



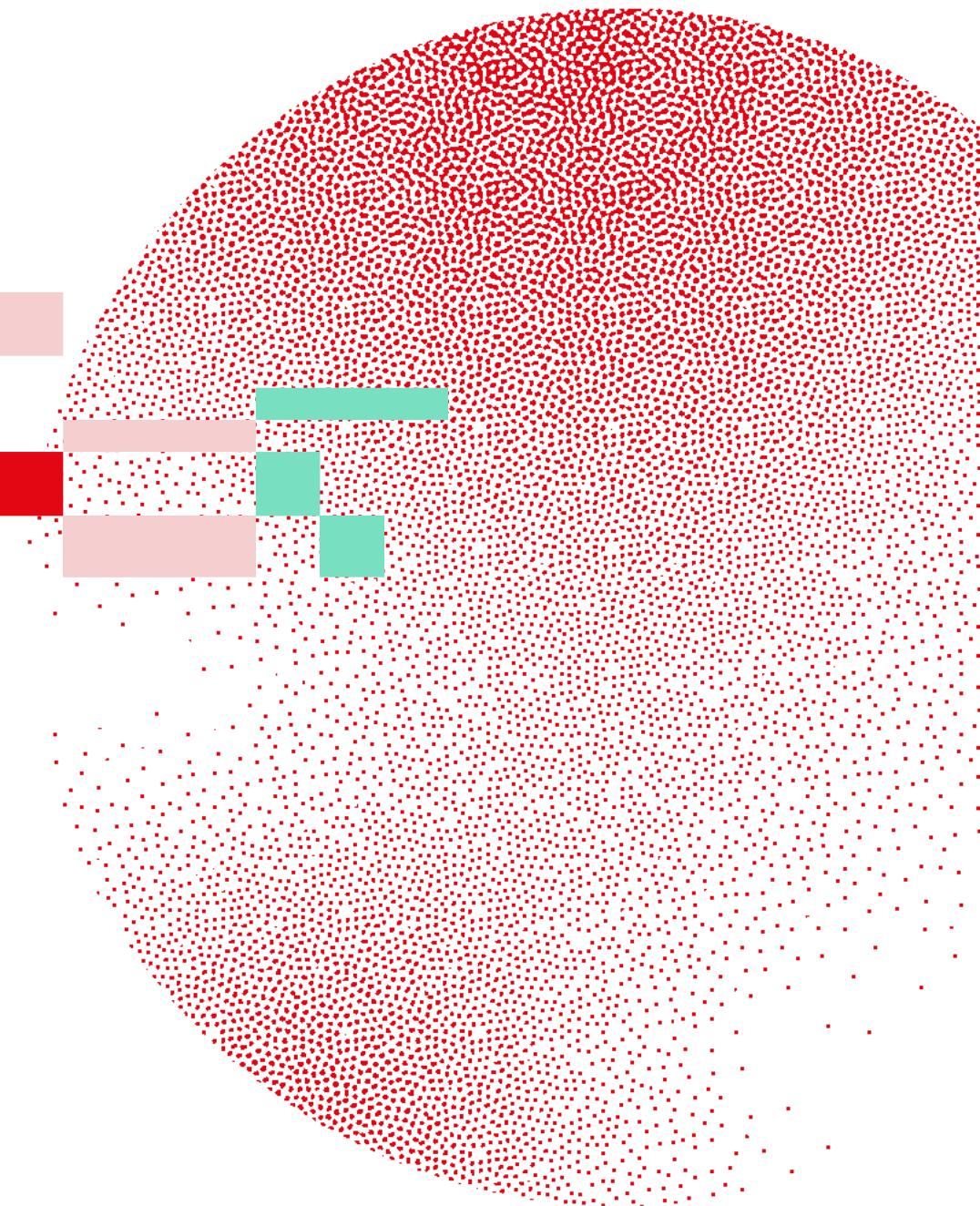
Swiss Institute of  
Bioinformatics

BIOLOGY-INFORMED INTEGRATION AND VISUALIZATION OF  
MULTIOMICS DATA

# Multi-omics data

Deepak Tanwar

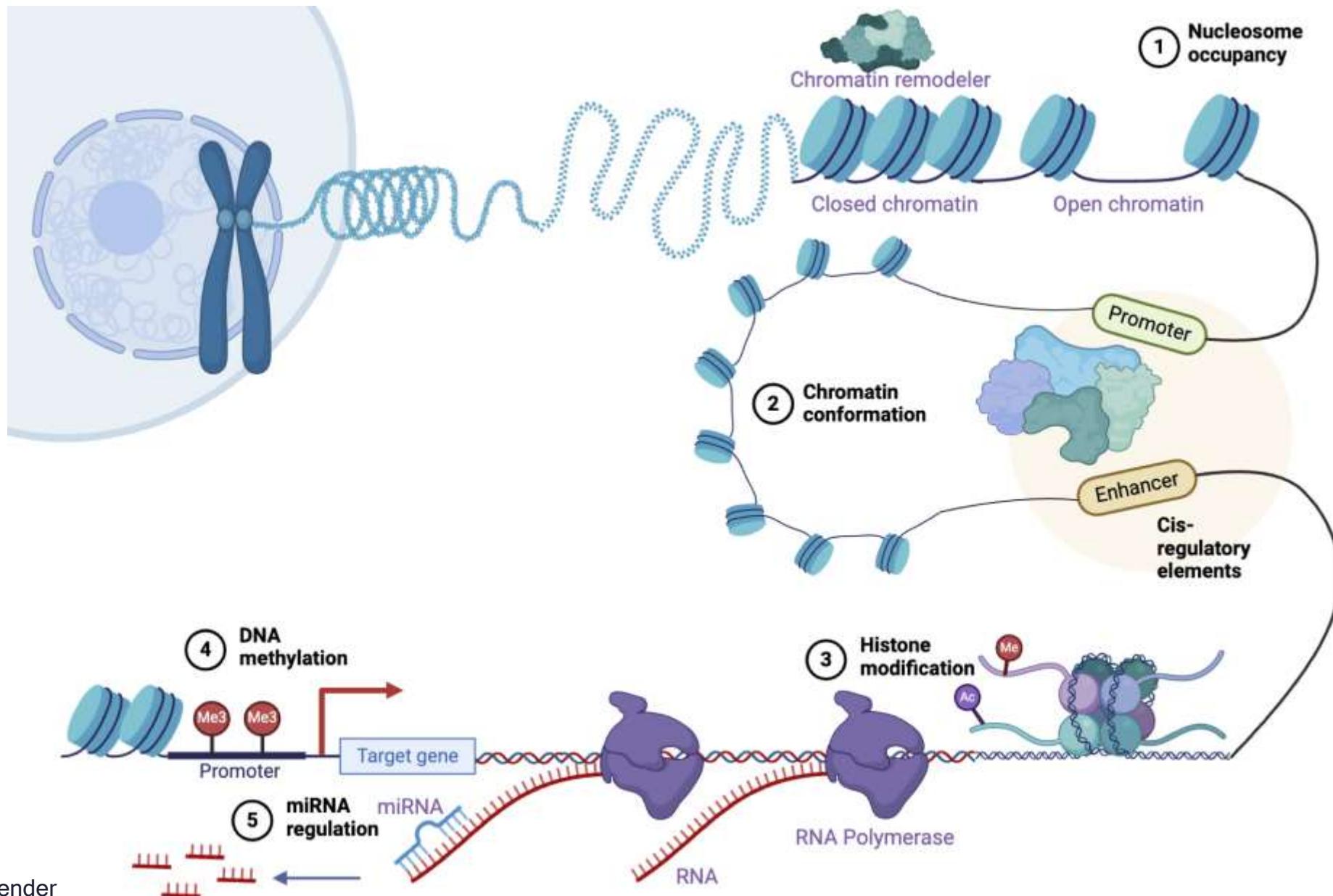
February 17-19, 2026



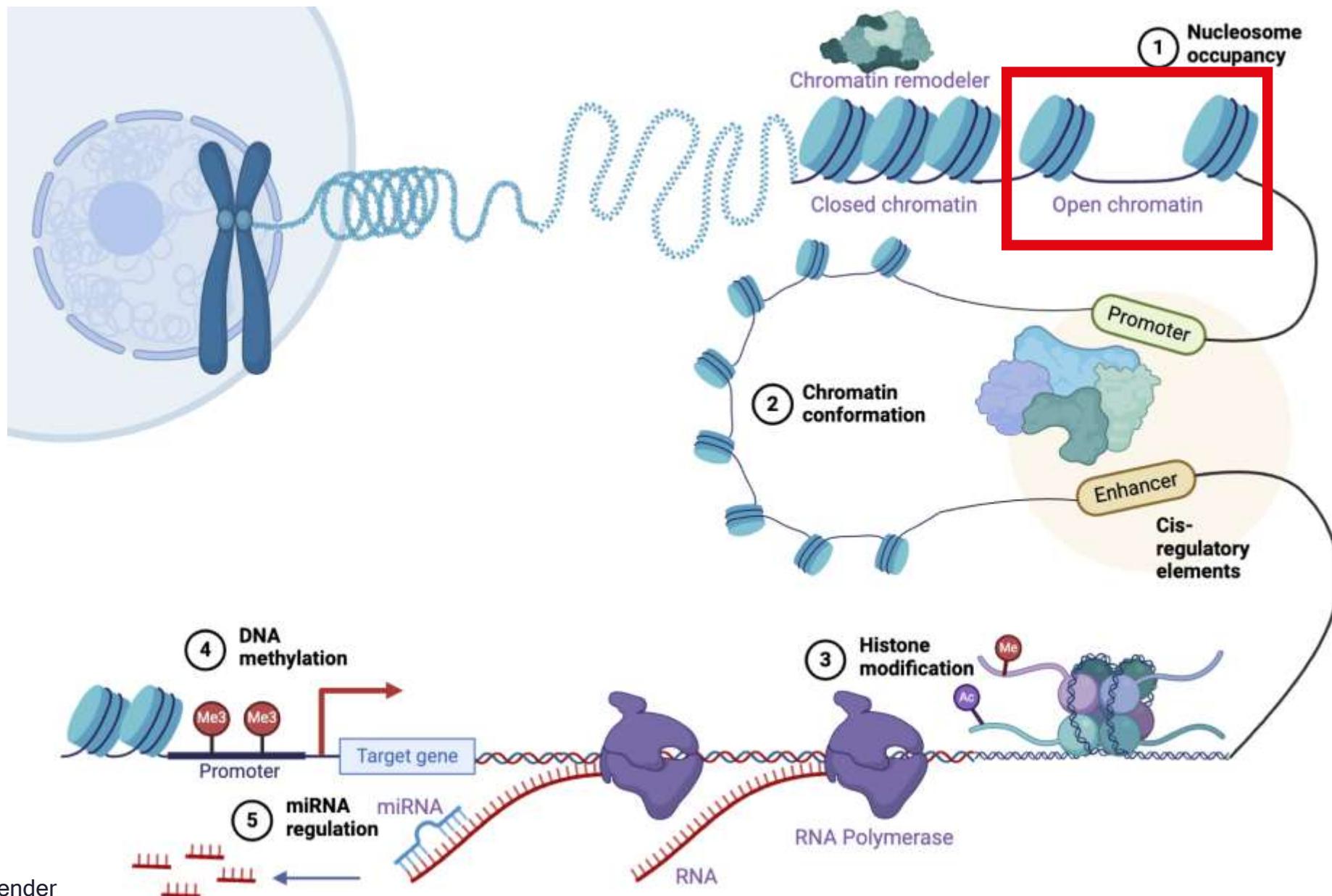
# Learning outcomes

- Different layers of genome activity
- Basic pipeline for data generation
- Basic pipeline for the data processing

