



Swiss Institute of
Bioinformatics

BIOLOGY-INFORMED INTEGRATION AND VISUALIZATION OF
MULTIOMICS DATA

Multi-omics data

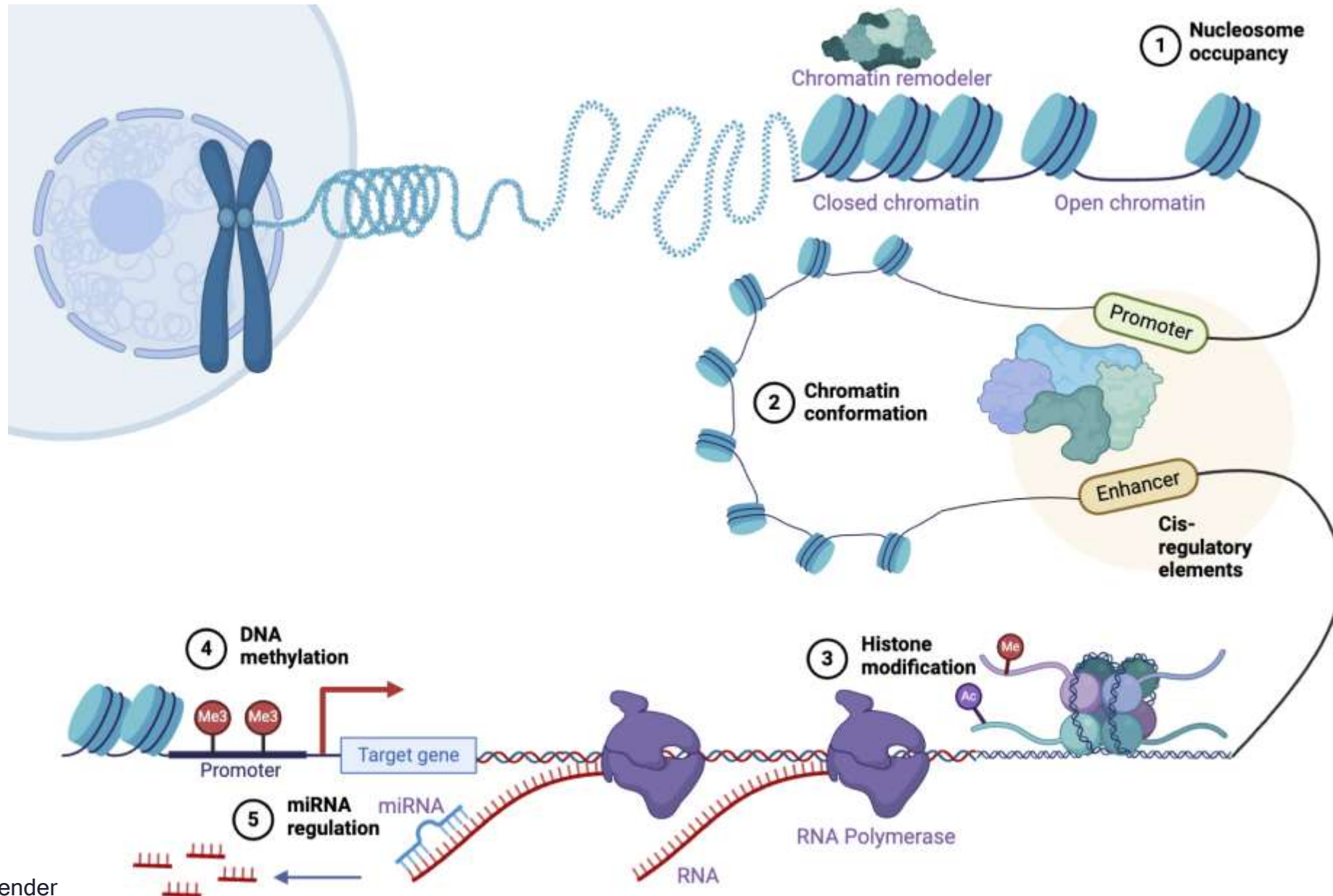
Deepak Tanwar

February 17-19, 2026

