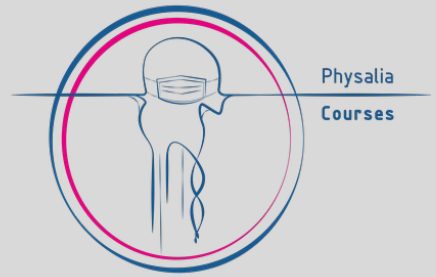
Introduction to epigenomics

Or how genes are regulated...

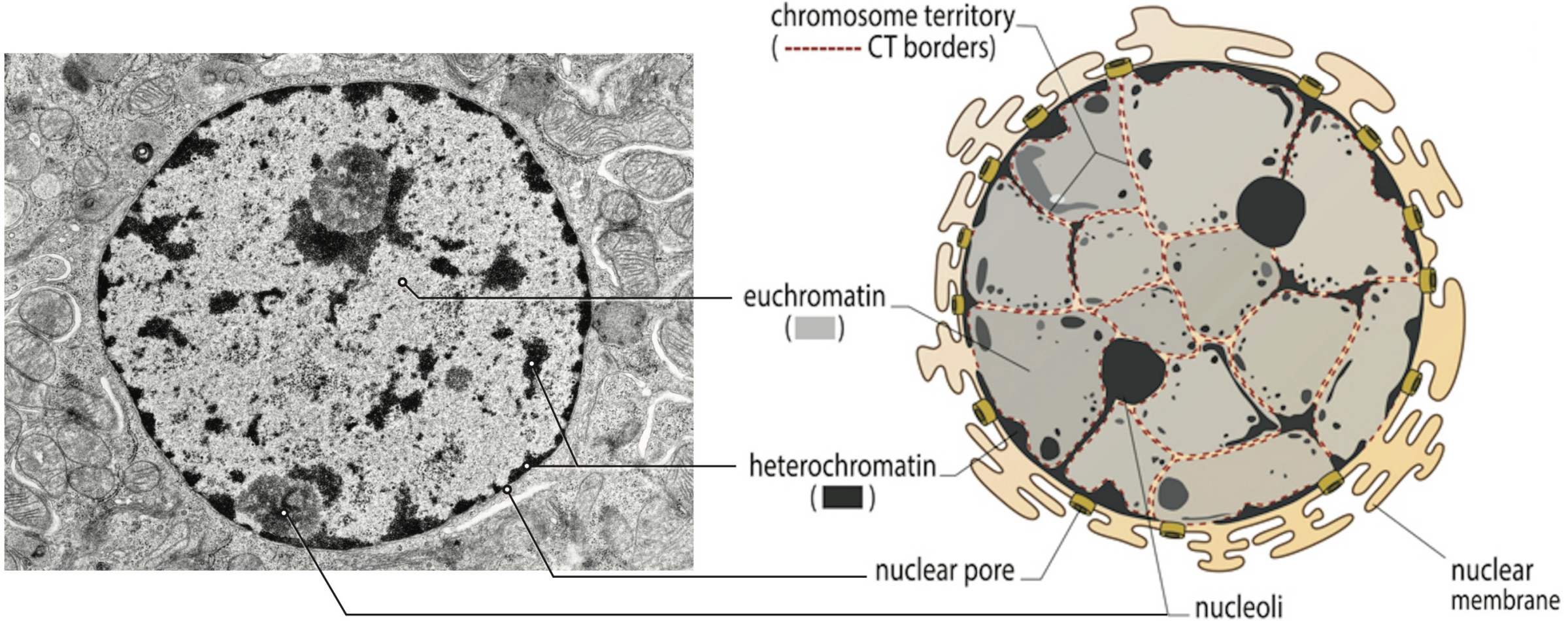
Epigenomics Data Analysis

Jacques Serizay

Physalia 2025



Chromatin is complex



Chromatin composition varies along the genome

DNA

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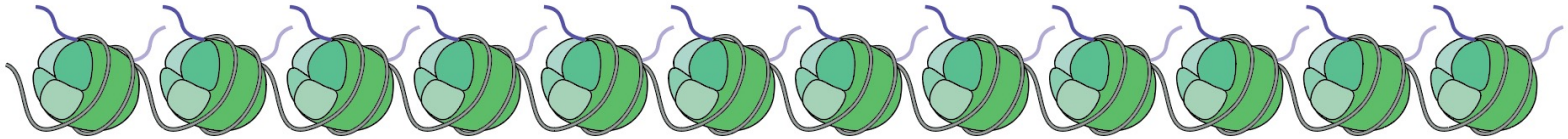
DNA

+ Histone cores

} Nucleosomes: core chromatin structural unit



Chromatin composition varies along the genome

DNA

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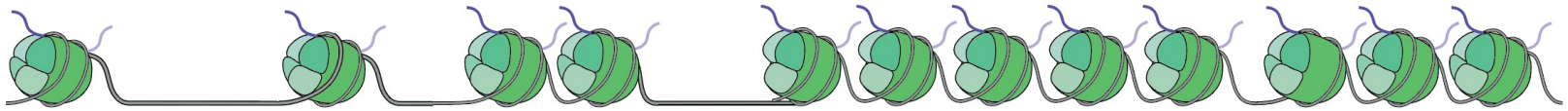
+ nucleosome positioning



