

Prediction of Regulatory Networks from Expression and Chromatin Data

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Overview

| Time | Topic | Who |
|-------------|--|-------------|
| 2:30 - 2:45 | Introduction / gene regulation / transcription / chromatin | IC |
| 2:45 - 3:00 | Introduction ChIP-seq peak calling | MH |
| 3:00 - 3:50 | Practical peak calling | MH & JH |
| 4:15 - 4:30 | Introduction Footprints | IC |
| 4:30 - 4:45 | Introduction Regulatory networks | MS |
| 4:45 - 5:50 | Practical Regulatory Networks | IG, MS & FS |
| 5:50 - 6:00 | Q & A session | all |

Material - <https://github.com/SchulzLab/EpigenomicsTutorial-ISMB2017>

Team



Ivan Costa (IC)



Matthias Heinig (MH)



Johann Hawe



Marcel Schulz(MH)



Florian Schmidt (FS)

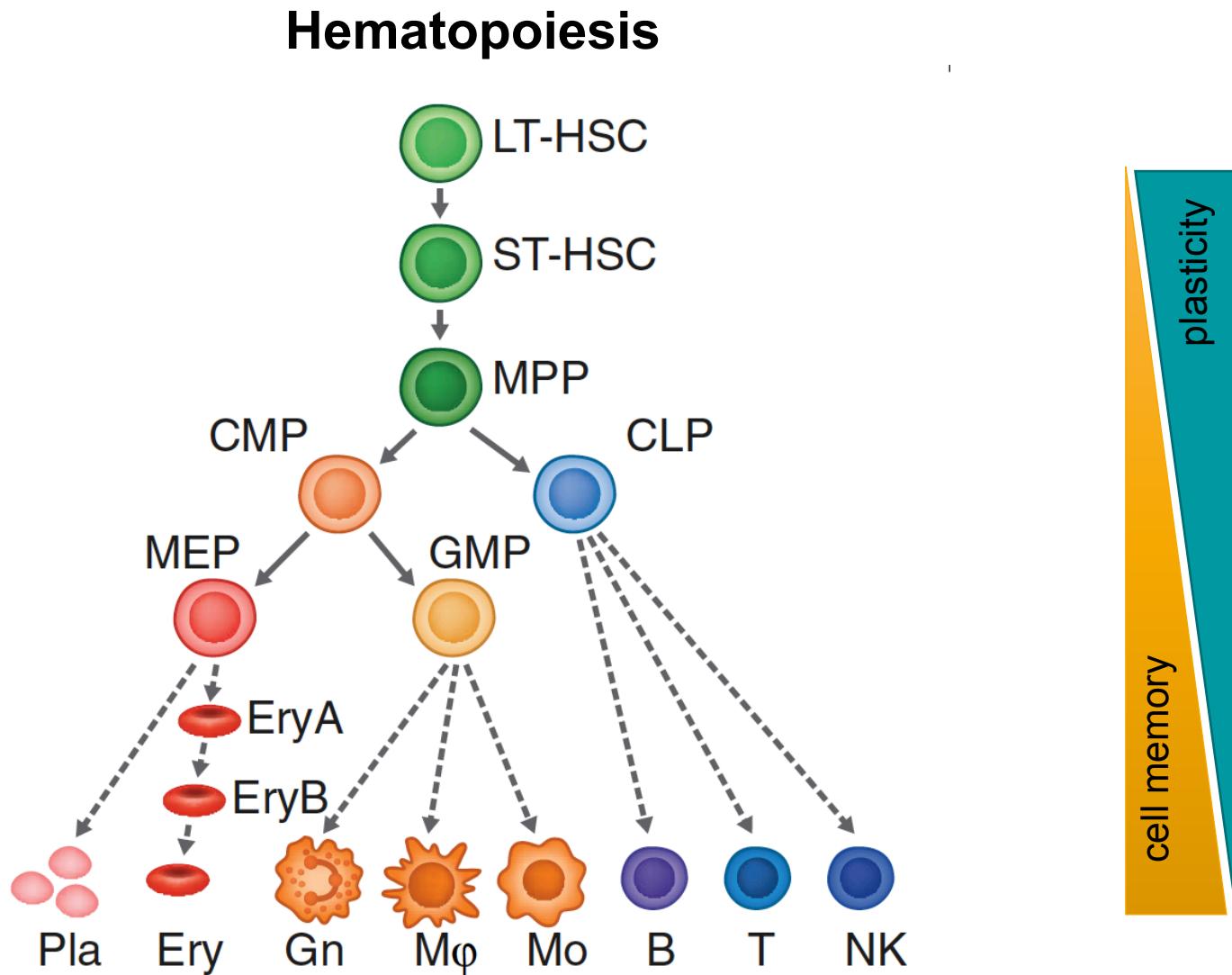
Introduction - Gene Regulation, Transcription and Chromatin

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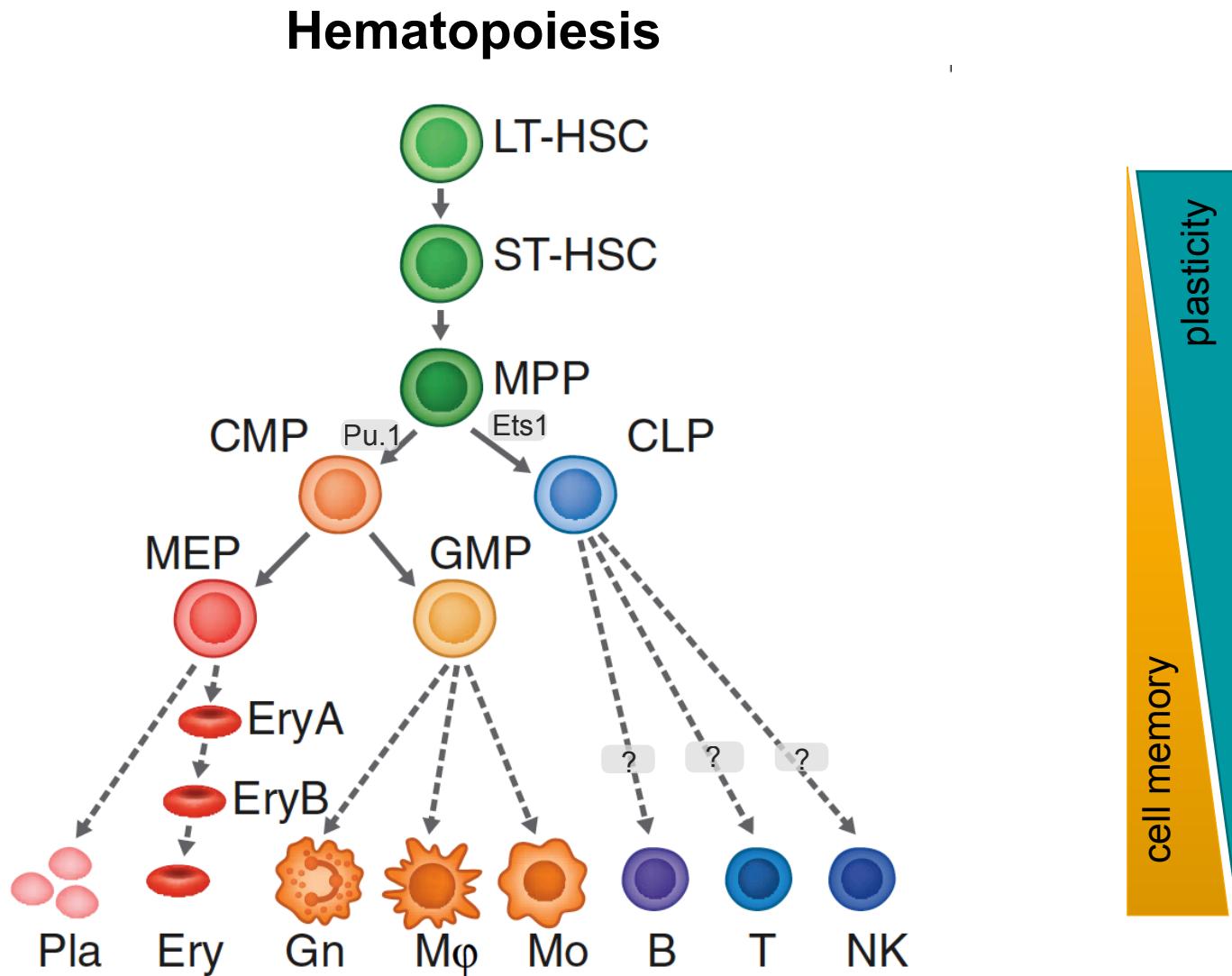


Cell Differentiation & Gene Regulation



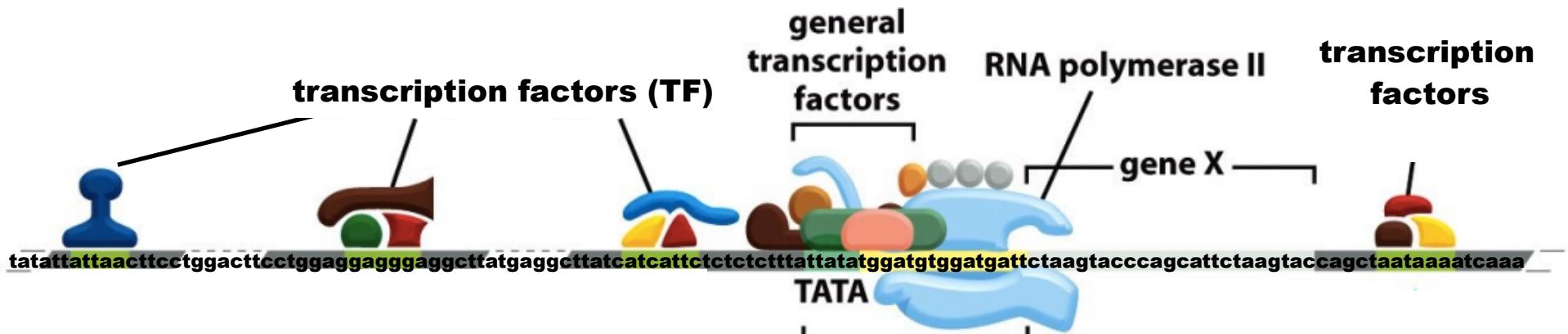
Adapted from Lara-Astiaso, Science, 2015.

