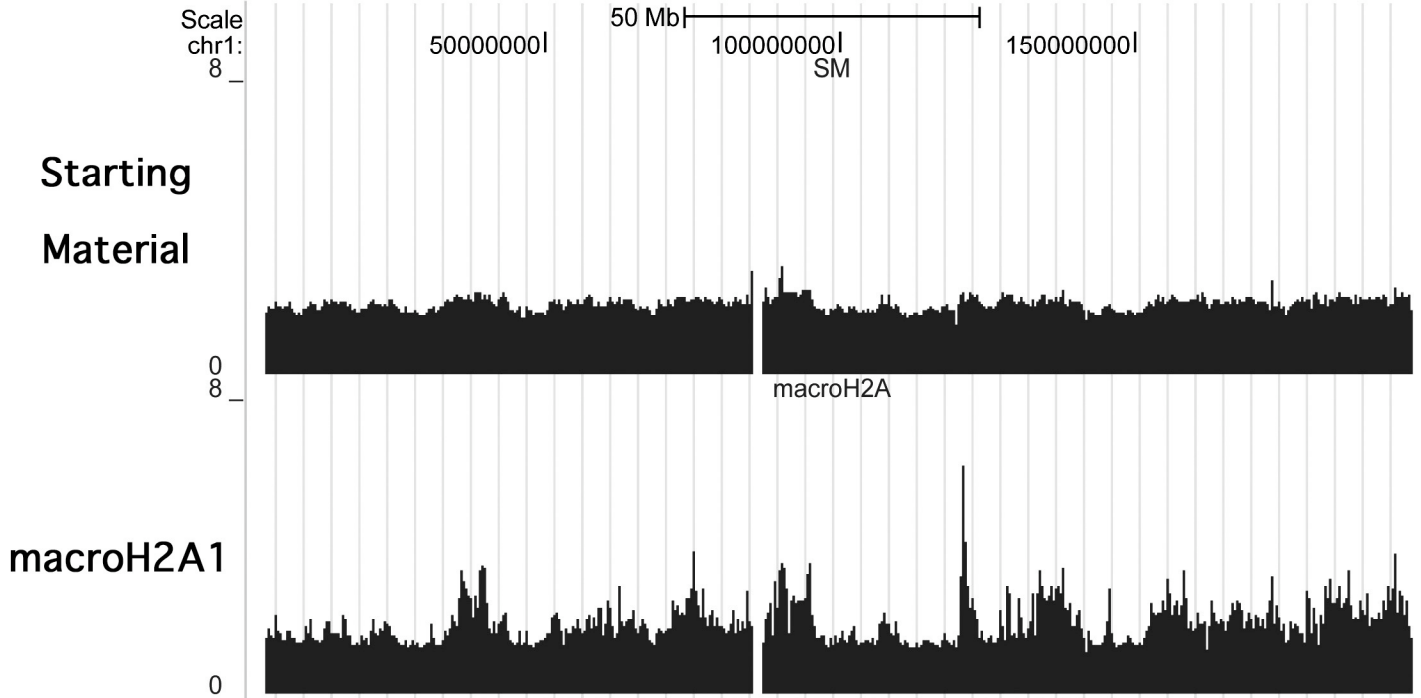
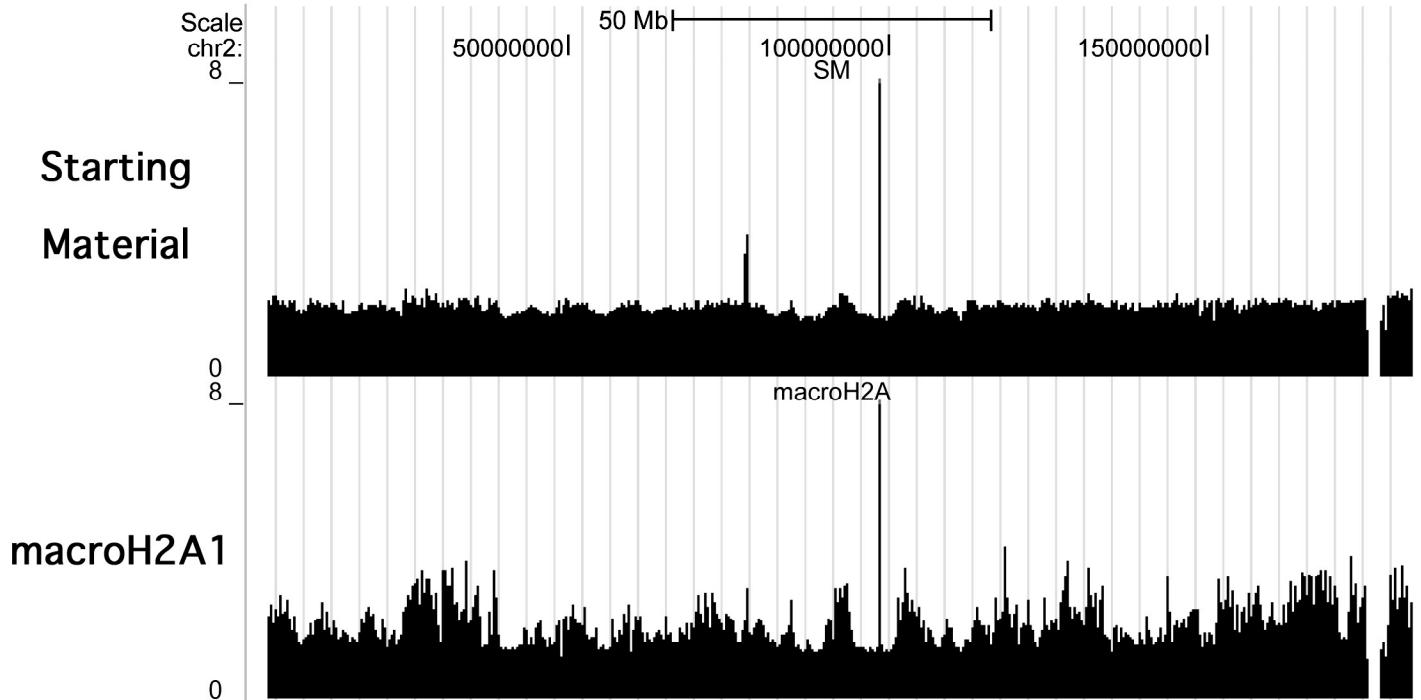