Chromatin composition varies along the genome

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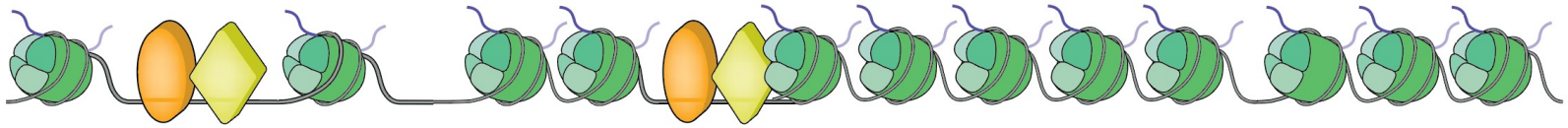
+ nucleosome positioning

+ transcription factors



Chromatin composition varies along the genome

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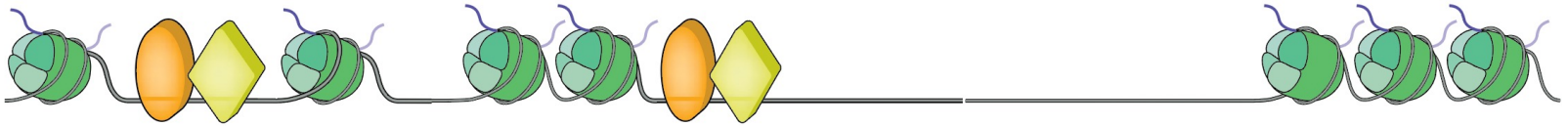
+ Promoter accessibility



Chromatin composition varies along the genome

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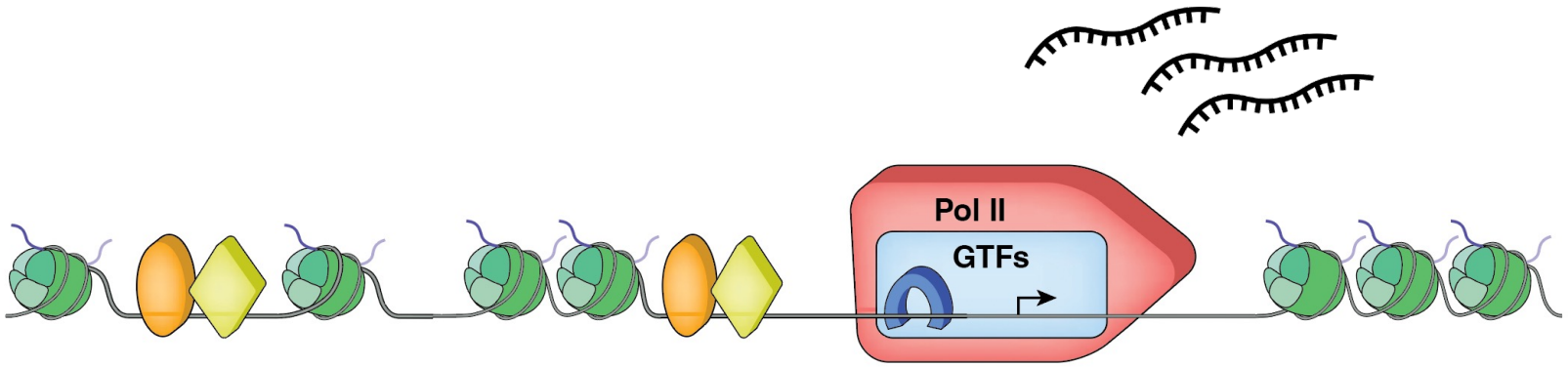
+ Polymerase



Chromatin composition varies along the genome

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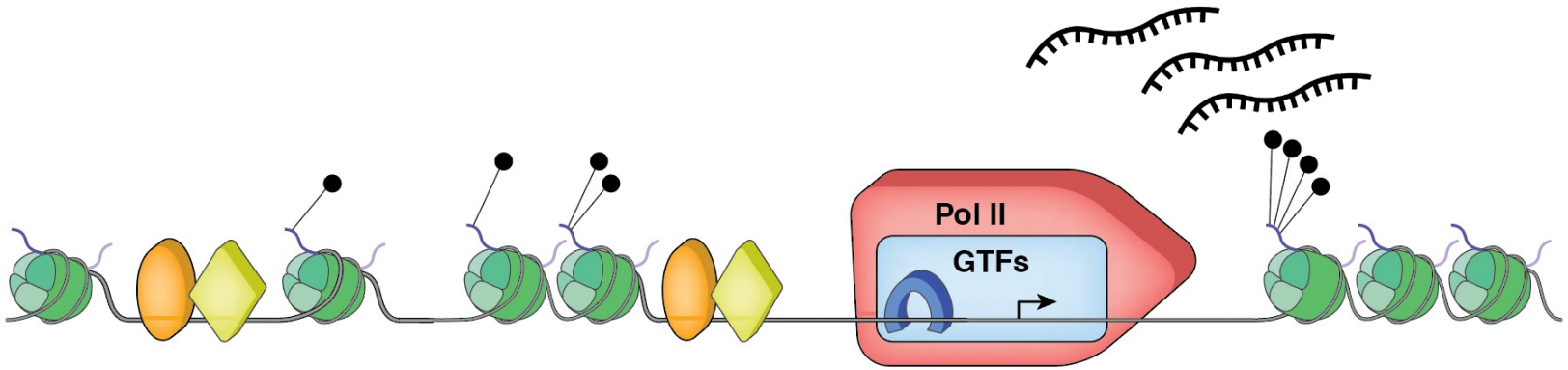
+ Histone PTMs