Cell Differentiation & Gene Regulation



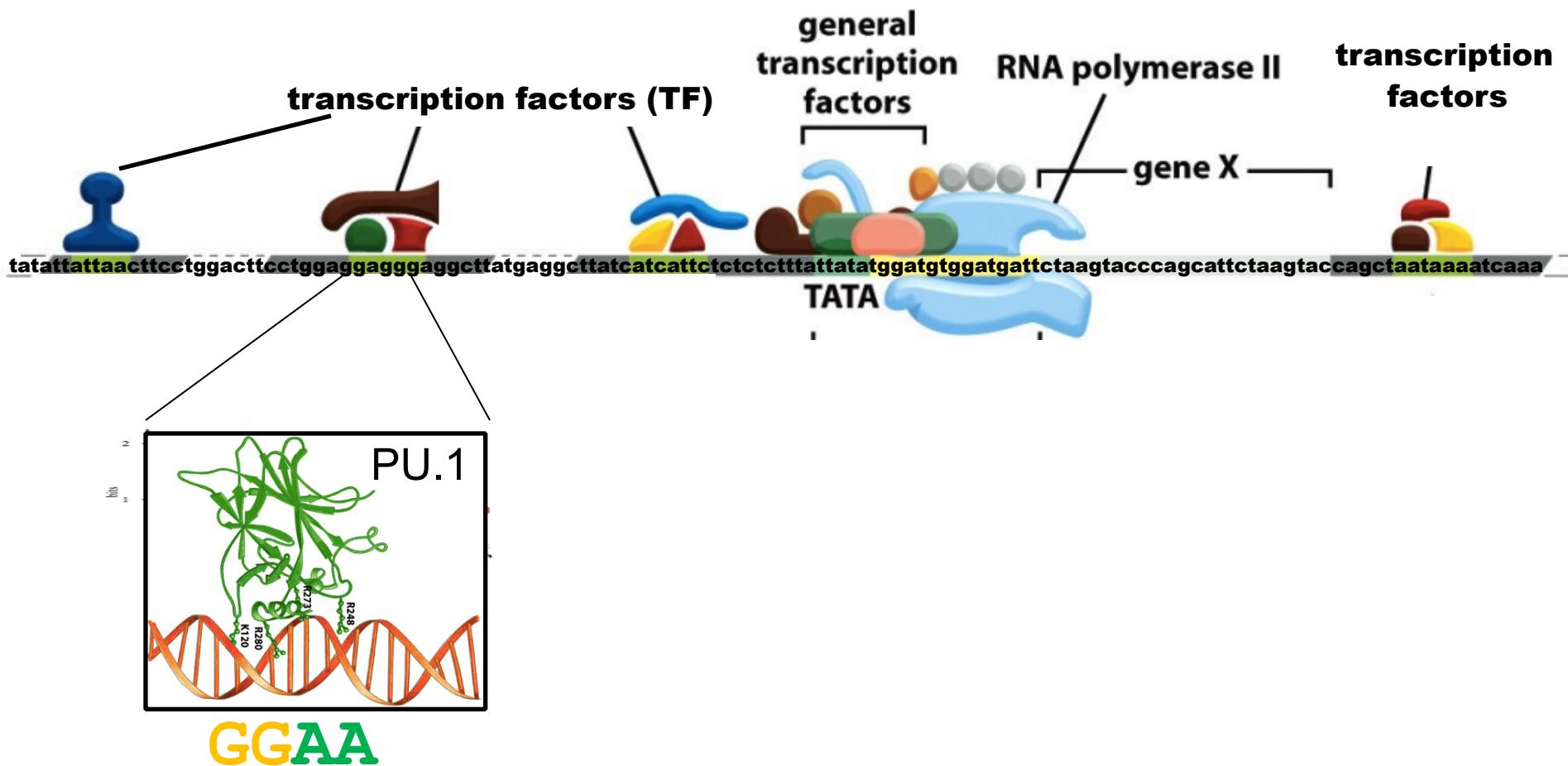
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Regulatory Control – Protein-DNA interaction



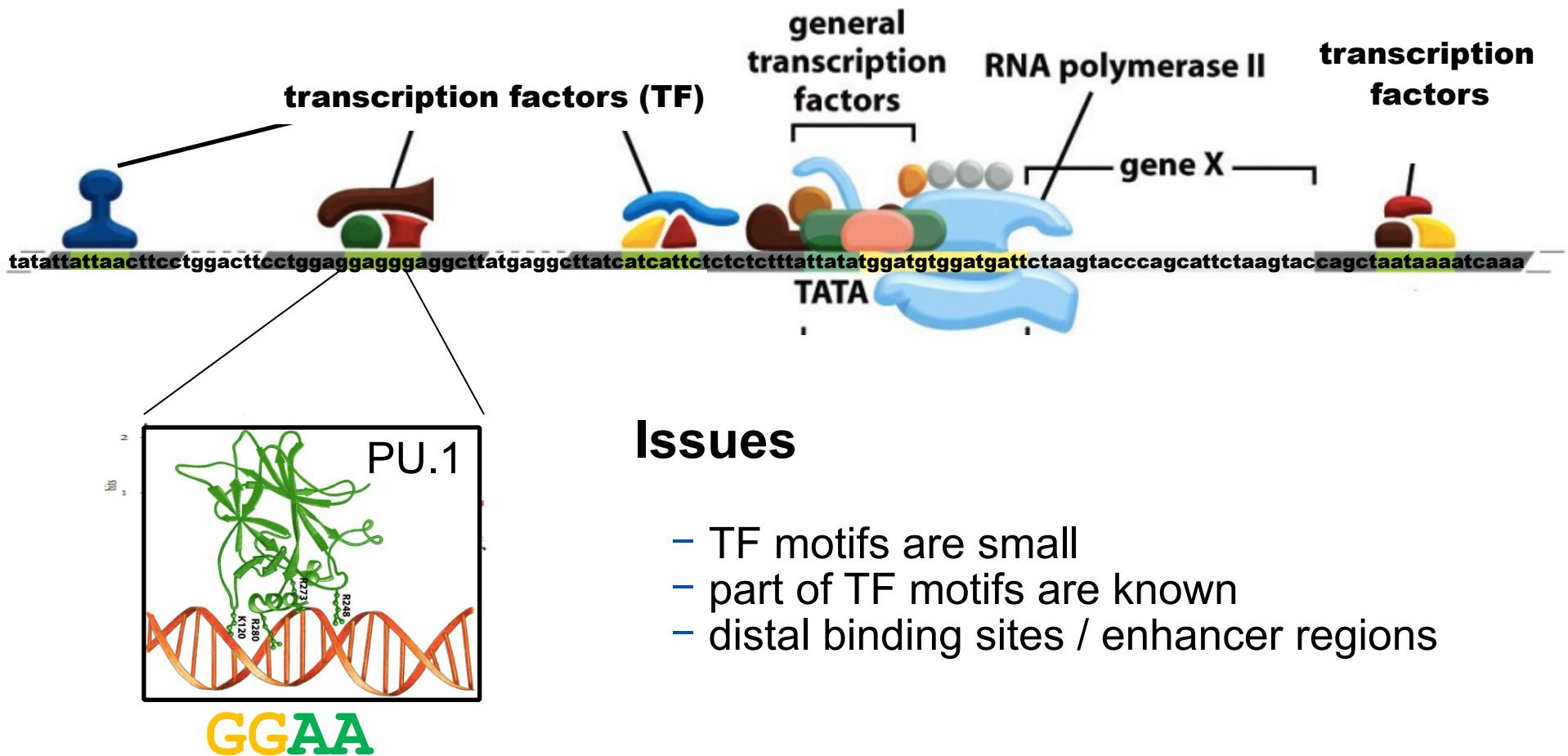
Adapted from Alberts, B. et al. (2008) Garland Science, 5th ed.

Regulatory Control – Protein-DNA interaction



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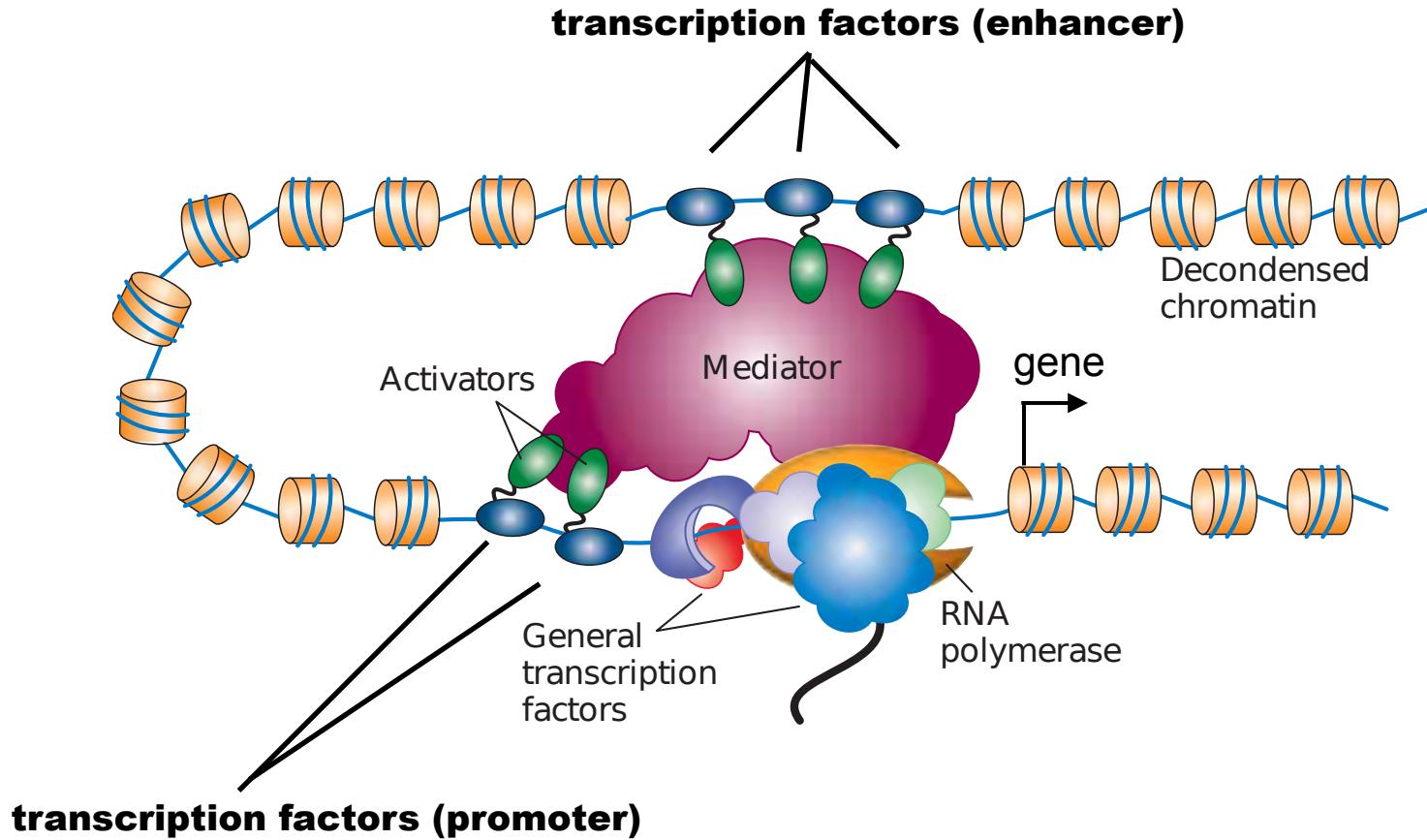
Regulatory Control – Protein-DNA interaction