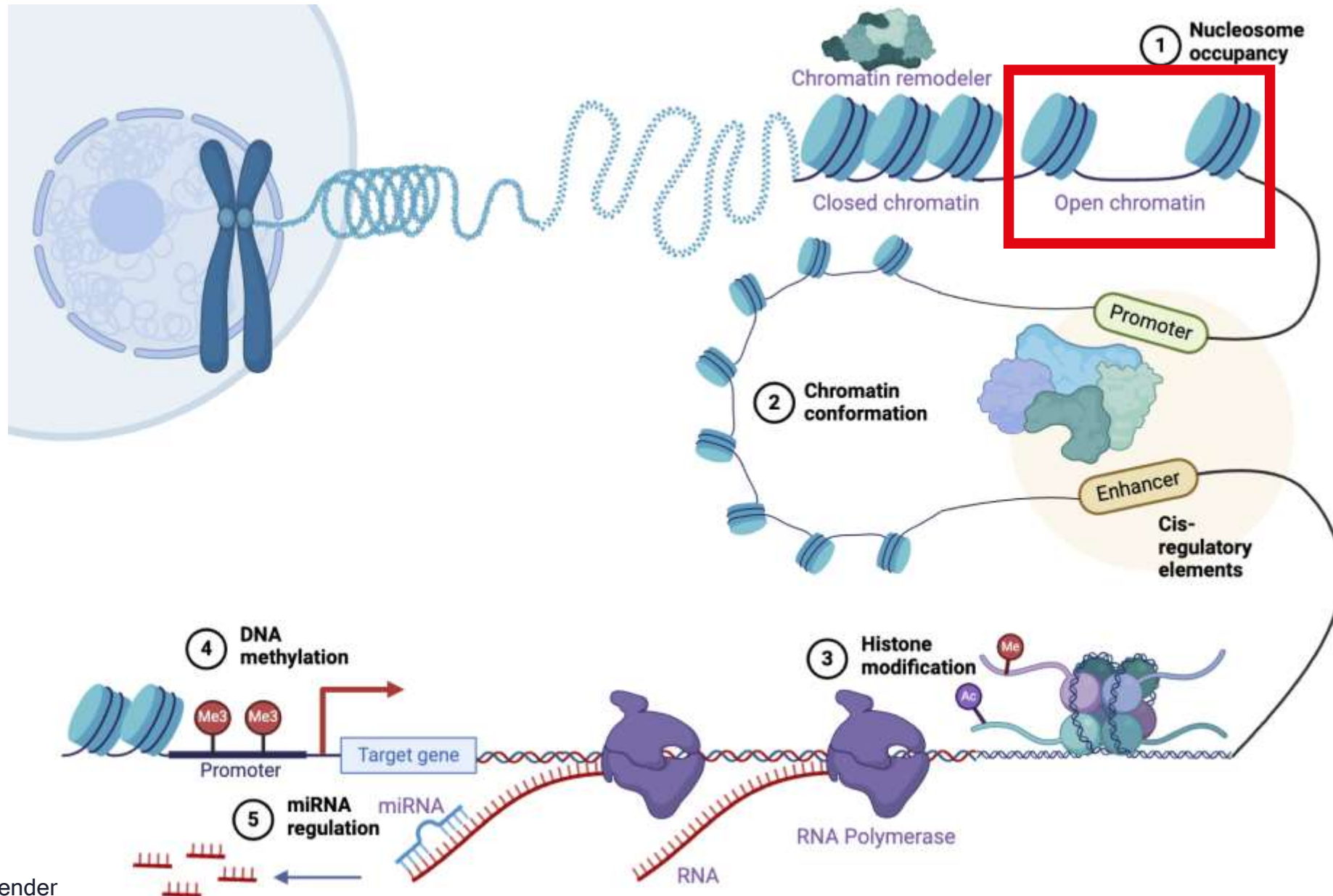
Learning outcomes

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

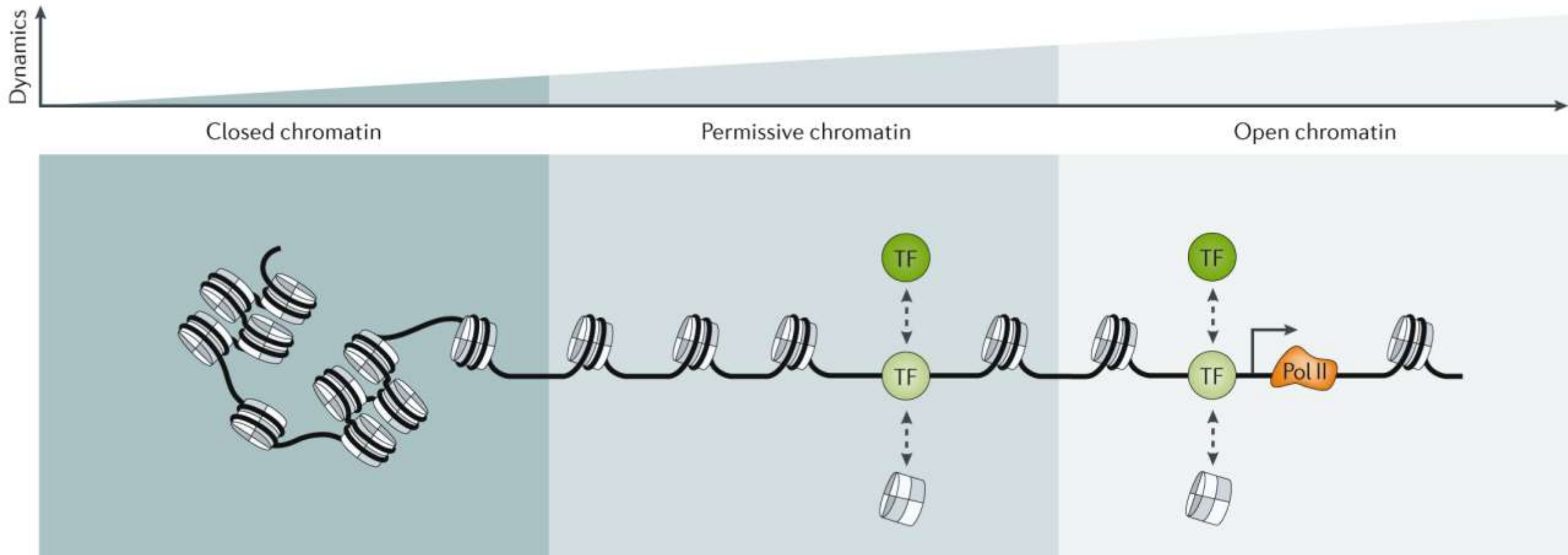
Simplified illustration of transcriptional regulation



