Chromatin accessibility: local chromatin architecture and regulatory elements

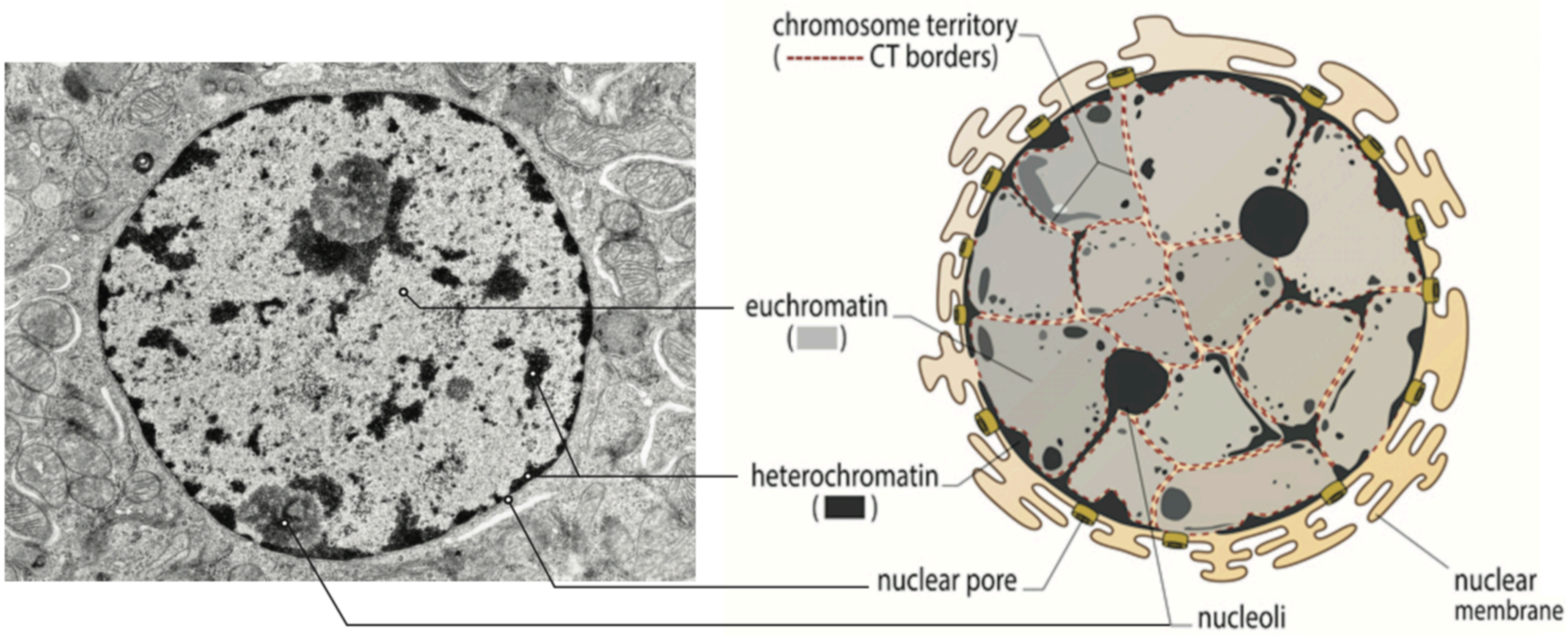
NGS analysis for gene regulation and epigenomics