Chromatin composition varies along the genome

DNA

+ Histone cores

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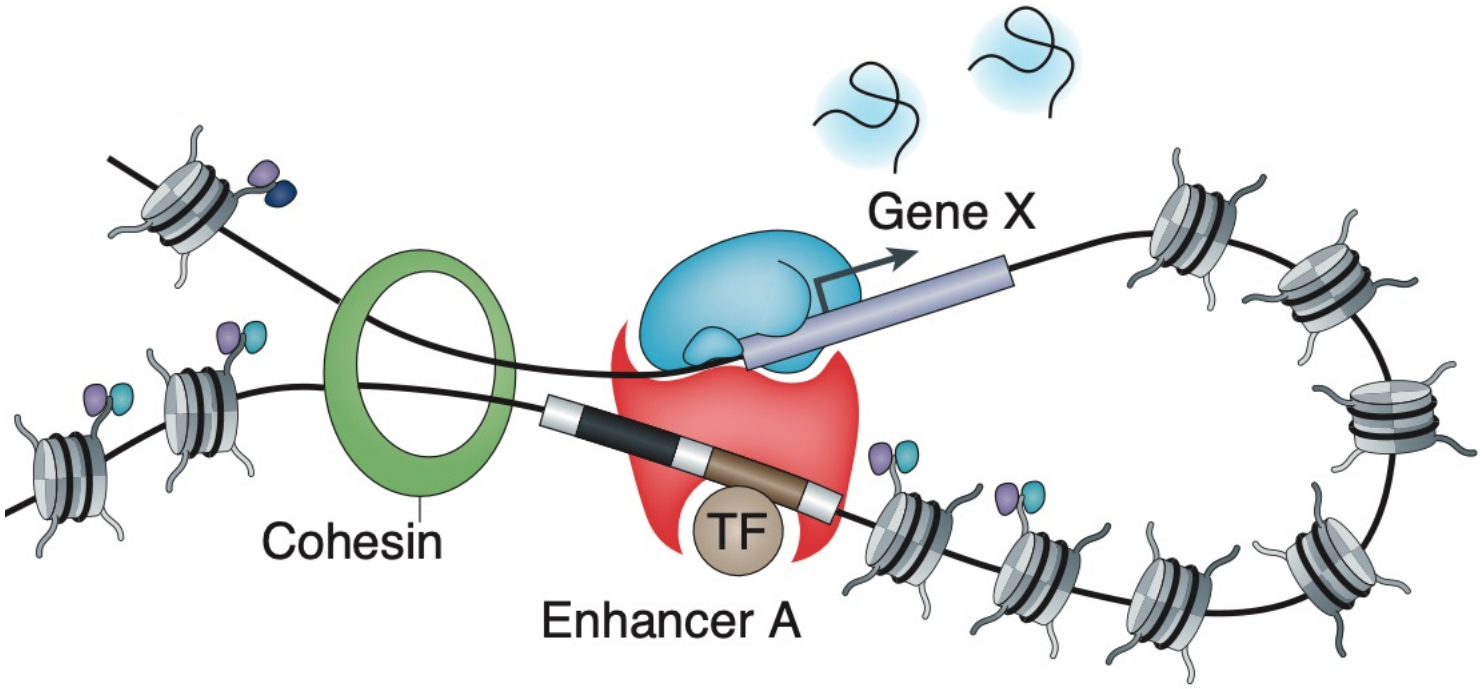
+ Polymerase