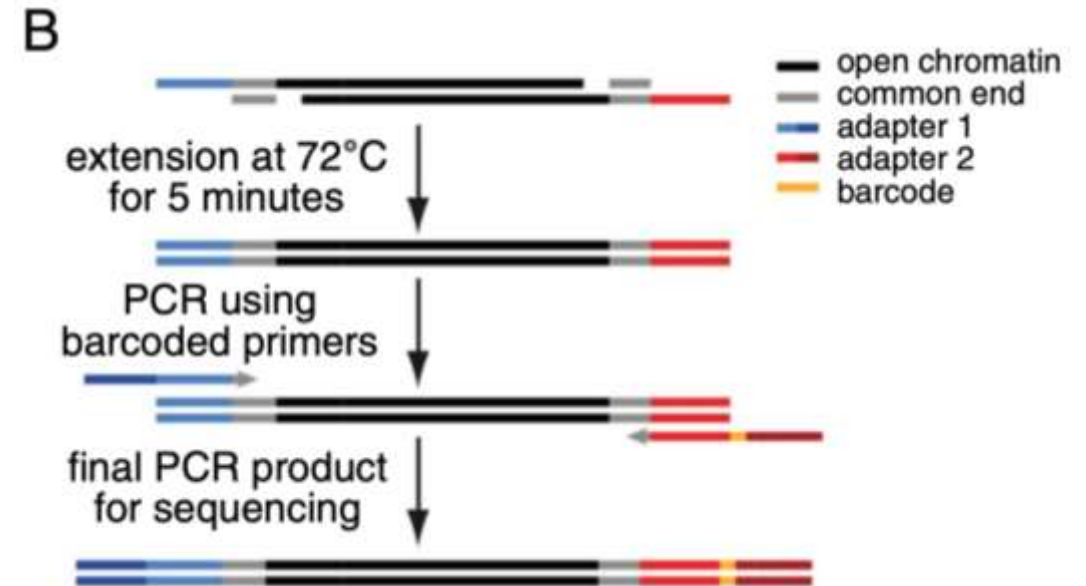
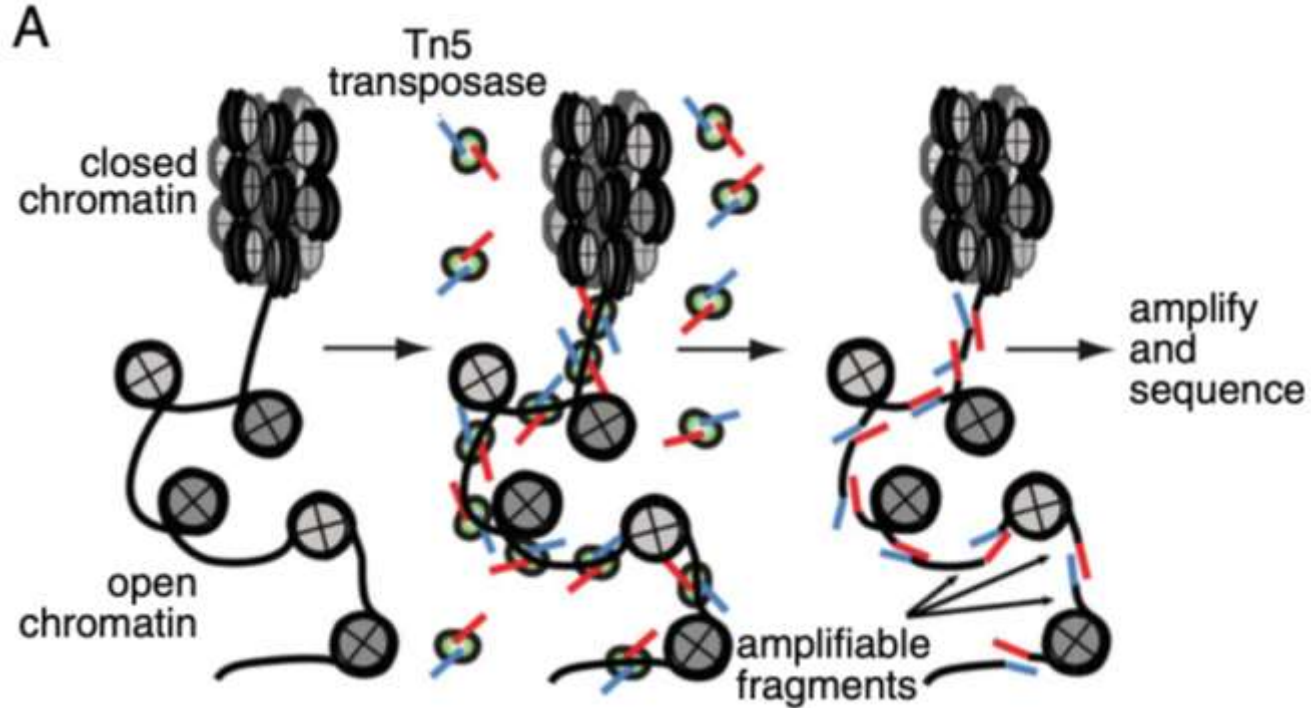
Simplified illustration of transcriptional regulation



