# 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. Wor kflow - 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 from the list of SnpEff databases. Genome data will be downloaded if it is not found. The list of databases depends on the SnpEff external tool version. | 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) |
| **Cannonical transcripts** | Use only cannonical 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** | *string* |
| **inp-format** | **Input format** | *string* |
| **out-format** | **Output format** | *string* |
| **genome** | **Genome** | *string* |
| **updown-length** | **Upstream/downstream length** | *numeric* |
| **canon** | **Cannonical transcripts** | *boolean* |
| **hgvs** | **HGVS nomenclature** | *boolean* |
| **lof** | **Annotate loss of function** | *boolean* |
| **motif** | **Annotate TFBSs motifs** | *boolean* |

# 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** | *string* |

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** | *variation* |