

± = Epigenome intensity percentage scale: 0% 100% PC1: -35.9 42.9 TADs: GeneHancer

222.91Mb 223.71Mb

promoter/enhancer  
Bcell-H3K27ac  
Bcell-H3K27ac  
Bcell-H3K27ac  
CLL-H3K27ac  
CLL-H3K27ac  
CLL-H3K27ac  
CLL-H3K27ac  
CLL-H3K27ac  
CLL-H3K27ac  
CLL-H3K27ac  
CLL-H3K27ac  
CLL-H3K27ac  
CLL-H3K27ac  
CLL-H3K27ac  
CLL-H3K27ac  
Bcell-H3K4me1  
Bcell-H3K4me1  
Bcell-H3K4me1  
CLL-H3K4me1  
CLL-H3K4me1  
CLL-H3K4me1  
CLL-H3K4me1  
CLL-H3K4me1  
CLL-H3K4me1  
CLL-H3K4me1  
CLL-H3K4me1  
CLL-H3K4me1  
CLL-H3K4me1  
CLL-H3K4me1

Each bin by default is 2kb. The bin colours represent the normalised intensities, which range from grey (lowest) to red (highest). The bins whose intensities are absent are coloured in green.