Visualization of customized XCI escape gene annotations

Step 1: Create a template

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

1. CREATE A TEMPLATE Template Type Template 1 (gene, state, start, end) Template 2 (gene, state, sample, start, end) Download Template

Template 1:

GENE	STATE	START	END

Example data:

GENE	STATE	START	END
CD99	escape	2691187	2741309
ZFX	escape	24149173	24216255
IDS	inactive	149476988	149521096

For template 2, the term "SAMPLE" refers to the sample or tissue of the observed gene status.

Template 2:

GEN	1E	STATE	SAMPLE	START	END

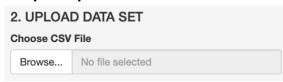
Example data:

GENE	STATE	SAMPLE	START	END	
CD99	escape	STMACH	2691187	2741309	
CD99	escape	SKINS	2691187	2741309	
CD99	inactive	LUNG	2691187	2741309	

Click the Download Template button to download the template in csv format.

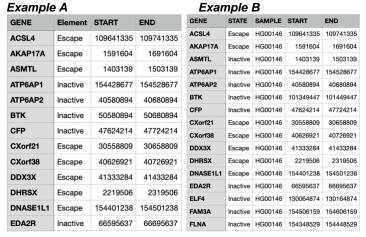
Click the Download Example button to download an example study in csv format.

Step 2: Upload data set



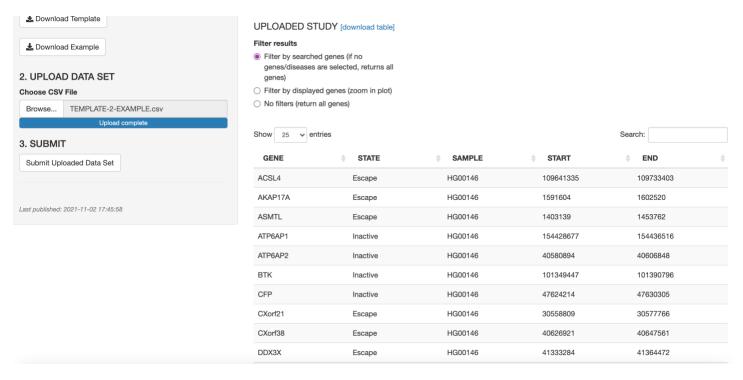
Populate the downloaded template with the necessary data. Note, the final file **must include the column names which reflect one of the available templates**.

Example csv files:



Click Browse... to select your csv file and upload to the application. Once uploaded, a preview of your data set should be displayed.

Preview of upload:



Step 3: Submit data set

Once you've verified your data set, select

Submit Uploaded Data Set

The application will produce the following levels of information:

Escape frequencies and escape status based upon STATE

GENE	STATE	SAMPLE	START		
ACSL4	escape	HG00146	109641335	109733403	1
AKAP17A	escape	HG00146	1591604	1602520	1
ASMTL	escape	HG00146	1403139	1453762	1
ATP6AP1	inactive	HG00146	154428677	154436516	0
ATP6AP2	inactive	HG00146	40580894	40606848	0
втк	inactive	HG00146	101349447	101390796	0
CFP	inactive	HG00146	47624214	47630305	0
CXorf21	escape	HG00146	30558809	30577766	1
CXorf38	escape	HG00146	40626921	40647561	1
DDX3X	escape	HG00146	41333284	41364472	1
DHRSX	escape	HG00146	2219506	2500976	1
DNASE1L1	escape	HG00146	154401238	154412090	1

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 Association Data tab
 - 2. Select genes of interest in left side panel

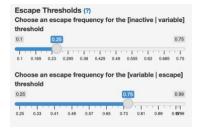


3. Results:



3. SUBMIT

Submit Uploaded Data Set



Visual annotation of XCI status

X-Chromosome Escape Profile