+ Histone PTMs

+ Chromatin folding



Chromatin composition varies along the genome

DNA **WGS**

} Nucleosomes: core chromatin structural unit

+ Histone cores **ChIP-seq**

+ nucleosome positioning **MNase-seq**

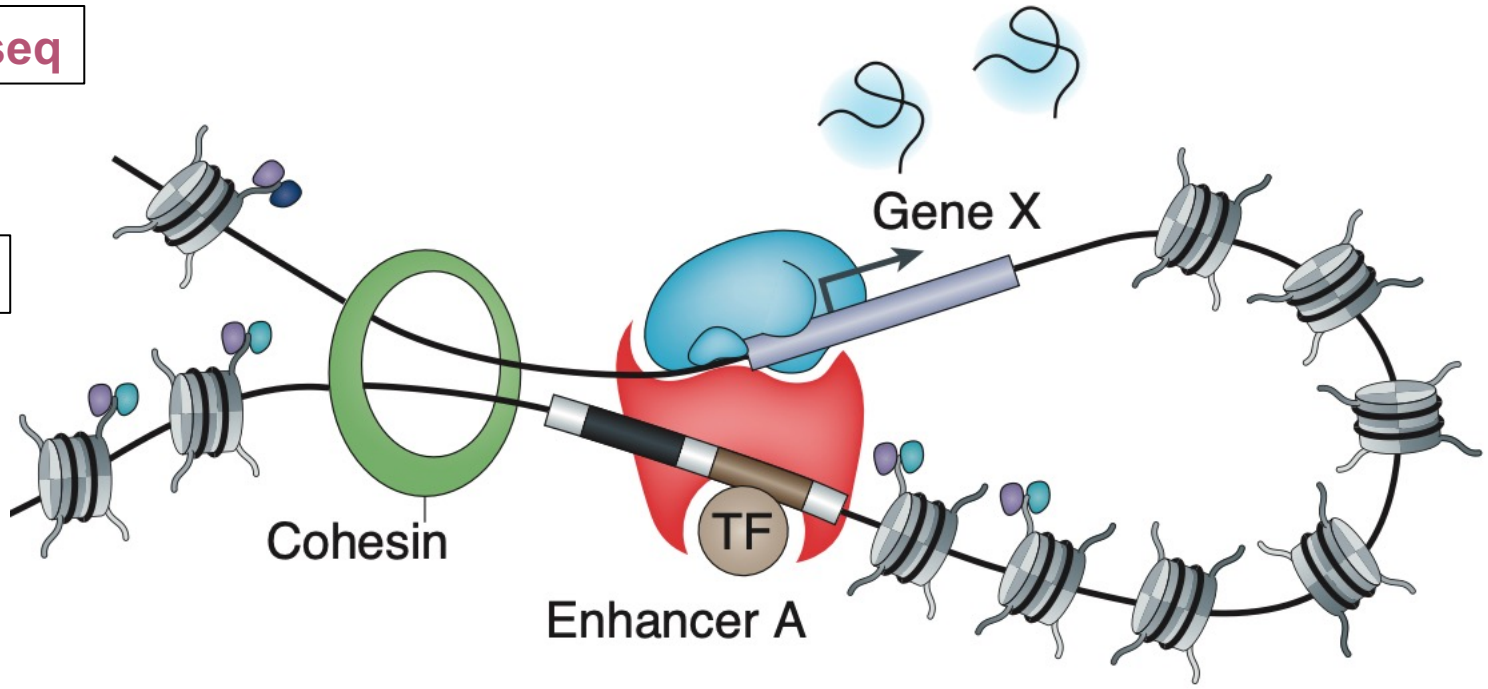
+ transcription factors **ChIP-seq**

+ Promoter accessibility **ATAC-seq**

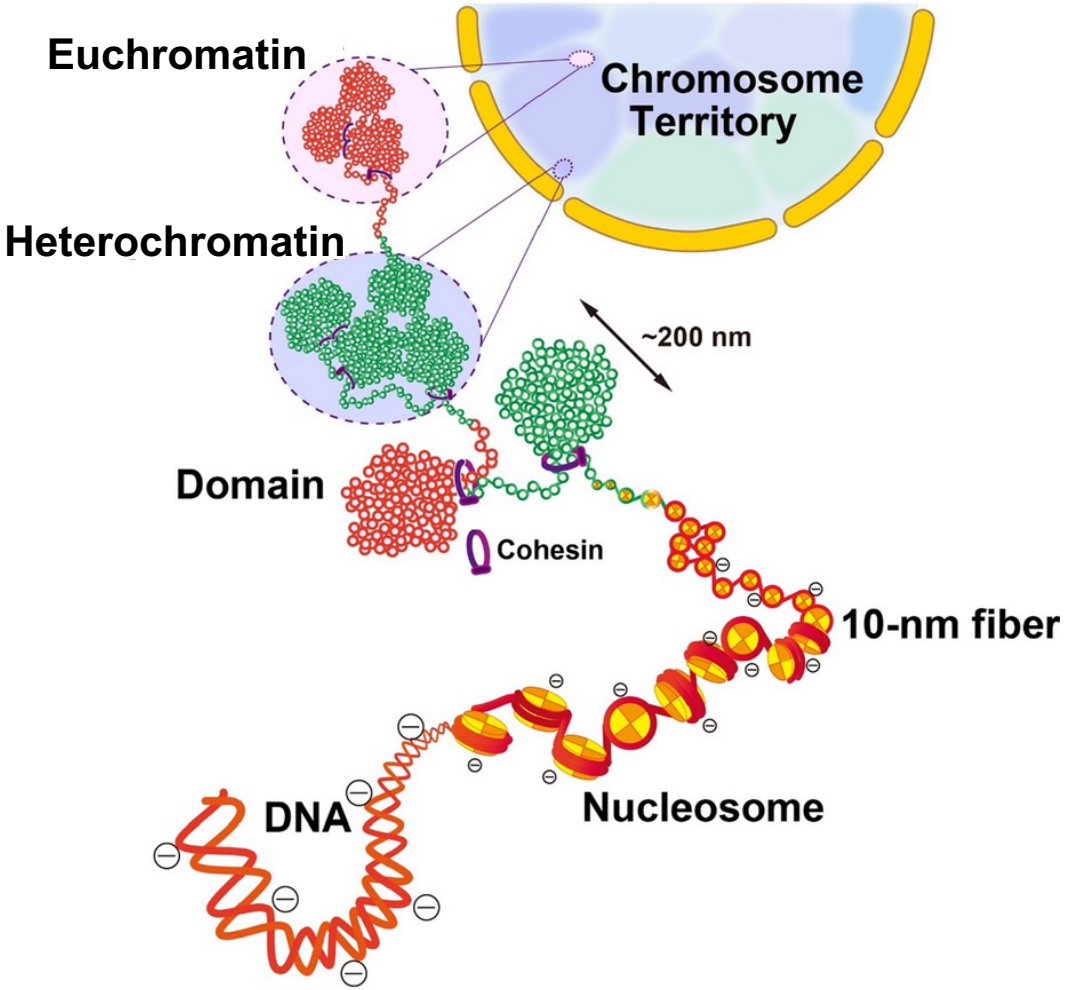
+ Polymerase **RNA-seq**

+ Histone PTMs **ChIP-seq**

+ Chromatin folding **Hi-C**



Chromatin is organized in hierarchical structure to enable transcriptional regulation