Issues

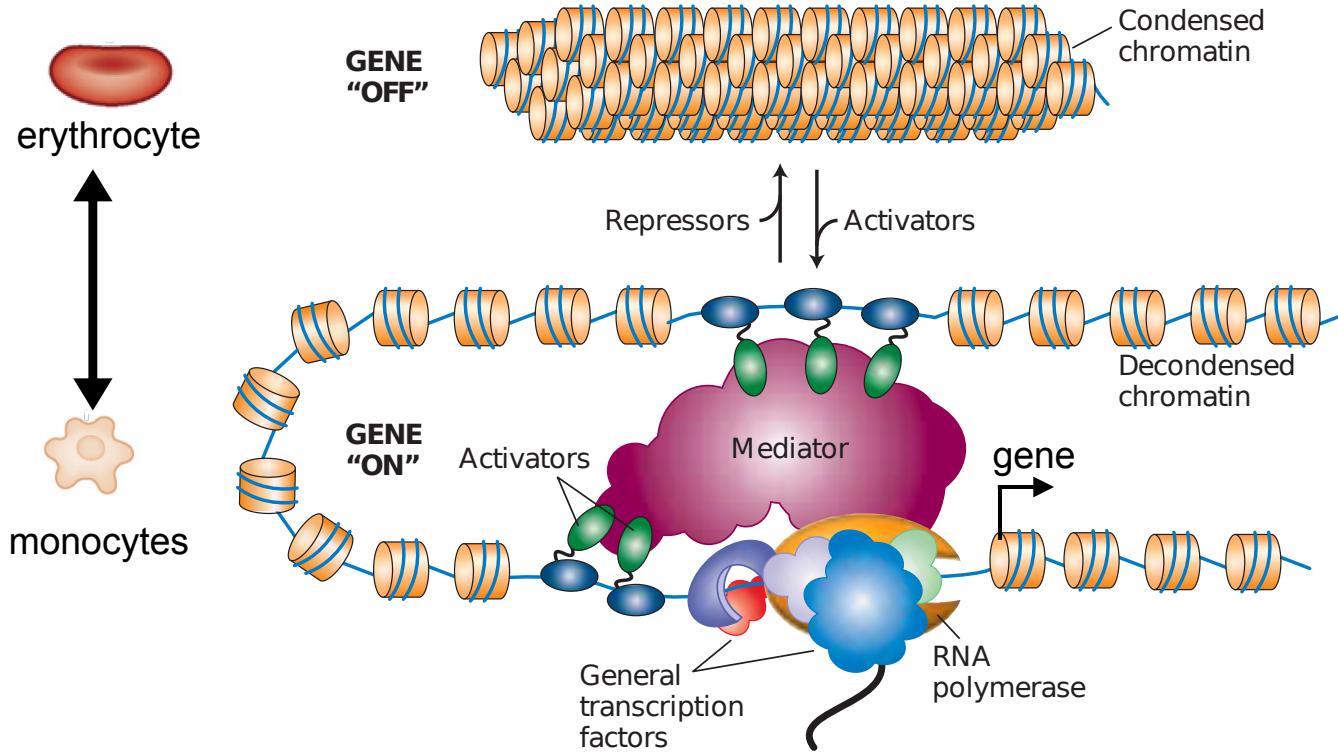
- TF motifs are small
- part of TF motifs are known
- distal binding sites / enhancer regions

Chromatin and Gene Regulation



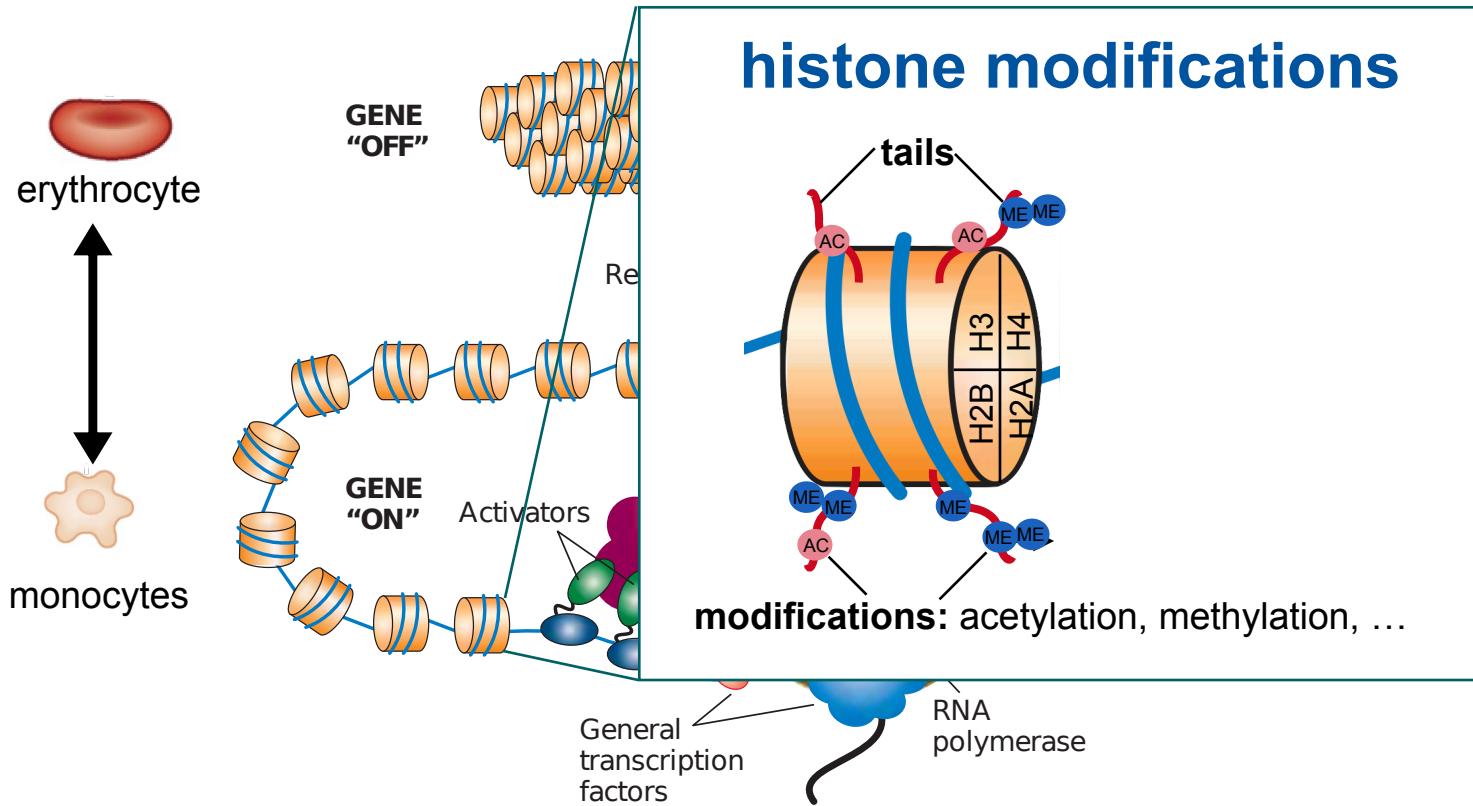
Adapted from Lodish, B. et al. (2004) 5th ed.

Chromatin and Cell Memory/Plasticity



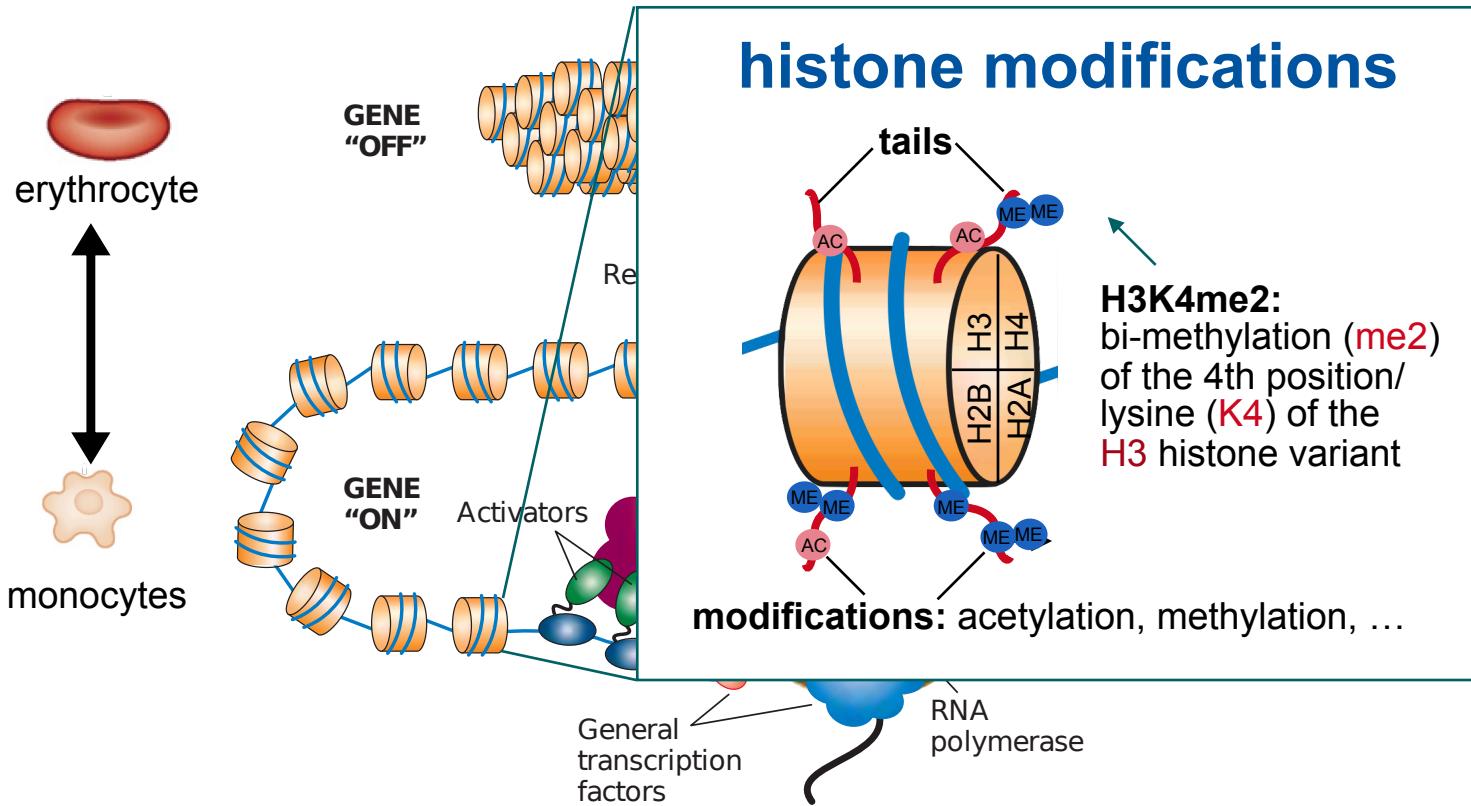
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Chromatin and Histones