Physalia 2021

Jacques Serizay

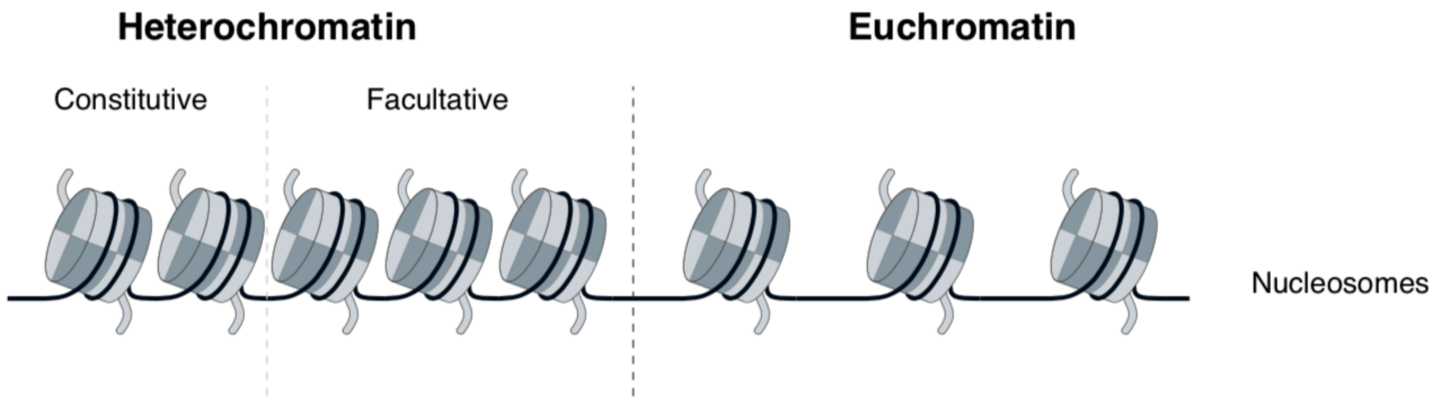
Euchromatin vs. heterochromatin

- Chromatin has different conformations in the nucleus



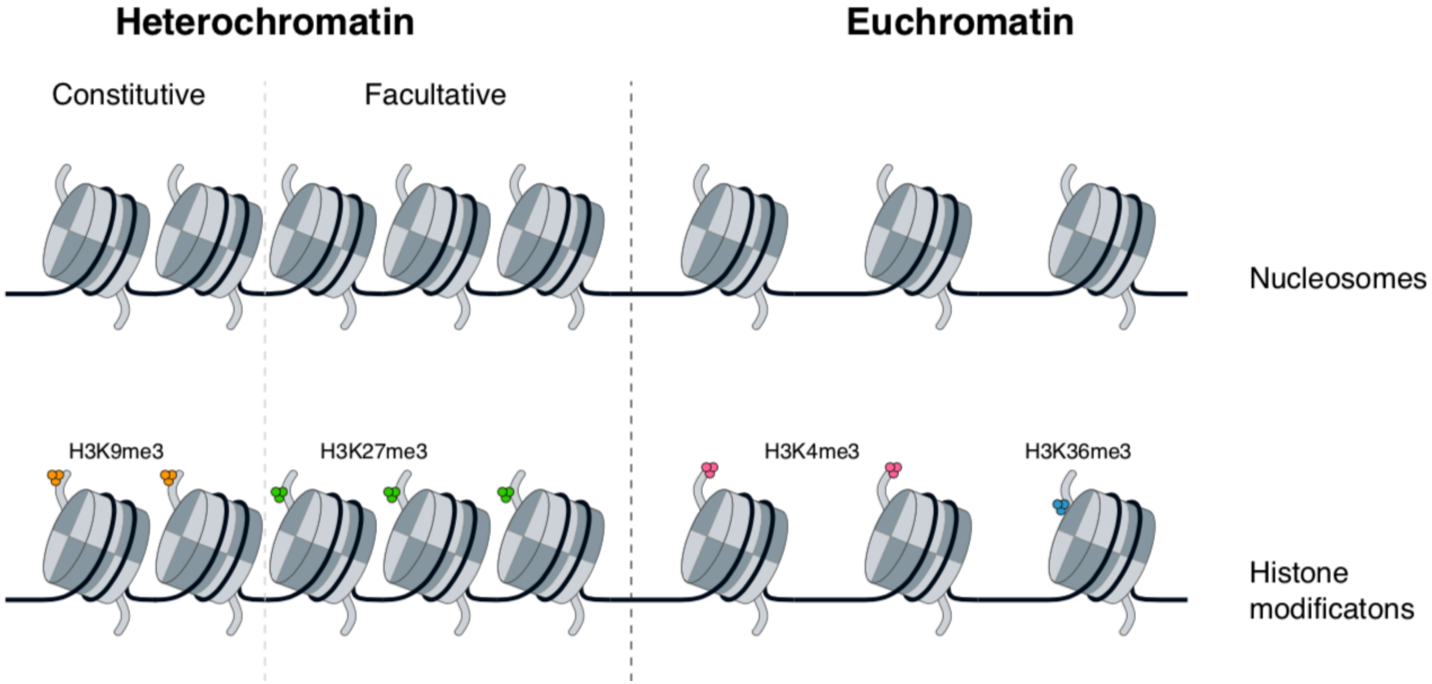
Euchromatin vs. heterochromatin

