Change Chromosome Notation for VCF Element

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

Parameters in GUI

Parameter	Description	Default value
Replace prefixes	Input the list of chromosome prefixes that you would like to replace. For example "NC_000". Separate different prefixes by semicolons.	
Replace by	Input the prefix that should be set instead, for example "chr".	

Parameters in Workflow File

Type: rename-chromosome-in-variation

Parameter	Parameter in the GUI	Type
prefixes-to-replace	**Replace prefixes**	*string*
prefix-replace-with	**Replace by**	*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*