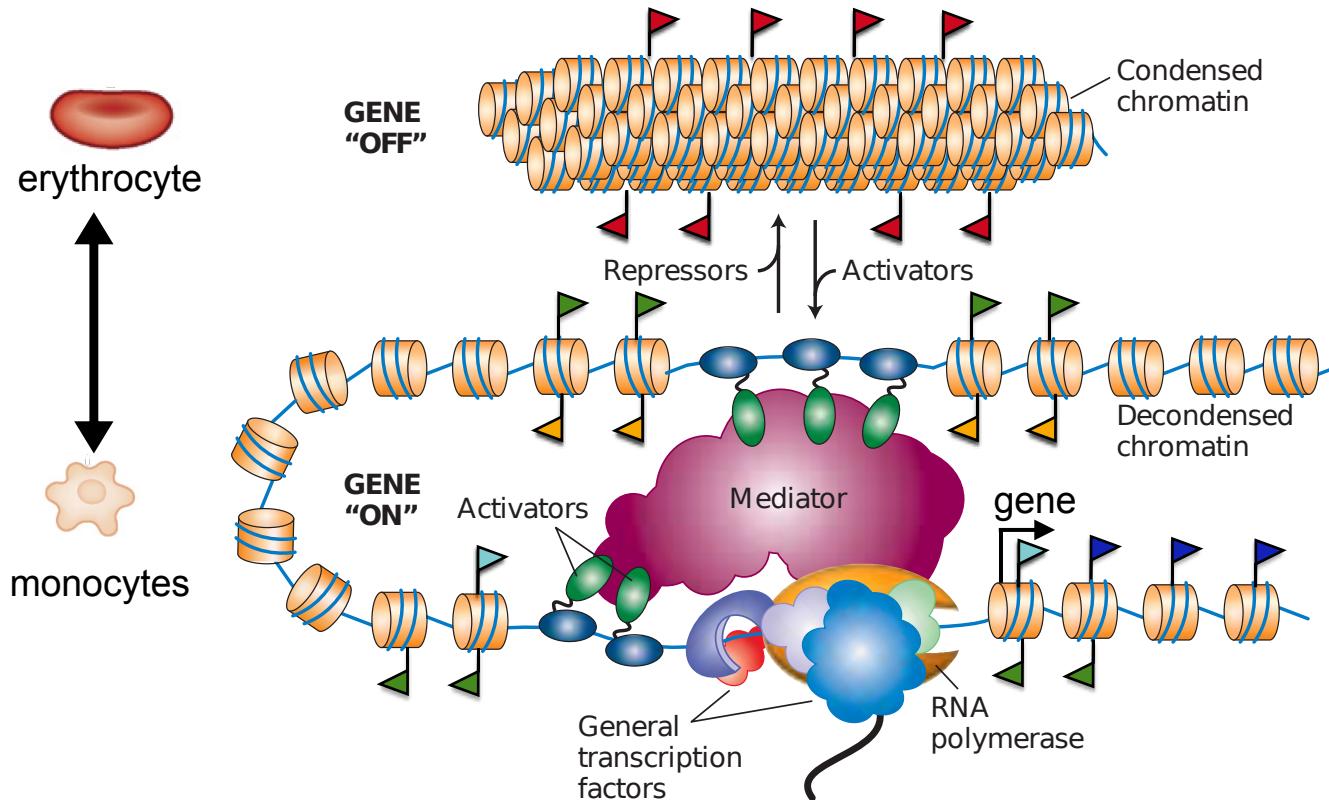
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Chromatin and Histones



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Chromatin and Cell Memory/Plasticity



Histone Code

► Transcription

H3K79me2, H3k36me3

► Active Regions

H3K27ac, H3K9ac

► Active Promoters

H3K4me3

► Active Enhancers

H3K4me1

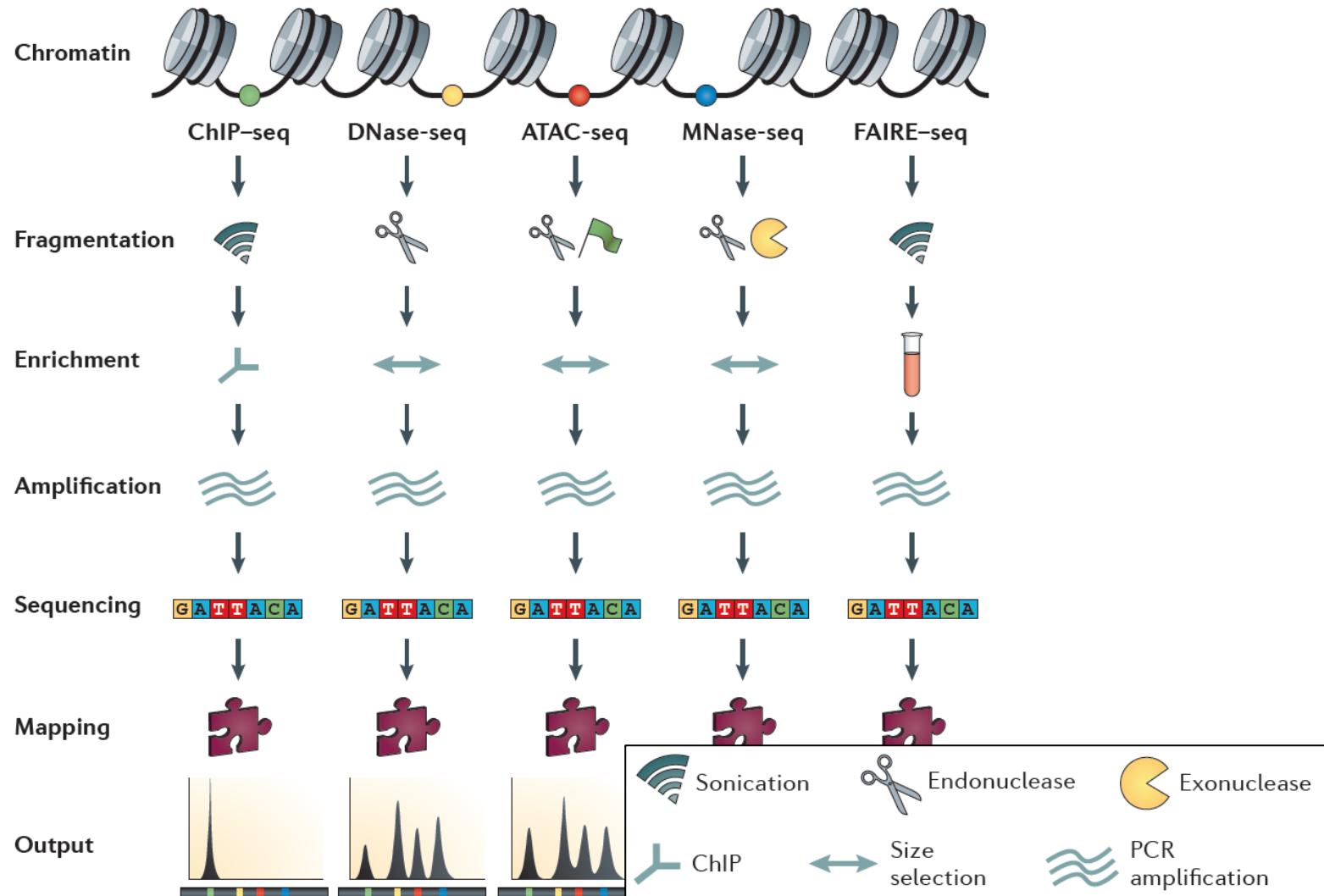
► Repressed Prom.