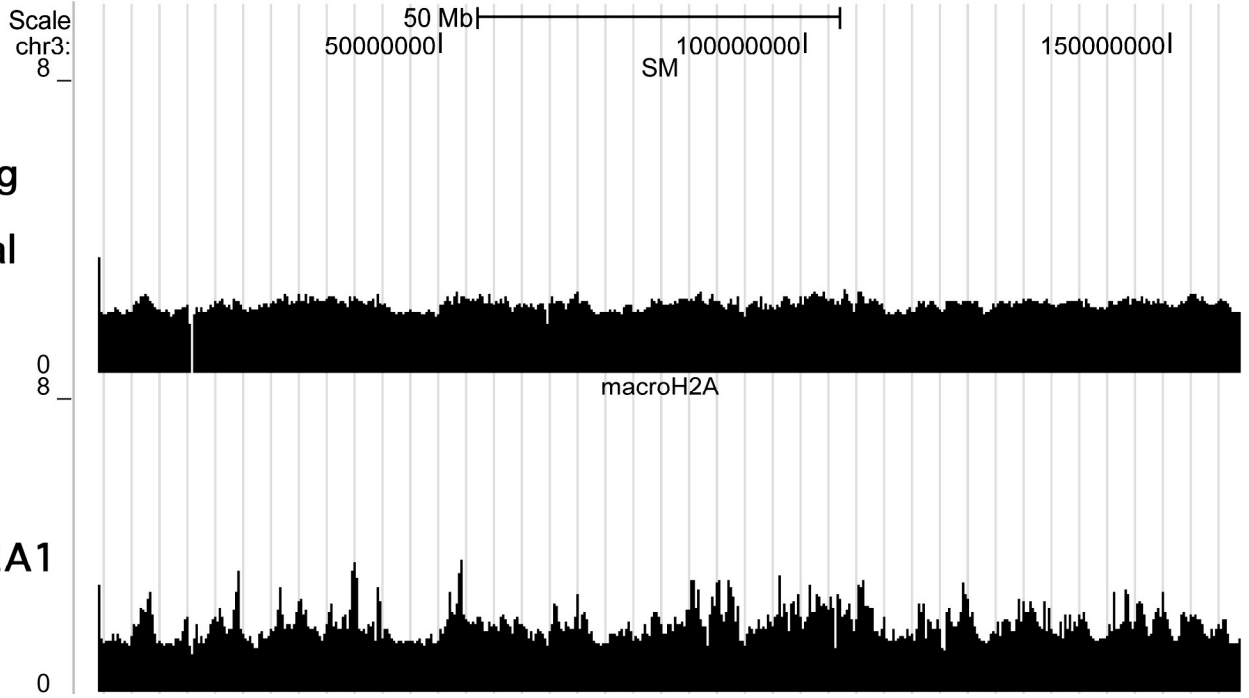
# Chromosome 1



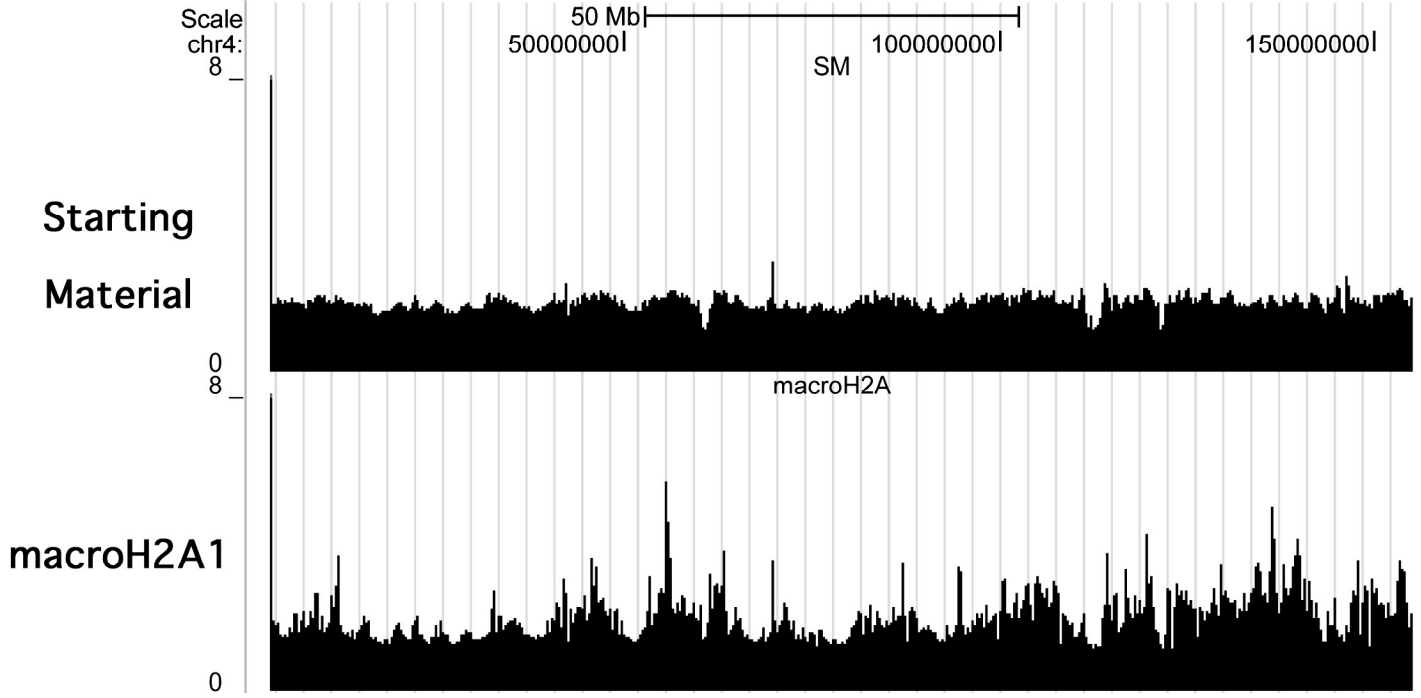
# Chromosome 2



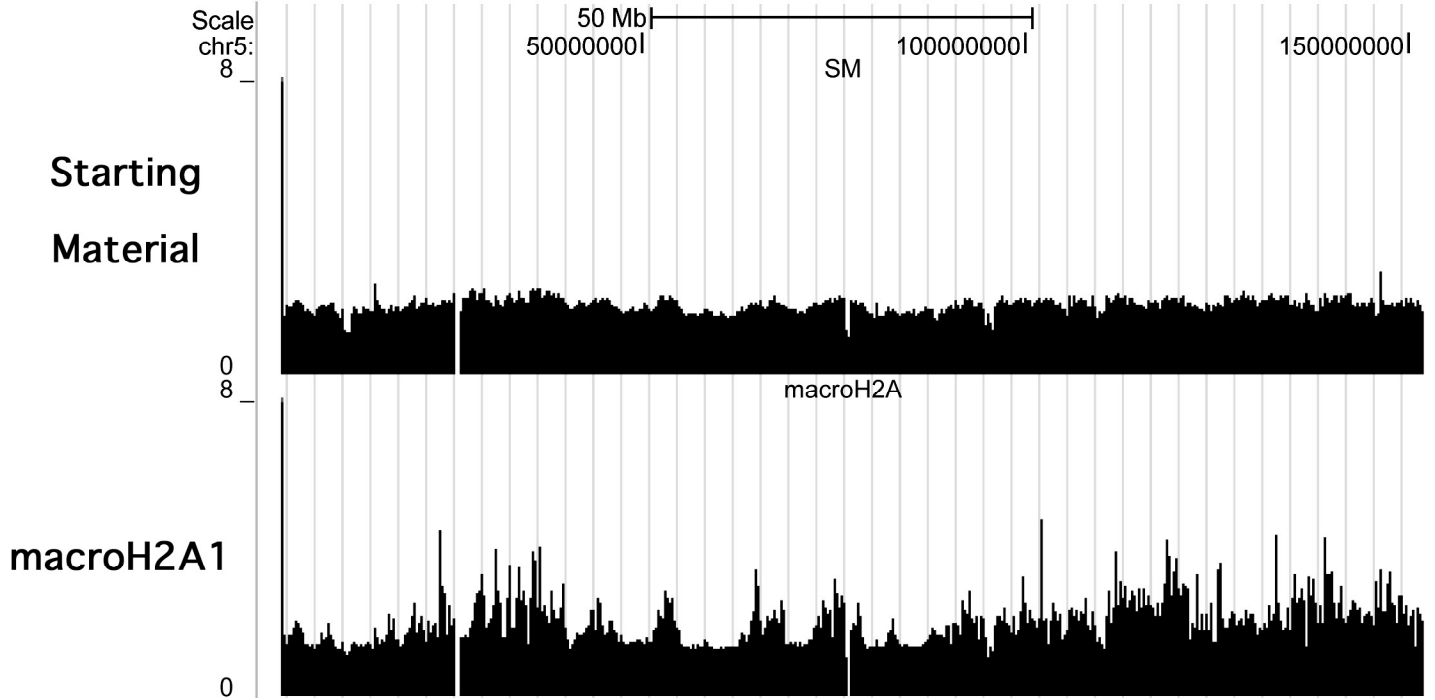
# Chromosome 3



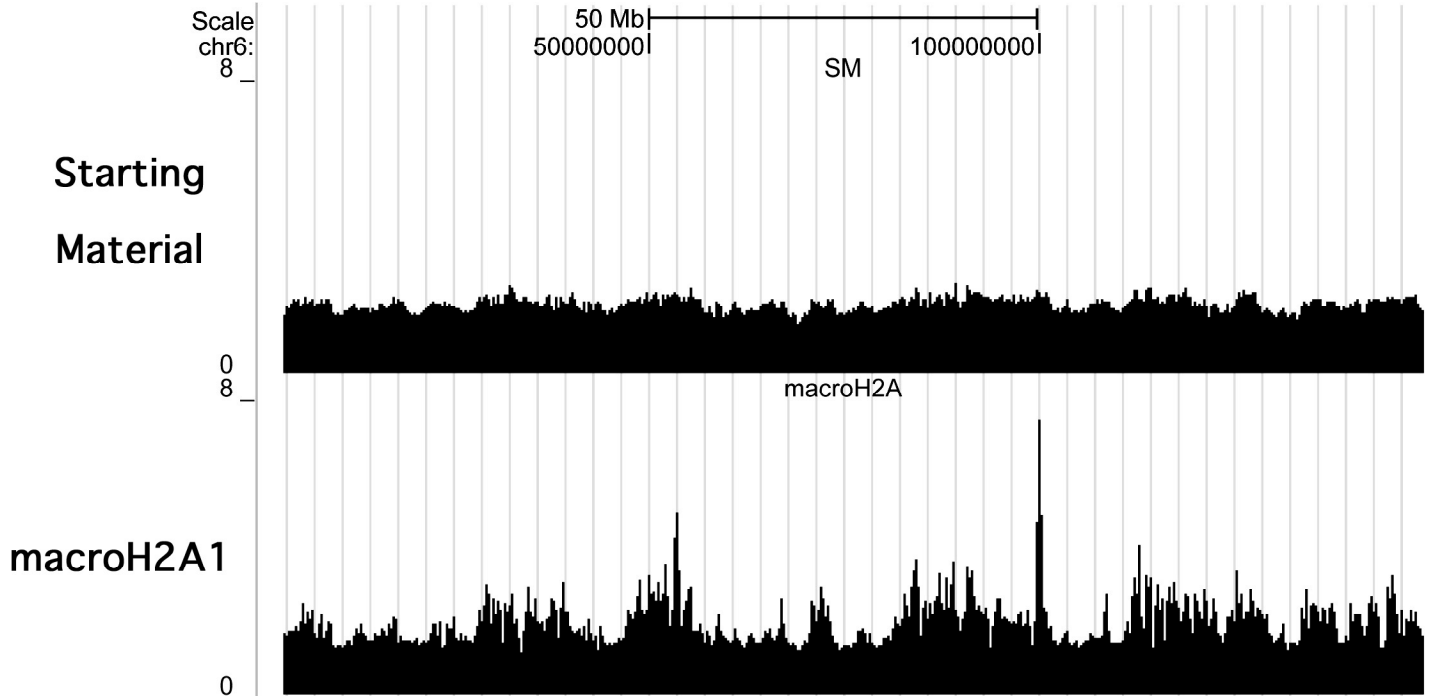
