</i>
<b>Custom directory</b>	Specify the output directory.		<b>custom-dir</b>	<i>string</i>
<b>Output file name</b>	A name of an output file. If default of empty value is provided the output name is the name of the first file with additional extention.		<b>out-name</b>	<i>string</i>
<b>Quality threshold</b>	Quality threshold for trimming.	30	<b>qual-id</b>	<i>numeric</i>
<b>Min Length</b>	Too short reads are discarded by the filter.	0	<b>len-id</b>	<i>numeric</i>
<b>Trim both ends</b>	Trim the both ends of a read or not. Usually, you need to set True for Sanger sequencing and False for NGS	True	<b>both-ends</b>	<i>boolean</i>

## Input/Output Ports

The element has 1 *input port*.

**Name in GUI:** Input File

**Name in Workflow File:** in-file

**Slots:**

Slot In GUI	Slot in Workflow File	Type
<b>Source URL</b>	url	<i>string</i>

And 1 *output port*.

**Name in GUI:** Output File

**Name in Workflow File:** out-file

**Slots:**

Slot In GUI	Slot in Workflow File	Type
<b>Source URL</b>	url	<i>string</i>