H3K27me3

► Repressed Regions

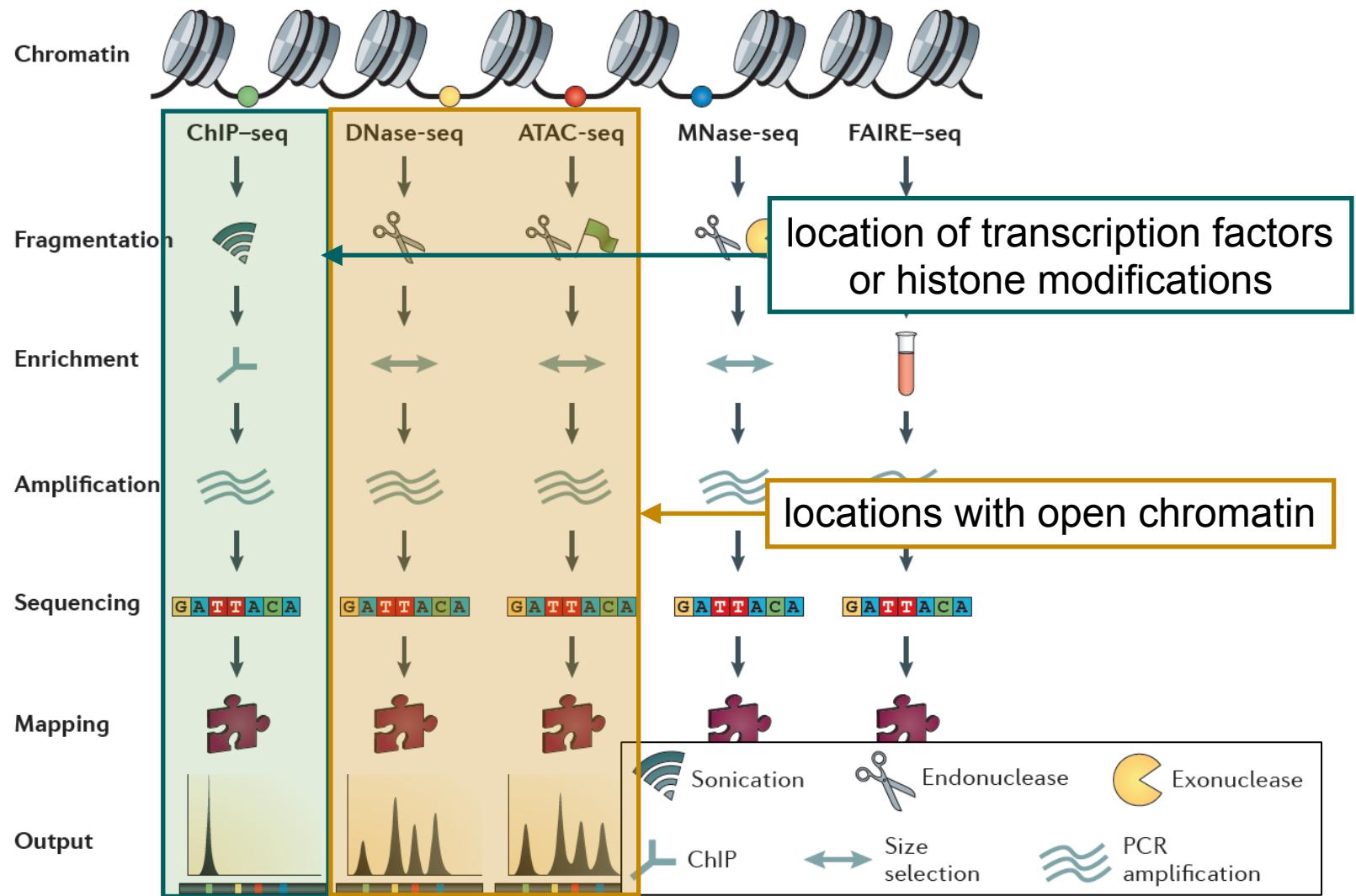
H3K9me3

NGS and Chromatin



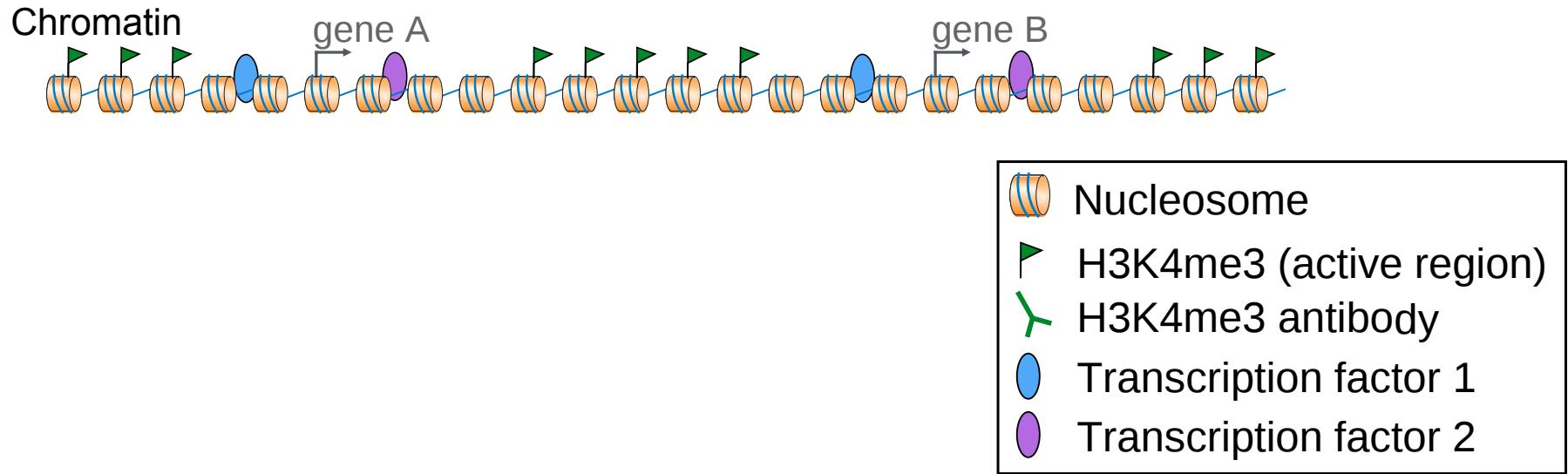
Source: Meyer, C.A. and Liu X.S. (2014). *Nature Reviews Genetics*.

NGS and Chromatin

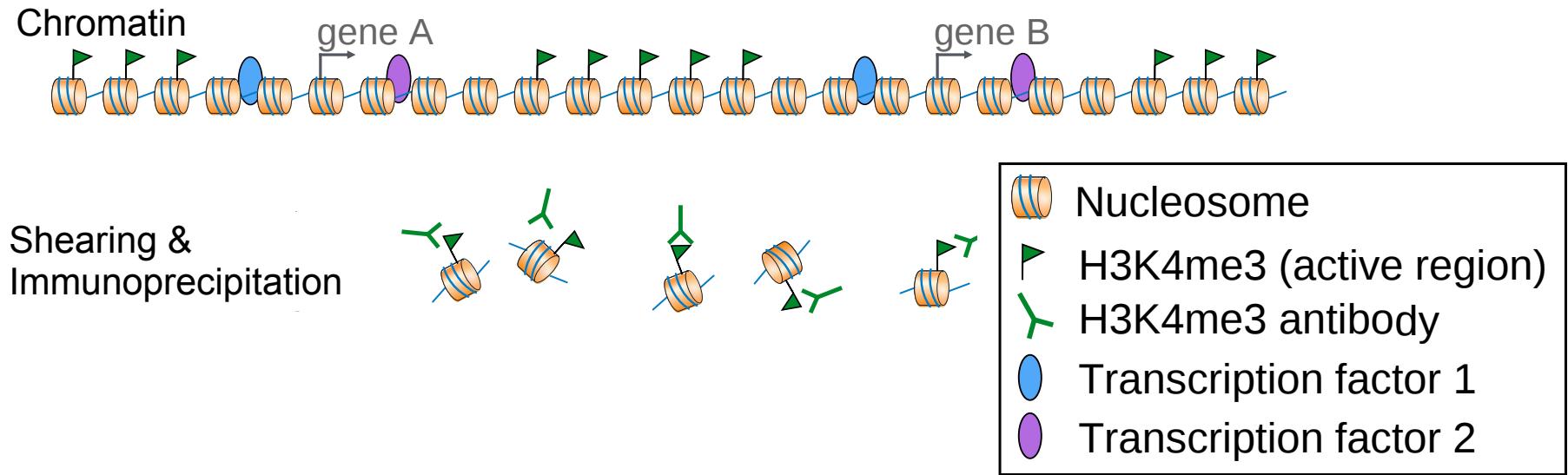


Source: Meyer, C.A. and Liu X.S. (2014). *Nature Reviews Genetics*.

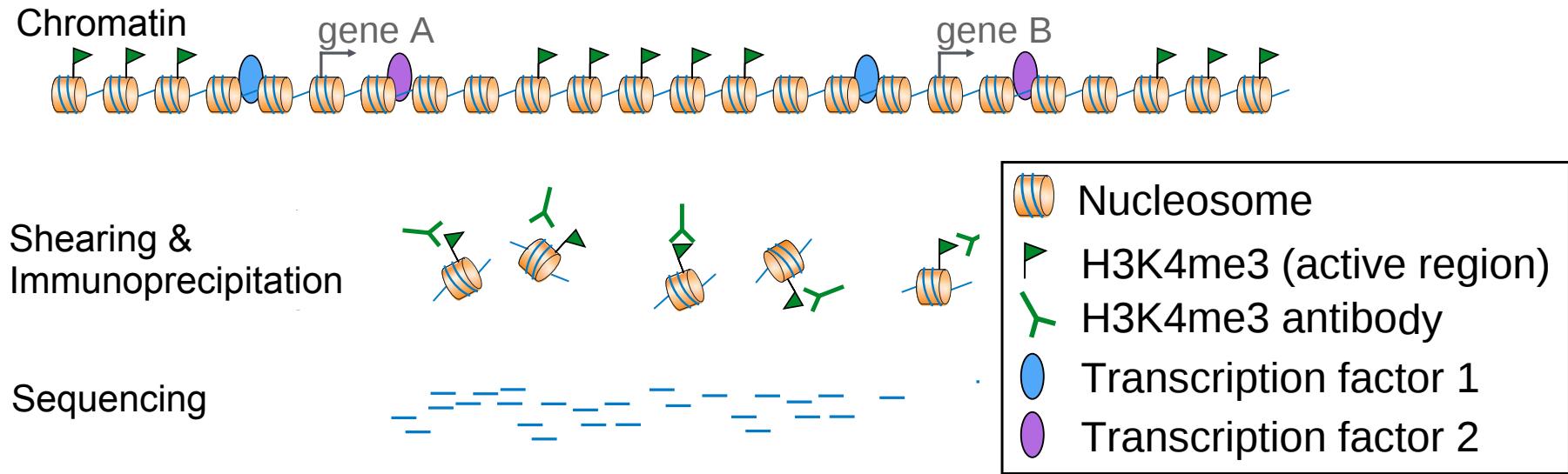
DNA - Protein interactions with ChIP-Seq



