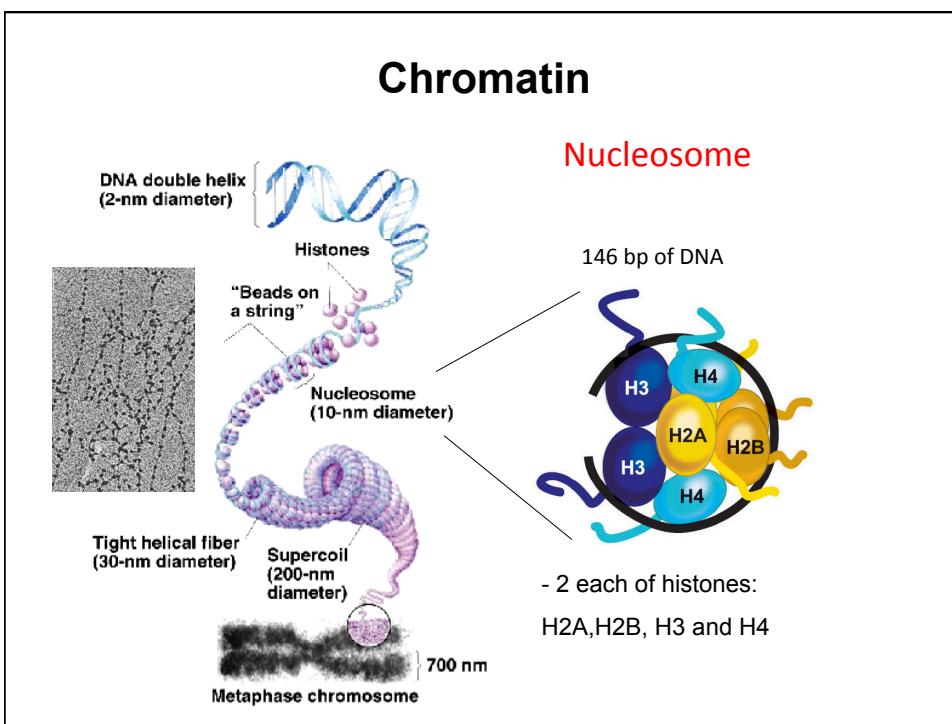
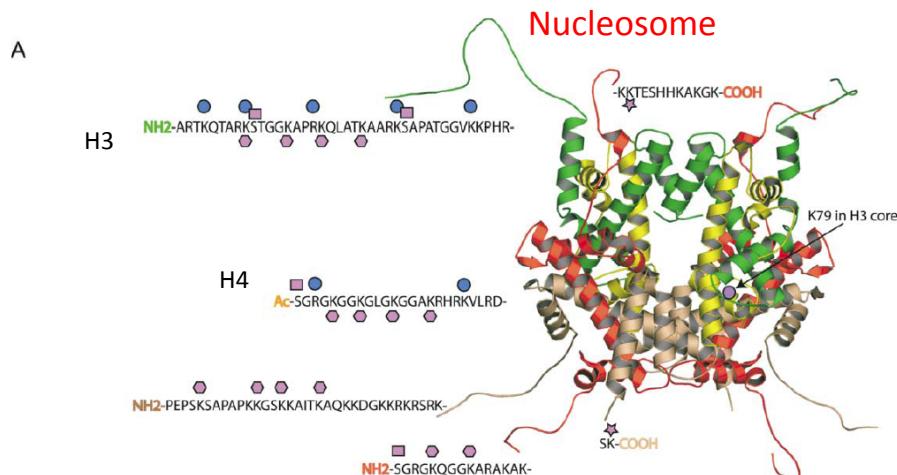


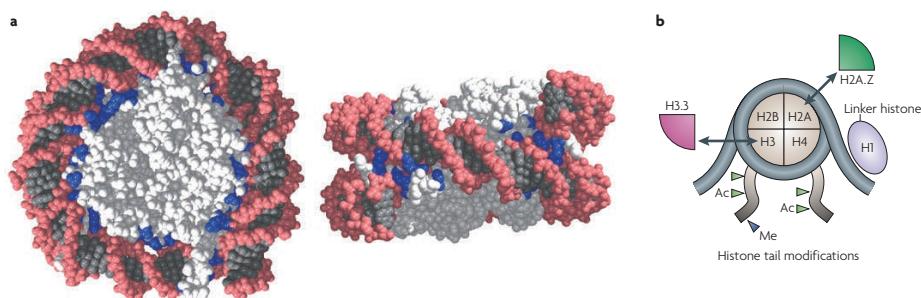
“Your current situation is no indication of your ultimate potential.”
-- Tony Robbins



