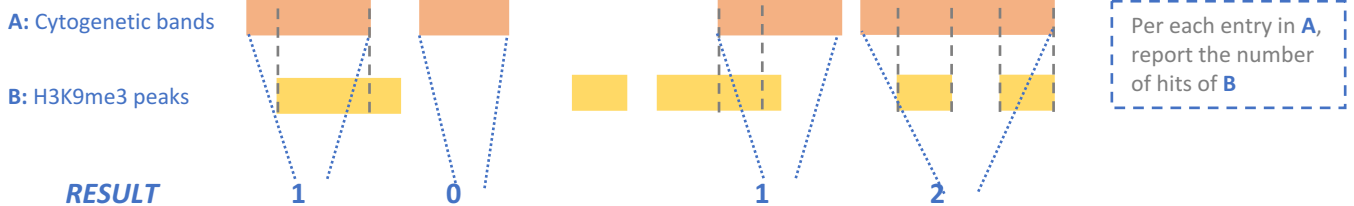
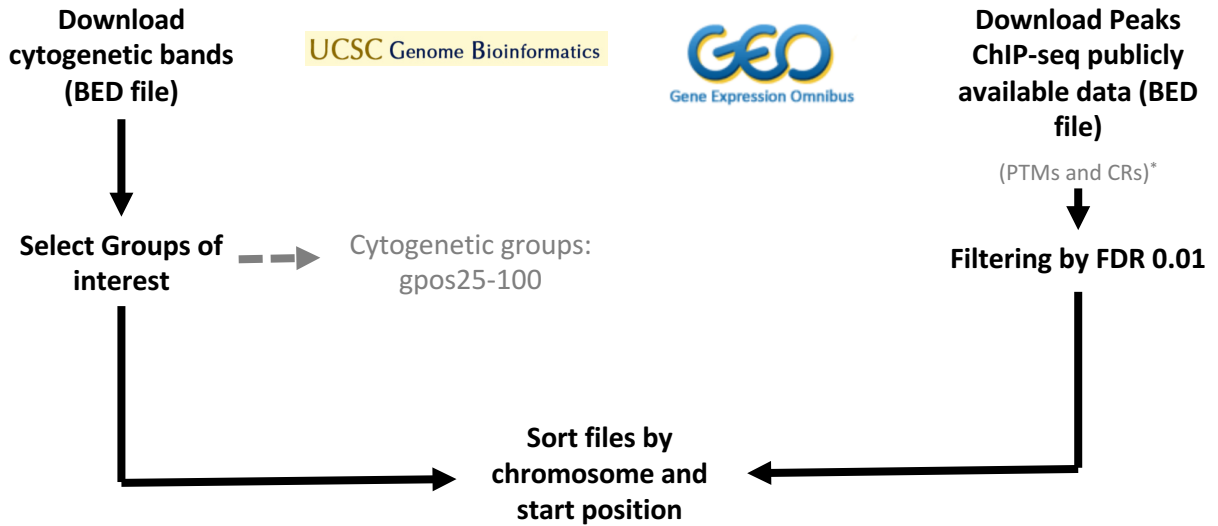


Cytogenetic Band Classification Pipeline



Output BED file

Scale values by cytogenetic band length

Read all files generated (for all of the Peaks ChIP-seq data of interest)

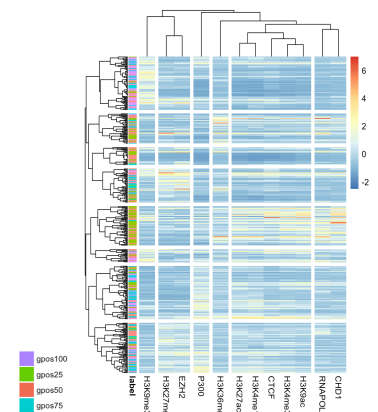
Scale the data (to have comparable values among different datasets)

**Perform Hierarchical clustering
(Decide clustering distance)**

Do Heatmap

Correlation
distance for
cytogenetic bands

Euclidean
distance for
PTMs and CRs



* *Post-translational Modifications (PTMs) and Chromatin Regulators (CRs)*