

# Change Chromosome Notation for VCF Element

Changes chromosome notation for each variant from the input, VCF or other variation files.

**Element type:** rename-chromosome-in-variation

## Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
<b>Replace prefixes</b>	Input the list of chromosome prefixes that you would like to replace. For example "NC_000". Separate different prefixes by semicolons.		prefixes-to-replace	<i>string</i>
<b>Replace by</b>	Input the prefix that should be set instead, for example "chr".		prefix-replace-with	<i>string</i>

## Input/Output Ports

The element has 1 *input ports*:

**Name in GUI:** Input file URL

**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 URL

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

**Slots:**

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