- Nucleosomes are differently arranged in euchromatin or in heterochromatin



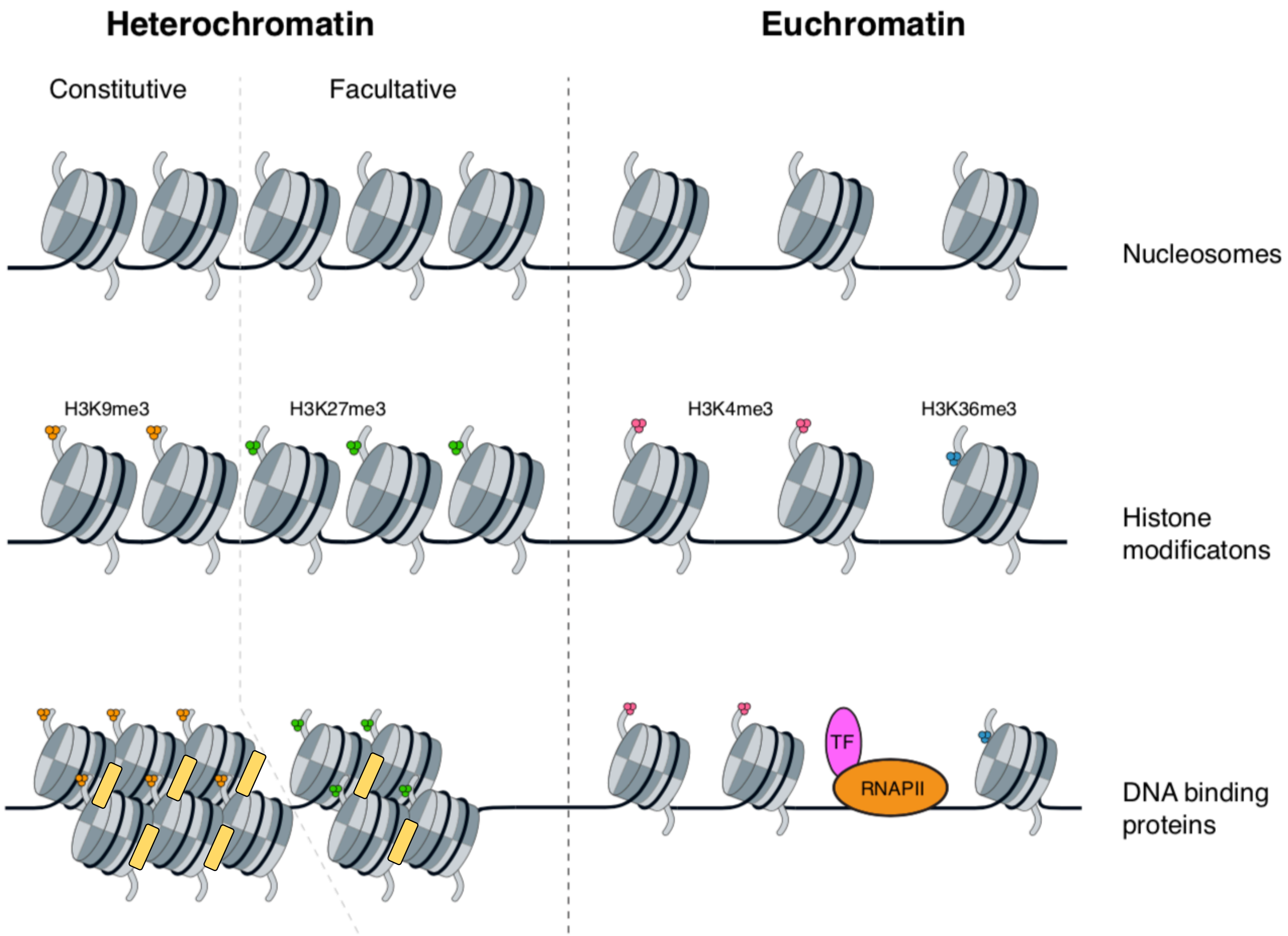
Euchromatin vs. heterochromatin

- Nucleosomes are differently arranged in euchromatin or in heterochromatin
- Nucleosomes also have different PTMs in euK/heteroK