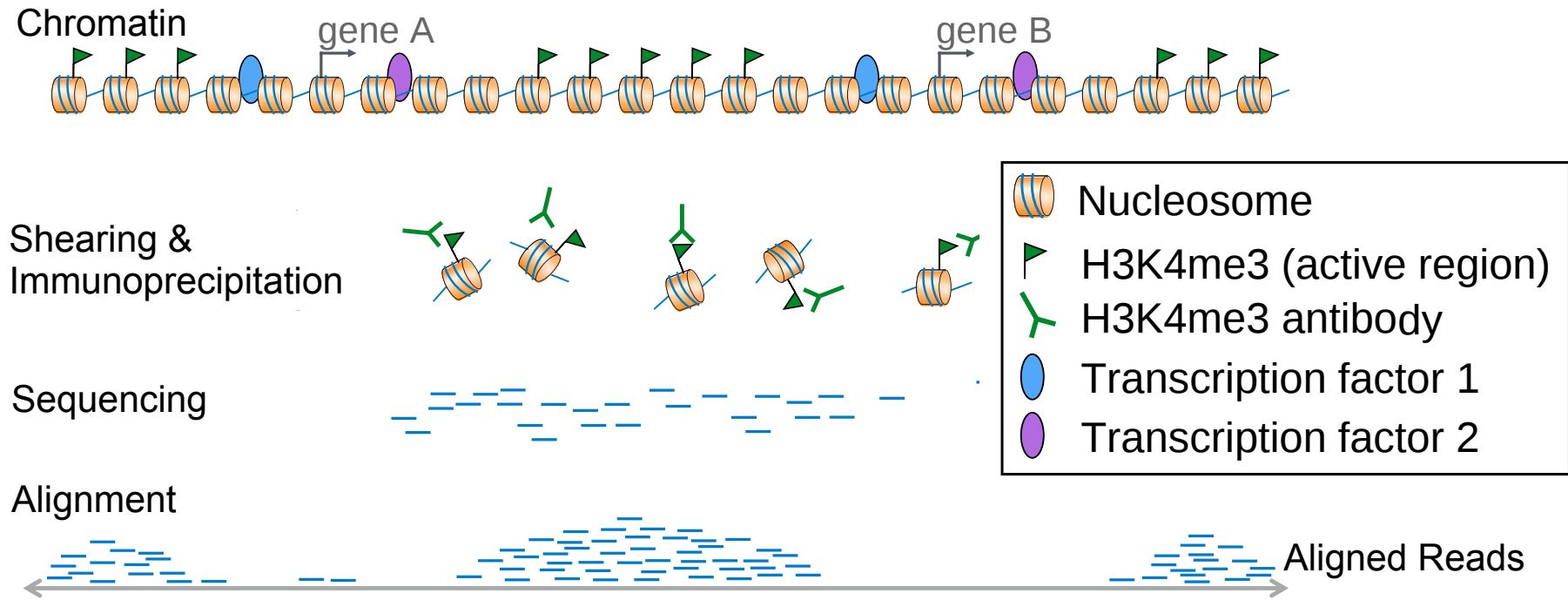
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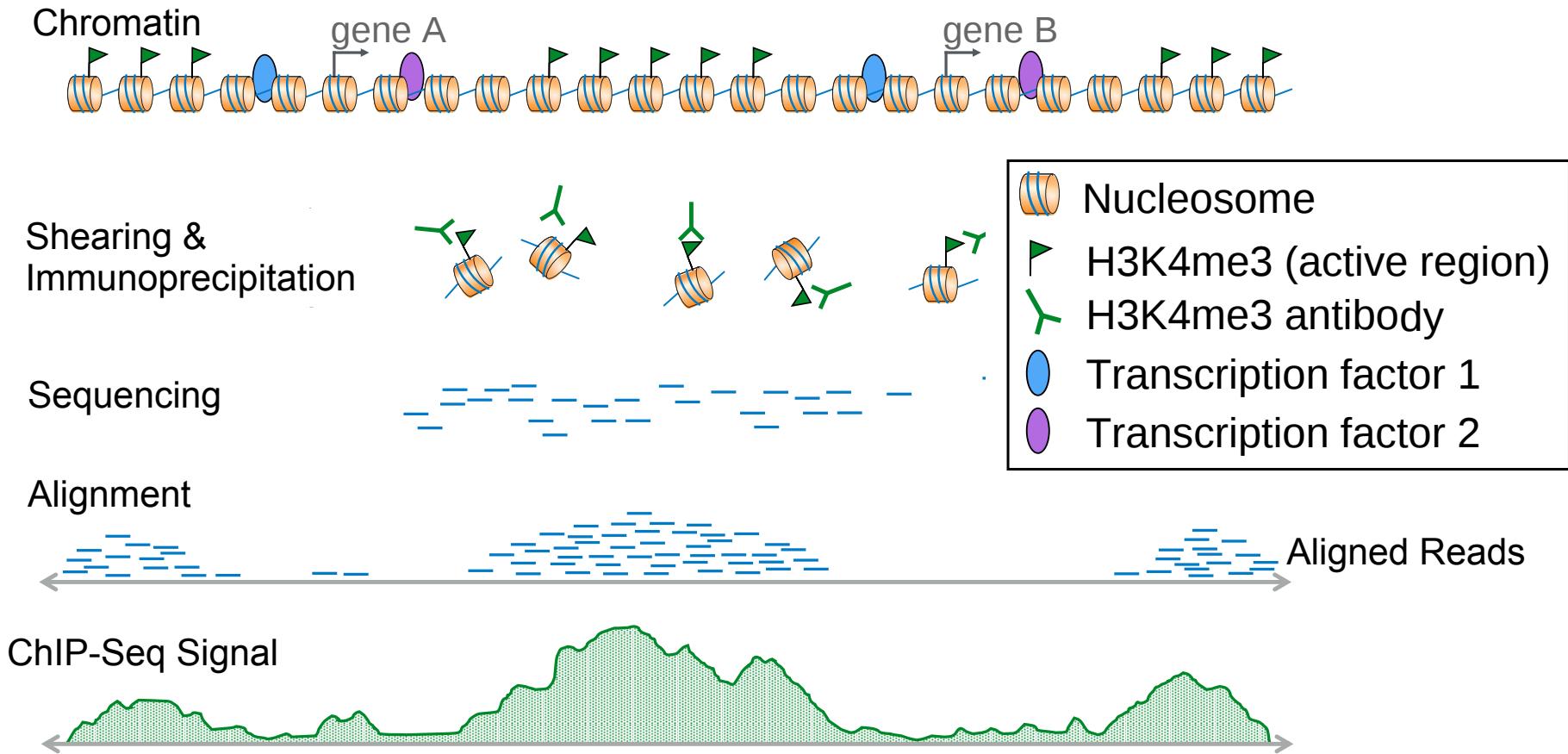
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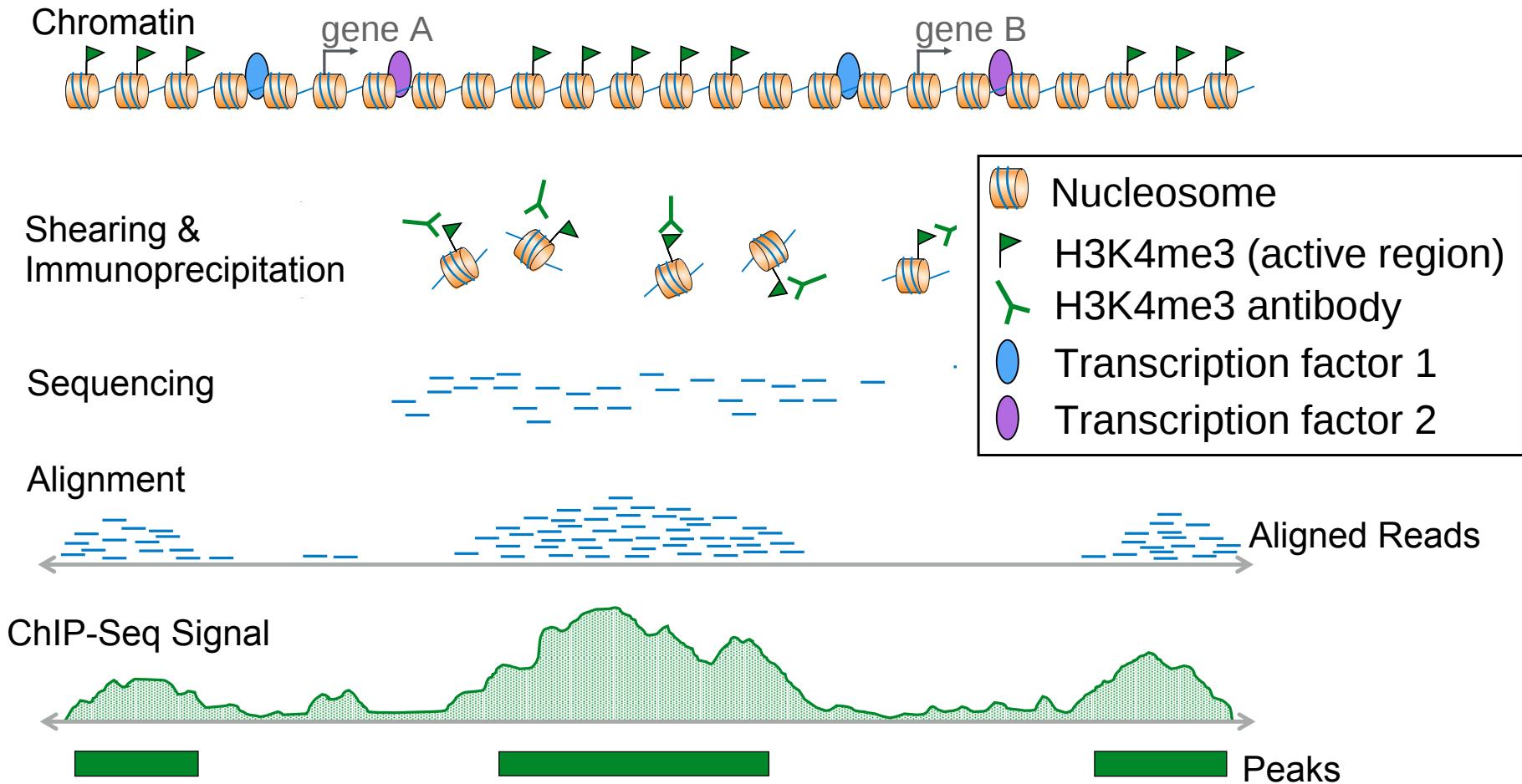
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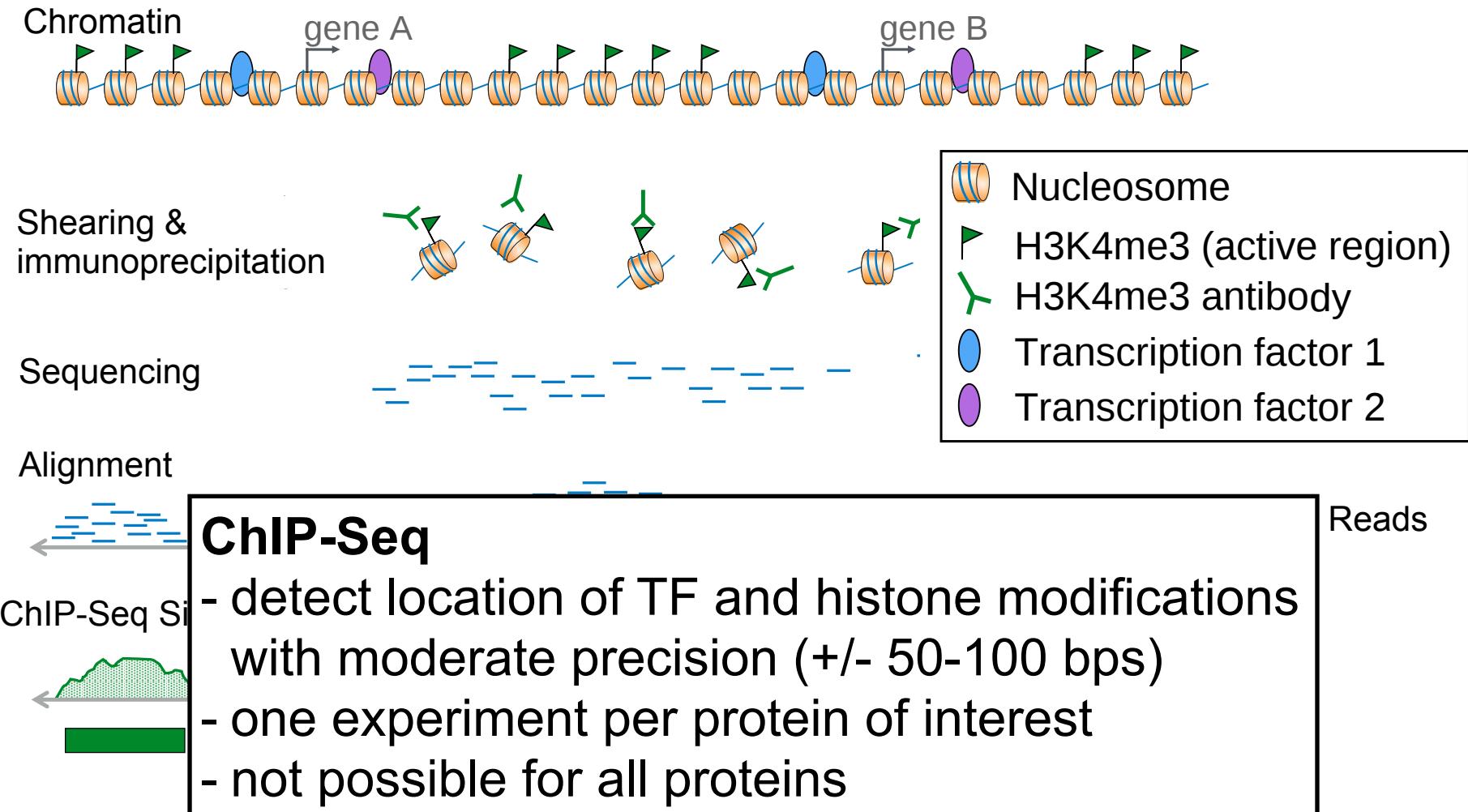
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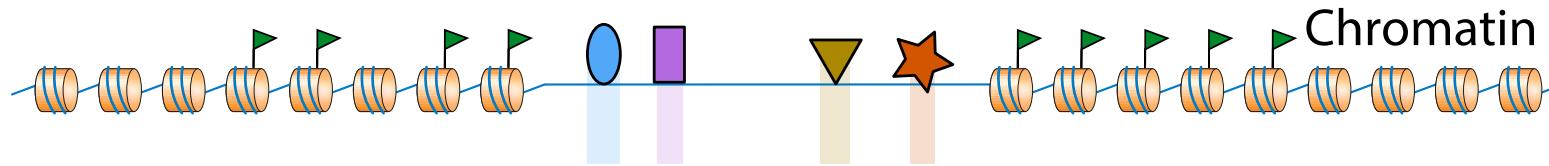
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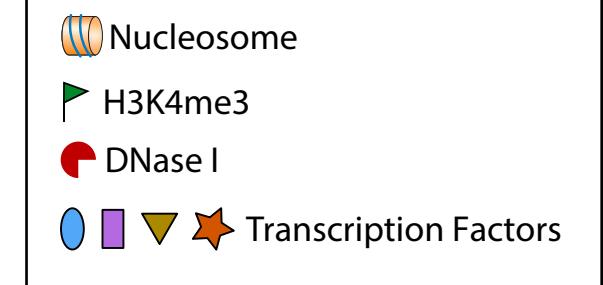
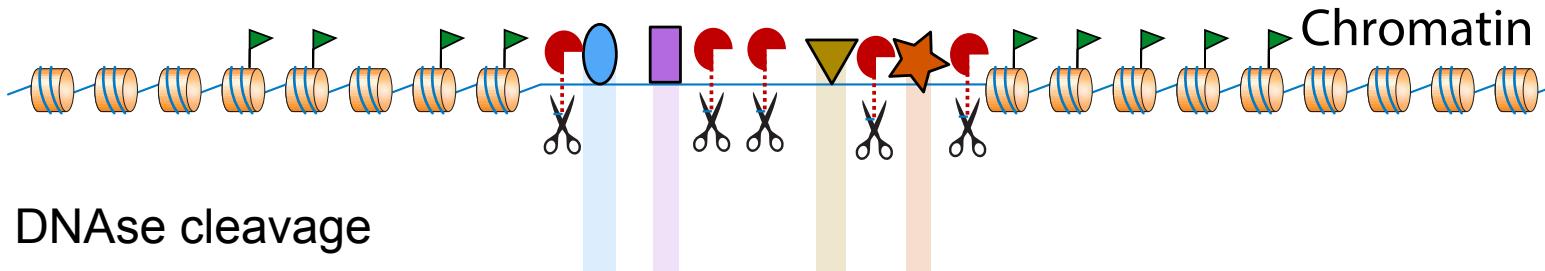