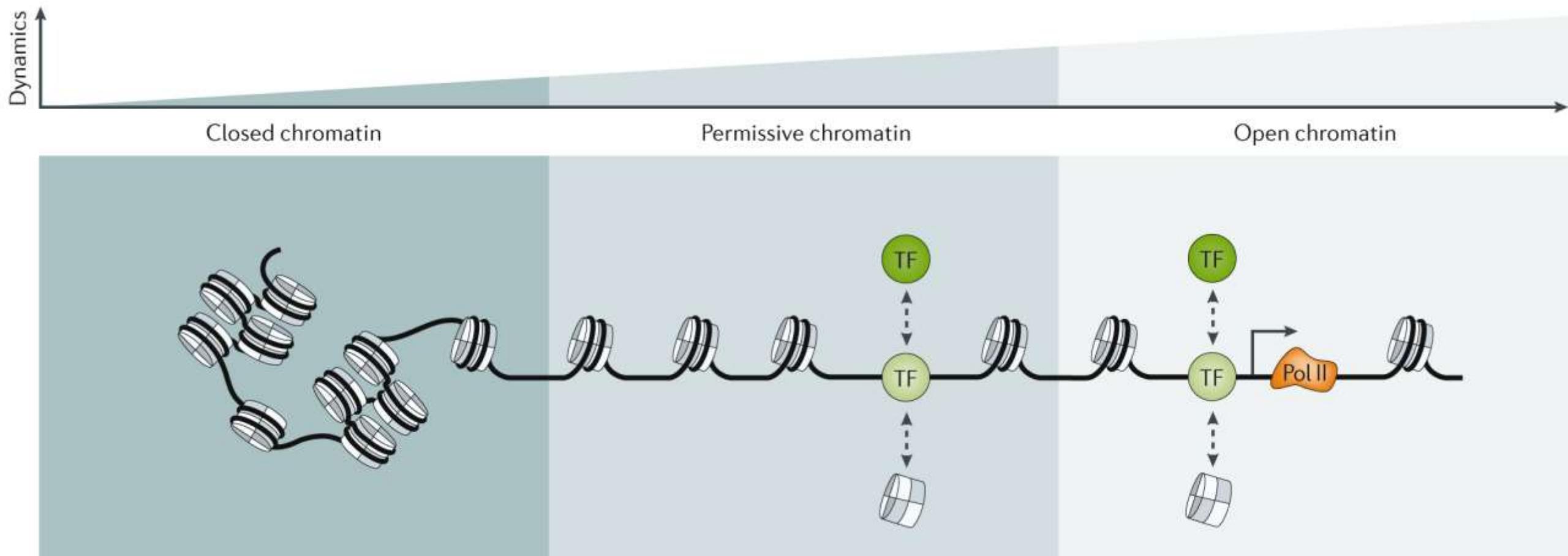
# Simplified illustration of transcriptional regulation



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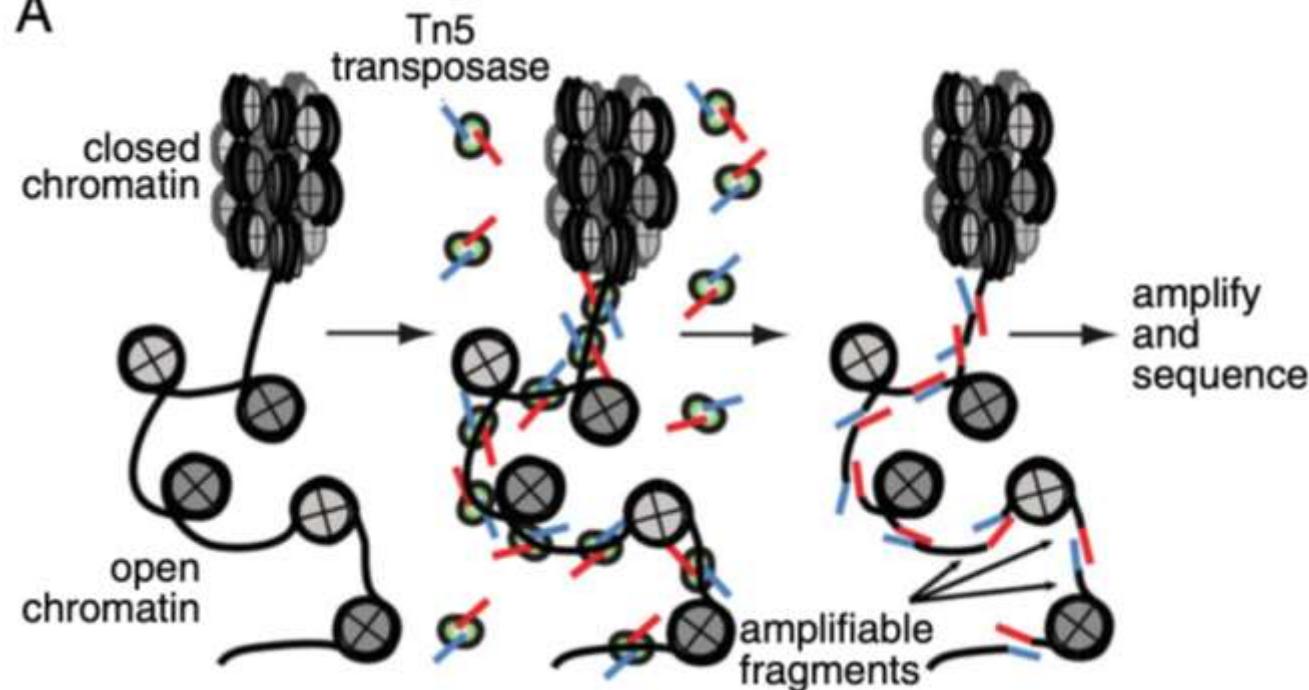


