

## heatmapper

heatmapper (version 1.0.3)

**Matrix file from the computeMatrix tool:**  
85: computeMatrix on data 5, data 82, and data 53: Matrix

**Show advanced output settings:**  
no

**Show advanced options:**  
yes

**Sort regions:**  
descending order  
Whether the heatmap should present the regions sorted. The default is to sort in descending order based on the mean value per region.

**Method used for sorting:**  
region length  
*instead of mean, we choose to sort according to the regions' length (just to show you an alternative sorting)*  
For each row the method is computed.

**Type of statistic that should be plotted in the summary image above the heatmap:**  
mean

**What to show:**  
heatmap and colorbar  
The default is to include a summary or profile plot on top of the heatmap and a heatmap colorbar.

**Label for the region start:**  
TSS  
[only for scale-regions mode] Label shown in the plot for the start of the region. Default is TSS (transcription start site), but could be changed to anything, e.g. "peak start".

**Label for the region end:**  
TES  
[only for scale-regions mode] Label shown in the plot for the region end. Default is TES (transcription end site).

**Reference point label:**  
TSS  
[only for scale-regions mode] Label shown in the plot for the reference-point. Default is the same as the reference point selected (e.g. TSS), but could be anything, e.g. "peak start" etc.

**Labels for the regions plotted in the heatmap:**  
no Pol II, Pol II at promoter  
*2 clusters <-> 2 names*  
If more than one region is being plotted a list of labels separated by comma and limited by quotes, is required. For example, label1, label2.

**Title of the plot:**  
Pol II  
Title of the plot, to be printed on top of the generated image. Leave blank for no title.

**Do one plot per group:**  
☐  
When computeMatrix was used on more than one group of genes, the average plots for all the groups will be drawn in one panel by default. If this option is set, each group will get its own plot, stacked on top of each other.

**Did you used multiple regions in ComputeMatrix?:**  
No, I used only one region.  
*clustering will overwrite any user-specified groups of regions which is why we recommend to use it only for cases where you supplied just one BED file to computeMatrix*  
Would you like to cluster the regions according to the similarity of the signal distribution? This is only possible if you used computeMatrix on only one group of regions.

**Clustering algorithm:**  
Kmeans clustering

**Number of clusters to compute:**  
2  
When this option is set, then the matrix is split into clusters using the kmeans algorithm. Only works for data that is not grouped, otherwise only the first group will be clustered. If more specific clustering methods are required it is advisable to save the underlying matrix and run the clustering using other software. The plotting of the clustering may fail (Error: Segmentation fault) if a cluster has very few members compared to the total number of regions. (default: None).

Execute