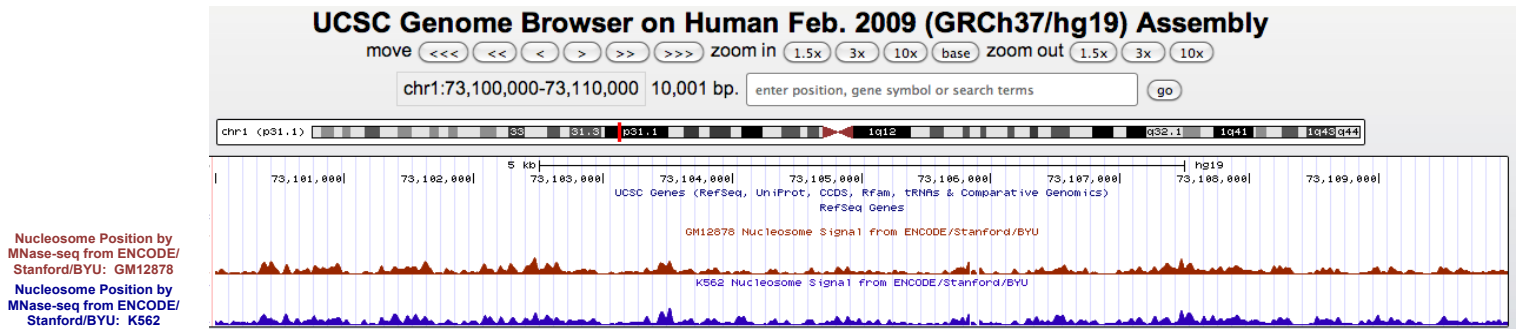


## Sexton et al. \_ Supplementary Figure 18



Supp. Fig. 18. Nucleosome position data by MNase-seq from the ENCODE project for both GM12878 (red) and K562 (blue) cell lines. The x-axis represents genomic position, this region was randomly selected, spanning from 73,100,000 bp to 73,110,000 bp on chromosome 1. The y-axis is the number of reads for each data set. This whole genome study reveals that nucleosome occupancies are remarkably similar between GM12878 and K562 (<http://genome.ucsc.edu/encode/>).