# Chromatin accessibility

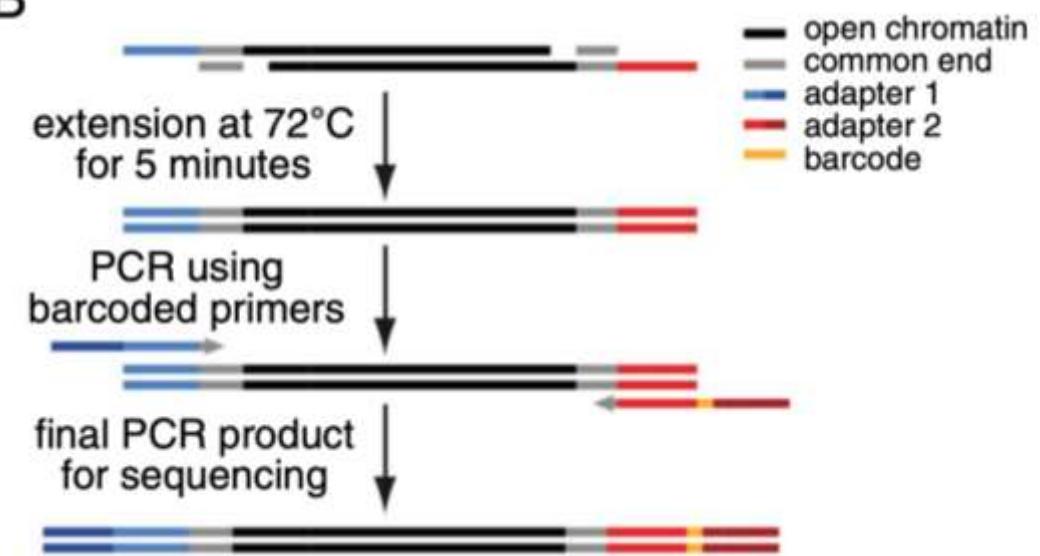


# Library preparation for ATAC-seq

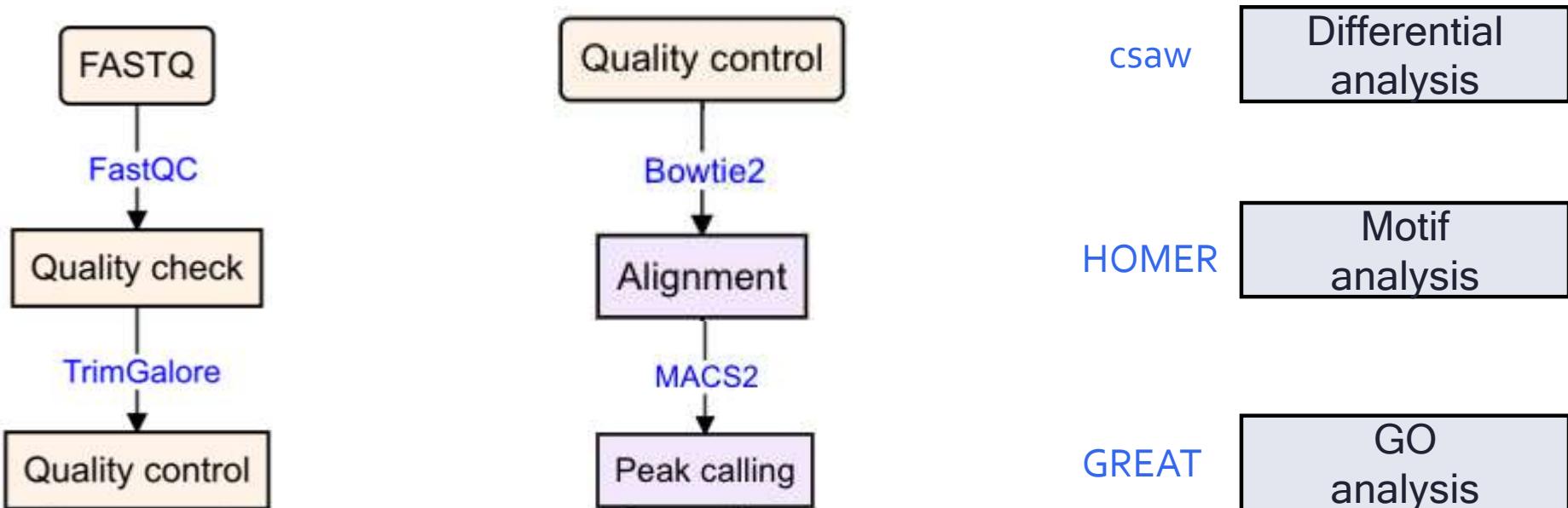
A



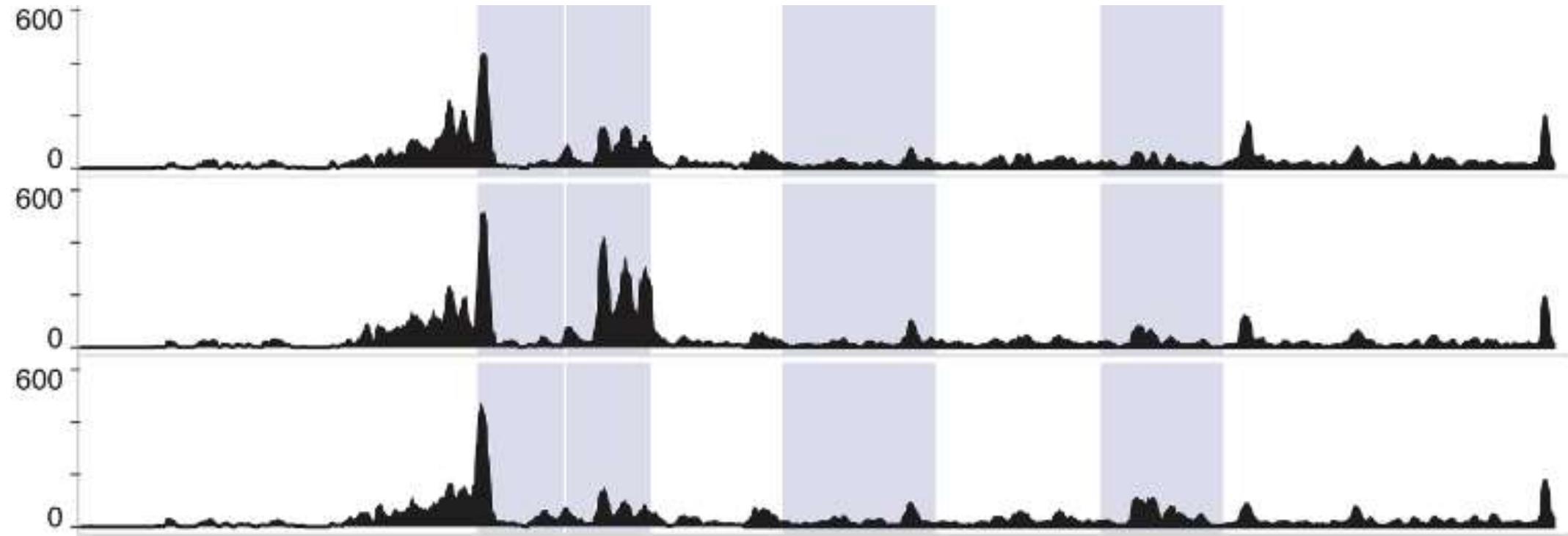
B



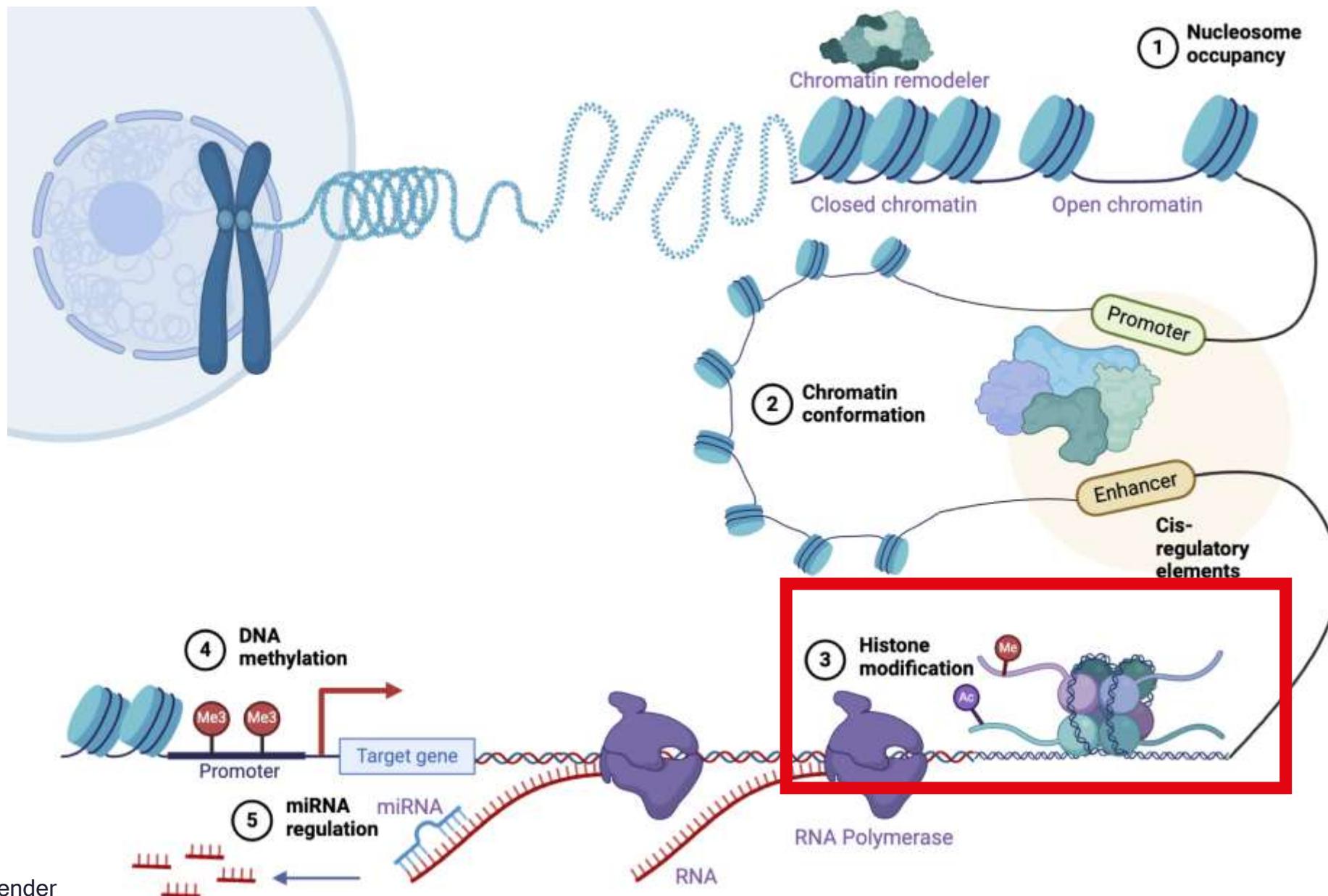
# ATAC-seq data analysis pipeline



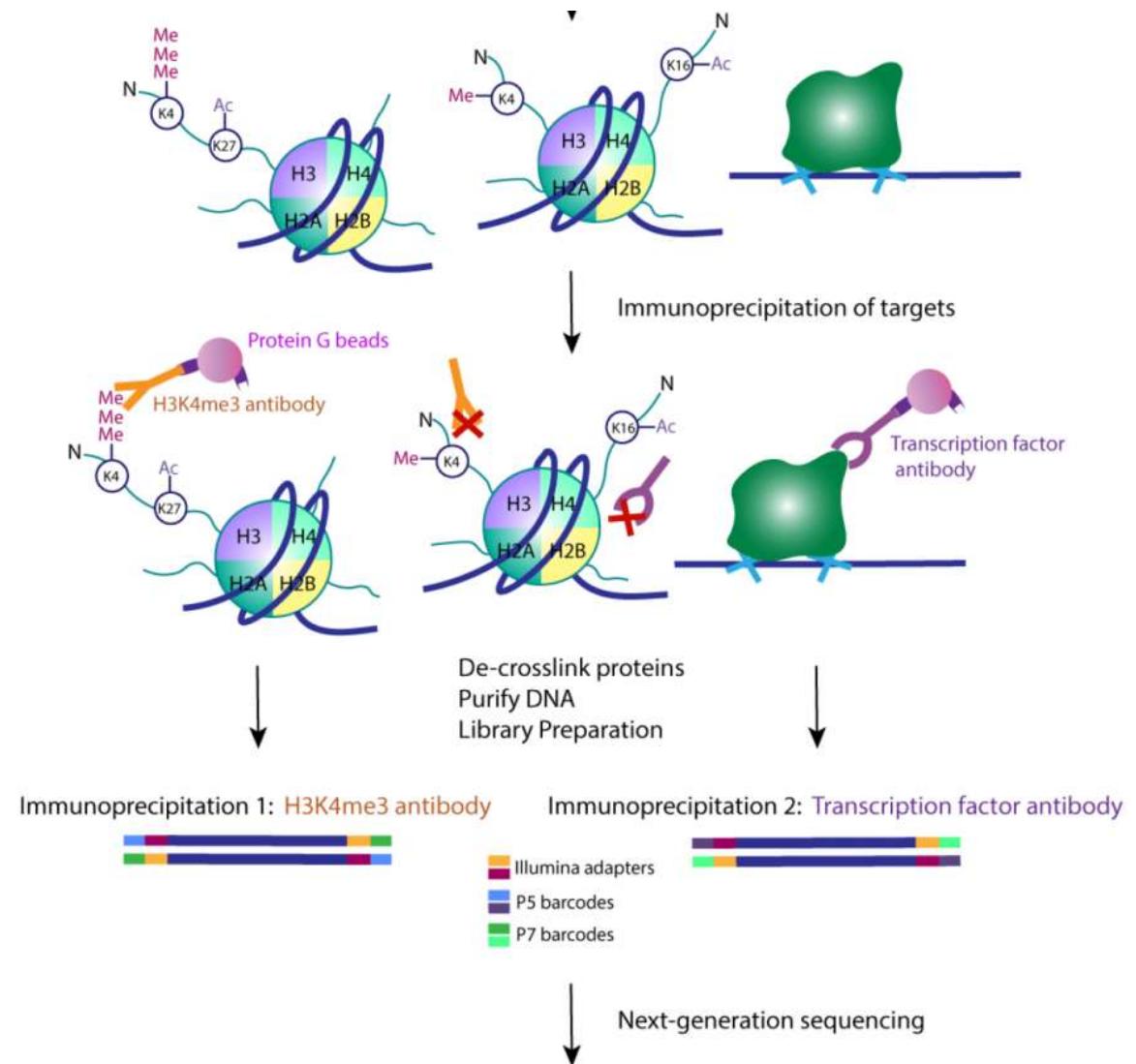
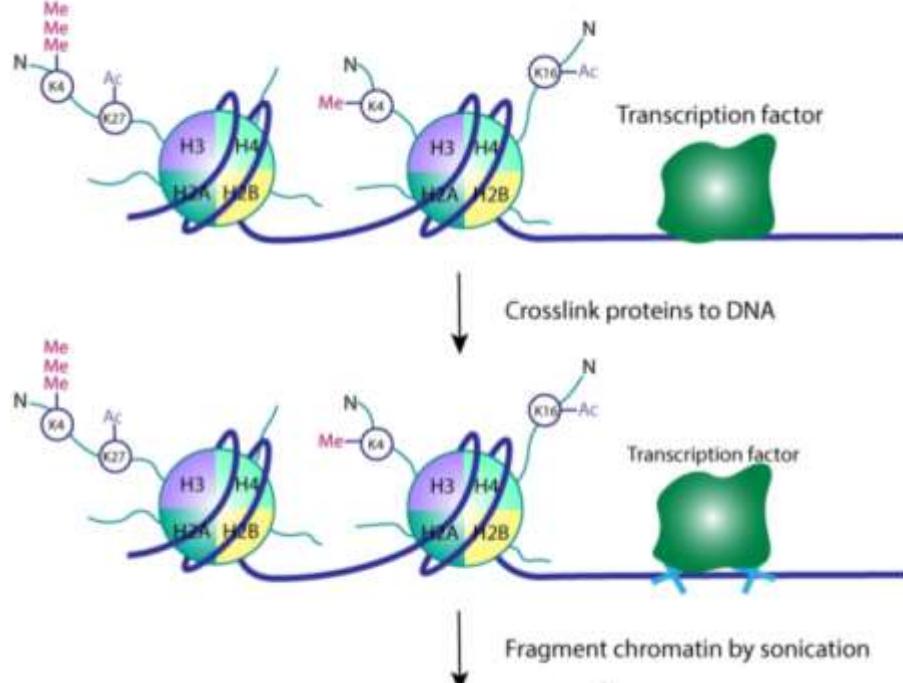
# Example snapshot of chromatin accessibility