Lafontain et al., Current Protocols 2021

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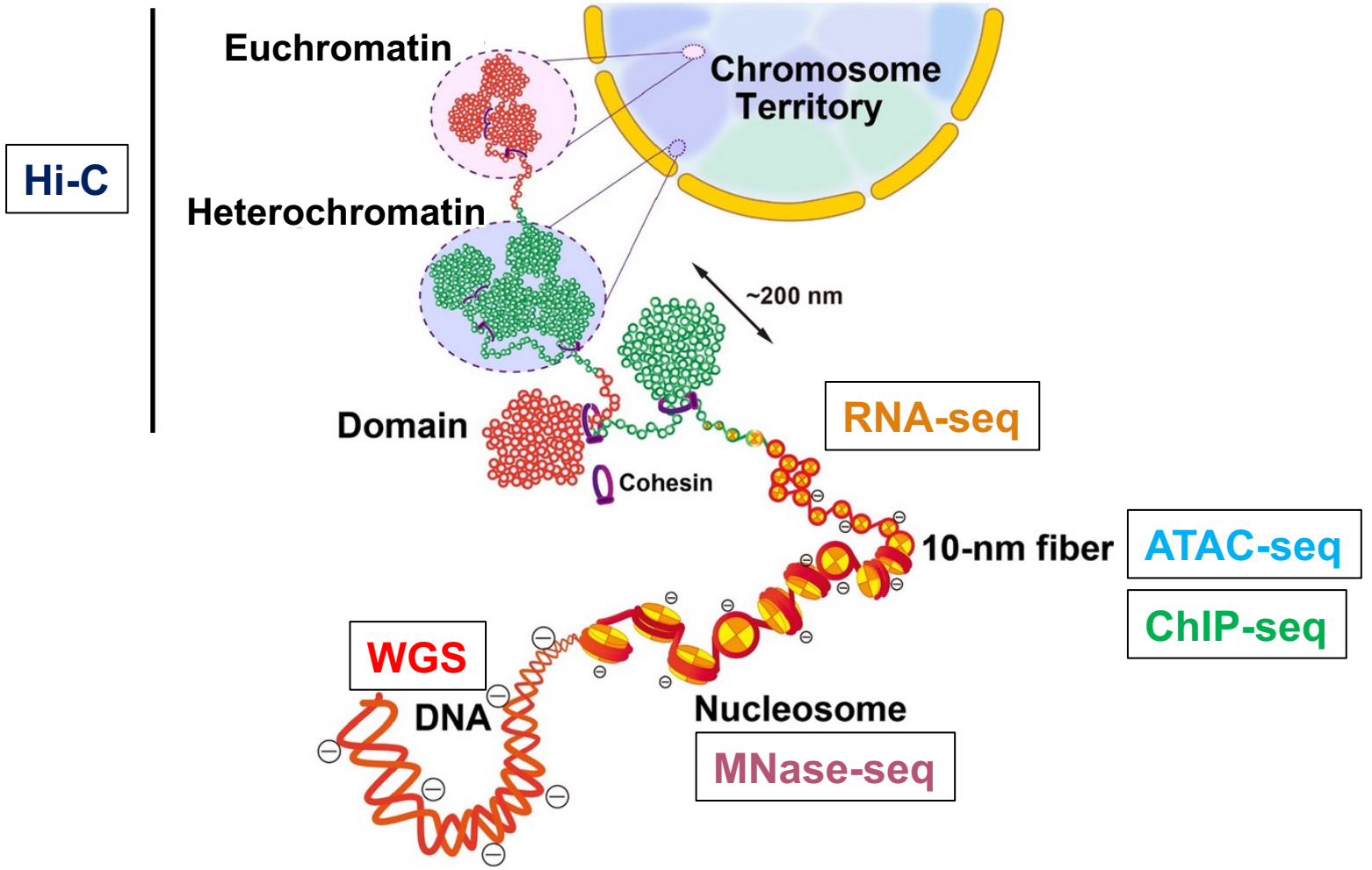
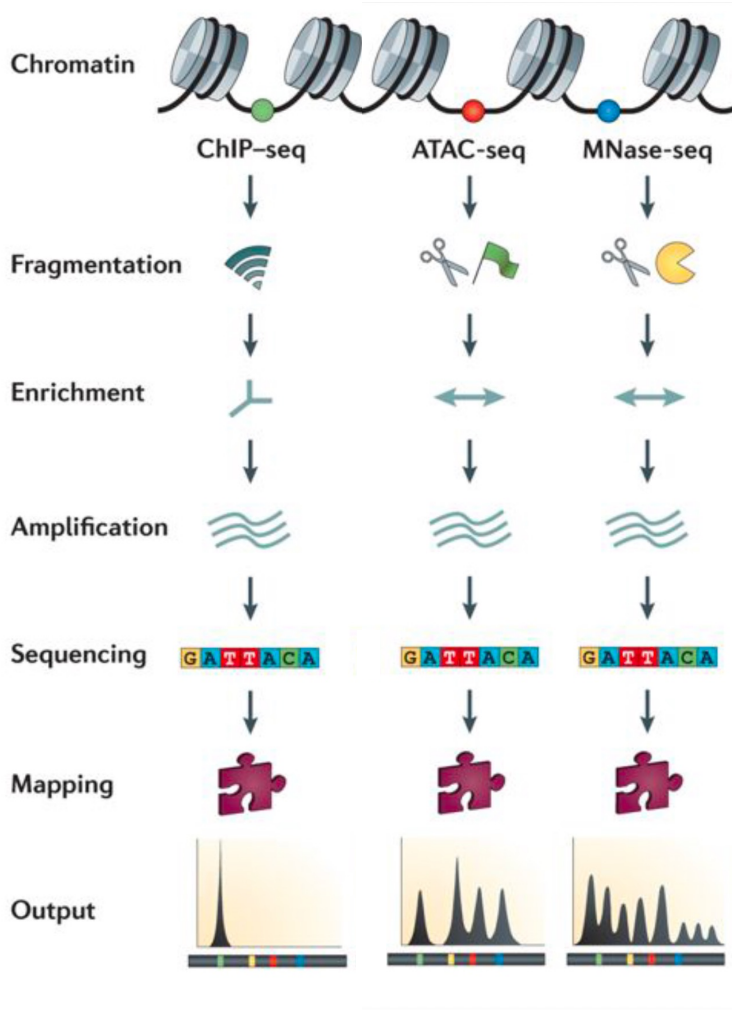
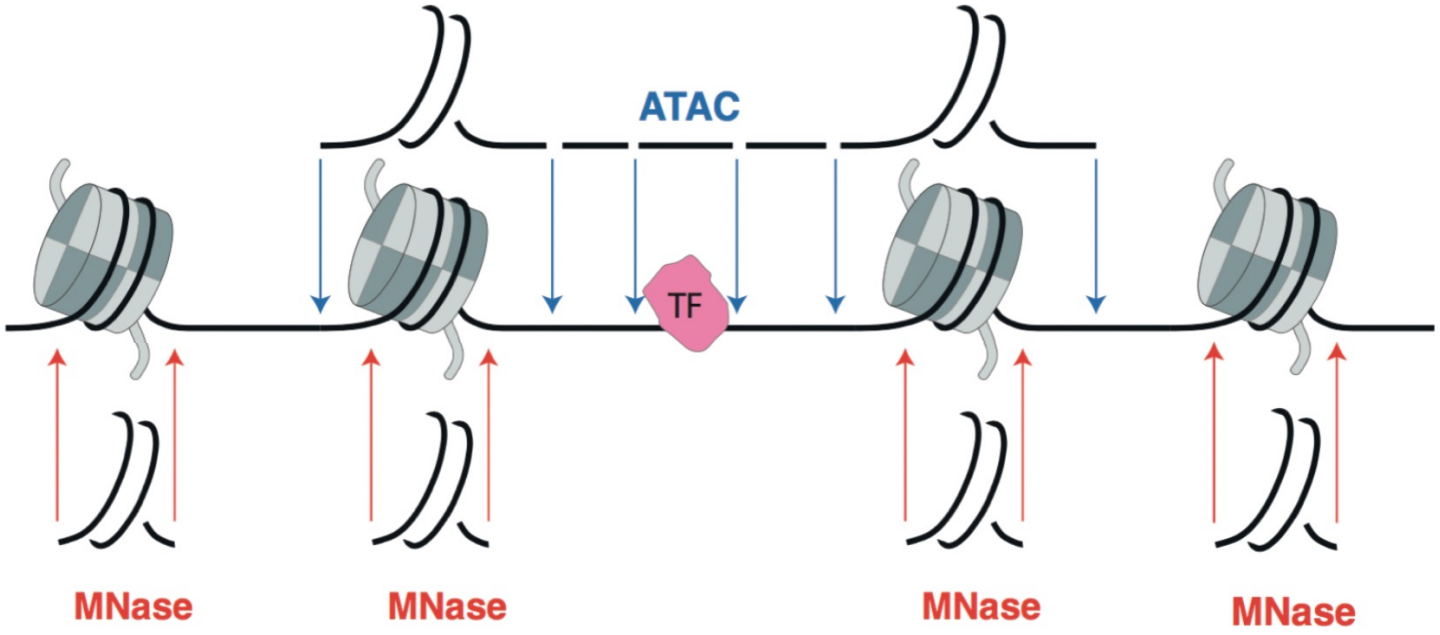