The Nucleosome core particle



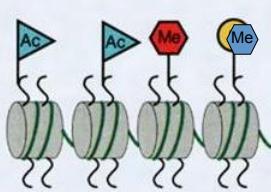
Structure of histones



Structure & Epigenetics of Euchromatin versus Heterochromatin

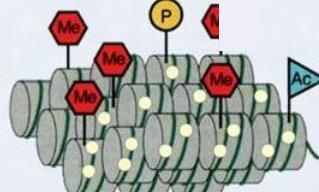
DNA methylation and histone modifications help to compartmentalize the genome into domains of different transcriptional potentials

Euchromatin



- High histone acetylation
- Low DNA methylation
- H3-K4 methylation

Heterochromatin



- Low histone acetylation
- Dense DNA methylation
- H3-K9 methylation

Paula Vertino, Henry Stewart Talks

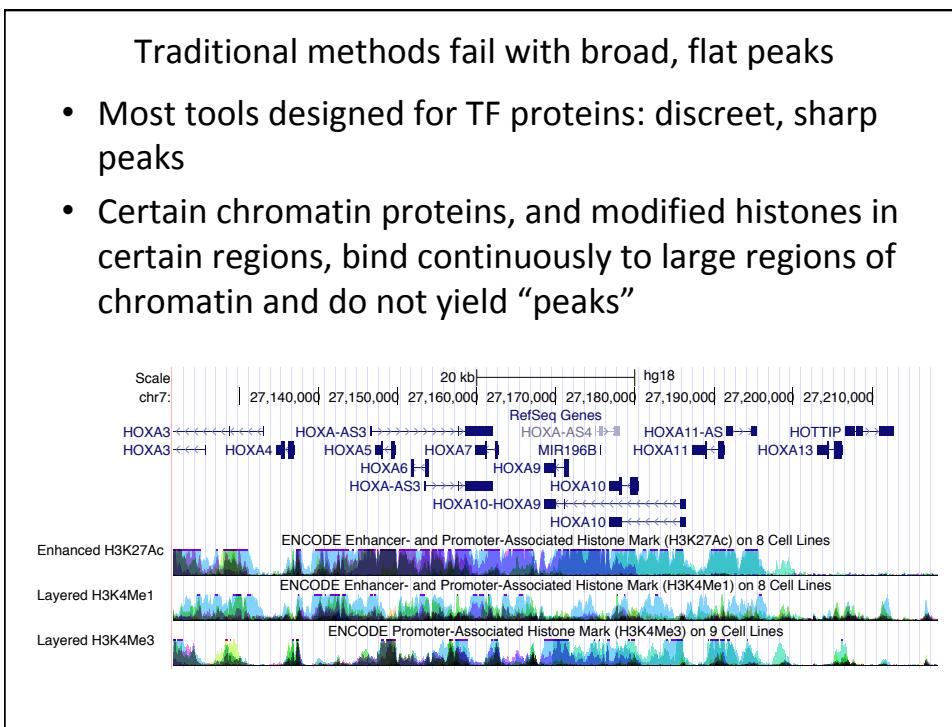
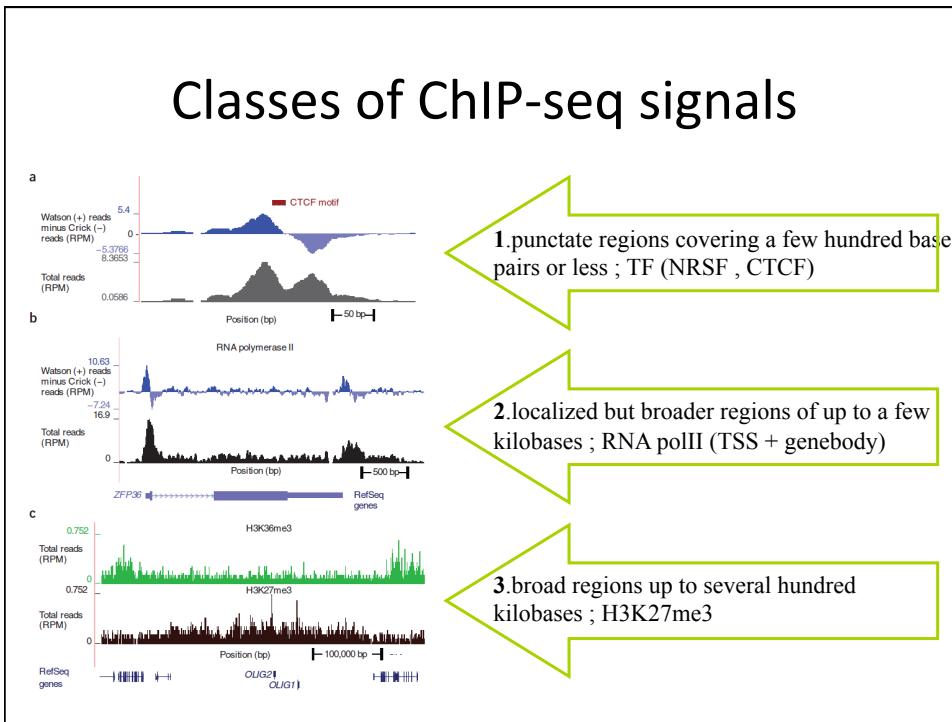
Two ways of measuring chromatin

