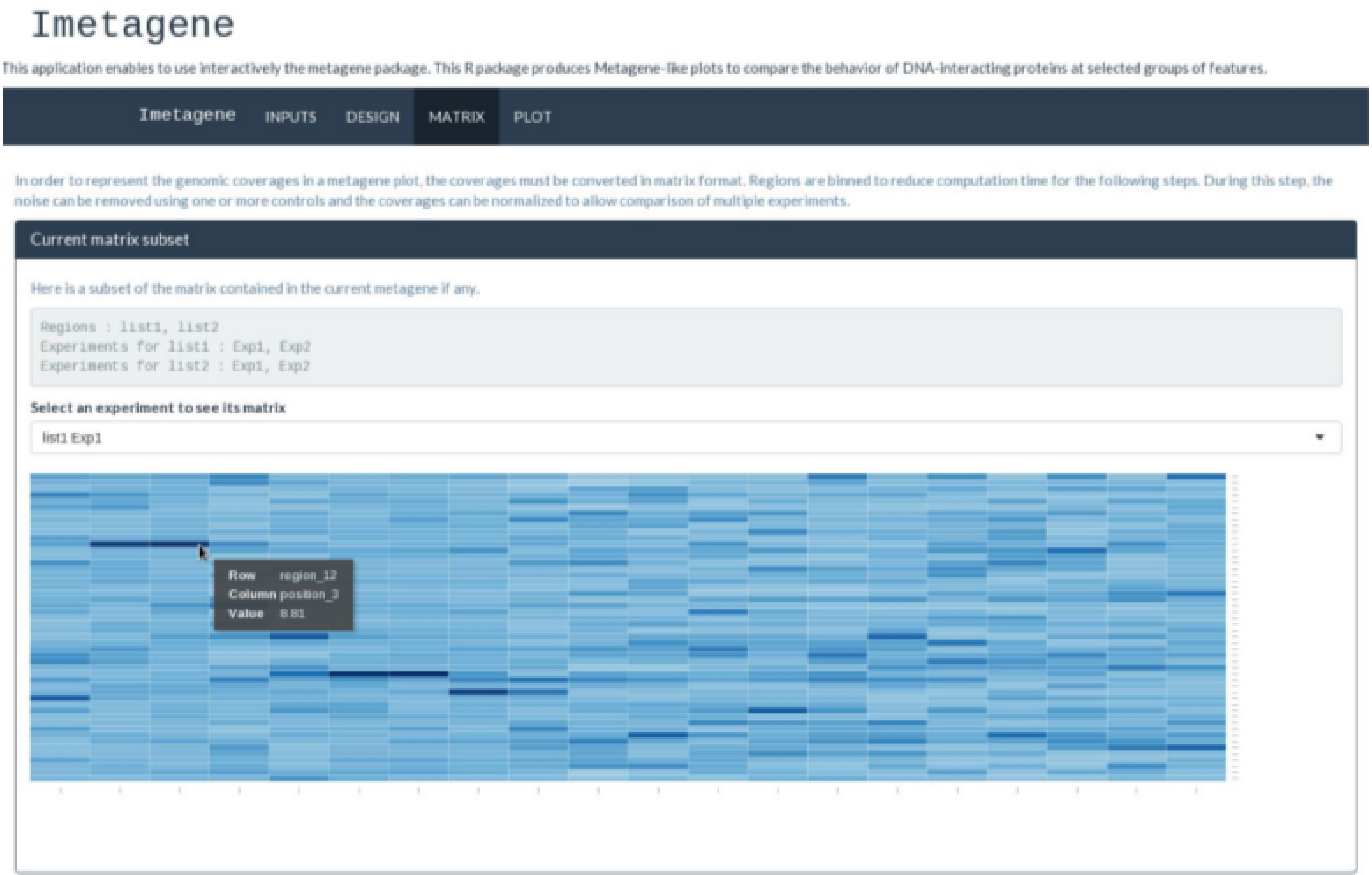
S1 Fig. Imetagene interactive heatmap representation



Imetagene

This application enables to use interactively the metagene package. This R package produces Metagene-like plots to compare the behavior of DNA-interacting proteins at selected groups of features.

In order to represent the genomic coverages in a metagene plot, the coverages must be converted in matrix format. Regions are binned to reduce computation time for the following steps. During this step, the noise can be removed using one or more controls and the coverages can be normalized to allow comparison of multiple experiments.

Current matrix subset

Here is a subset of the matrix contained in the current metagene if any.

```
Regions : list1, list2
Experiments for list1 : Exp1, Exp2
Experiments for list2 : Exp1, Exp2
```

Select an experiment to see its matrix: list1 Exp1

Row region_12
Column position_3
Value 8.81