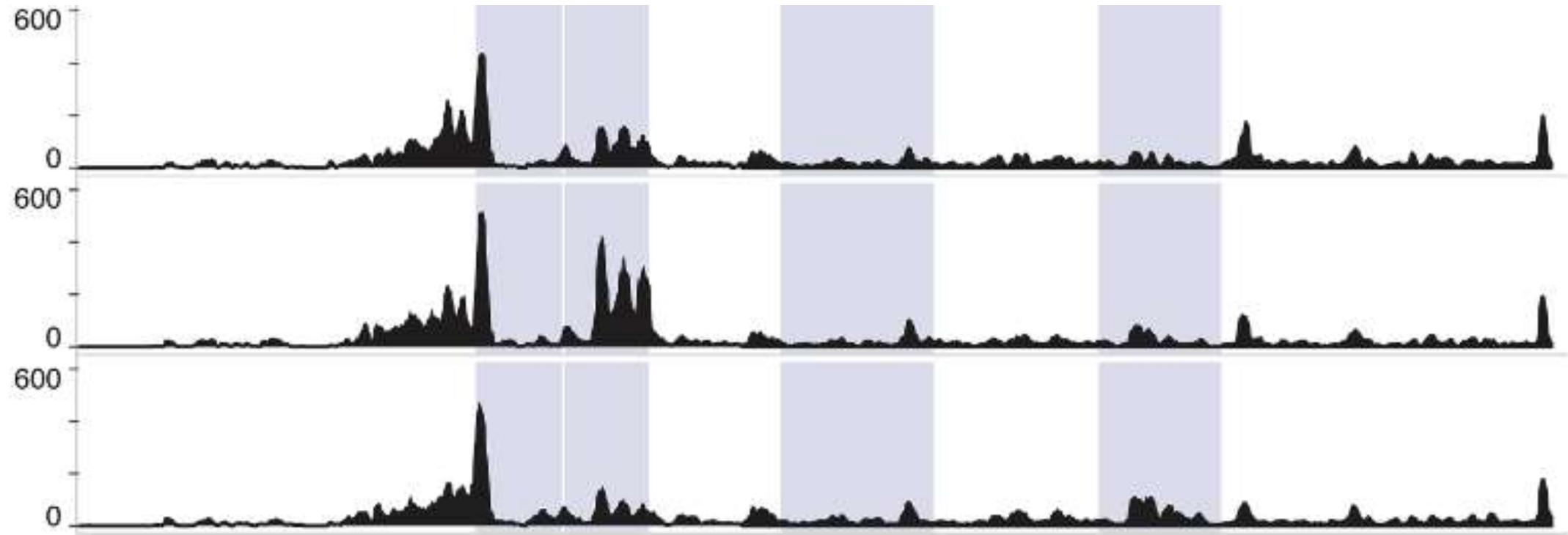
# Simplified illustration of transcriptional regulation



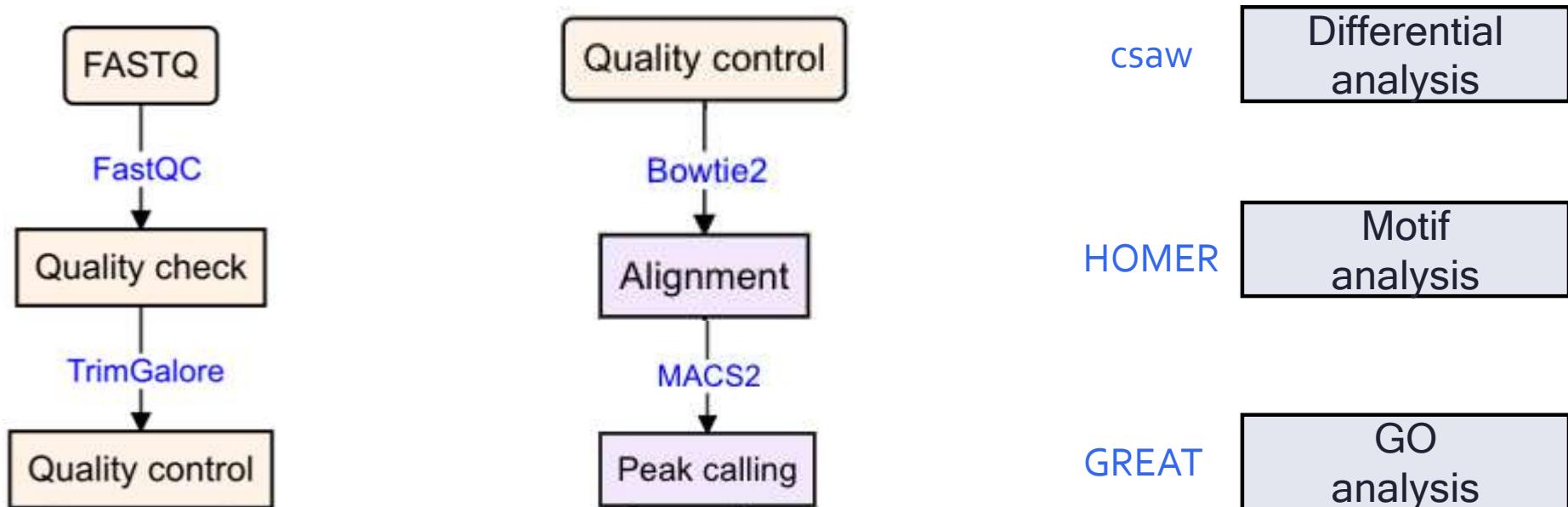
# Chromatin Immunoprecipitation sequencing



