

## **Combining Chexmix+Genetrack\_top500.R**

R script to combine ChExMix and Genetracks peaks to a single file. Script removes duplicate peaks calls, sorts the remaining peaks by occupancy, and then outputs this data. Additionally, the top 500 peaks by occupancy are output as a separate file to be used for MEME motif discovery.

## **correlation\_coeff\_v2.py**

Calculates the correlation coefficient between datasets and generates the corresponding heatmaps.

## **genetrack.py**

Genetrack peak-caller script used for genetrack peak calls

## **sum\_Row\_CDT.pl**

Calculates the sum of the individual peaks across a given matrix. Used to create the composite plots shown in the paper.