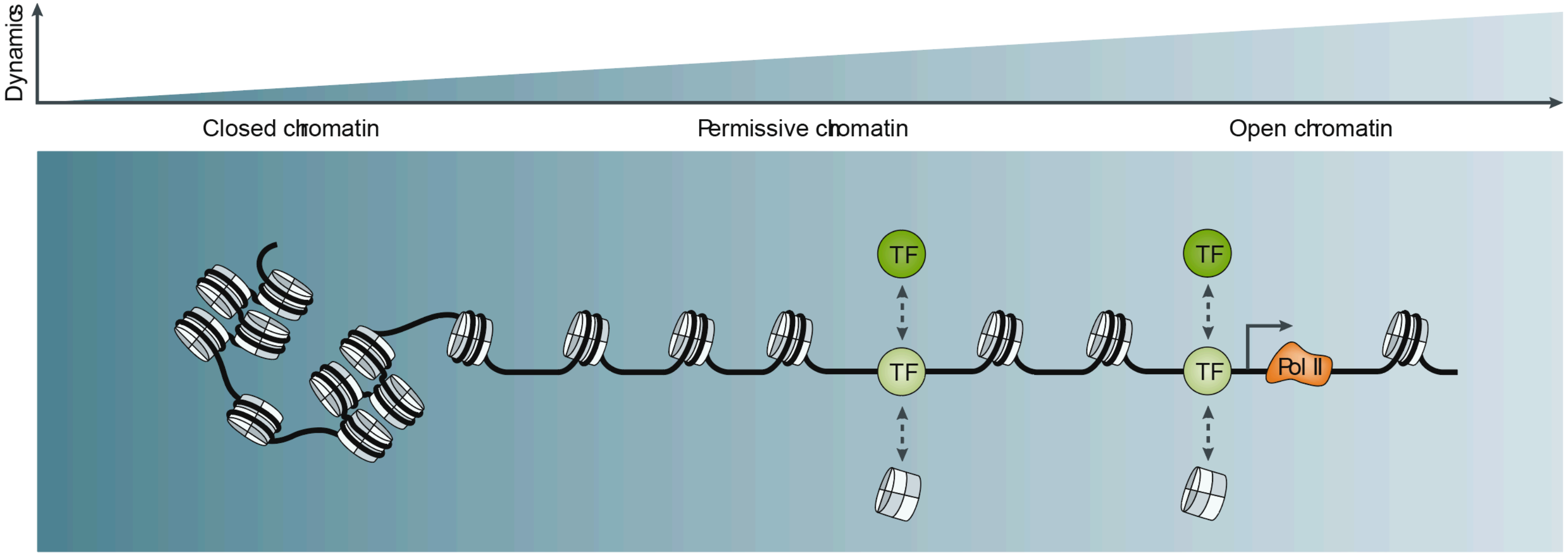
Euchromatin vs. heterochromatin

- Nucleosomes are differently arranged in euchromatin or in heterochromatin
- Nucleosomes also have different PTMs in euK/heteroK
- Finally, DNA-binding proteins are specific to euK/heteroK



Beyond textbook statements: a spectrum of regulatory capacity

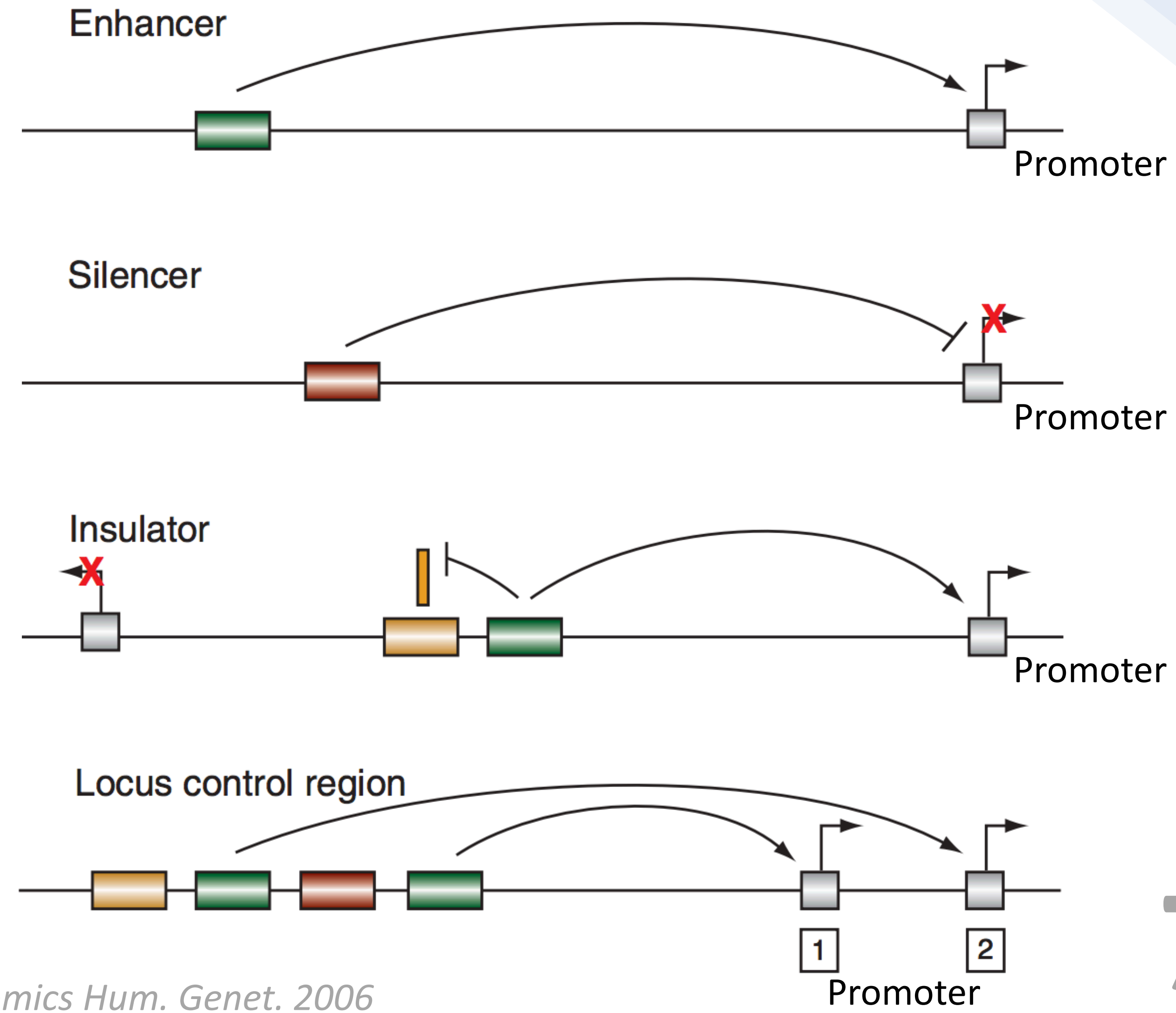
- Chromatin accessibility continuum that ranges from closed chromatin to highly dynamic, accessible or permissive chromatin
- This landscape of chromatin accessibility reflects the spectrum of regulatory capacity — rather than a bistate organization