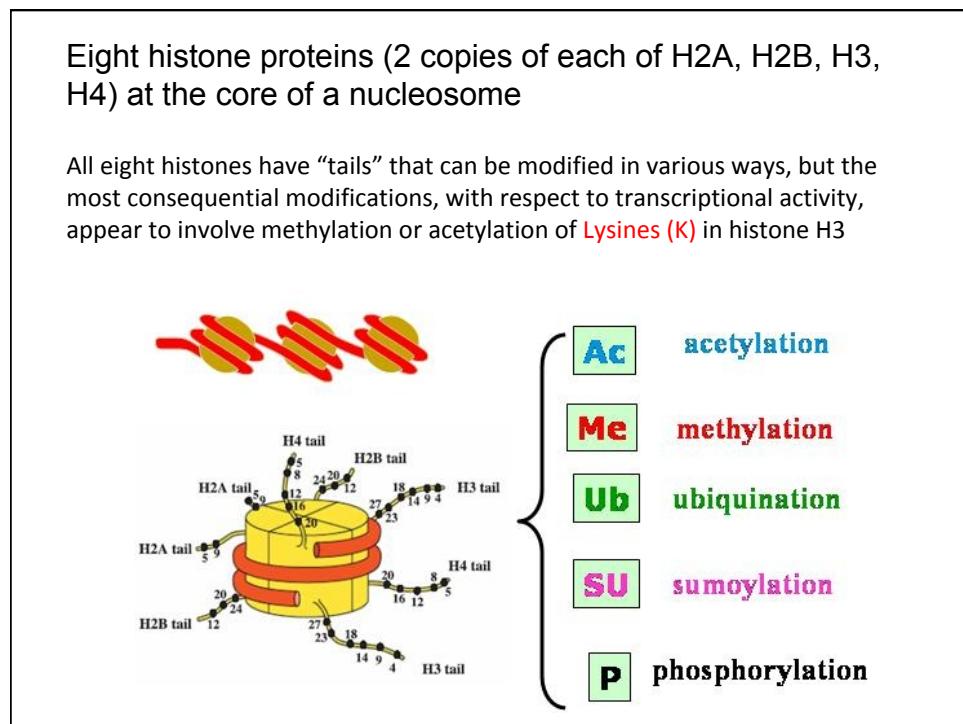
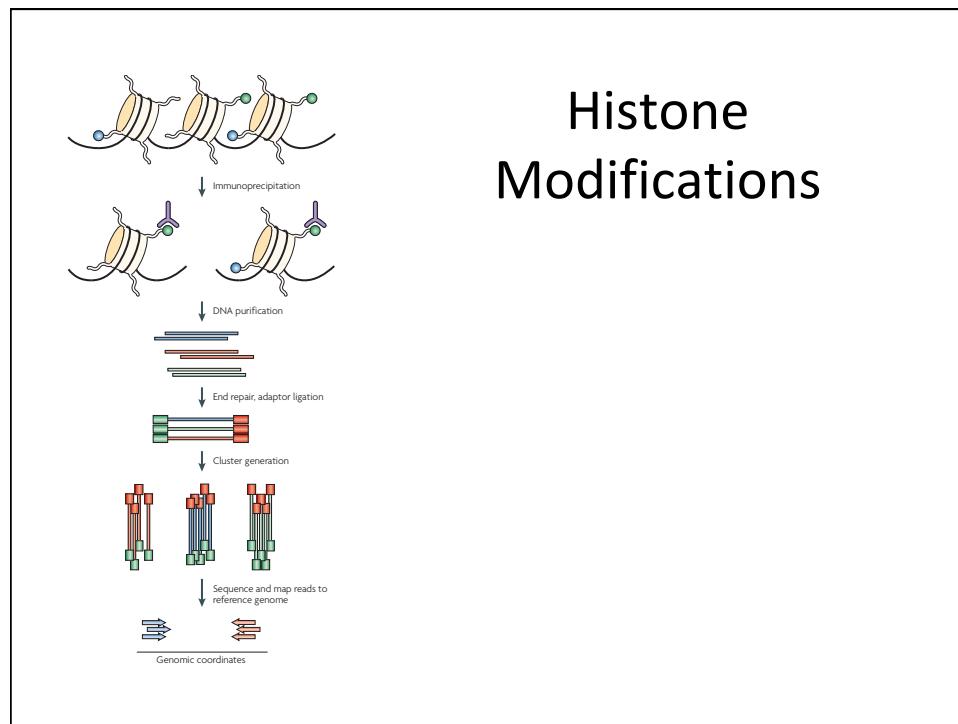
- Where are nucleosomes (or marks)?

