

# Filter BAM SAM Files Element

Filters BAM/SAM files using SAMTools view.

**Element type:** filter-bam

## 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.		<b>out-mode</b>	<i>numeric</i>
<b>Custom directory</b>	Custom output directory.		<b>custom-dir</b>	<i>string</i>
<b>Output name</b>	A name of an output BAM/SAM file. If default of empty value is provided the output name is the name of the first BAM/SAM file with .filtered extension.		<b>out-name</b>	<i>string</i>
<b>Output format</b>	Format of an output assembly file.	bam	<b>out-format</b>	<i>string</i>
<b>Region</b>	Regions to filter. For BAM output only. chr2 to output the whole chr2. <a href="#">chr2:1000</a> to output regions of chr 2 starting from 1000. <a href="#">chr2:1000-2000</a> to output regions of chr2 between 1000 and 2000 including the end point. To input multiple regions use the space separator (e.g. chr1 chr2 <a href="#">chr3:1000-2000</a> ).		<b>region</b>	<i>string</i>
<b>MAPQ threshold</b>	Minimum MAPQ quality score.	0	<b>mapq</b>	<i>numeric</i>
<b>Skip flag</b>	Skip alignment with the selected items. Select the items in the combobox to configure bit flag. Do not select the items to avoid filtration by this parameter.		<b>flag</b>	<i>string</i>

## Input/Output Ports

The element has 1 *input port*:

**Name in GUI:** BAM/SAM File

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

**Slots:**

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

And 1 *output port*:

**Name in GUI:** Filtered BAM/SAM files

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

**Slots:**

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