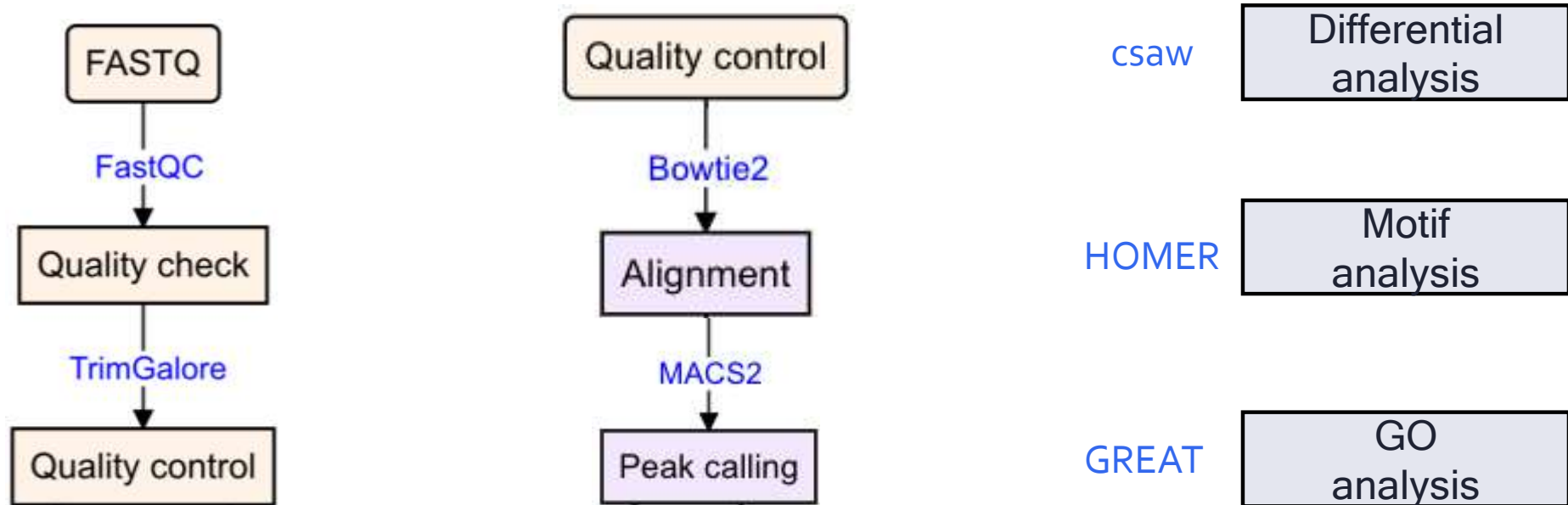
Chromatin accessibility



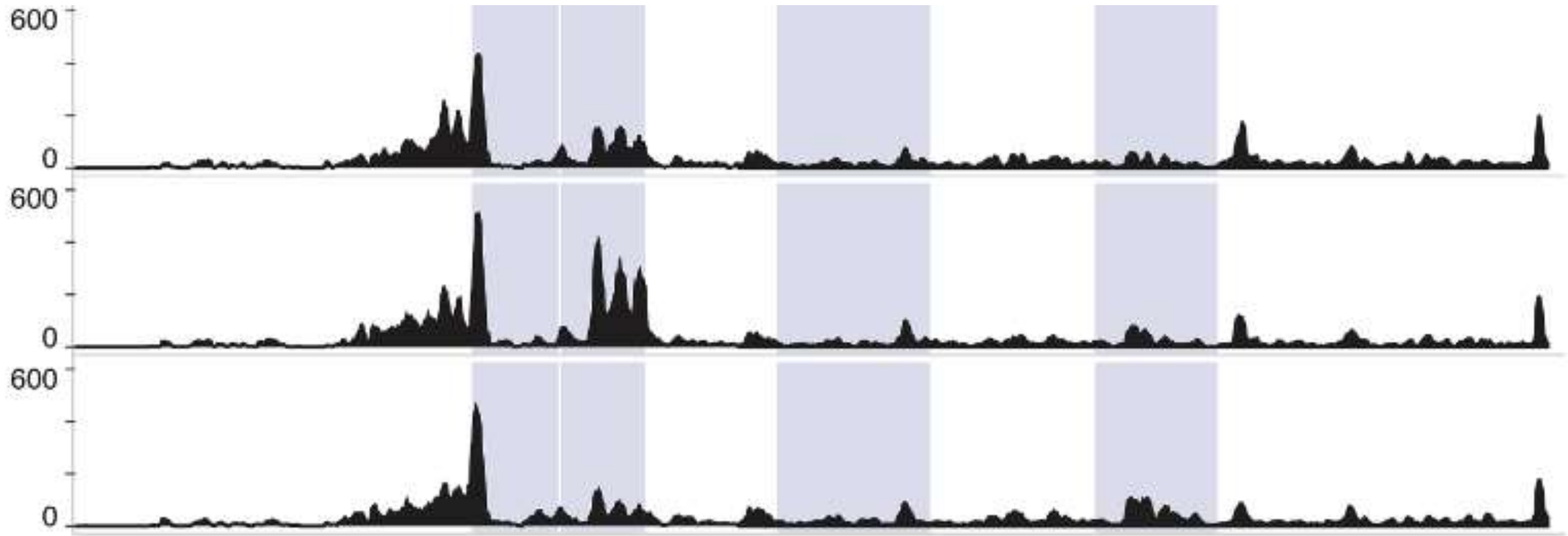