DNA - Protein interactions with DNase-Seq

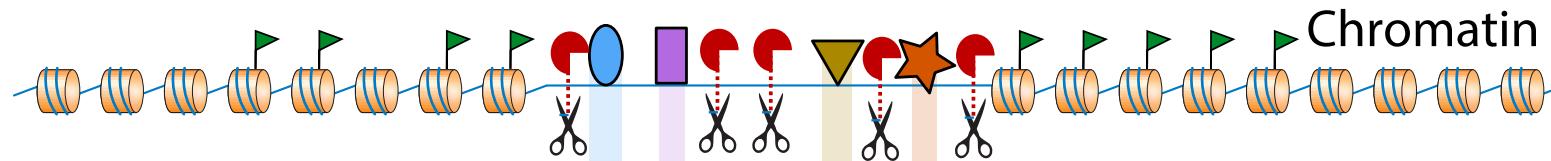


- Nucleosome
- H3K4me3
- DNase I
- Transcription Factors

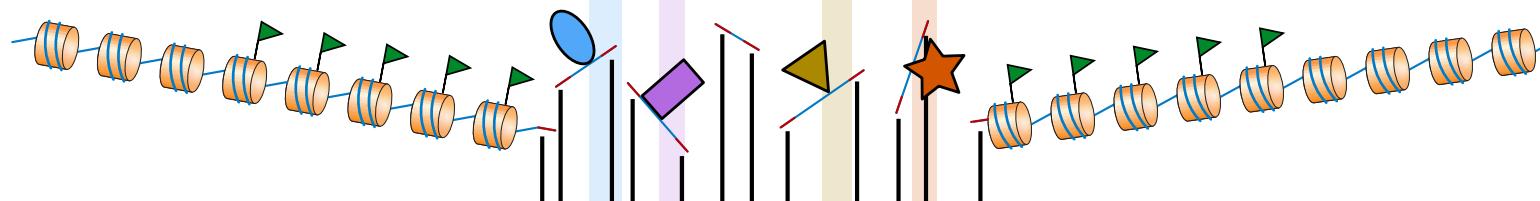
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DNA - Protein interactions with DNase-Seq

