

SnpEff Annotation and Filtration Element

Annotates and filters variations with SnpEff.

Parameters in GUI

Parameter	Description	Default value
Output directory	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
Input format	Select the input format of variations.	VCF
Output format	Select the format of annotated output files.	VCF
Genome	Select the target genome. Genome data will be downloaded if it is not found.	Homo sapiens
Upstream /downstream length	Upstream and downstream interval size. Eliminate any upstream and downstream effect by using 0 length.	No upstream /downstream interval (0 bases)
Canonical transcripts	Use only canonical transcripts.	False
HGVS nomenclature	Annotate using HGVS nomenclature.	False
Annotate loss of function	Annotate Loss of function (LOF) and Nonsense mediated decay (NMD).	False
Annotate TFBSS motifs	Annotate transcription factor binding site motifs (only available for latest GRCh37).	False

Parameters in Workflow File

Type: seff

Parameter	Parameter in the GUI	Type
out-mode	Output directory	<i>string</i>
inp-format	Input format	<i>string</i>
out-format	Output format	<i>string</i>
genome	Genome	<i>string</i>
updown-length	Upstream/downstream length	<i>numeric</i>
canon	Cannonical transcripts	<i>boolean</i>
hgvs	HGVS nomenclature	<i>boolean</i>
lof	Annotate loss of function	<i>boolean</i>
motif	Annotate TFBSs motifs	<i>boolean</i>

Input/Output Ports

The element has 1 *input port*:

Name in GUI: Variations

Name in Workflow File: in-file

Slots:

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

And 1 *output port*:

Name in GUI: Annotated variations

Name in Workflow File: out-file

Slots:

Slot In GUI	Slot in Workflow File	Type
Source url	url	<i>variation</i>