# Chromosome 4



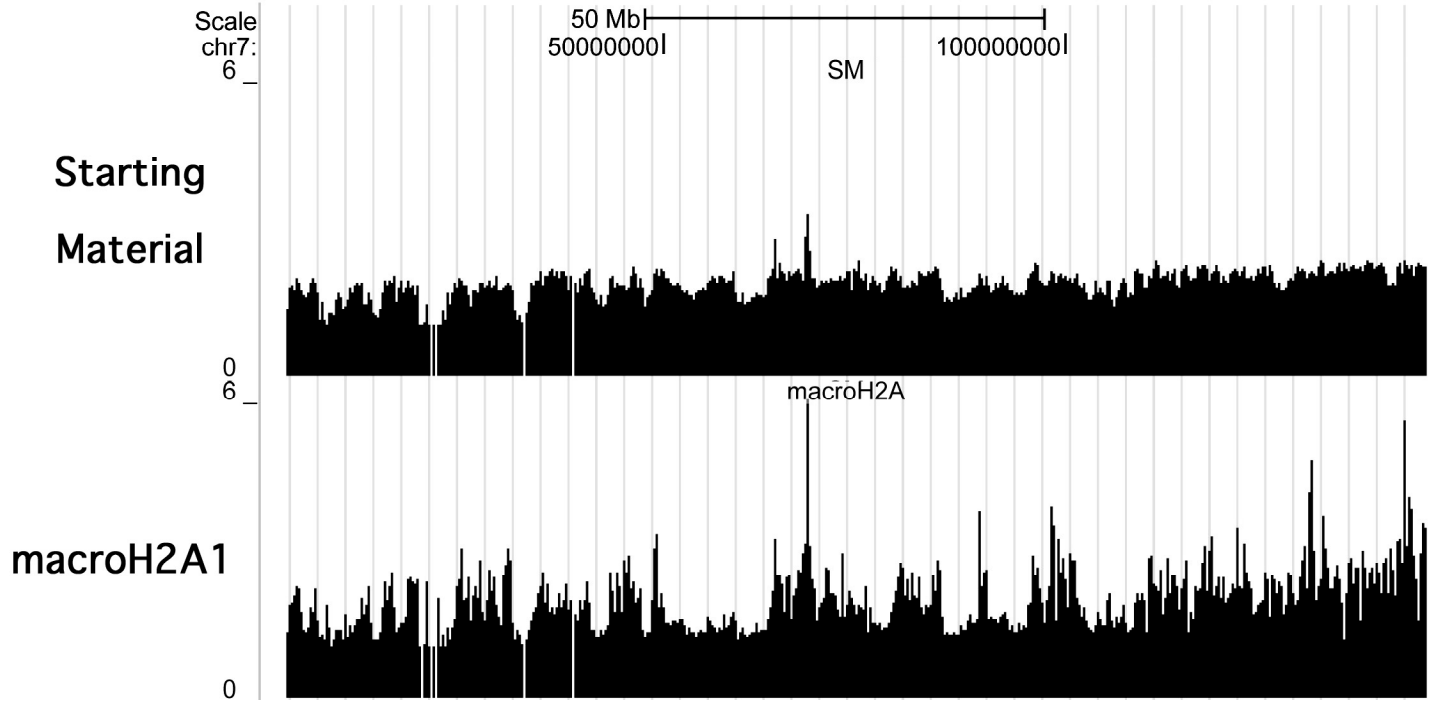
# Chromosome 5



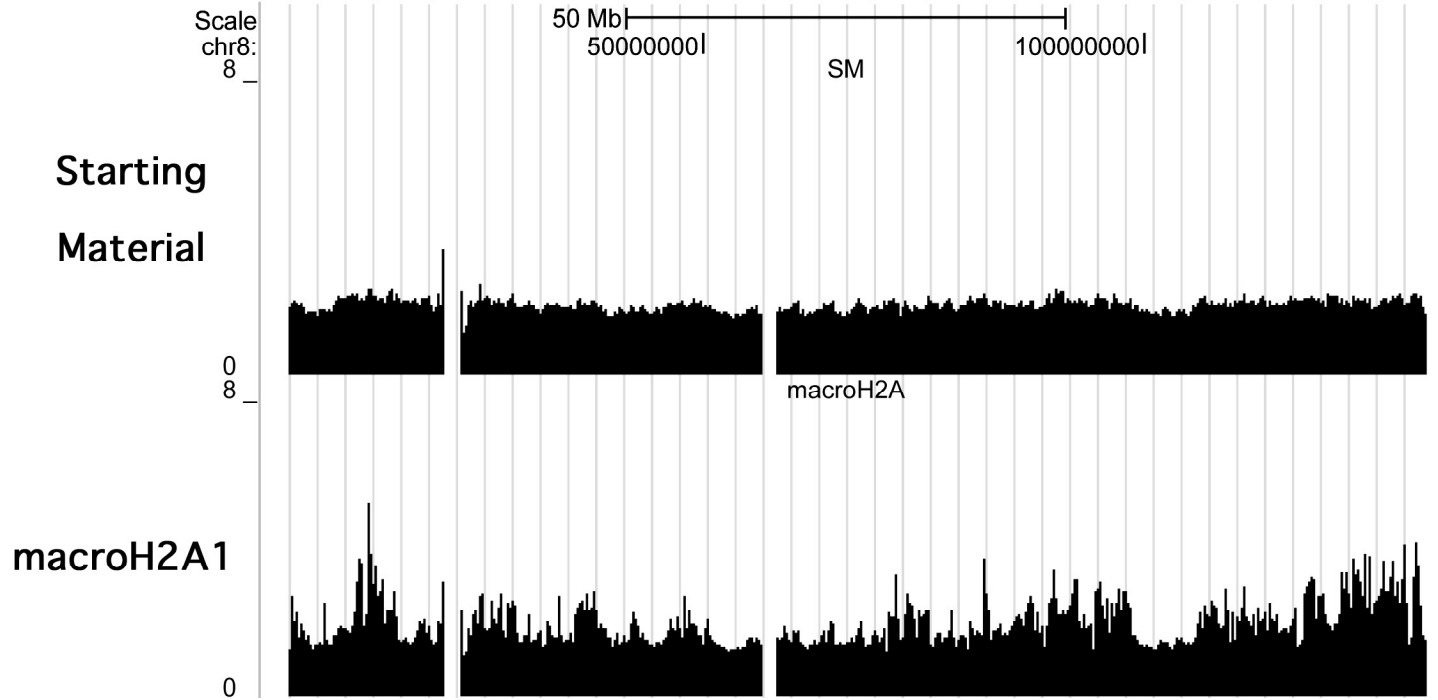
# Chromosome 6



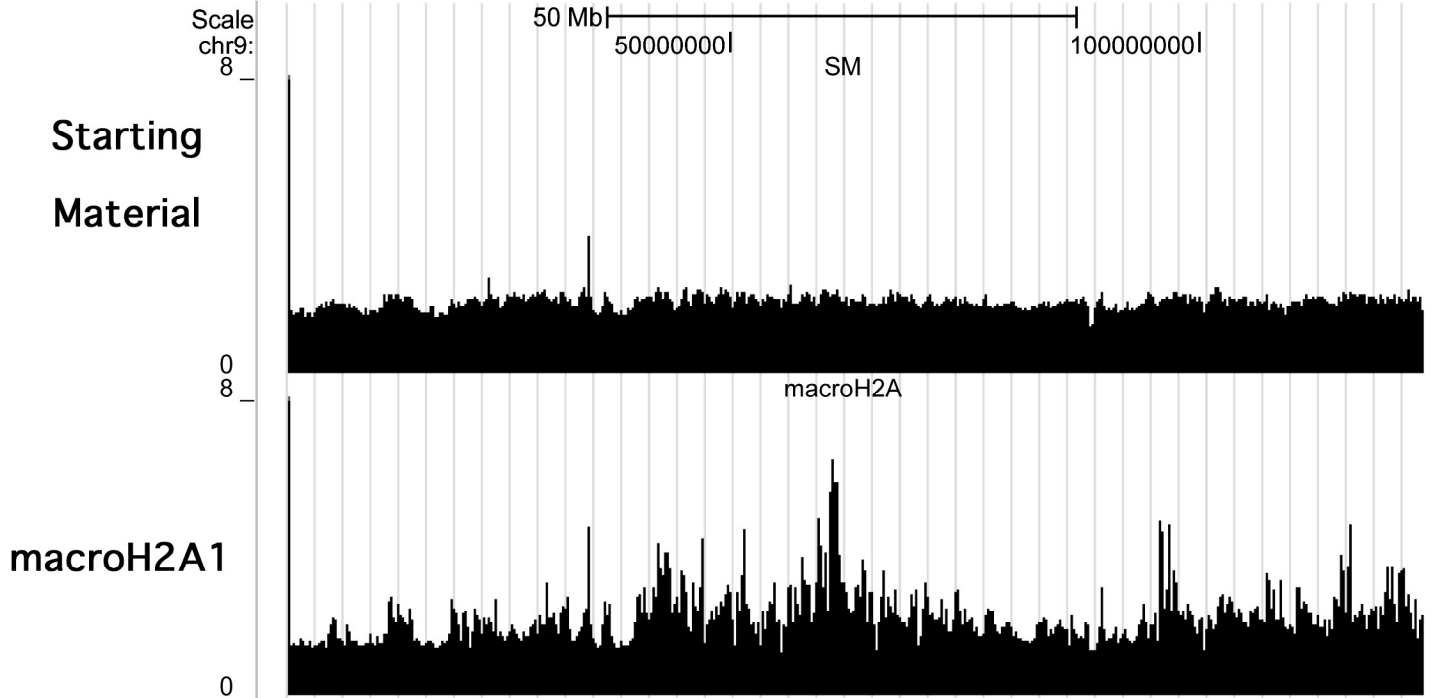
# Chromosome 7



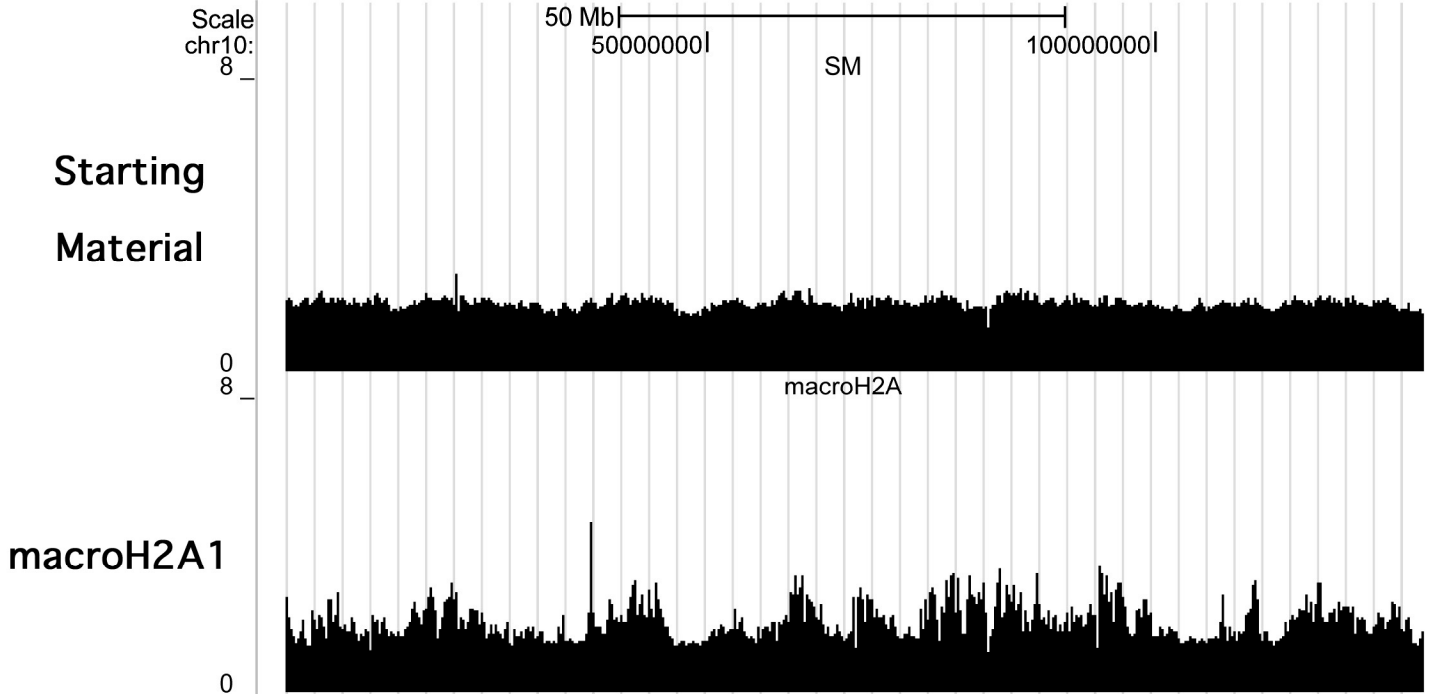