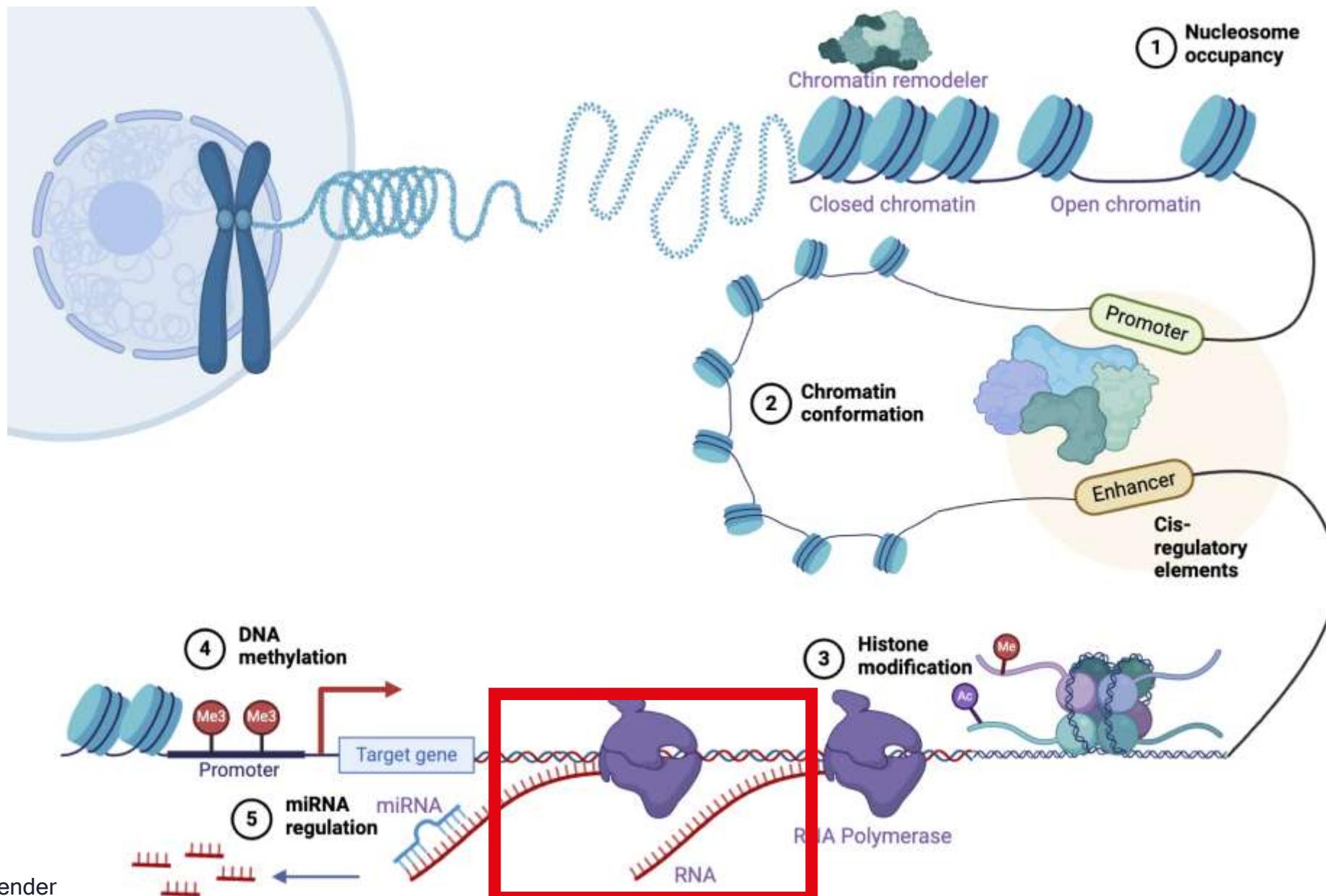
# Example snapshot of enrichment



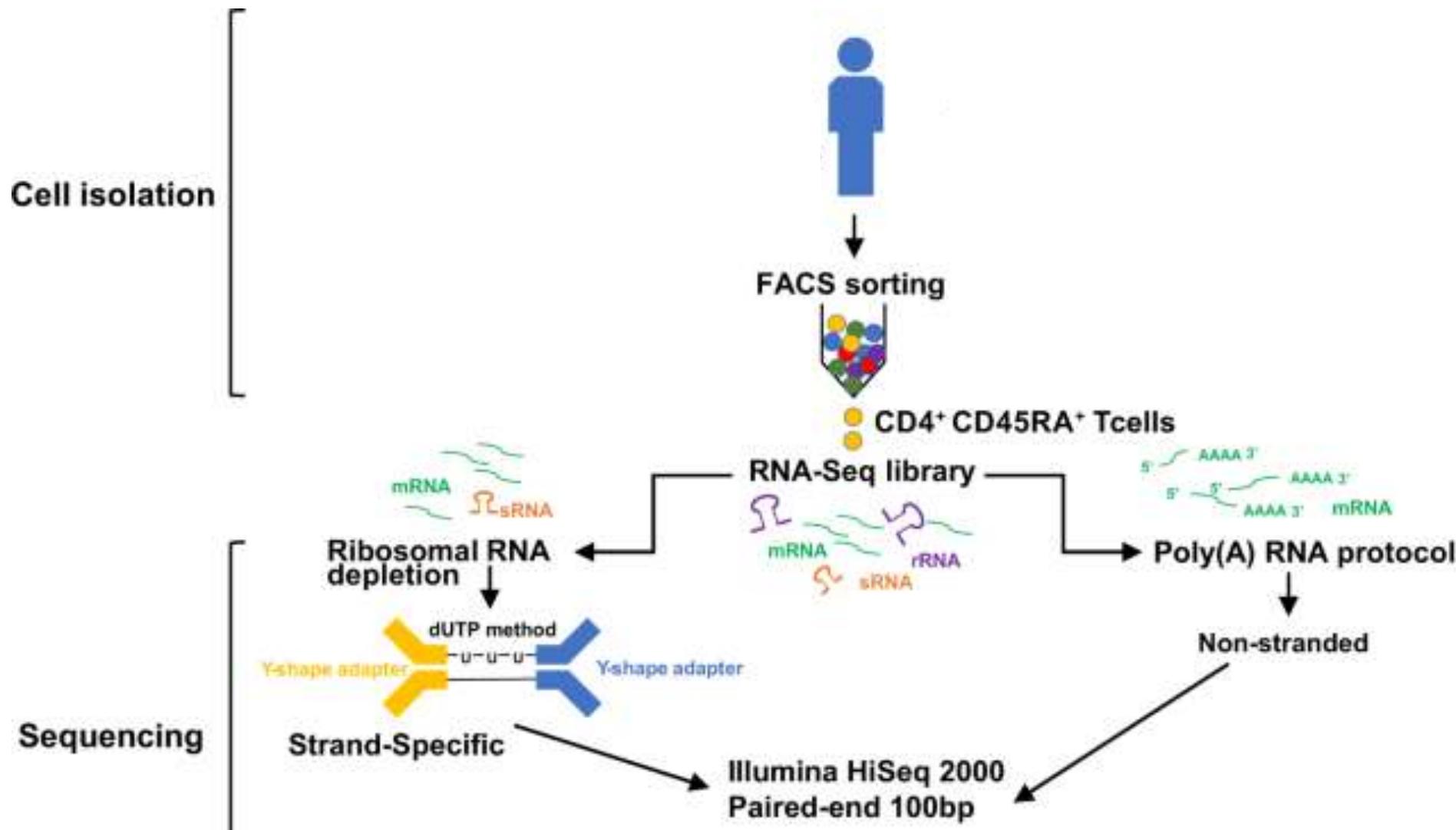
# ChIP-seq data analysis pipeline



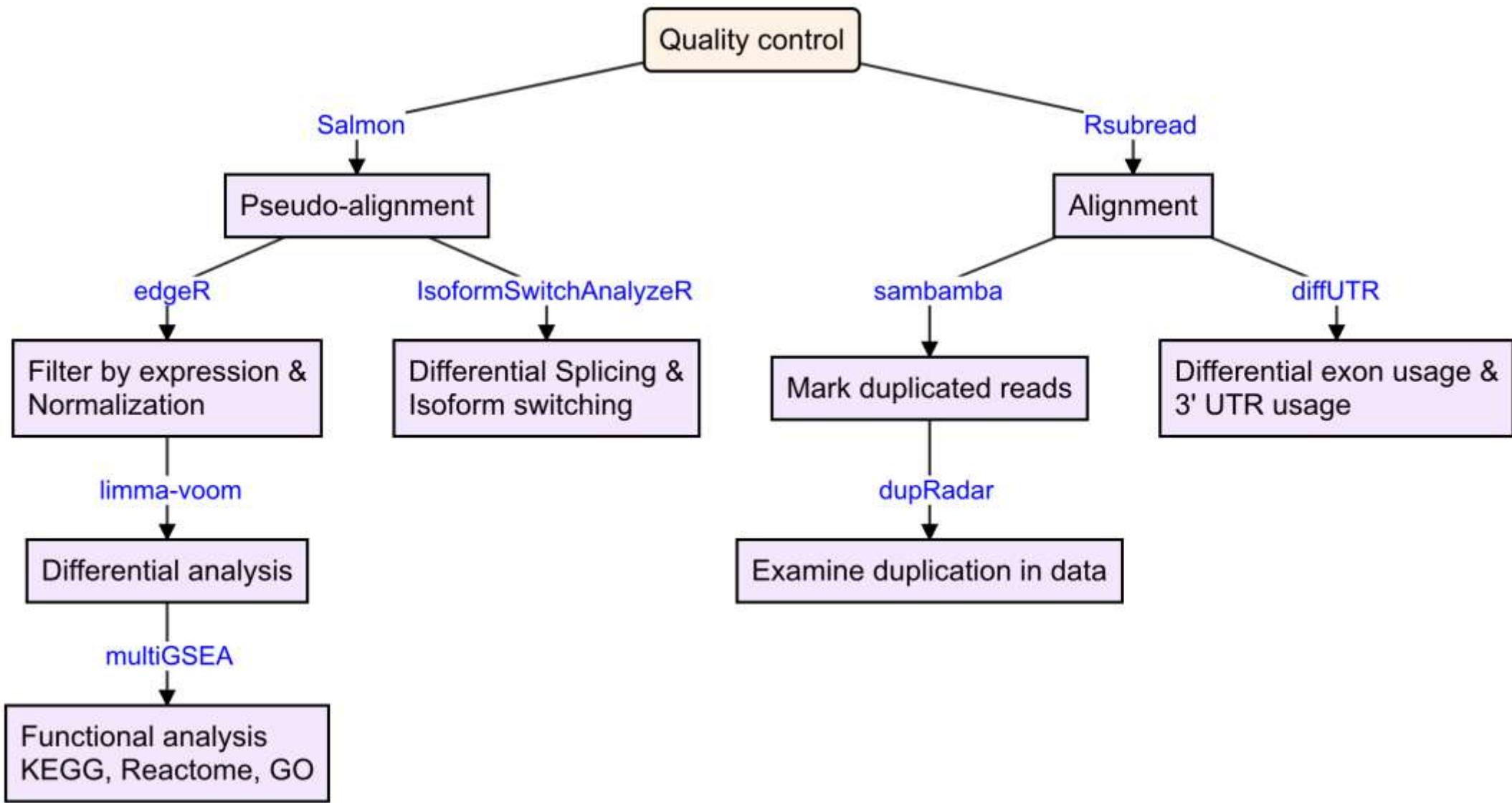
# Simplified illustration of transcriptional regulation



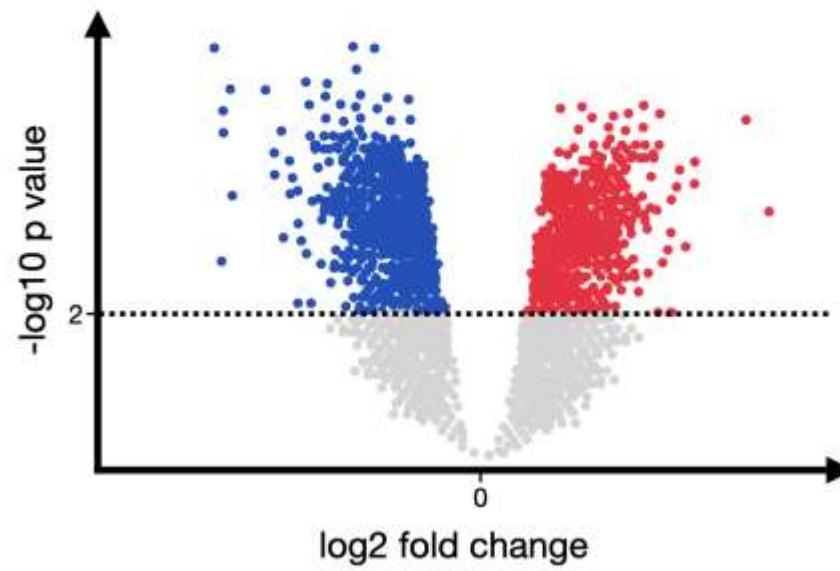
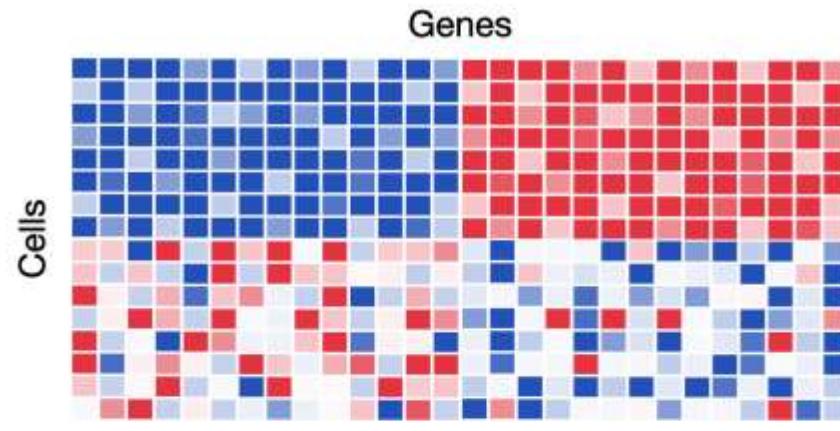
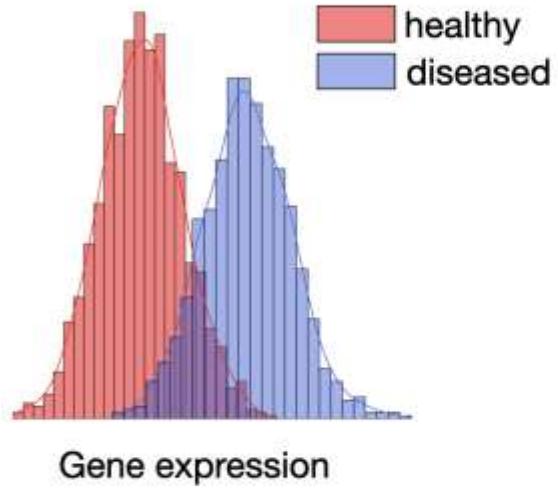
# Gene expression