Library preparation for ATAC-seq



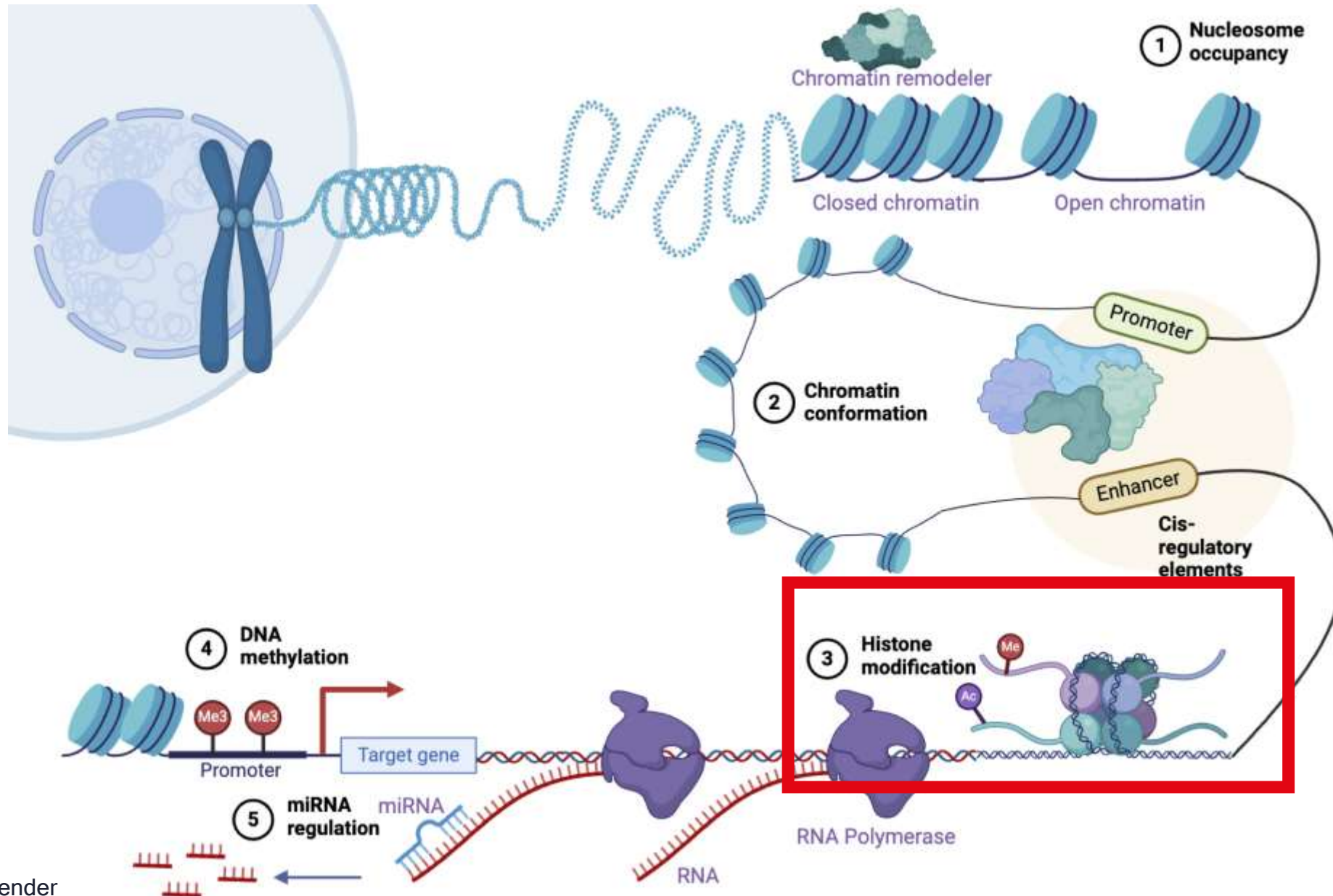
ATAC-seq data analysis pipeline