Klemm et al., Nat .Rev. Genet 2019

Regulatory elements

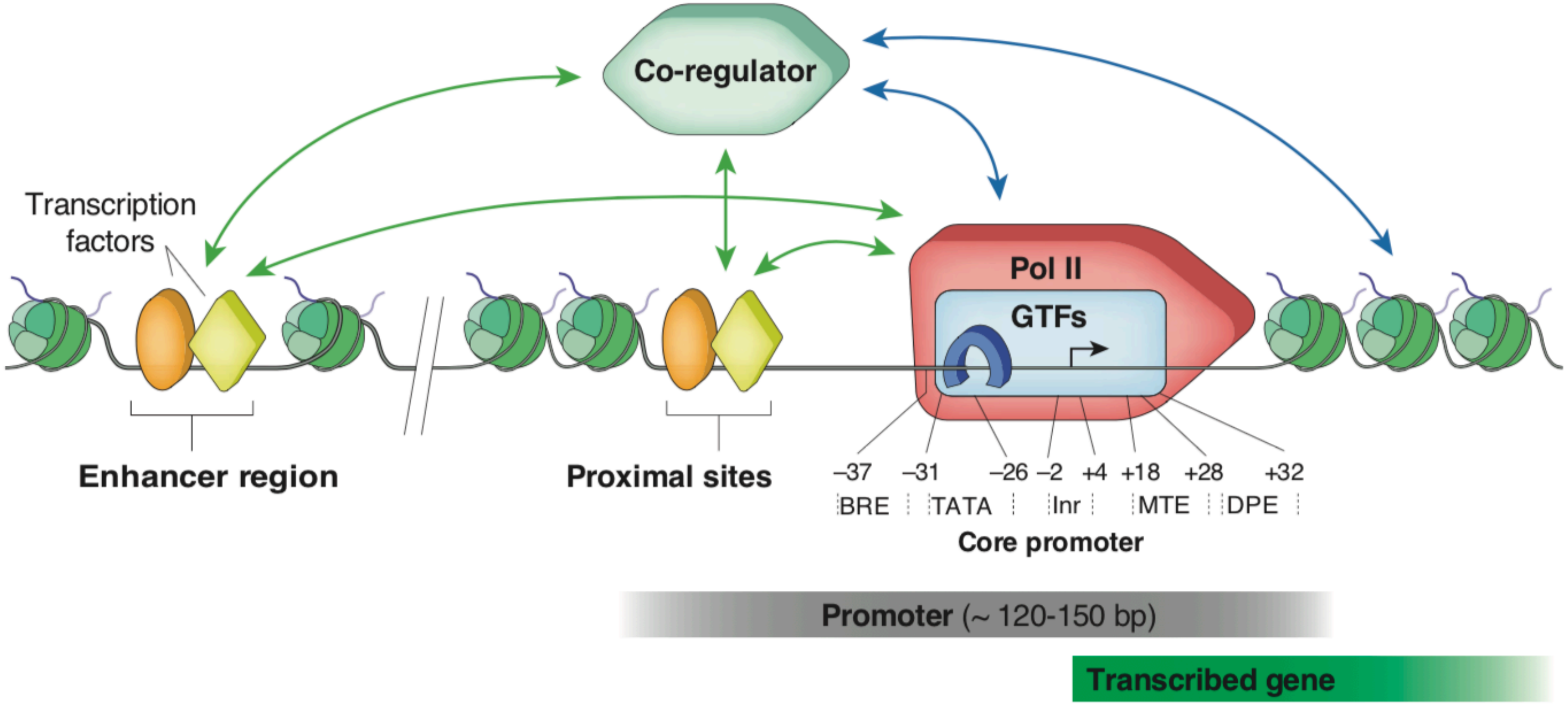
- Short genomic loci
- Chromatin may be accessible
- Play a role in regulation of gene expression
- Usually conserved across species



Maston et al., Annu. Rev. Genomics Hum. Genet. 2006

Regulatory elements

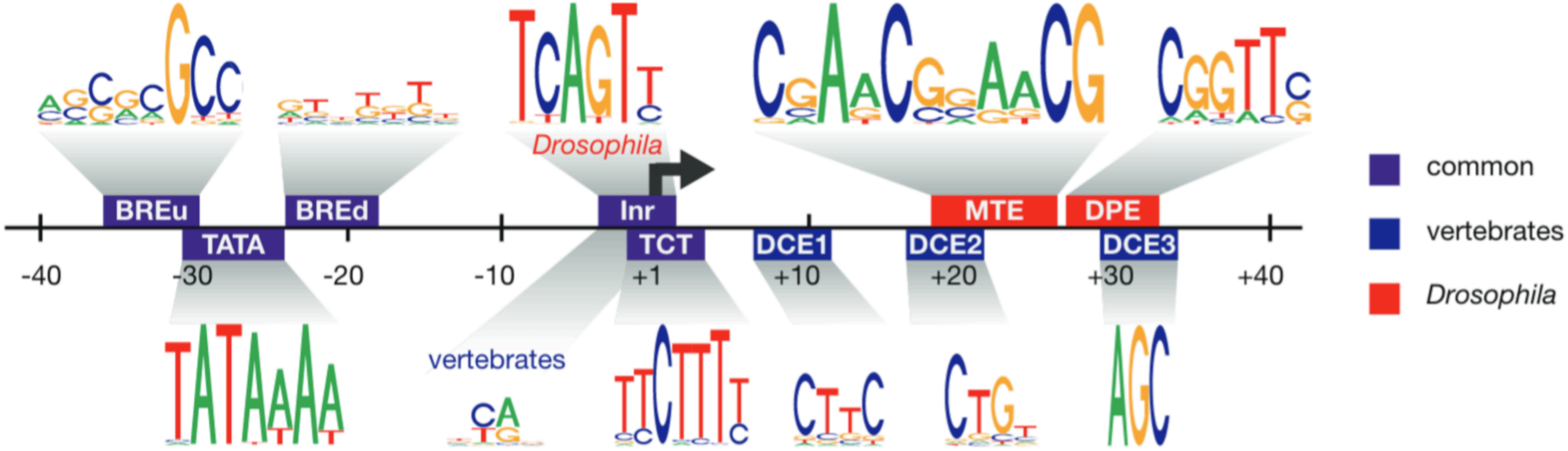
- Promoters and proximal enhancers are the most important REs for gene expression



