

# 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   |
|------------------|----------------------------------------------------------------------------------------------------------------------------------------|---------------|----------------------------|--------|
| Replace prefixes | Input the list of chromosome prefixes that you would like to replace. For example "NC_000". Separate different prefixes by semicolons. |               | prefixes-to-replace        | string |
| Replace by       | Input the prefix that should be set instead, for example "chr".                                                                        |               | prefix-replace-with        | string |

## 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   |
|-------------|-----------------------|--------|
| Source URL  | url                   | string |

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   |
|--------------|-----------------------|--------|
| Produced URL | url                   | string |