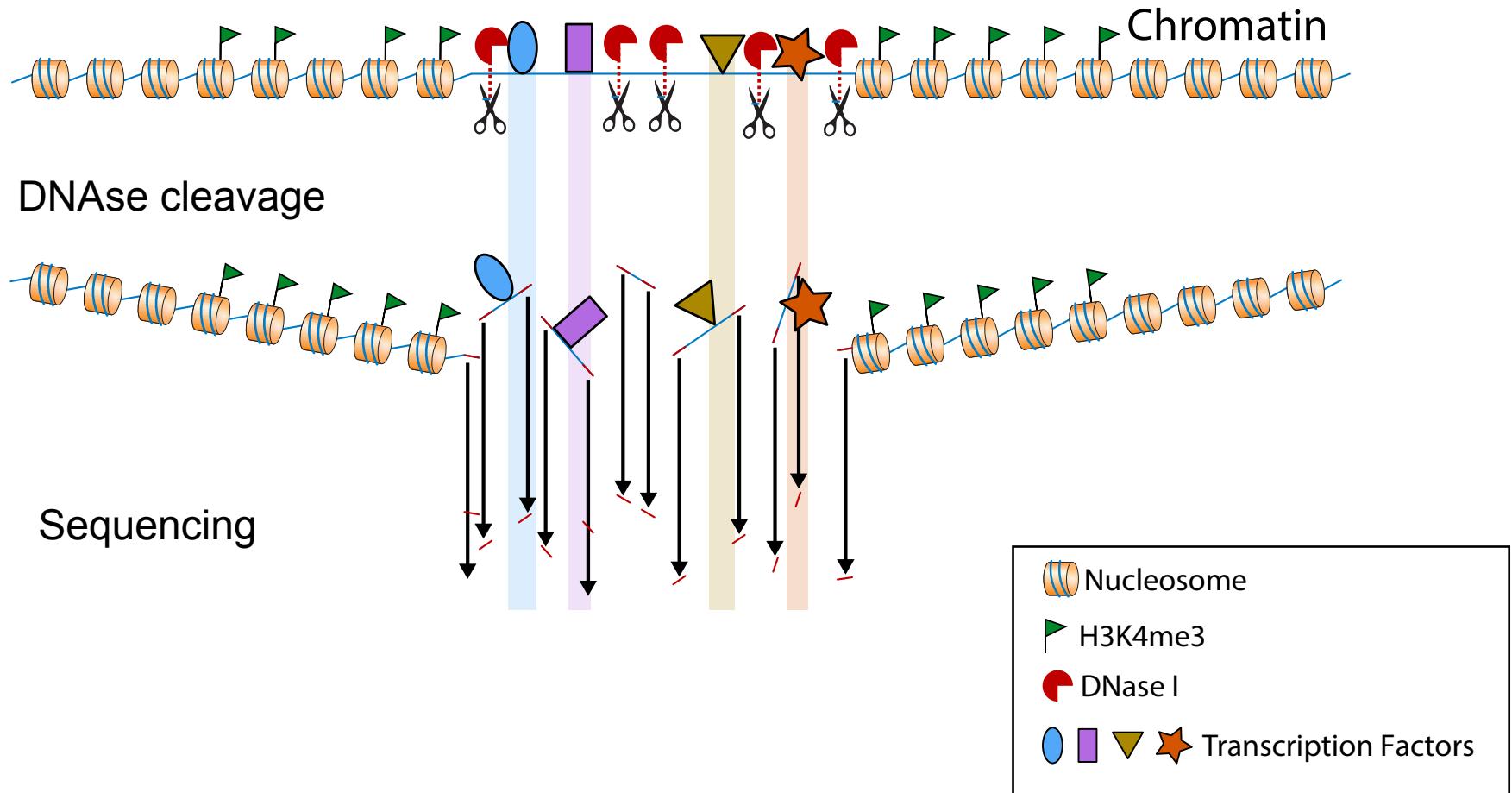


DNAse cleavage

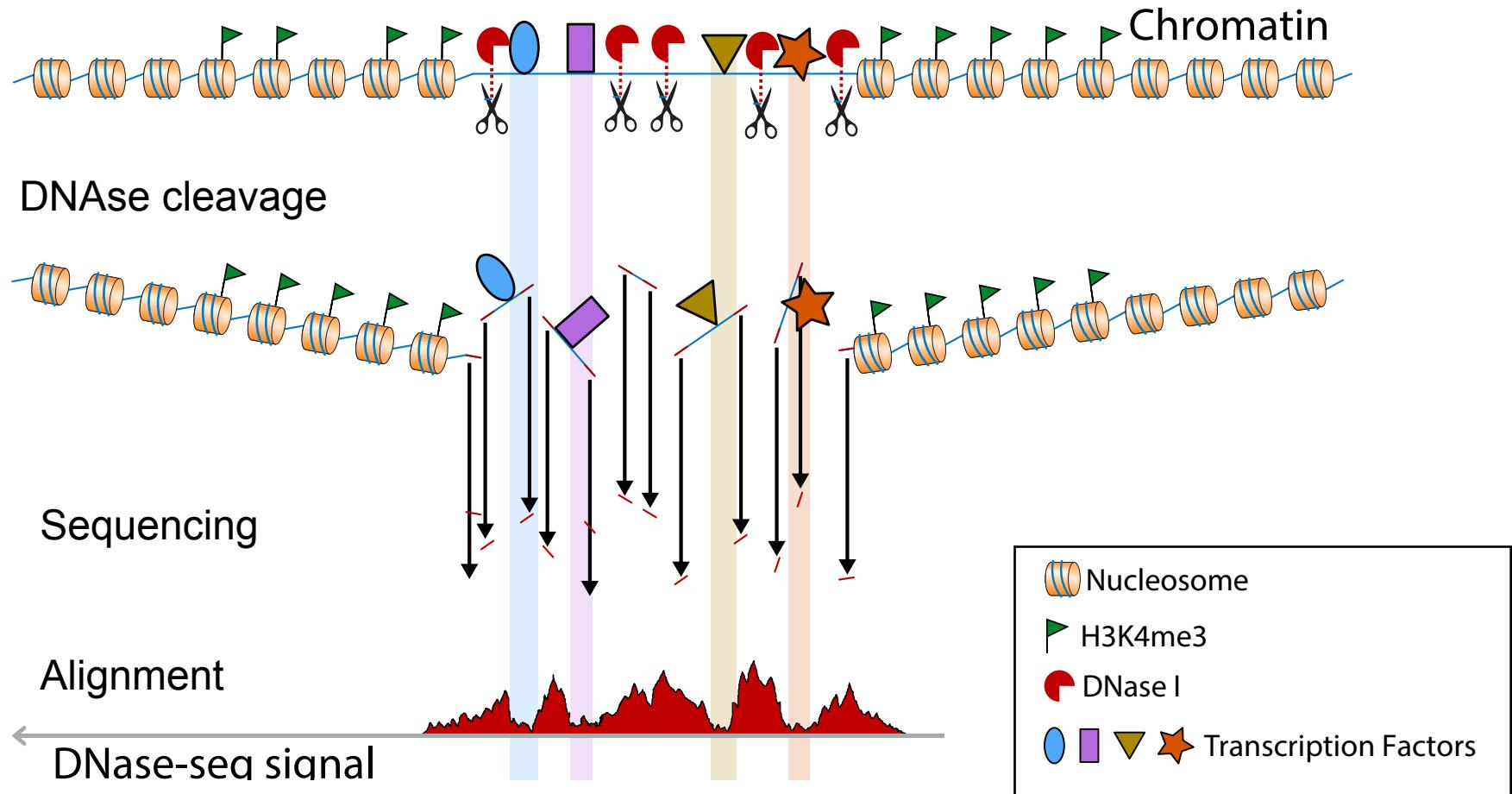


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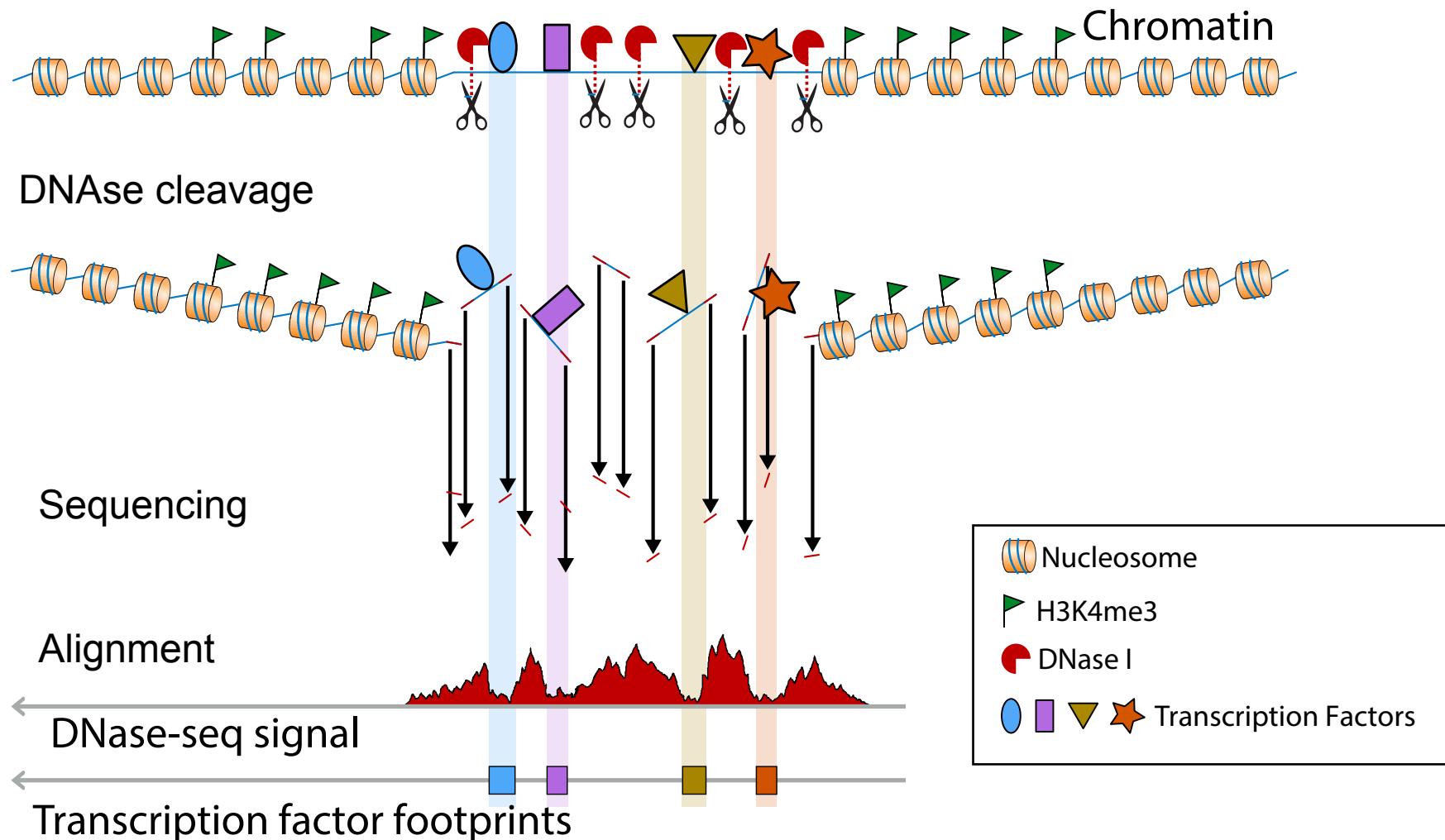
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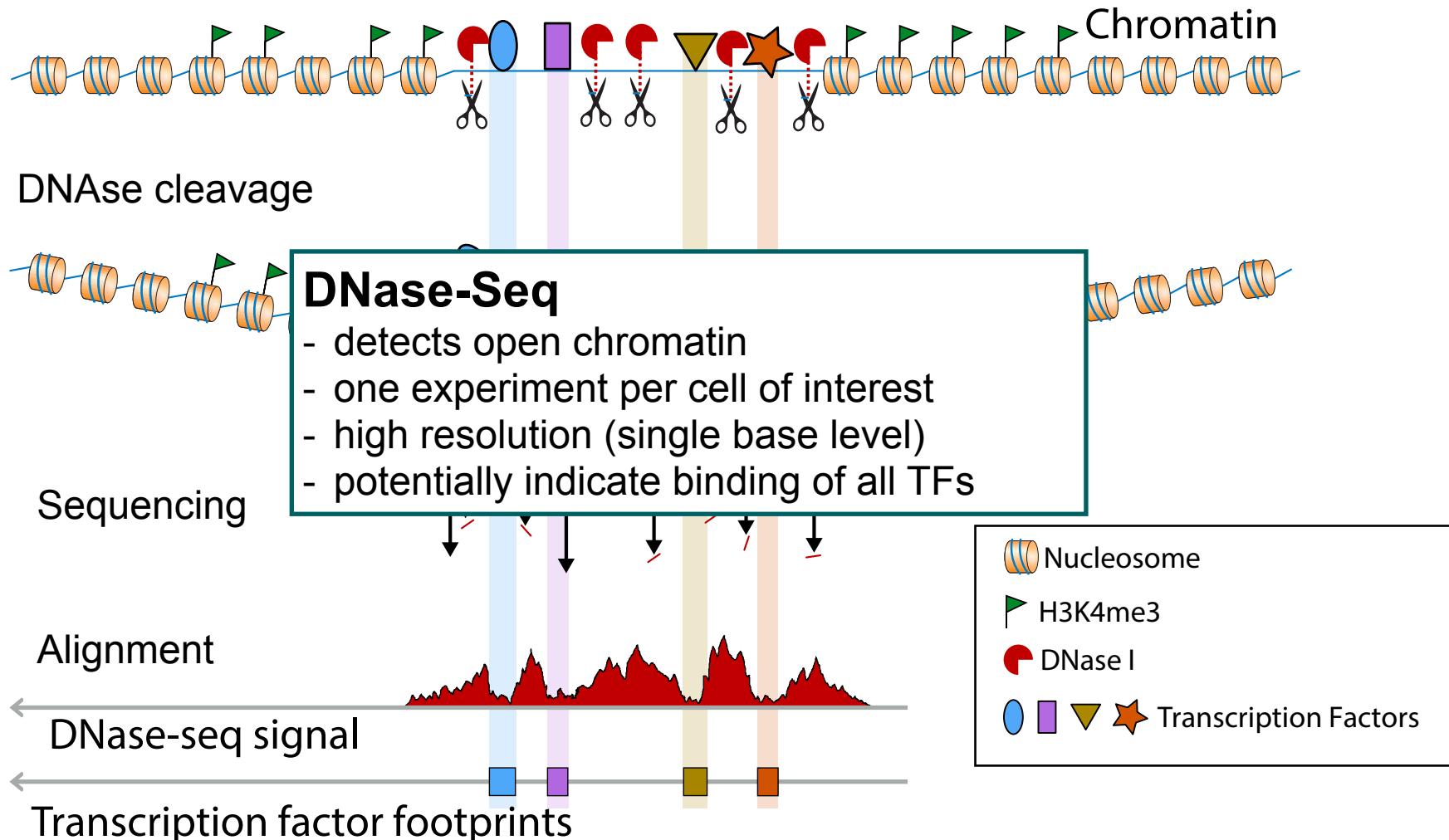
DNA - Protein interactions with DNase-Seq



DNA - Protein interactions with DNase-Seq



DNA - Protein interactions with DNase-Seq



Overview

Transcription factors

- main player of gene regulation/transcription

Chromatin/histones

- organization of chromatin conformation and controls cellular memory/plasticity

Histone modifications

- affect interaction of histones with DNA and other histones
- indicate regulatory status of genomic regions

Next generation sequencing

- TF binding and histone modifications (ChIP-seq)
- open chromatin regions (DNase- & ATAC-seq)

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