Fuda et al., Nature 2009

Promoter organization

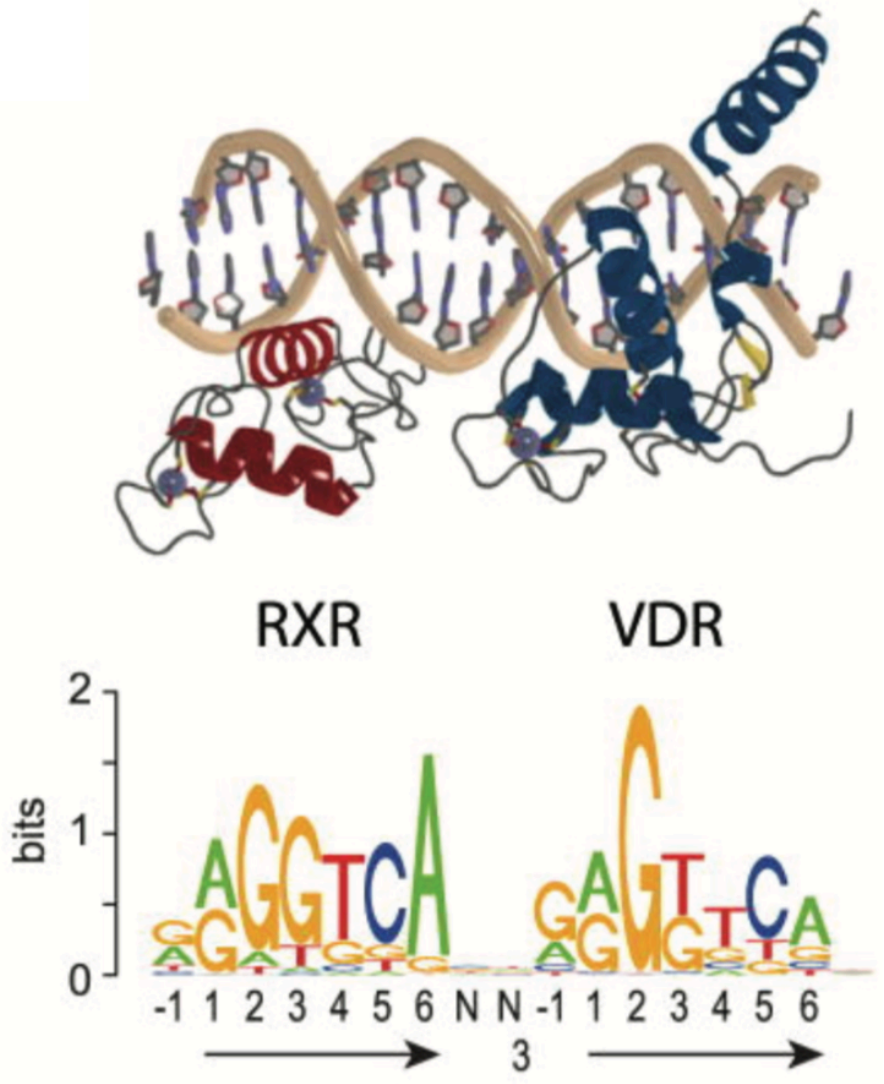
- Transcription machinery and general transcription factors need access to DNA to recognize their binding motif