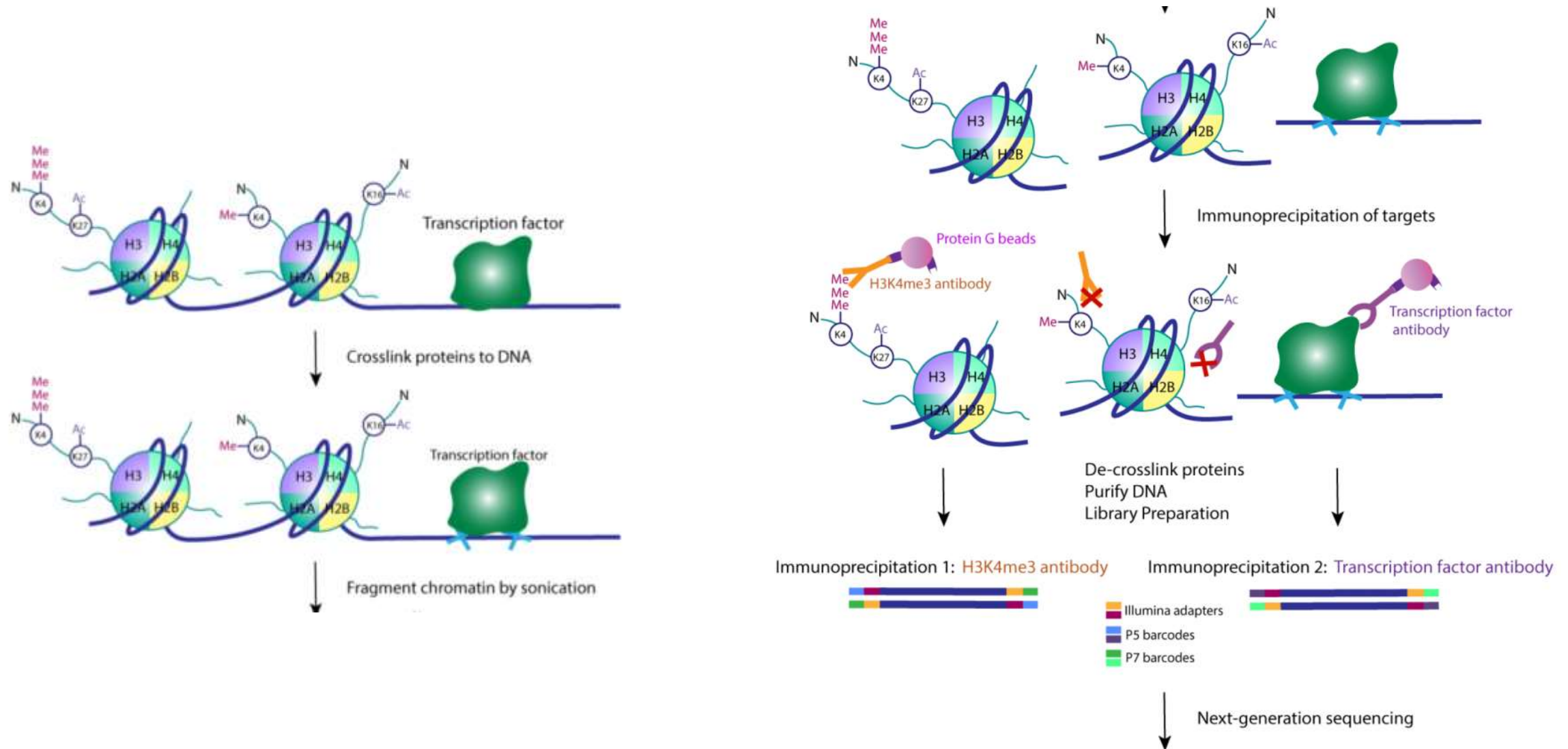
Example snapshot of chromatin accessibility