# Chromosome 8



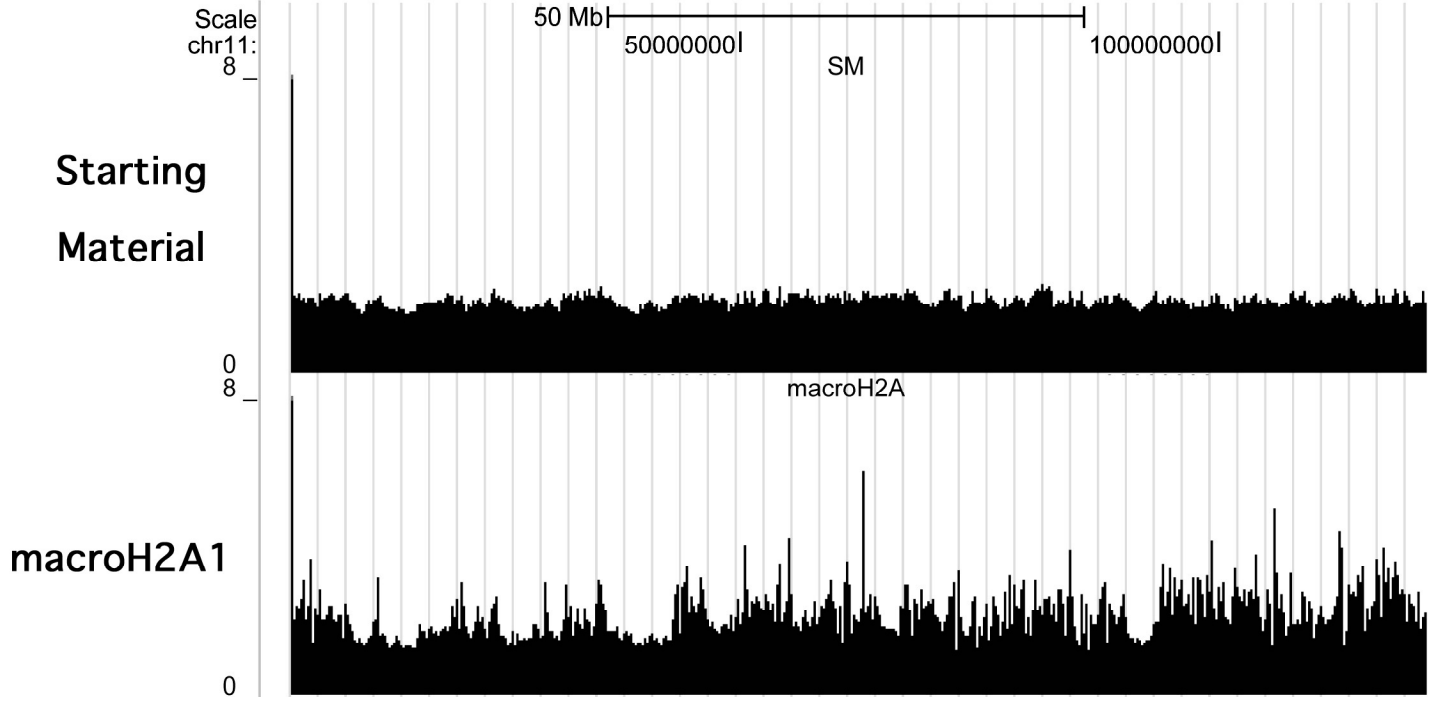
# Chromosome 9



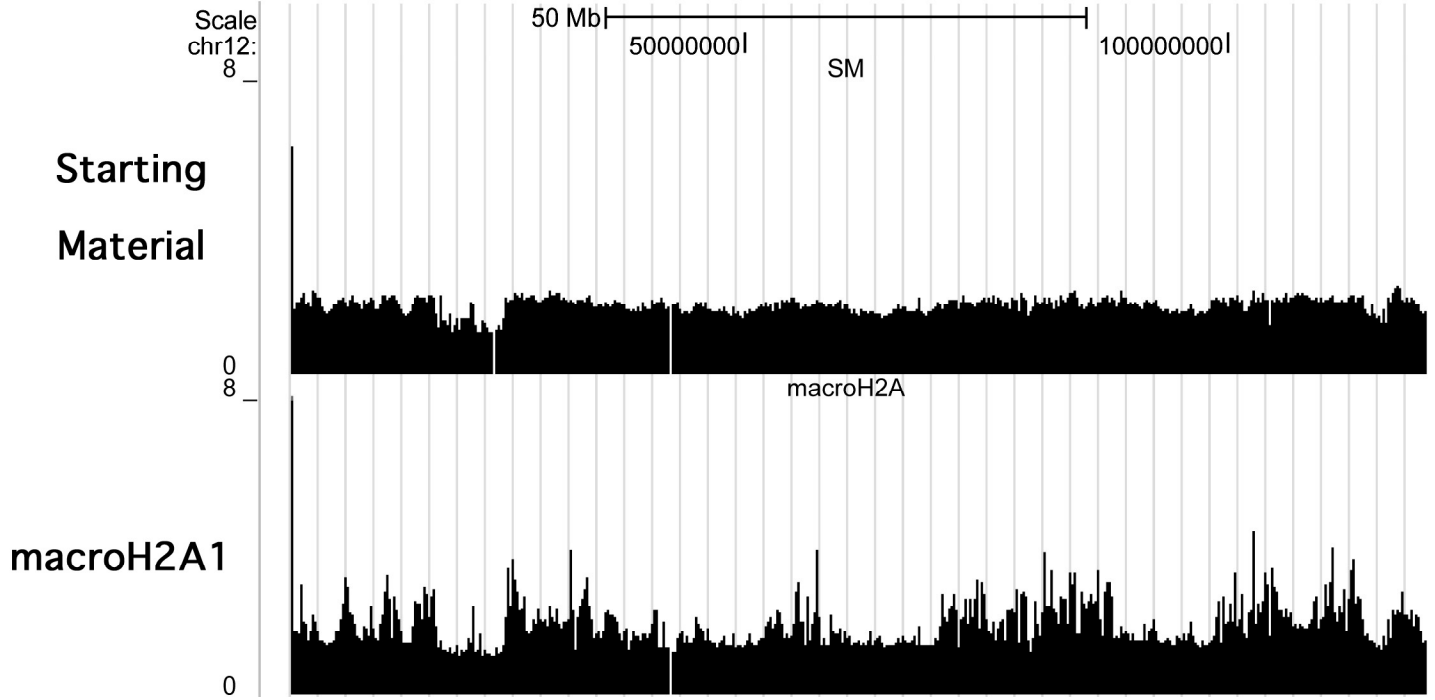
# Chromosome 10



# Chromosome 11



# Chromosome 12

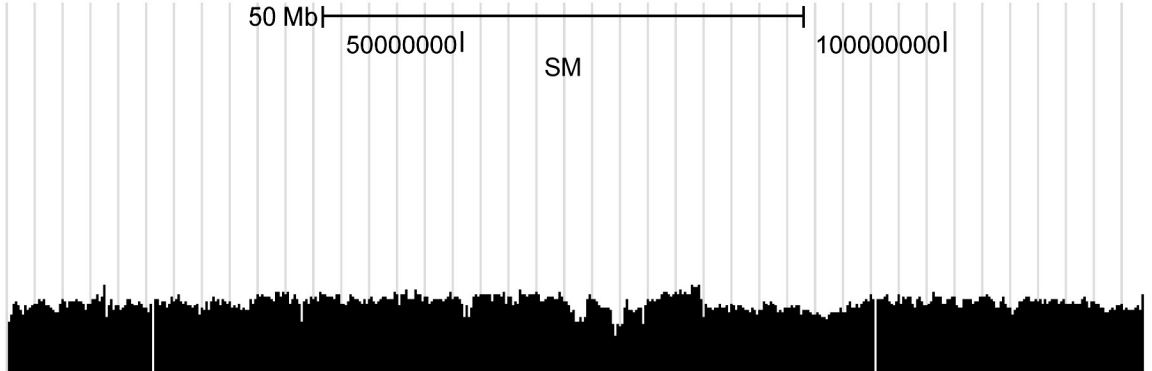