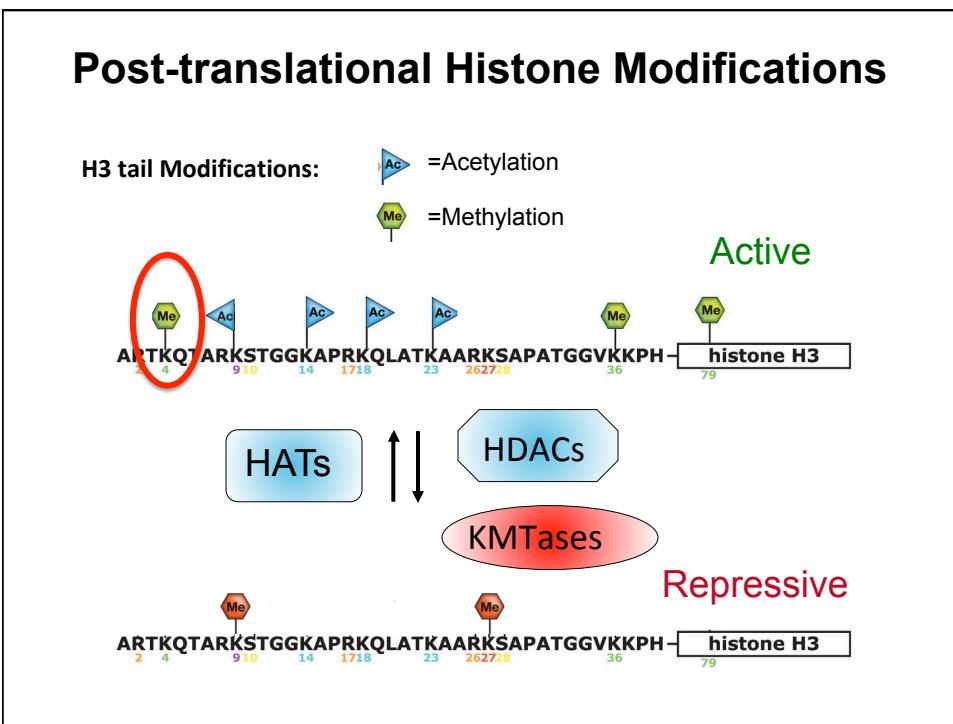
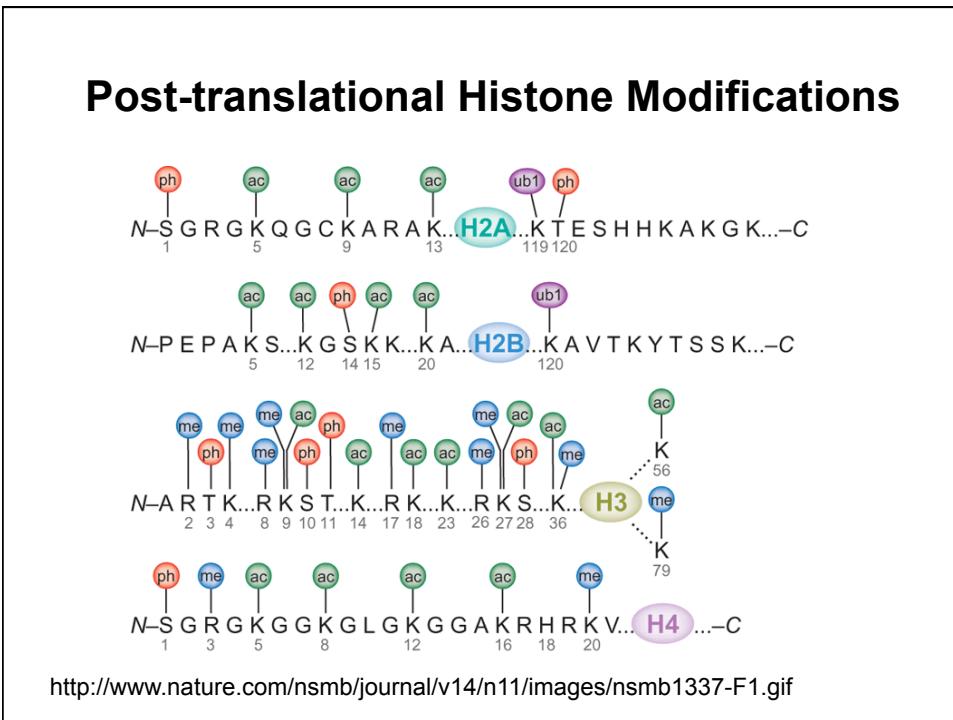
ChIP