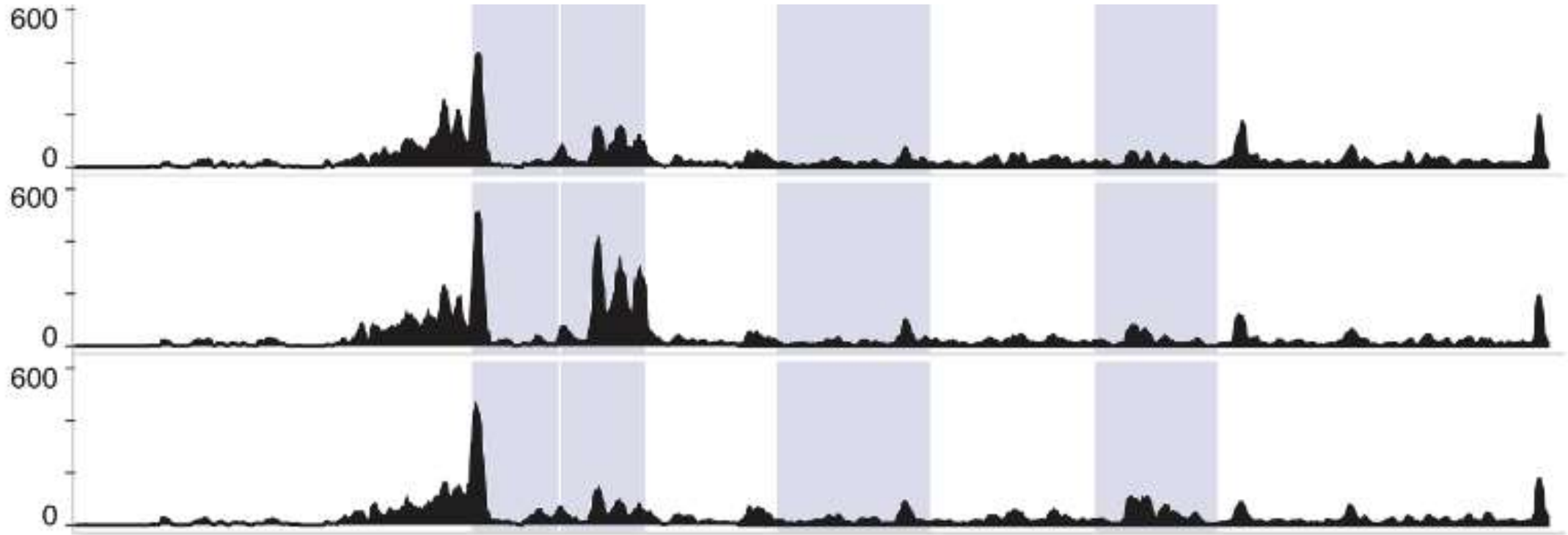
Simplified illustration of transcriptional regulation



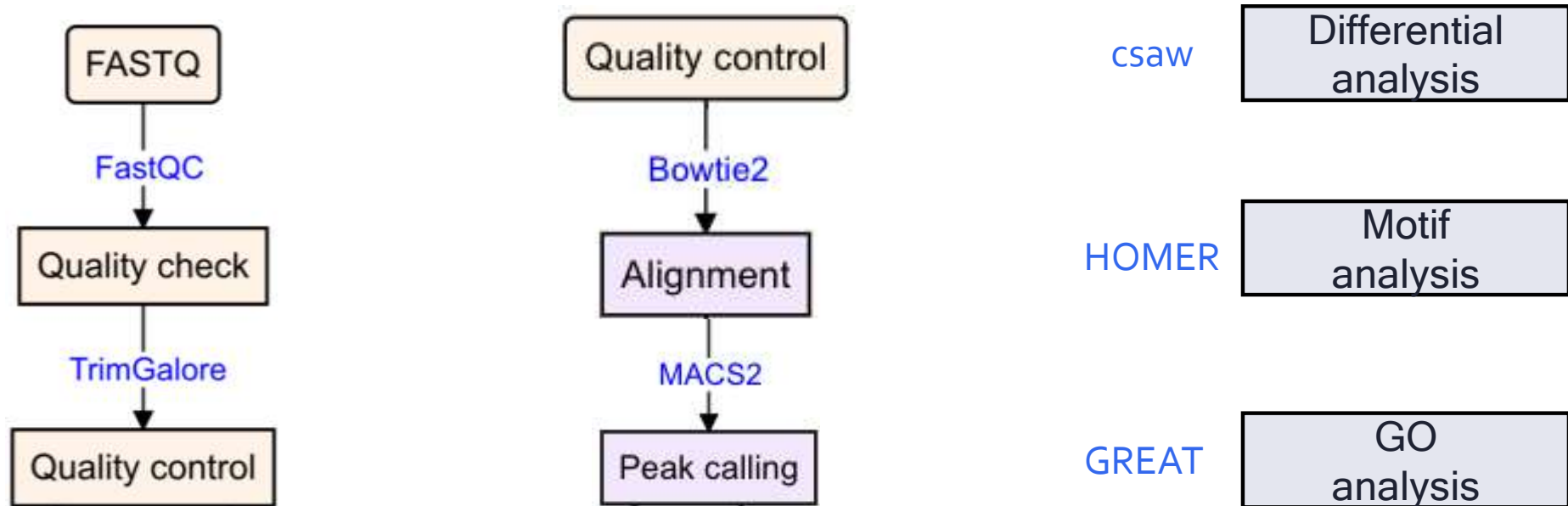
Chromatin Immunoprecipitation sequencing