# Chromosome 13

Scale  
chr13:  
8

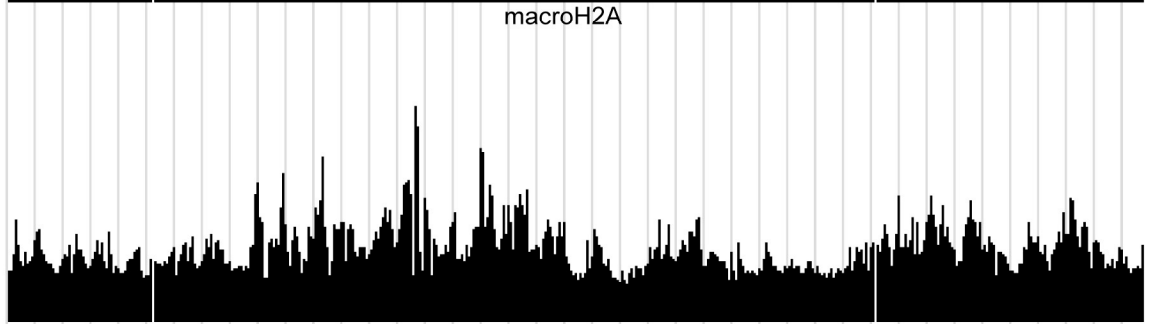
50 Mb | 50000000 | SM | 100000000

Starting  
Material



macroH2A

macroH2A1

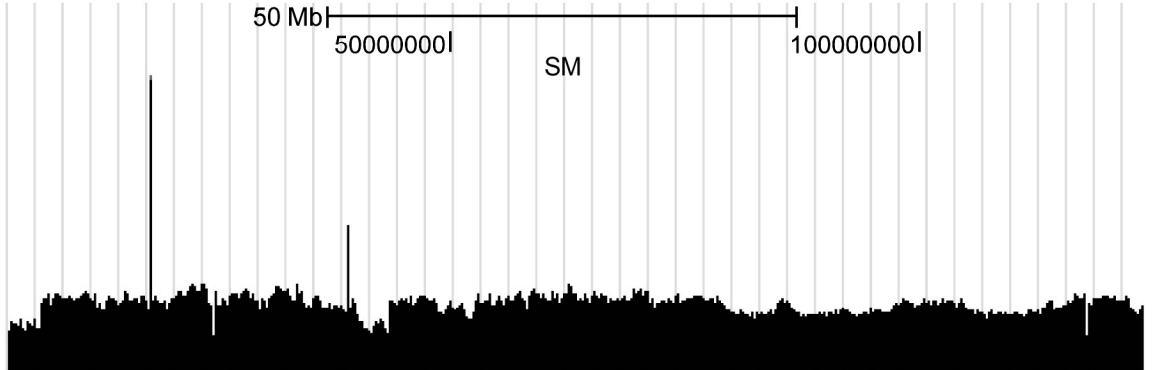


