

Tutorial: Escape Frequency Thresholds

BACKGROUND

The percent escape (PE) of a gene is the frequency of its escape status among samples.

For example, in the data set below *HCFC1* escapes in 3/10 of the samples, resulting in PE of 30%.

gene	samp_state	sample	start	escape_freq
HCFC1	escape	HG00146	153947557	0.3
HCFC1	inactive	HG00163	153947557	0.3
HCFC1	escape	NA20502	153947557	0.3
HCFC1	inactive	HG00231	153947557	0.3
HCFC1	inactive	HG00235	153947557	0.3
HCFC1	escape	HG00258	153947557	0.3
HCFC1	inactive	NA20756	153947557	0.3
HCFC1	inactive	NA20769	153947557	0.3
HCFC1	inactive	NA20795	153947557	0.3
HCFC1	inactive	NA20819	153947557	0.3

The PE of a gene is used to classify its escape status. Genes which escape in nearly all samples are classified as “escape”; genes which escape in some but not all samples are “variable”; genes which escape in few or no samples are “inactive”. **Escape Frequency Thresholds** are used to delineate each classification.

For example, the GEUVADIS lymphoblast study uses %25 and 75% thresholds.

- $\% \text{escape} \leq .25 \rightarrow$ Silenced (S)
- $.25 < \% \text{escape} < .75 \rightarrow$ Variable escape (VE)
- $\% \text{escape} \geq .75 \rightarrow$ Escape (E)

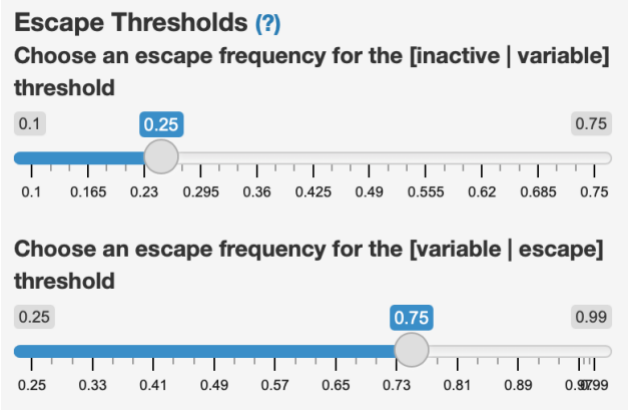
Applying these thresholds to our example data set will classify *HCFC1* as “variable”.

gene	samp_state	sample	start	escape_freq	state
HCFC1	escape	HG00146	153947557	0.3	variable
HCFC1	inactive	HG00163	153947557	0.3	variable
HCFC1	escape	NA20502	153947557	0.3	variable
HCFC1	inactive	HG00231	153947557	0.3	variable

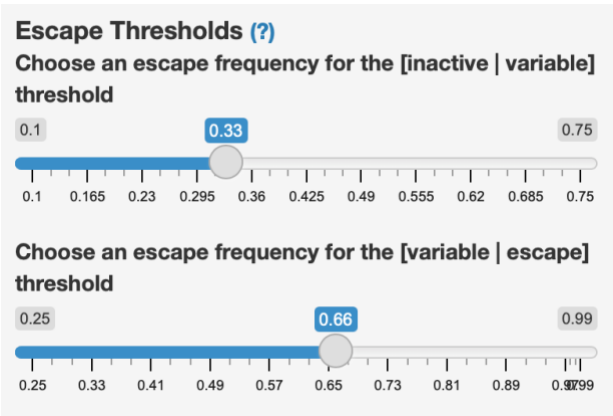
CHANGING ESCAPE FREQUENCY THRESHOLDS

The escape frequency thresholds of 25% and 75% arbitrarily selected and can be informed by biological information or study design. To allow for flexibility, the application gives users the freedom to change the escape frequency thresholds.

The left side panel contains sliders which modify the lower and upper thresholds. These sliders are available only for studies which contain sample level information of escape status.



Changing the escape thresholds will modify the classification sensitivity for the selected study. In our example data set, modifying the thresholds to 33% and 66% will re-classify the escape status of the *HCFC1* gene.