- What regions are accessible (not protected by chromatin)?

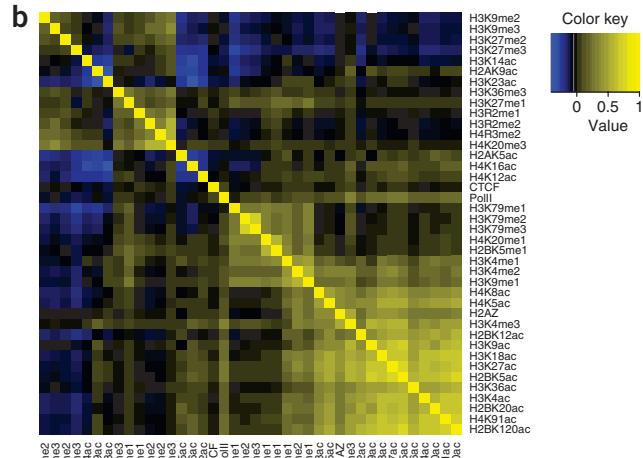
DNase I, MNase, ATAC



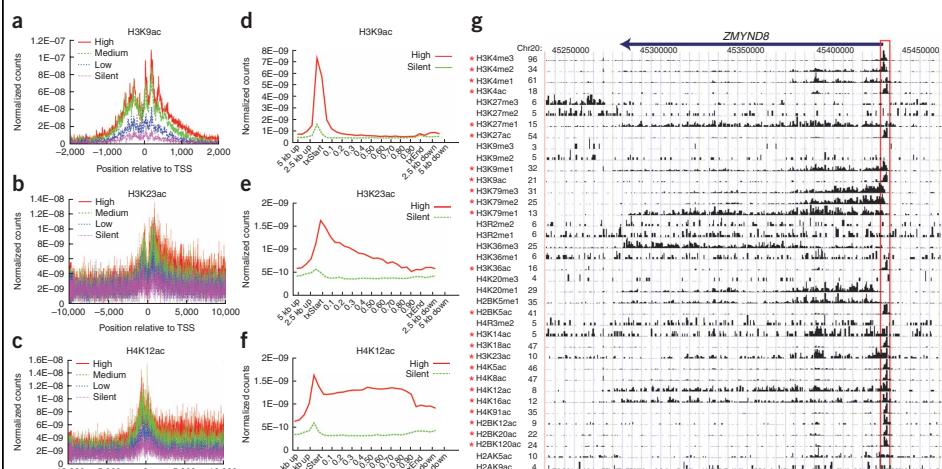