# Chromosome 14

Scale  
chr14:  
8

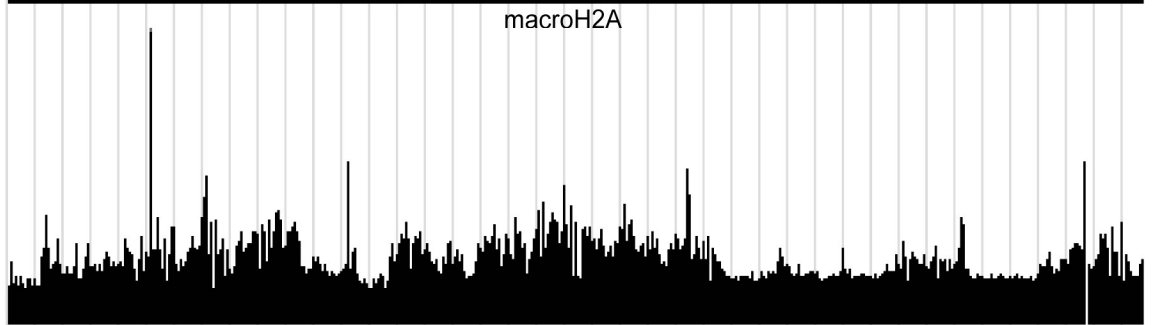
50 Mb | 50000000 | SM | 100000000

Starting  
Material



macroH2A

macroH2A1



# Chromosome 15

Scale  
chr15:  
8

50 Mb|

50000000|

SM

100000000|