Lafontain et al., Current Protocols 2021

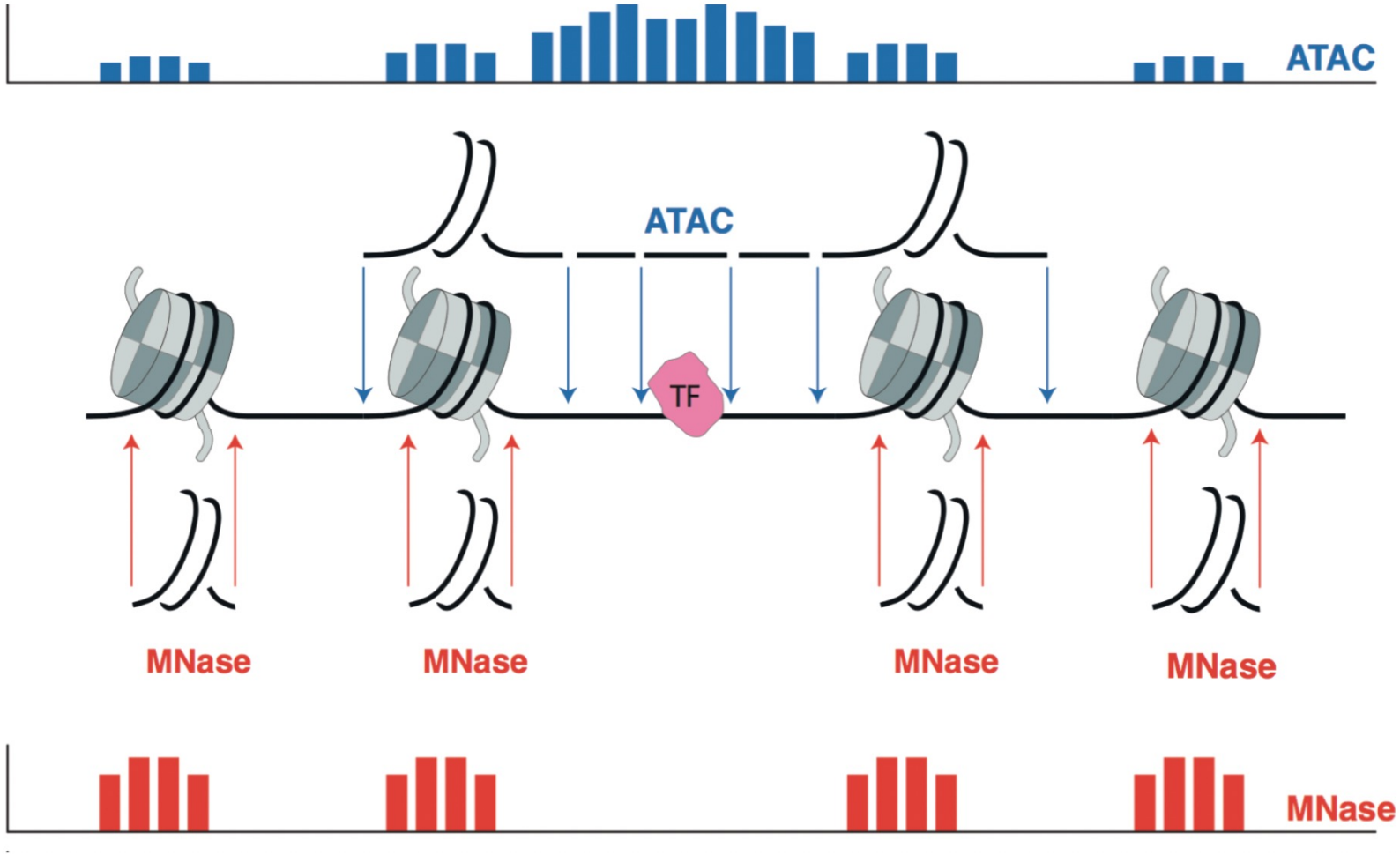
ChIP-seq vs. ATAC-seq vs MNase-seq



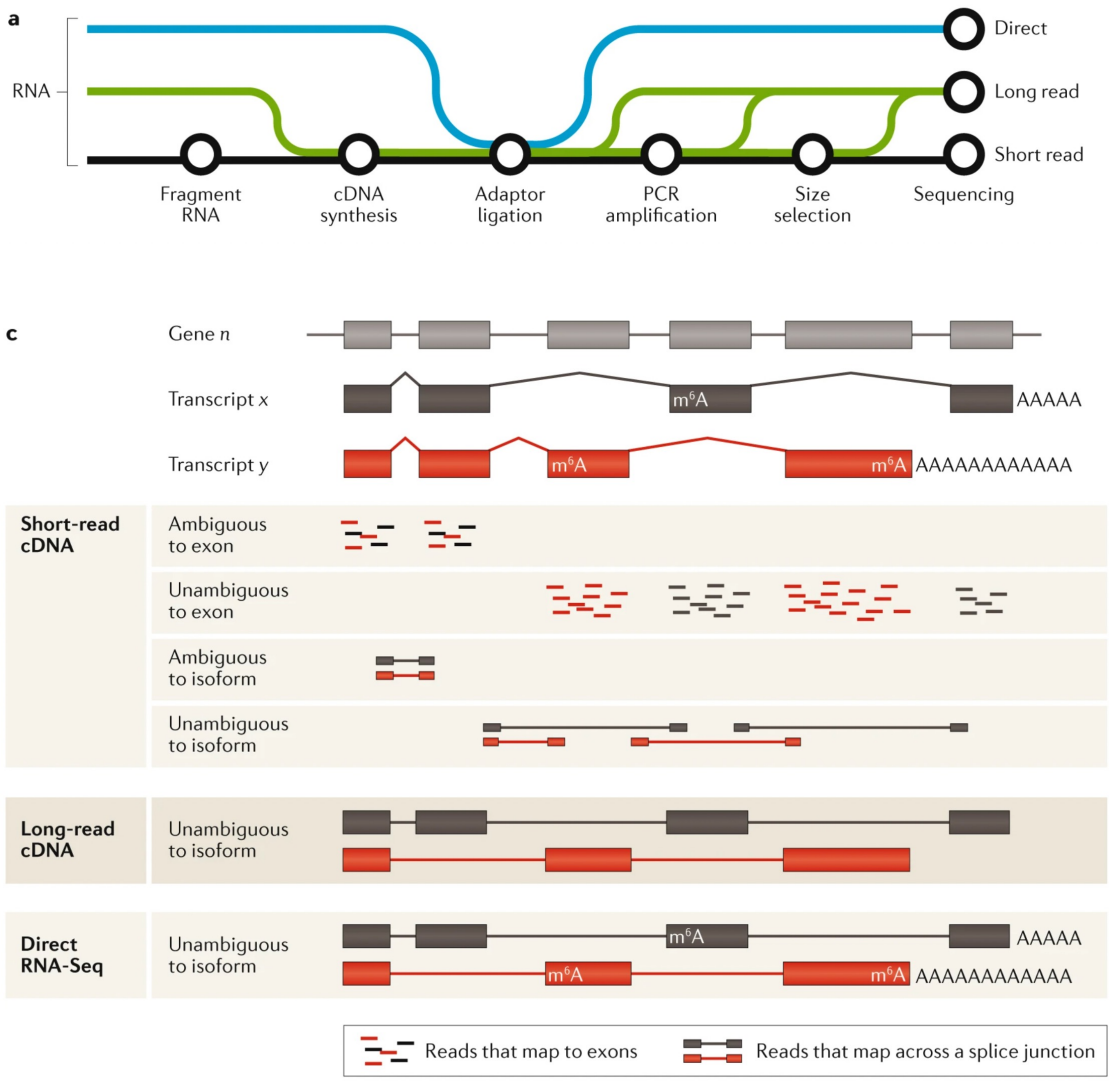
ATAC-seq vs MNase-seq