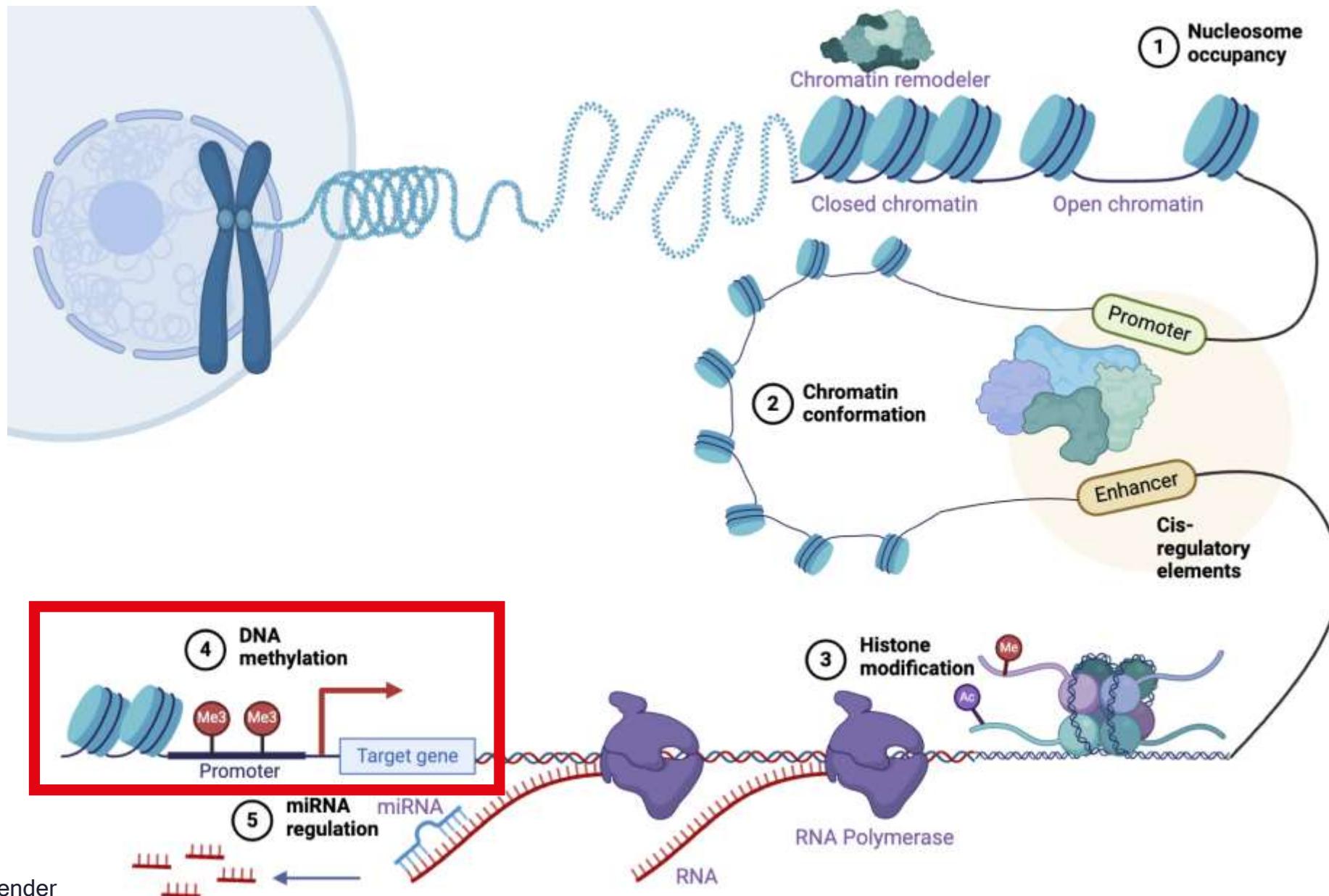
# RNA-seq data analysis pipeline



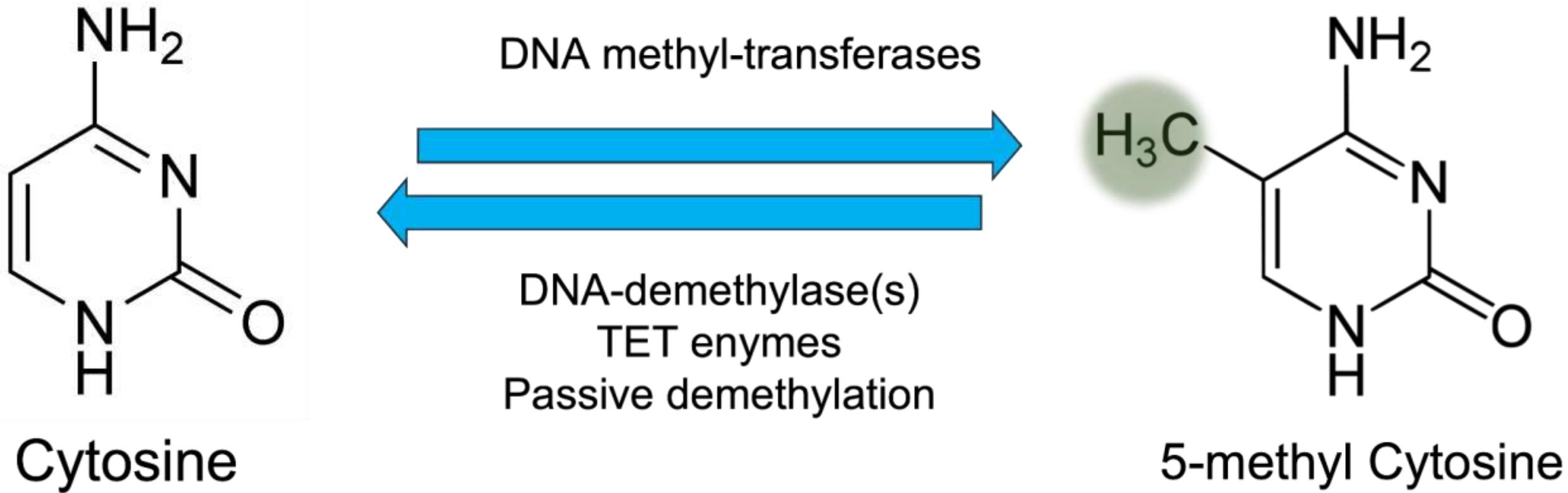
# Differences in gene expression



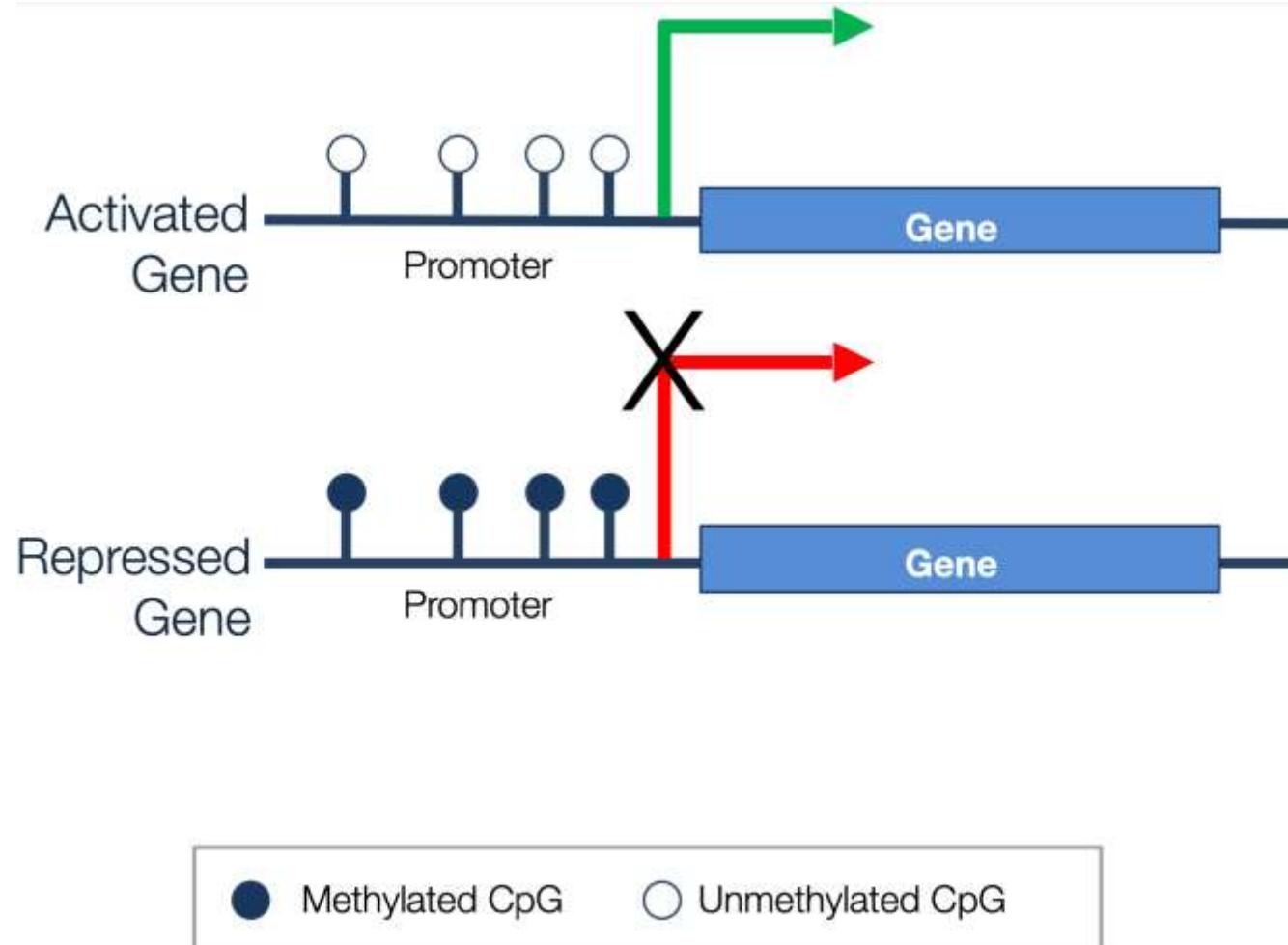
# Simplified illustration of transcriptional regulation



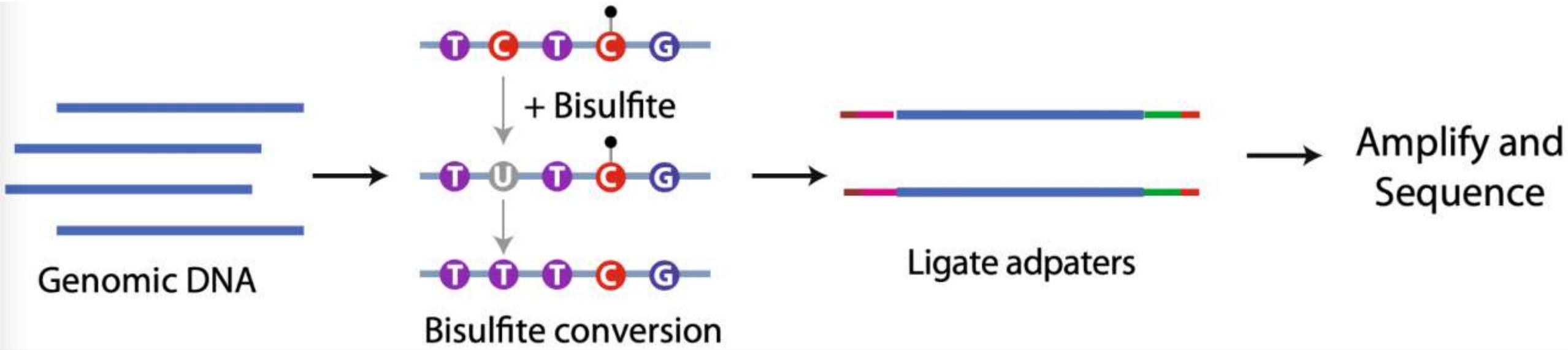
# DNA cytosine methylation is a biological process by which methyl groups are added to the DNA molecule



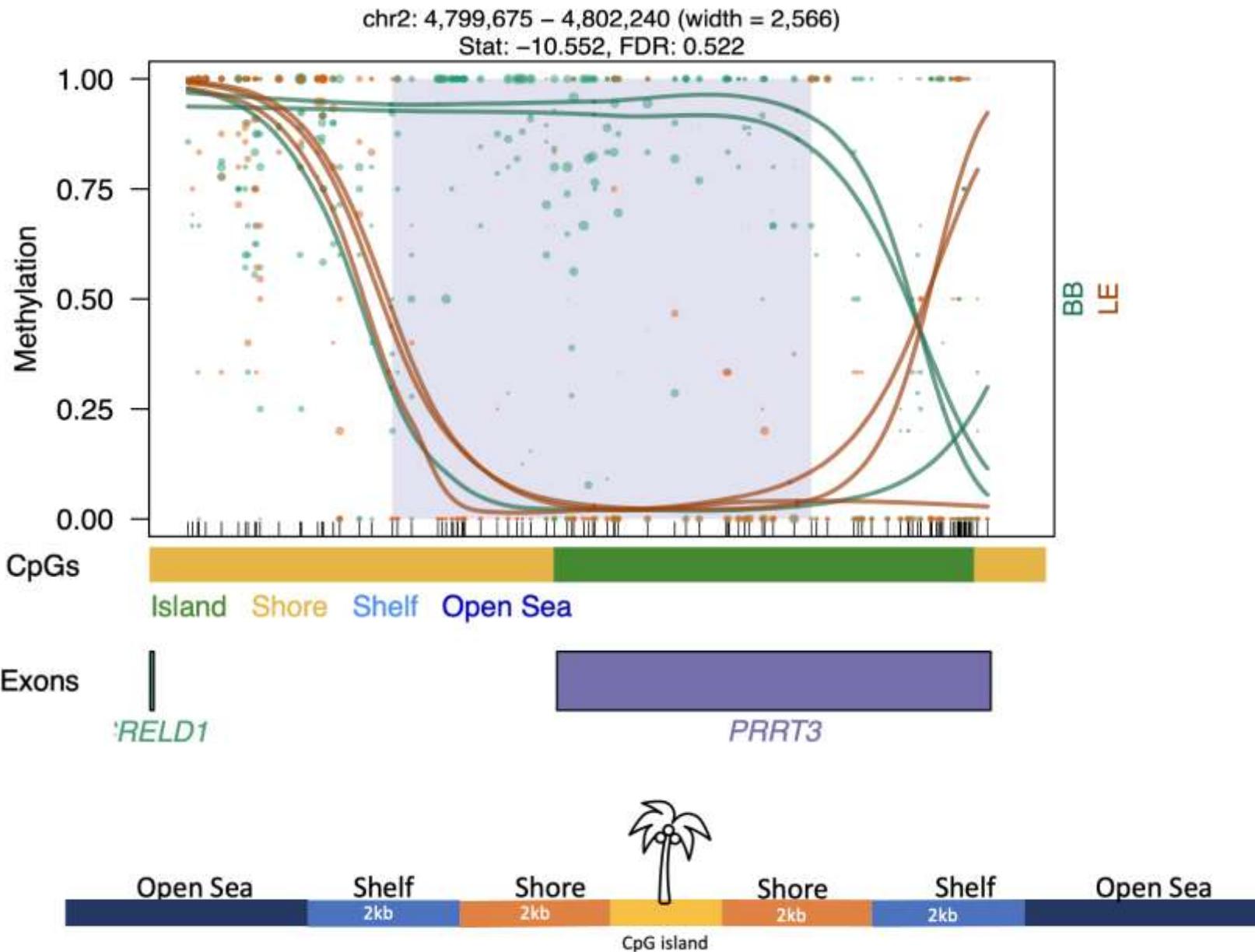
# Role of DNA methylation in transcriptional regulation