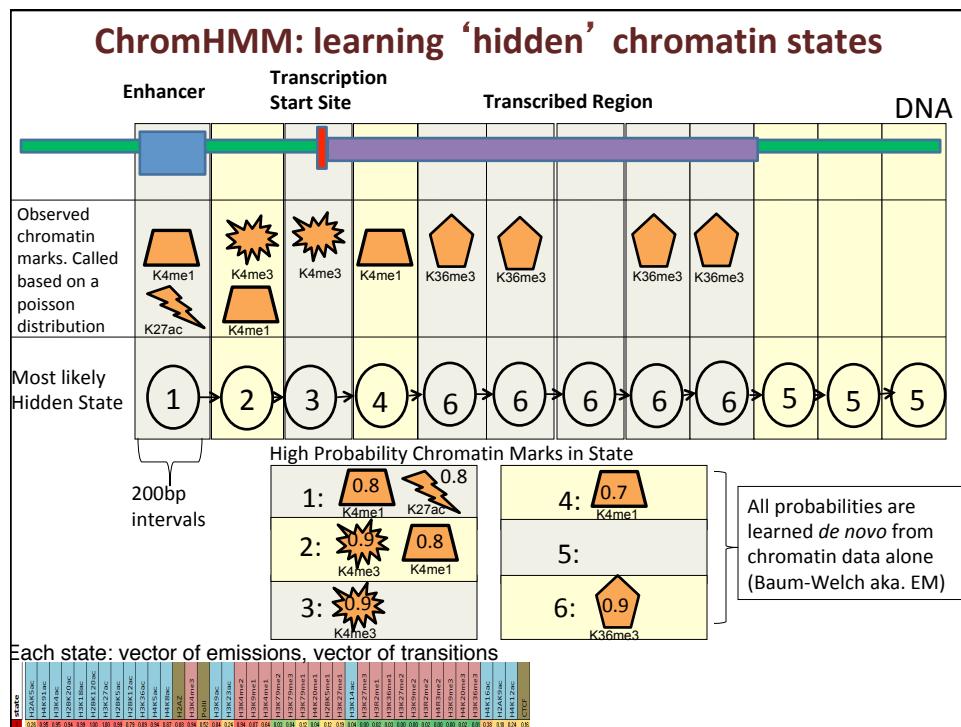
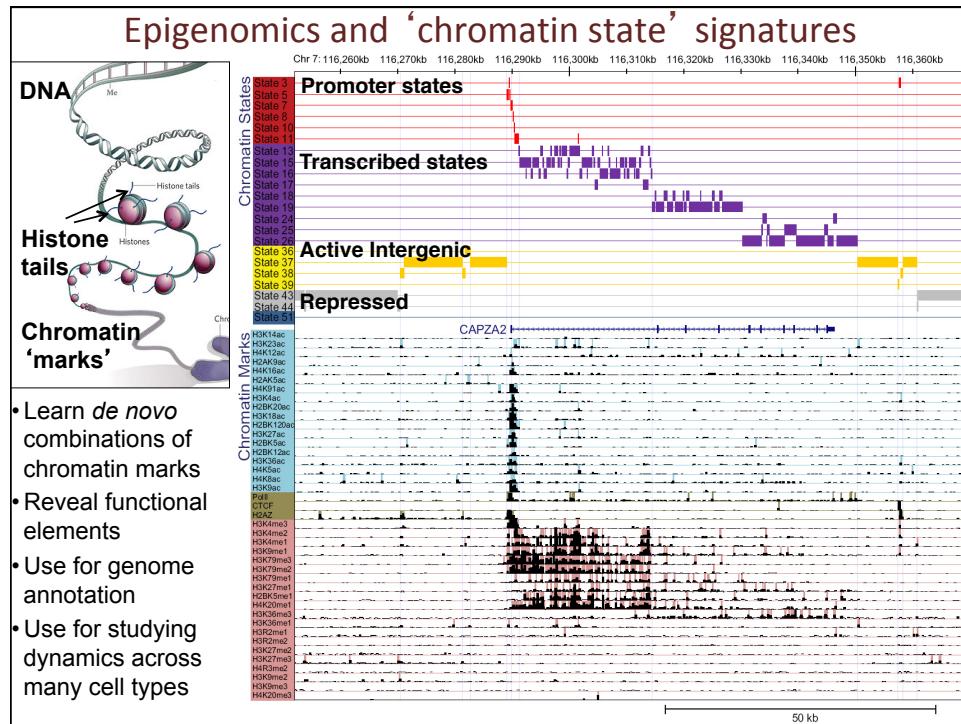


Marks are redundant .. So what do they do?