Haberle and Lenhard, Semin. Cell Dev. Biol. 2016

Promoter organization

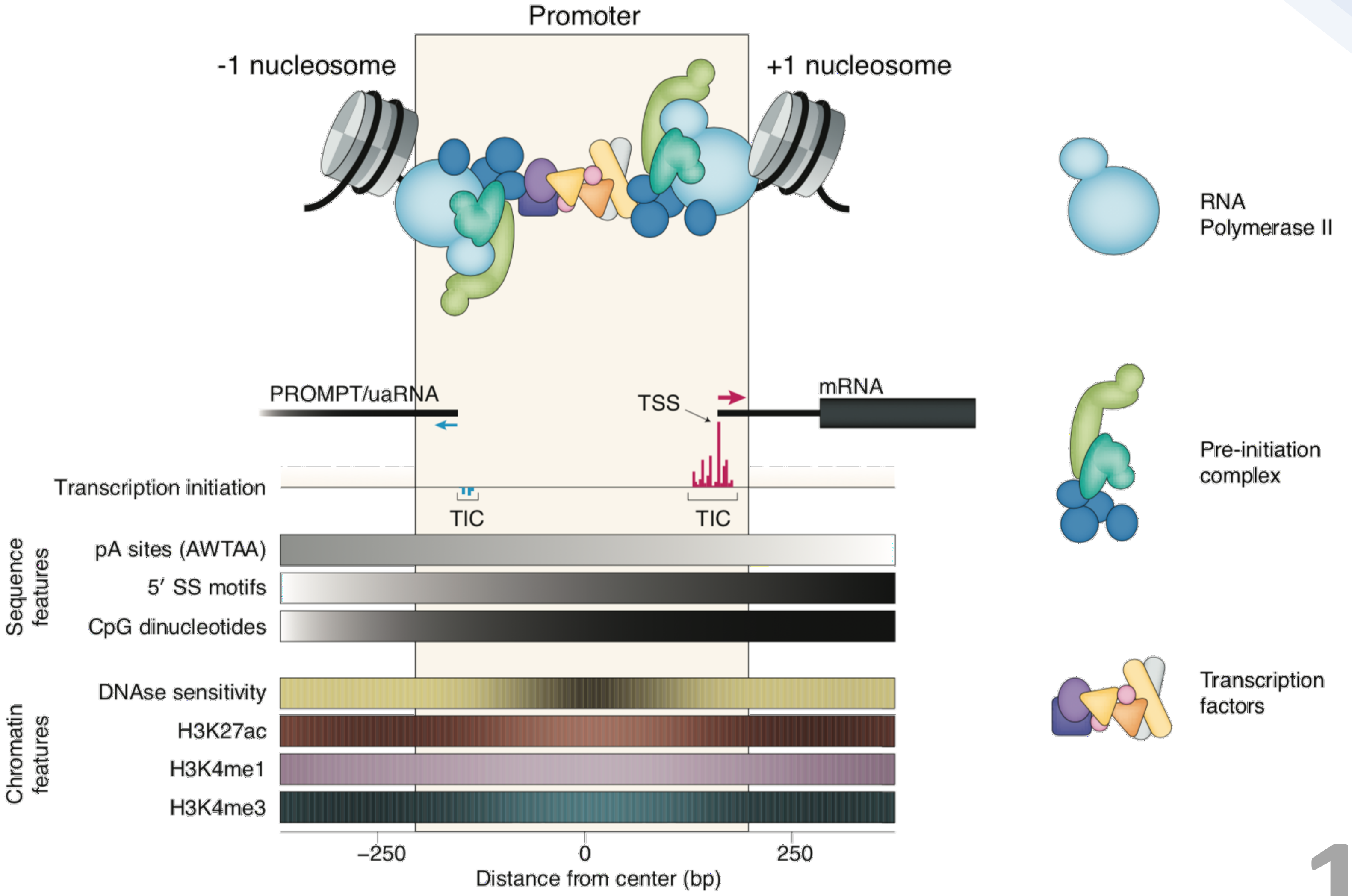
- Specific transcription factors also need access to DNA to recognize their binding motif