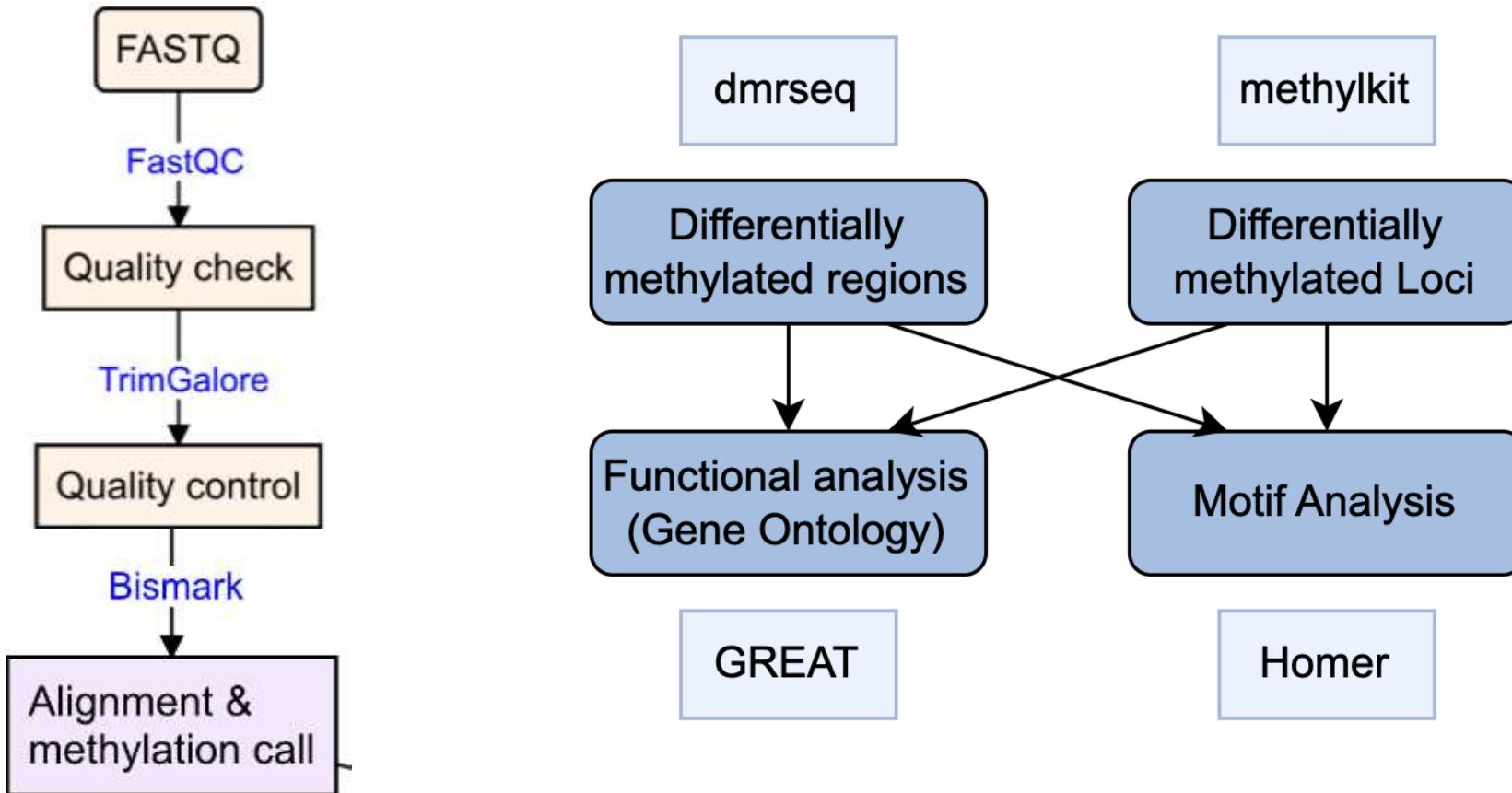
# Gold standard to study DNA methylation patterns across the genome: WGBS