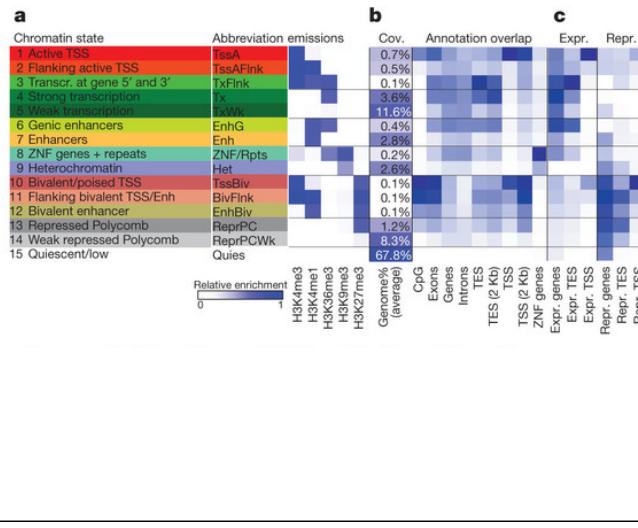
Patterns of Modifications



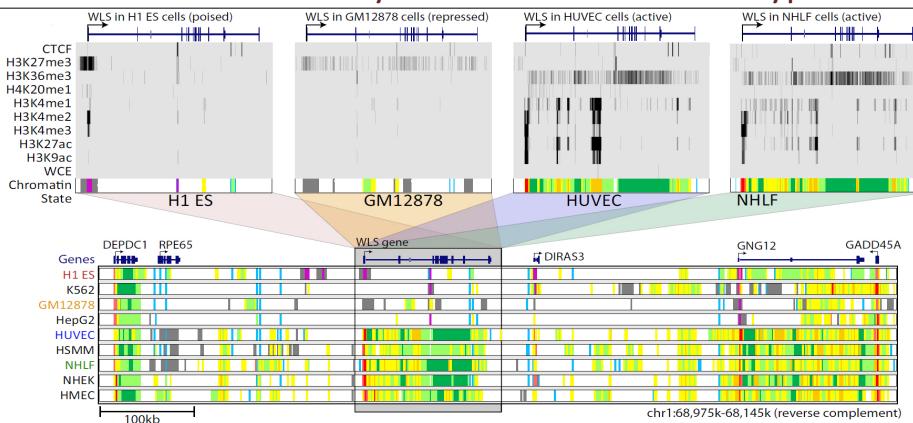


Chromatin “states”

- ChromHMM tool combines information from 38 different histone marks, Pol2 and CTCF profiles to identify different ‘states’
- States are labeled post-hoc
- Other tools exist, e.g., ChromaSig, Segway