Carlberg and Camp- bell, Steroids 2013

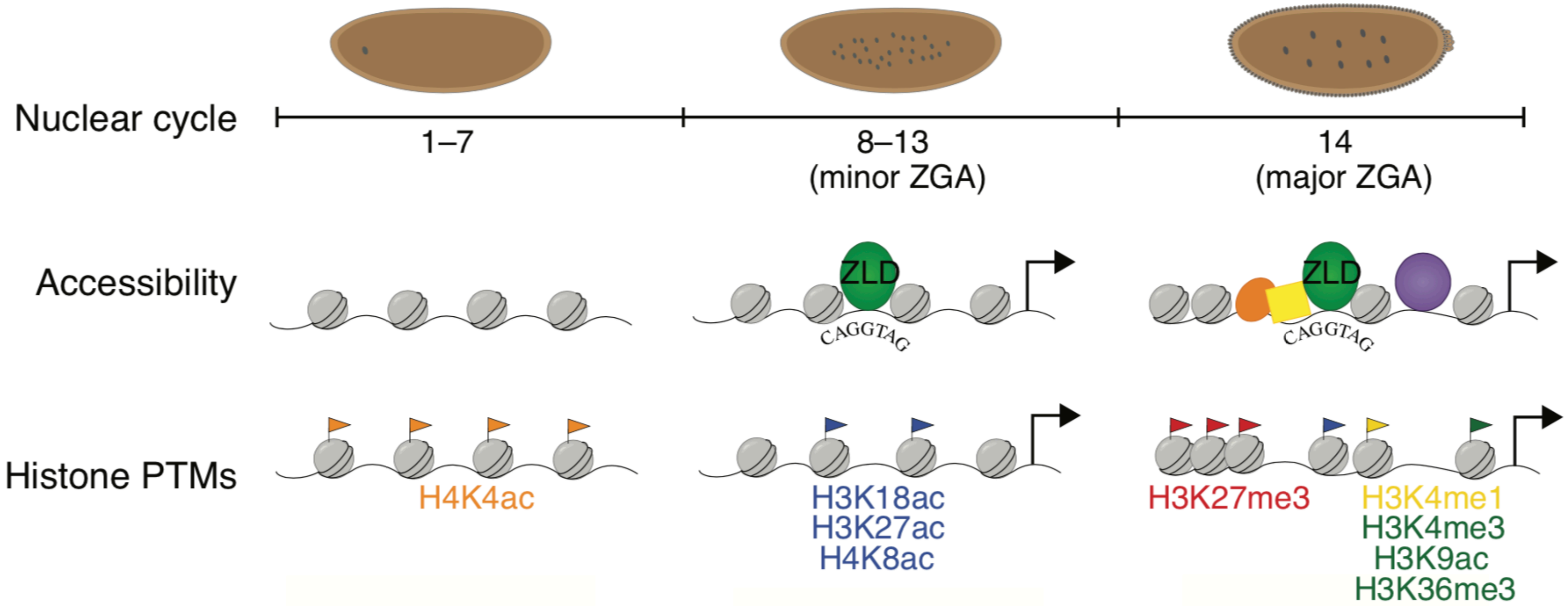
Promoter organization

- Promoters are crowded environments!



Chromatin accessibility is context-dependent

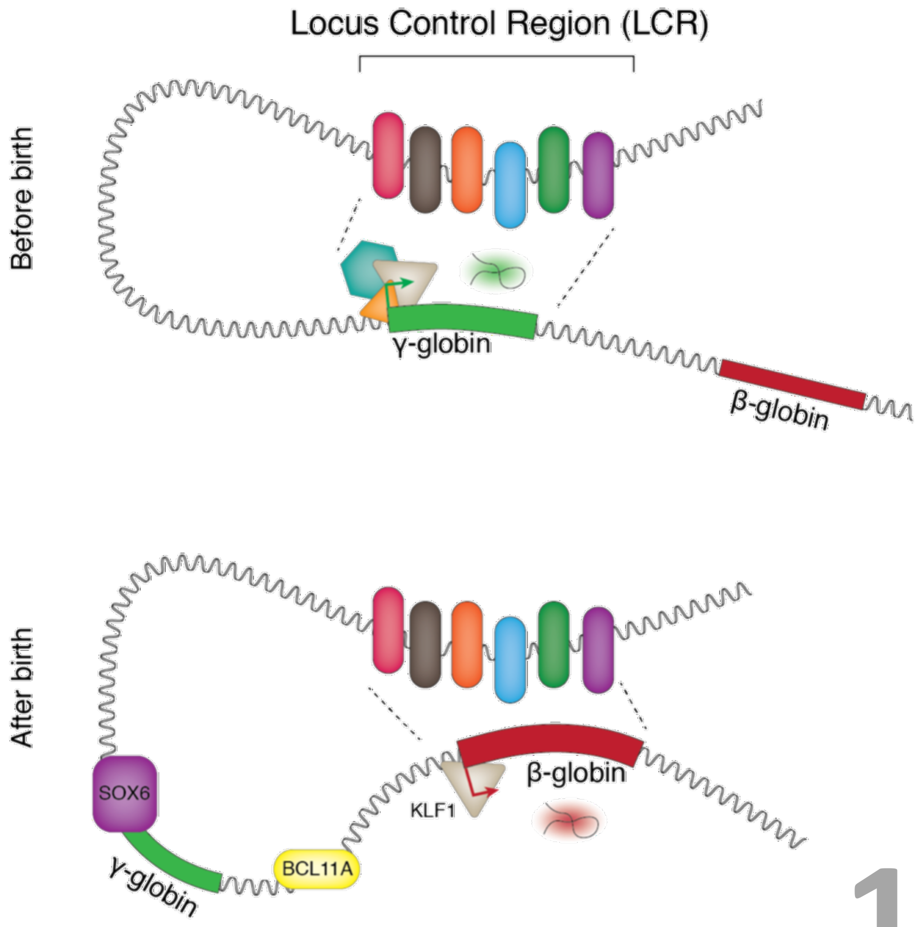
- During development, pioneer factors can bind nucleosomal DNA, displace nucleosomes and reveal specific transcription factor binding sites.



Hamm & Harrison, Open Biol. 2018

Chromatin accessibility remodeling regulates gene expression

- Changes in chromatin accessibility lead to regulatory network rewiring and modifications in patterns of gene expression



Documentation

- From reads to insight: a hitchhiker’s guide to ATAC-seq data analysis, *Yan et al., Genome Biol. 2019*

- https://epigeneticsandchromatin.biomedcentral.com/articles/10.1186/1756-8935-7-33