ATAC-seq vs MNase-seq

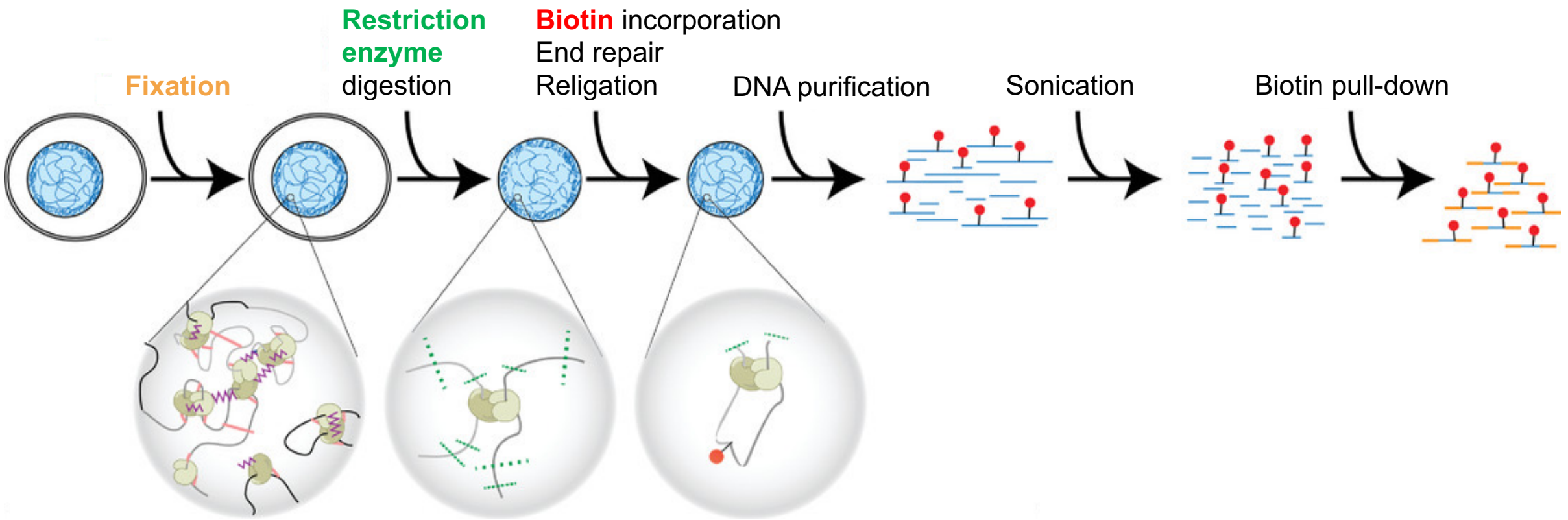


RNA-seq



Stark, Grzelak & Hadfield 2019

Hi-C



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