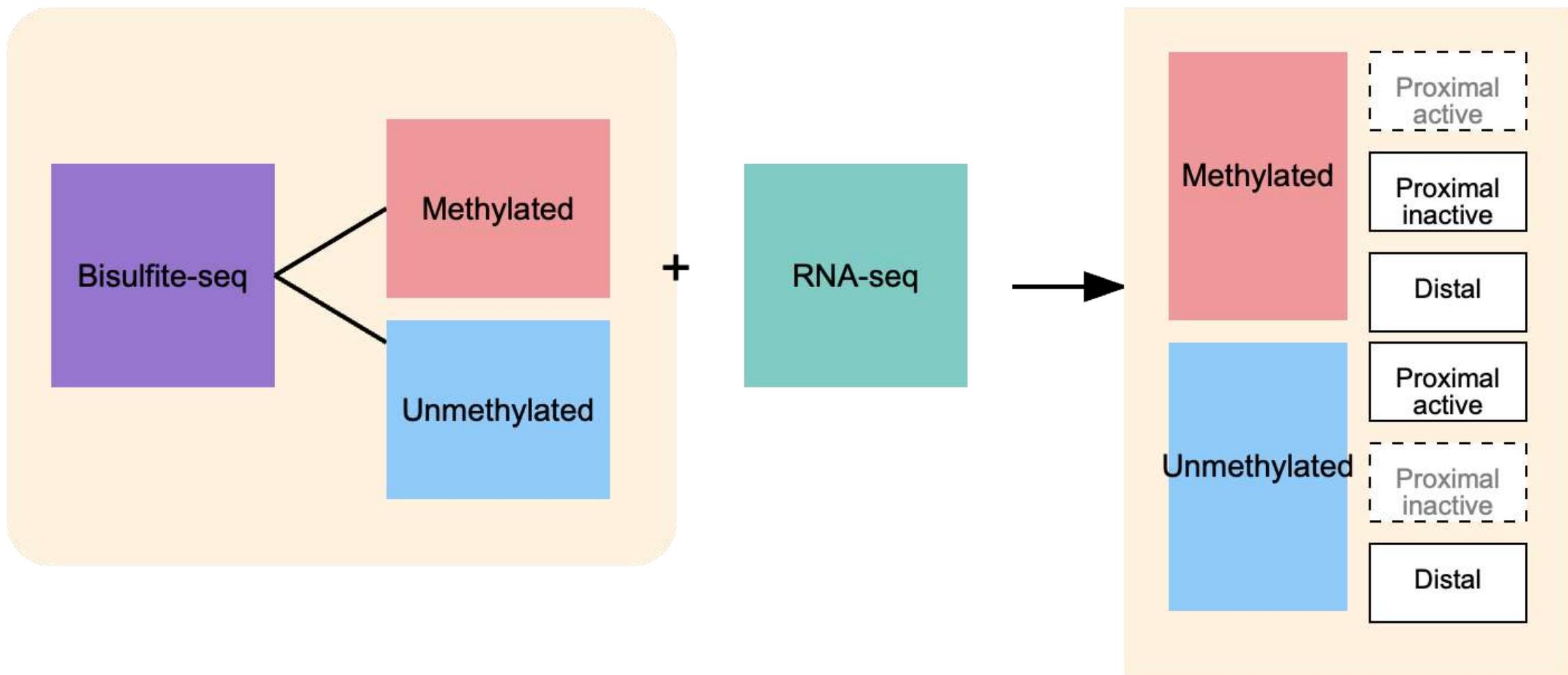
# Example plot for DNA methylation



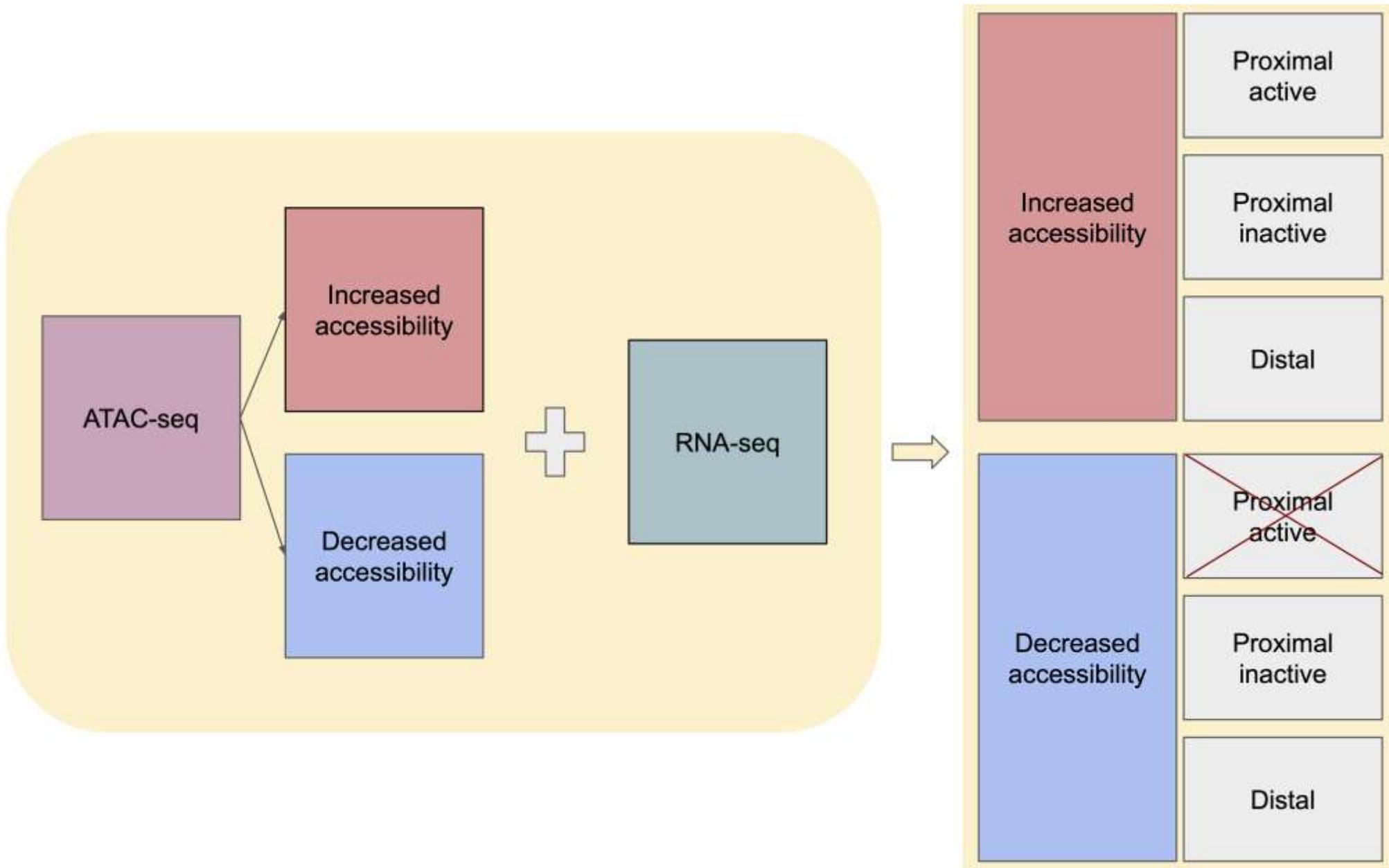
# DNAme data analysis pipeline



# Integration of RNA-seq and WGBS

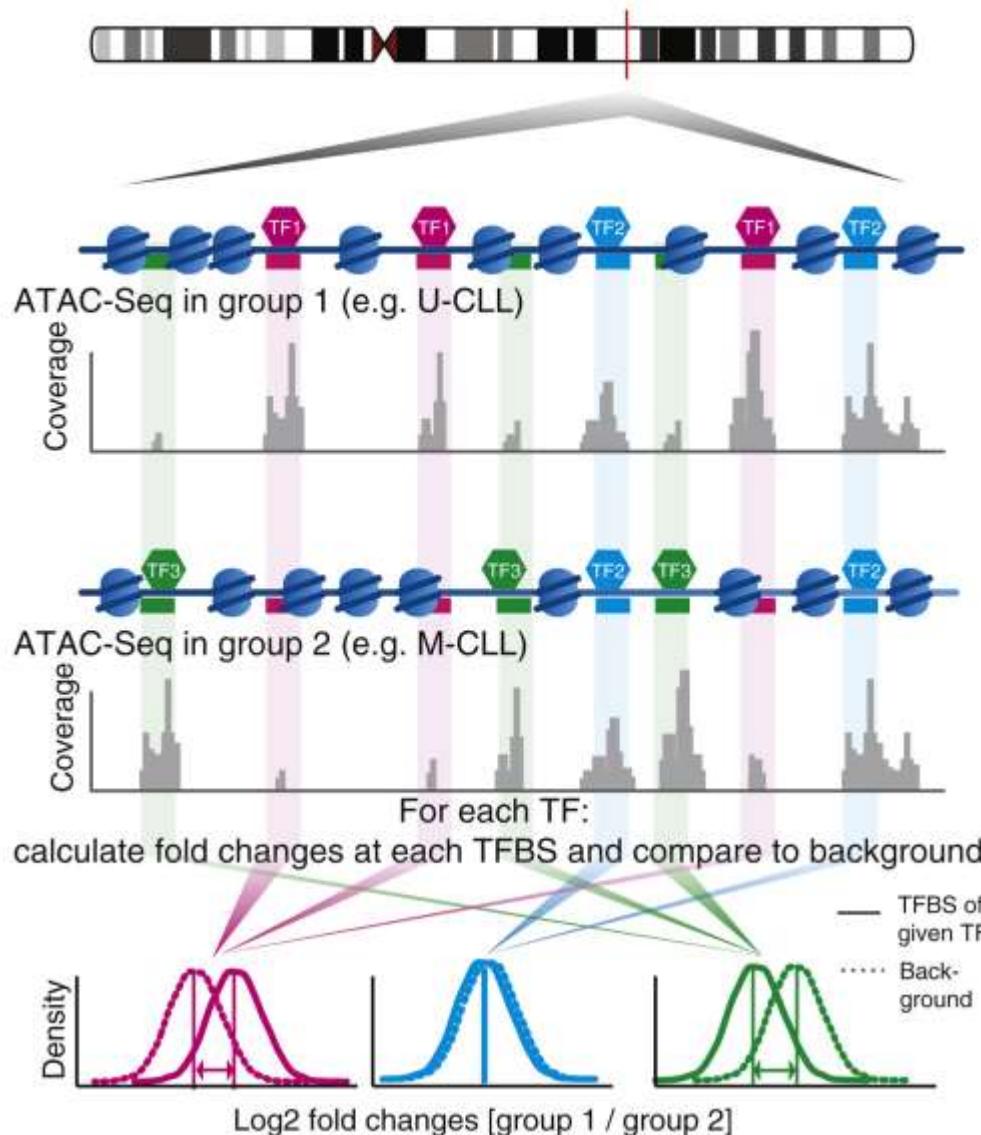


# Integration of RNA-seq and ATAC-seq

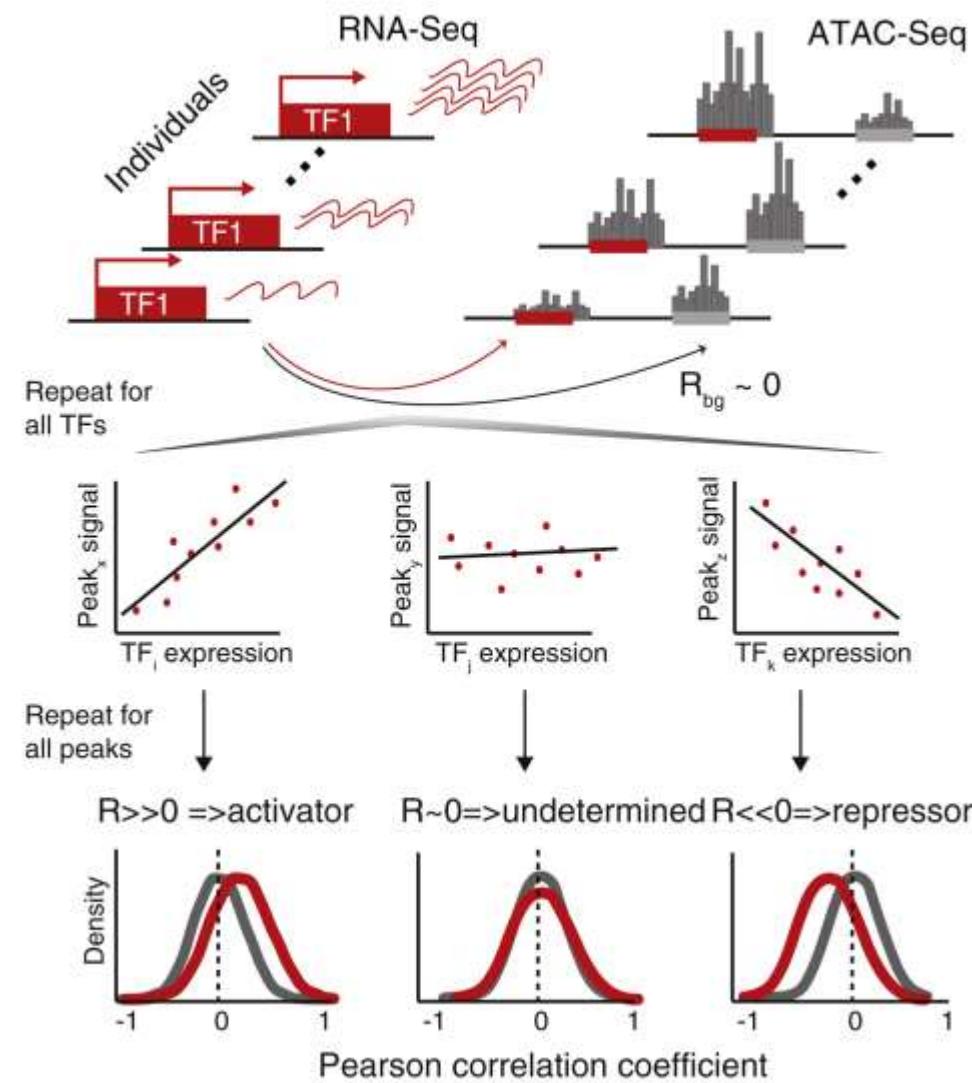


# Integration of RNA-seq and ATAC-seq: diffTF

**A** Schematic of diffTF - basic mode



**B** Schematic of diffTF - classification mode



# Multi-omics integration overview

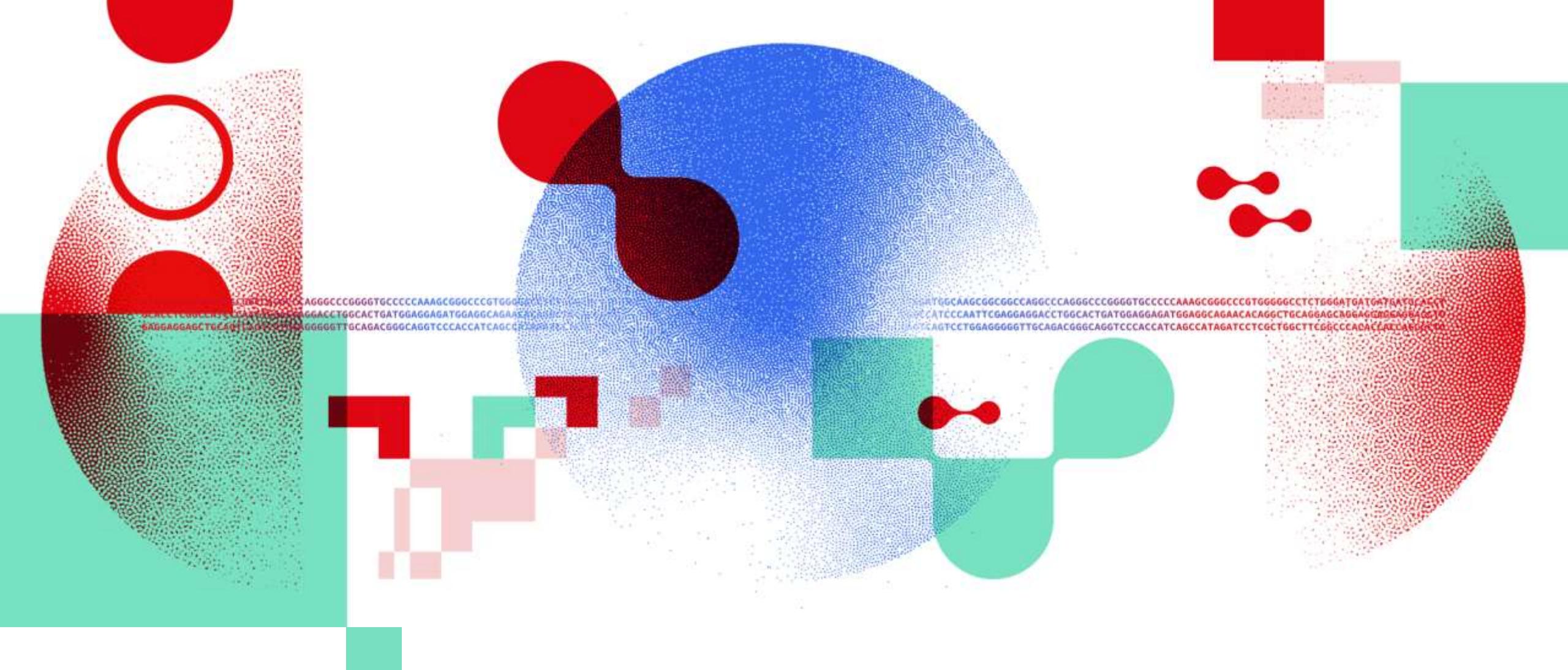
Feature	Systematic Approaches	Ad-hoc Approaches
Definition	Algorithmic frameworks for integrating multiple omics datasets using statistical or machine learning models.	Custom, hypothesis-driven integration of 1–2 omics datasets based on specific biological questions.
Tools	- mixOmics, DIABLO - MOFA - MINT - sGCCA	- diffTF - Custom R/Python scripts
Supervision	Supervised, unsupervised, or semi-supervised	Typically unsupervised or guided by prior biological knowledge
Omics Types	Multiple omics datasets ( $\geq 2$ ), can be diverse (transcriptomics, epigenomics, proteomics, etc.)	Usually 2 omics types (e.g., RNA-seq + ATAC-seq)
Advantages	- Scalable and reproducible - Handles complex data - Reveals hidden patterns - Supports biomarker discovery	- Biologically intuitive - Easy to prototype - Focused and hypothesis-driven
Interpretability	Moderate (depends on model complexity)	High (based on direct biological rationale)

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We will learn ad-hoc approaches for multi-omics in this course

# Quiz: 6-10



# Thank you

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