Starting  
Material

0

8

macroH2A

macroH2A1

0

# Chromosome 16

Scale  
chr16:  
8

20 Mb|

50000000|

SM

Starting  
Material

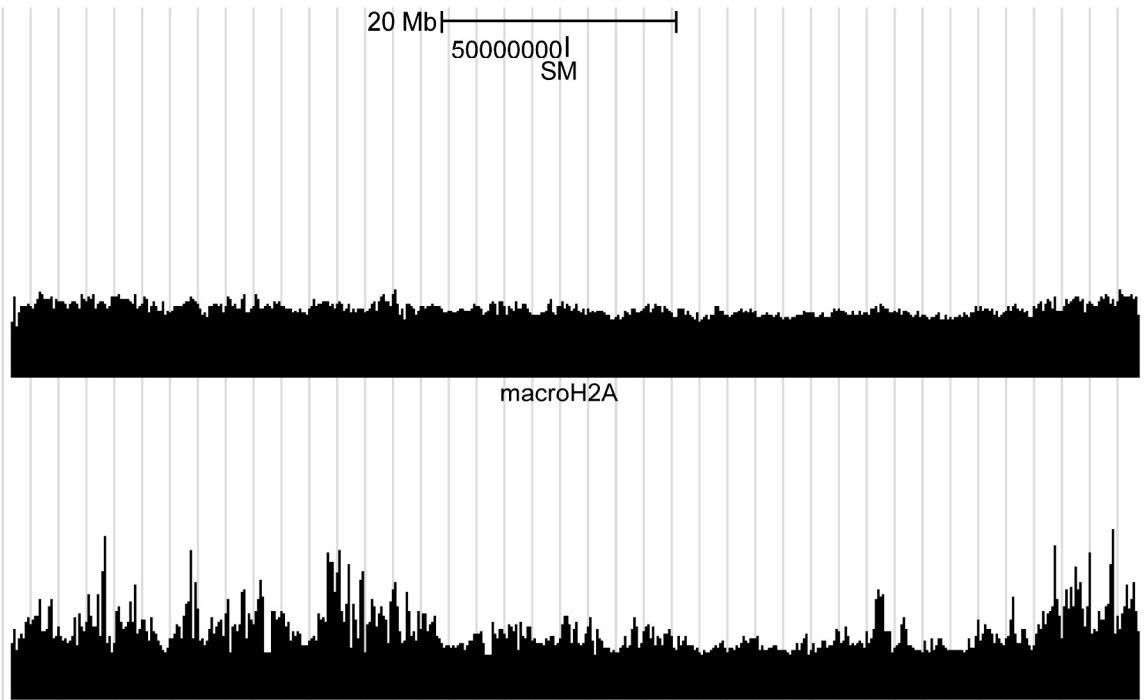
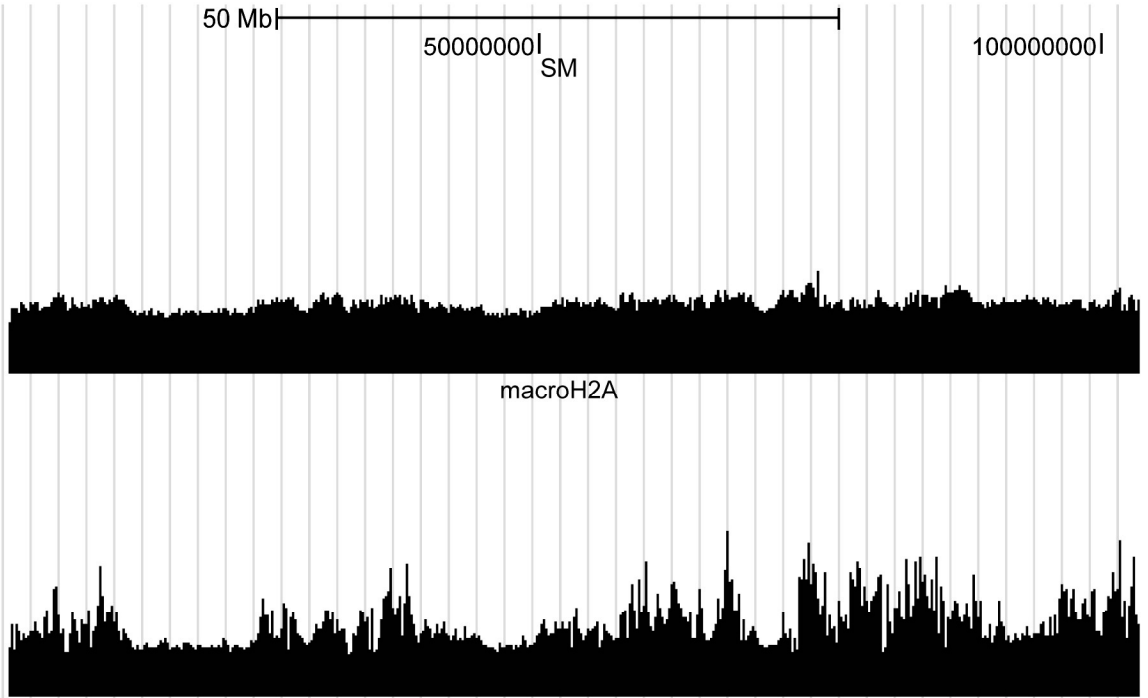
0