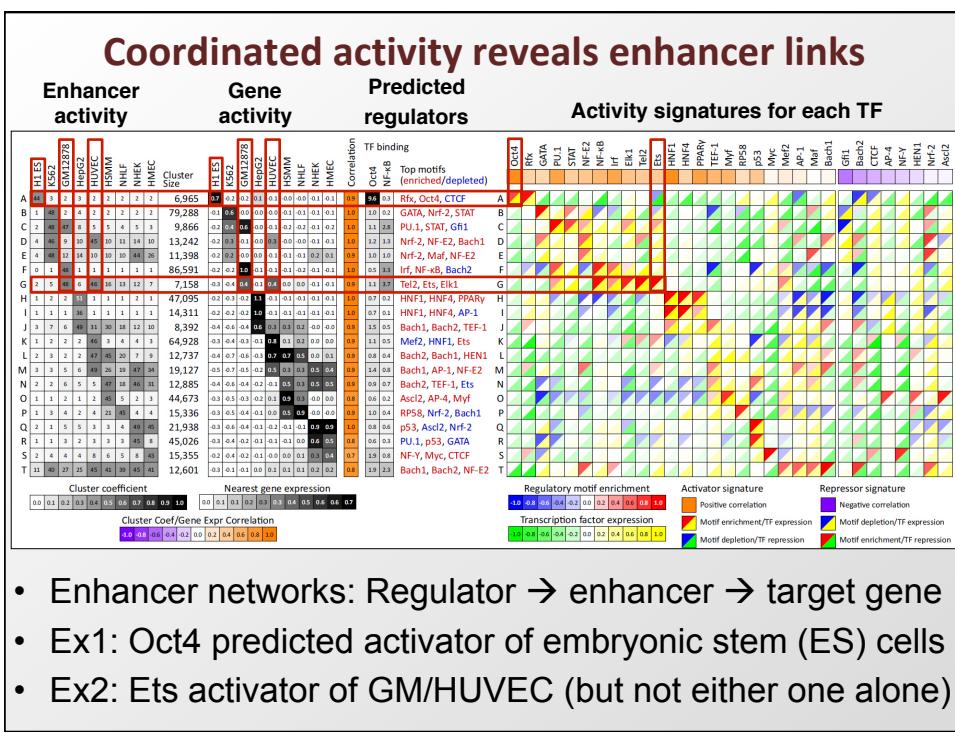
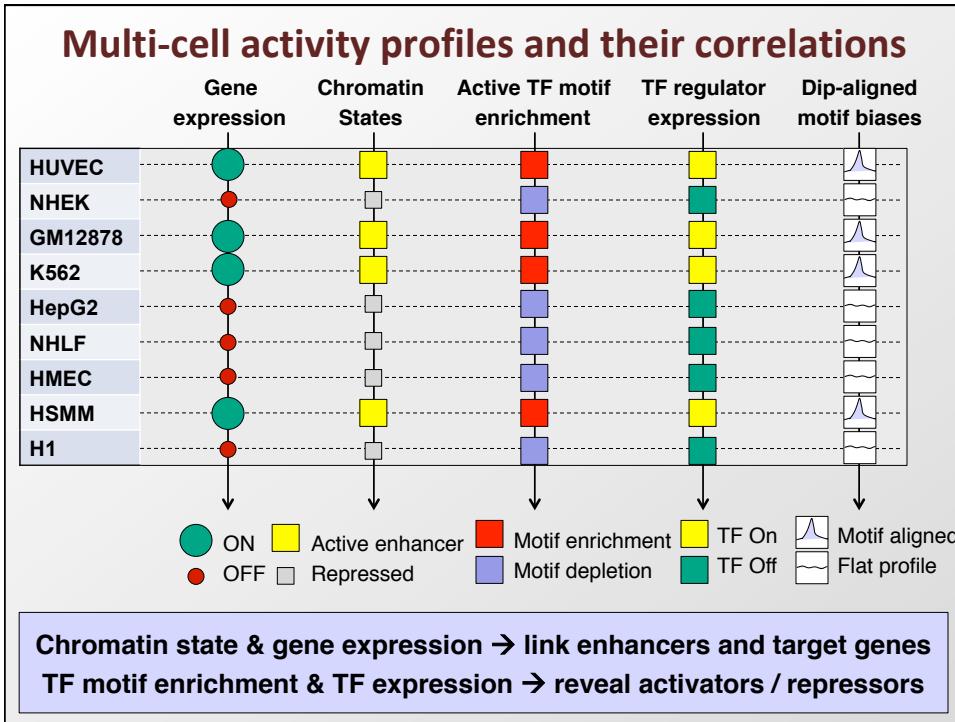


Chromatin states dynamics across nine cell types



- State definitions are cell-type invariant
 - Same combinations consistently found
- State locations are cell-type specific
 - Can study pair-wise or multi-way changes

State	State annotation
1	Active Promoter
2	Weak Promoter
3	Inactive/poised Promoter
4	Strong enhancer
5	Strong enhancer
6	Weak/poised enhancer
7	Weak/poised enhancer
8	Insulator
9	Transcriptional transition
10	Transcriptional elongation
11	Weak transcribed
12	Polycomb-repressed
13	Heterochrom; low signal
14	Repetitive/CNV
15	Repetitive/CNV



Many histone marks scale with Pol II density