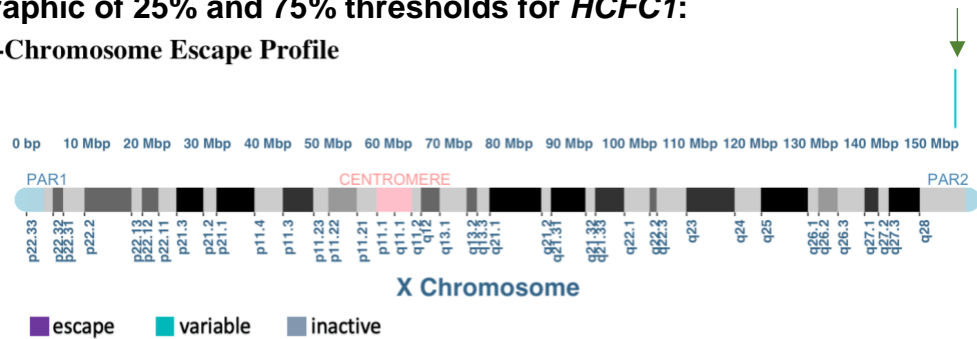


gene	samp_state	sample	start	escape_freq	state
HCFC1	escape	HG00146	153947557	0.3	inactive
HCFC1	inactive	HG00163	153947557	0.3	inactive
HCFC1	escape	NA20502	153947557	0.3	inactive
HCFC1	inactive	HG00231	153947557	0.3	inactive
HCFC1	inactive	HG00235	153947557	0.3	inactive
HCFC1	escape	HG00258	153947557	0.3	inactive

Modifying the escape thresholds will also update the gene position graphic. Note, this graphic is only available for studies which include positional data ("start" column).

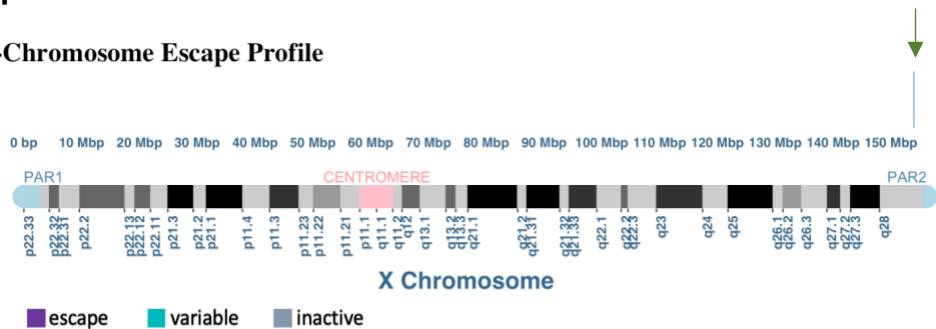
Graphic of 25% and 75% thresholds for *HCFC1*:

X-Chromosome Escape Profile



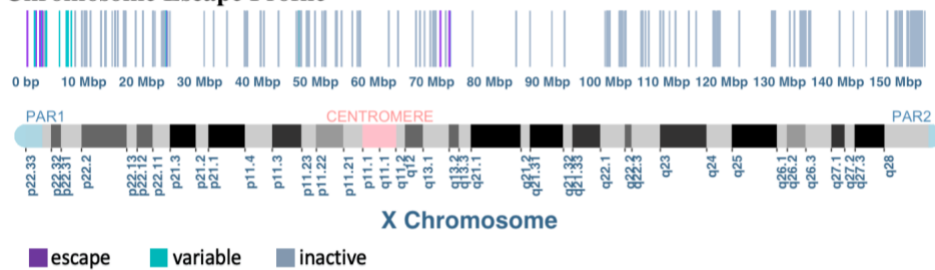
Graphic of 33% and 66% thresholds for *HCFC1*:

X-Chromosome Escape Profile



Graphic of 25% and 75% thresholds for *Tukiainen et al. GTEx study*:

X-Chromosome Escape Profile



Graphic of 33% and 66% thresholds for *Tukiainen et al. GTEx study*:

X-Chromosome Escape Profile