8

macroH2A

macroH2A1

0



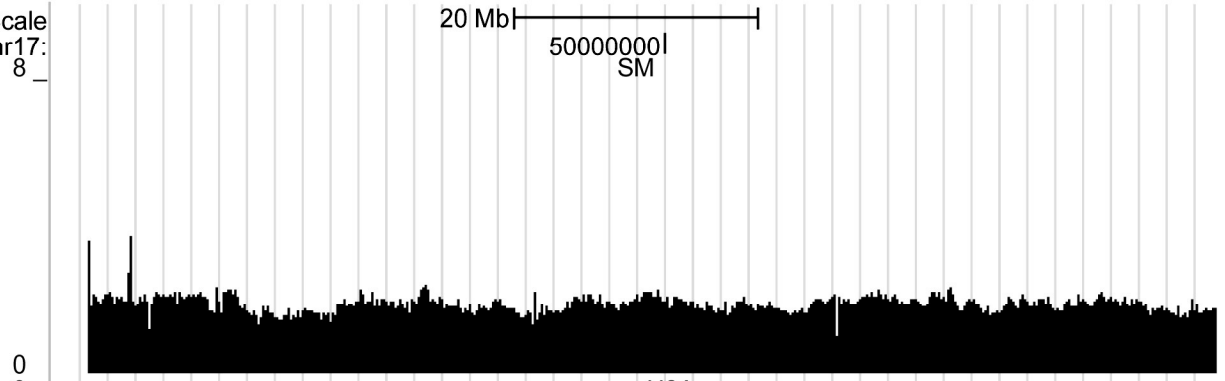


# Chromosome 17

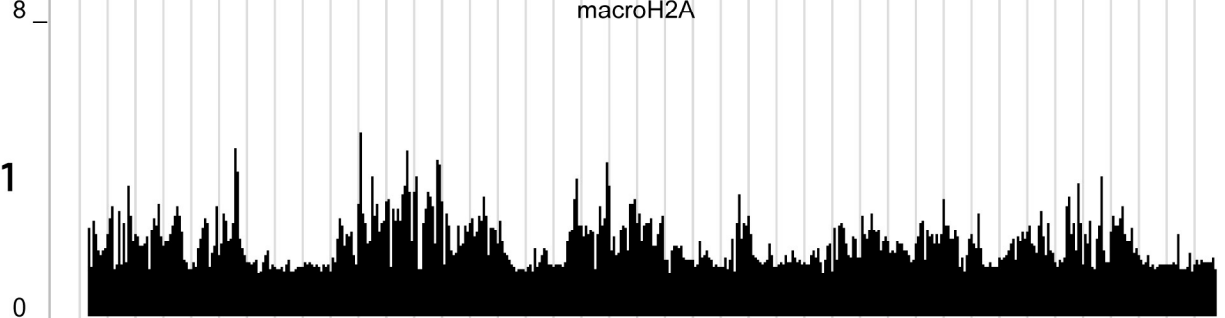
Scale  
chr17:  
8

20 Mb |-----|  
500000001  
SM

Starting  
Material



macroH2A1

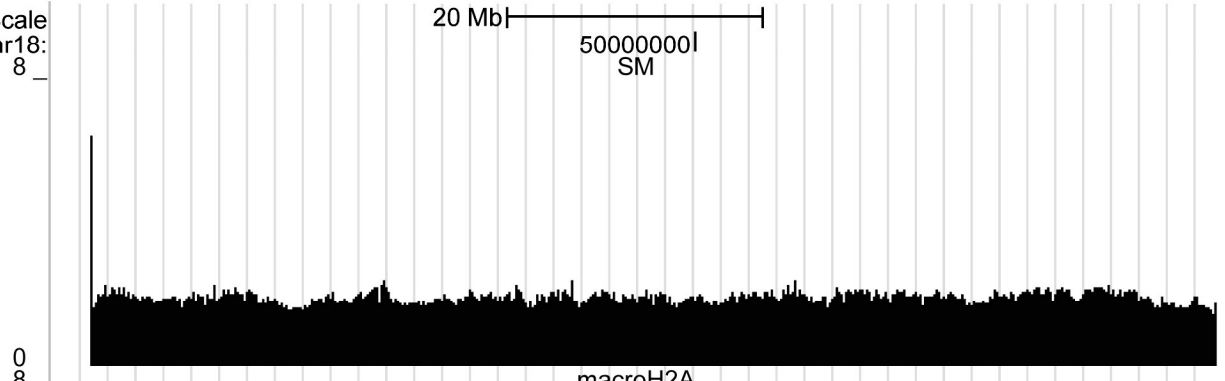


# Chromosome 18

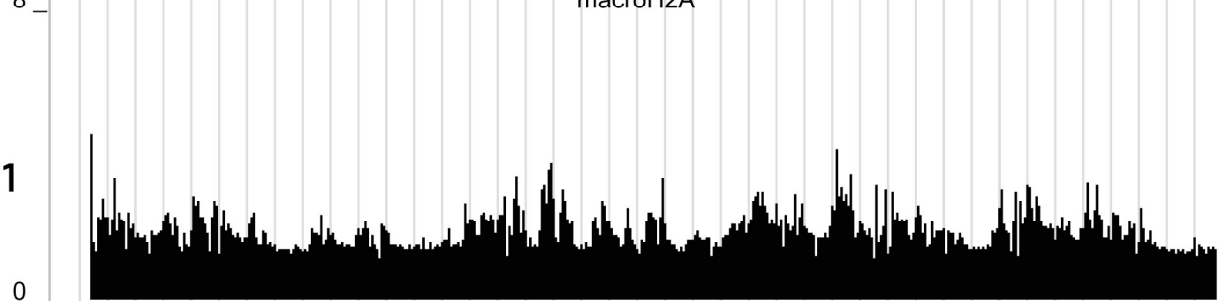
Scale  
chr18:  
8

20 Mb |-----|  
500000001  
SM

Starting  
Material



macroH2A1



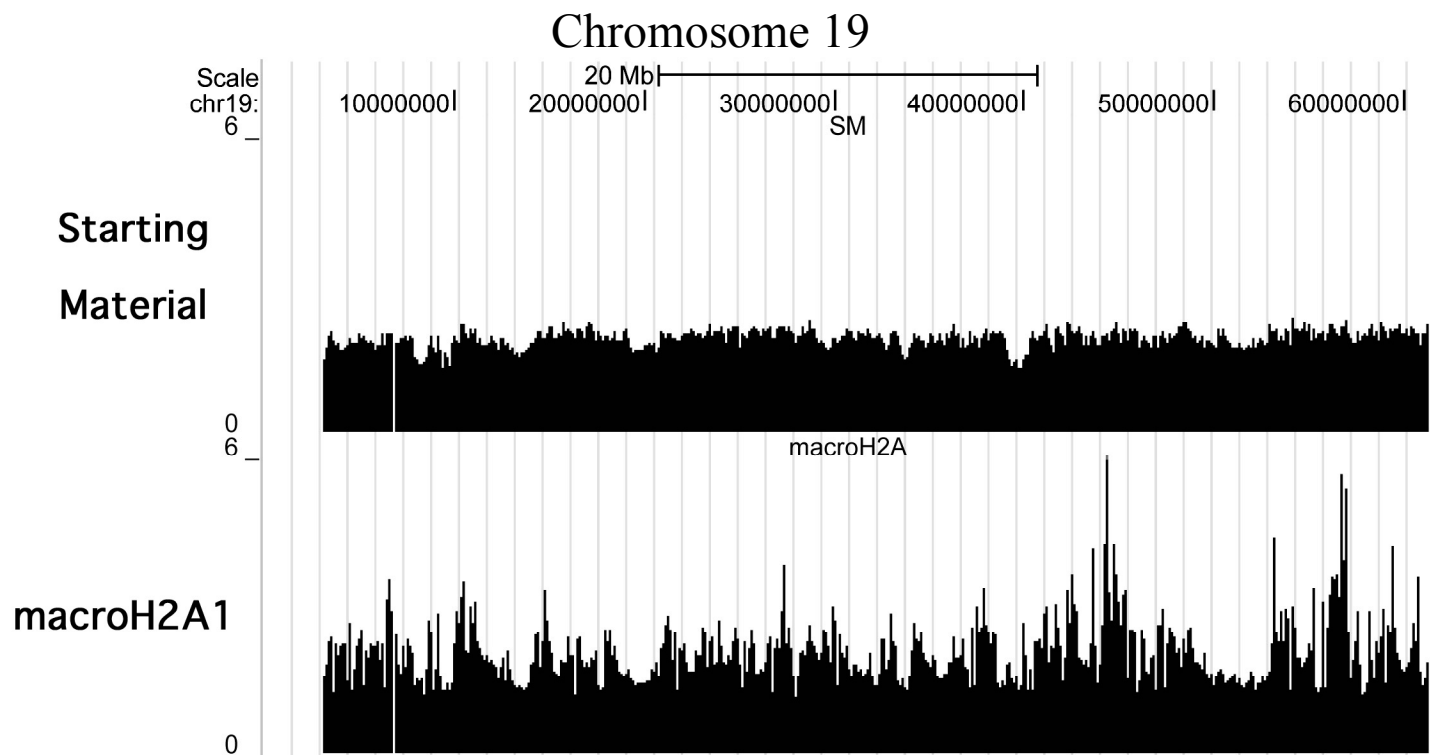


Figure 1, supplement. Distribution of macroH2A1 nucleosomes across autosomes in female mouse liver. macroH2A1 nucleosomes were purified by thioaffinity chromatography, see methods. Sequence tag maps for starting material and macroH2A1 mononucleosomal DNAs are shown. Data was uploaded in the UCSC genome browser [1] (NCBI 36/mm8).

1. Kent, W.J., C.W. Sugnet, T.S. Furey, K.M. Roskin, T.H. Pringle, A.M. Zahler, and D. Haussler, *The human genome browser at UCSC*. *Genome Res*, 2002. **12**(6): p. 996-1006.