# **Graphical user interface, text, application Description automatically generatedVisualization of customized XCI escape gene annotations**

**Step 1: Create a template**

The default template (template 1) includes columns for gene, escape state, and start position.

**Template 1:**

|  |  |  |
| --- | --- | --- |
| **gene** | **samp\_state** | **start** |
|  |  |  |

**Example data:**

|  |  |  |
| --- | --- | --- |
| **gene** | **samp\_state** | **start** |
| CD99 | escape | 154021573 |
| CD99 | escape | 154021573 |
| CD99 | inactive | 154021573 |

The term “samp\_state” refers to the state of the gene within a sample or tissue. The sample or tissue can be specified by using template 2.

**Template 2:**

|  |  |  |  |
| --- | --- | --- | --- |
| **gene** | **samp\_state** | **sample** | **start** |
|  |  |  |  |

**Example data:**

|  |  |  |  |
| --- | --- | --- | --- |
| **gene** | **samp\_state** | **sample** | **start** |
| CD99 | escape | STMACH | 154021573 |
| CD99 | escape | SKINS | 154021573 |
| CD99 | inactive | LUNG | 154021573 |

The “start” position is optional an only necessary for plotting the genes on the x chromosome coordinate system. Deselecting “Include ‘start’ position” will remove the ‘start’ column for both templates.

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Click the Text

Description automatically generated with low confidence button to download the template in csv format.

**Step 2: Upload data set**

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Populate the downloaded template with the necessary data. Note, the final file **must include the column names which reflect one of the available templates**.

**Example csv files:**

***Example A Example B***

Table

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Click Text

Description automatically generated with medium confidence to select your csv file and upload to the application. Once uploaded, a preview of your data set should be displayed.

**Preview of upload:**

Graphical user interface

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**Graphical user interface, text, application, chat or text message

Description automatically generatedStep 3: Submit data set**

Once you’ve verified your data set, select Text

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The application will produce the following levels of information:

* **Escape frequencies and escape statuses based upon samp\_state**

Application

Description automatically generated with medium confidenceTable

Description automatically generated

Note: the default thresholds applied are:

* %escape ≤ 25% → Silenced (S)
* 25% < %escape < 75%  → Variable escape (VE)
* %escape  ≥ 75% → Escape (E)

These can be changed with the sliders in the left side panel.

* **GWAS associations of selected genes of interest**

1. **Select the** Graphical user interface, application

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2. **Select genes of interest in left side panel**

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1. **Results:**

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* **Genomic positions of genes and escape statuses (if “start” position is included)**

**Timeline

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