

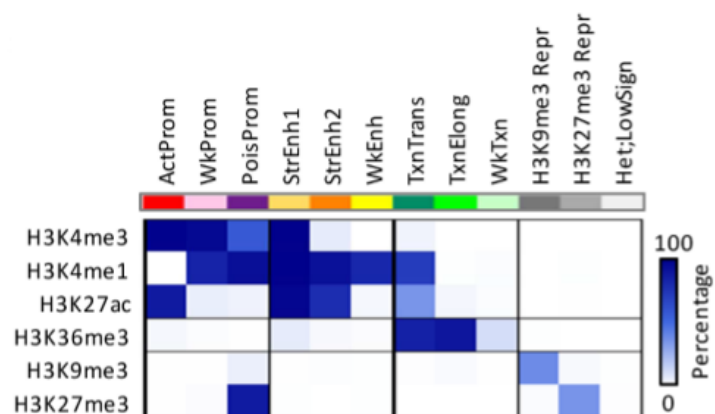
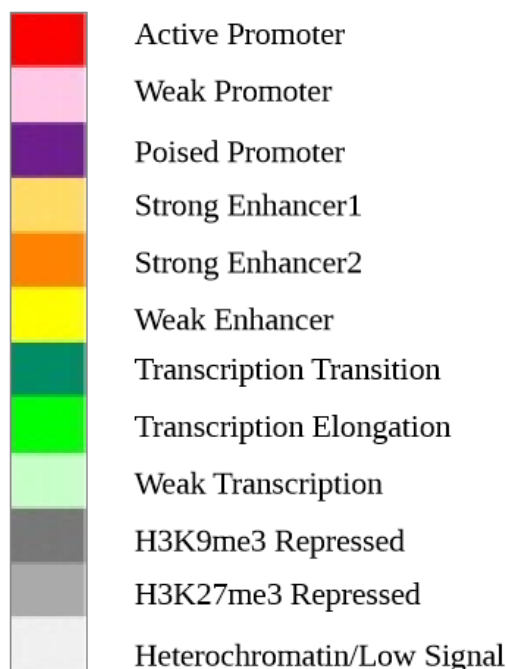
# Chromatin activation as a unifying principle underlying pathogenic mechanisms in multiple myeloma

## UCSC Genome Browser Tracks Description

### Individual tracks

#### ChromHMM

The ChromHMM track shows the chromatin states for the multiple myeloma and 15 normal B-cell samples from the reference epigenome. Colors codes are described below:



#### Epigenome MM

Individual sample signals of H3K4me3, H3K4me1, H3K27ac, H3K27me3, H3K9me3, H3K36me3, ATAC-seq, RNA-seq and DNA methylation can be shown in the browser. In order to configure this track, click on “Epigenome\_MM” and select the desired subtracks.