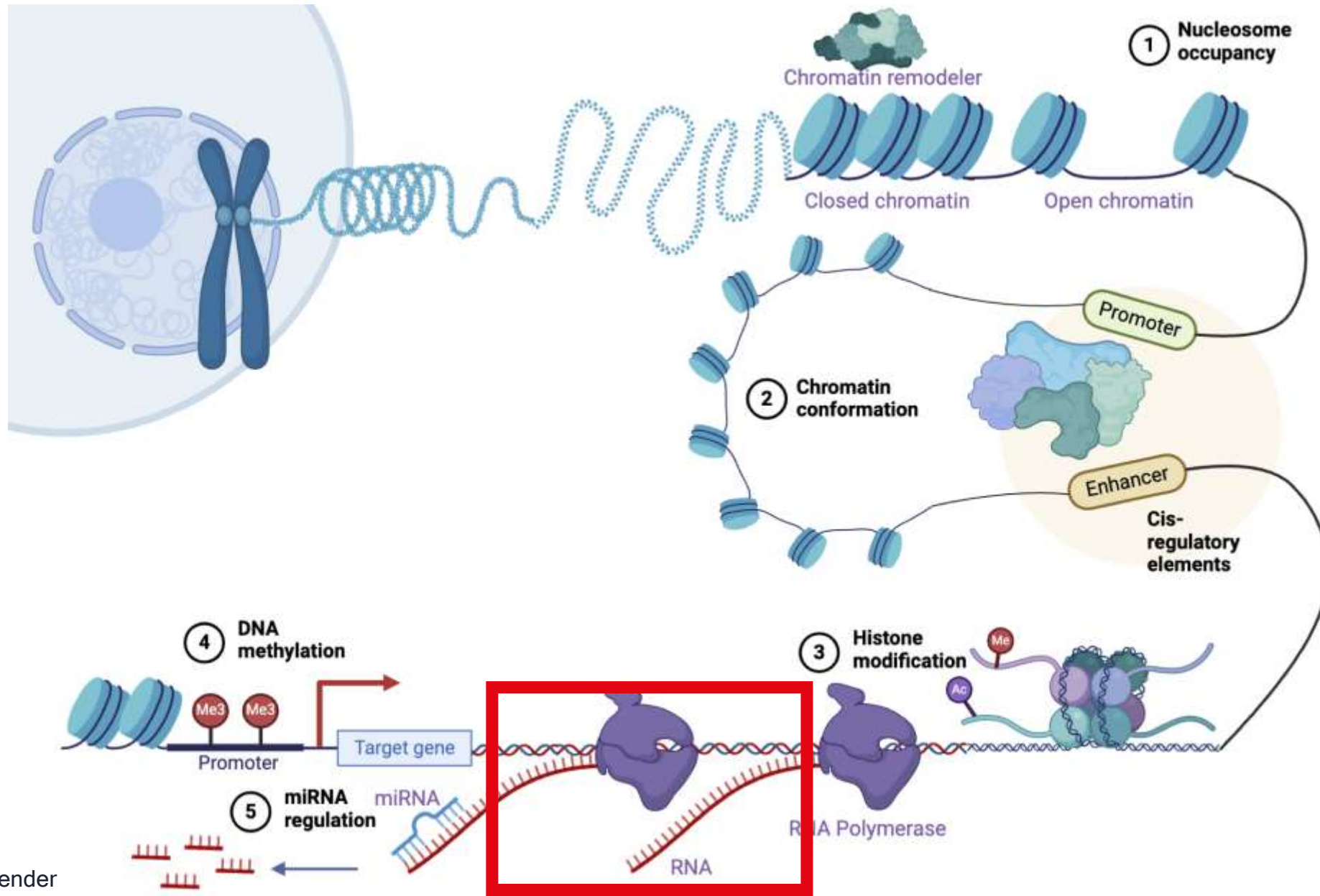
Example snapshot of enrichment



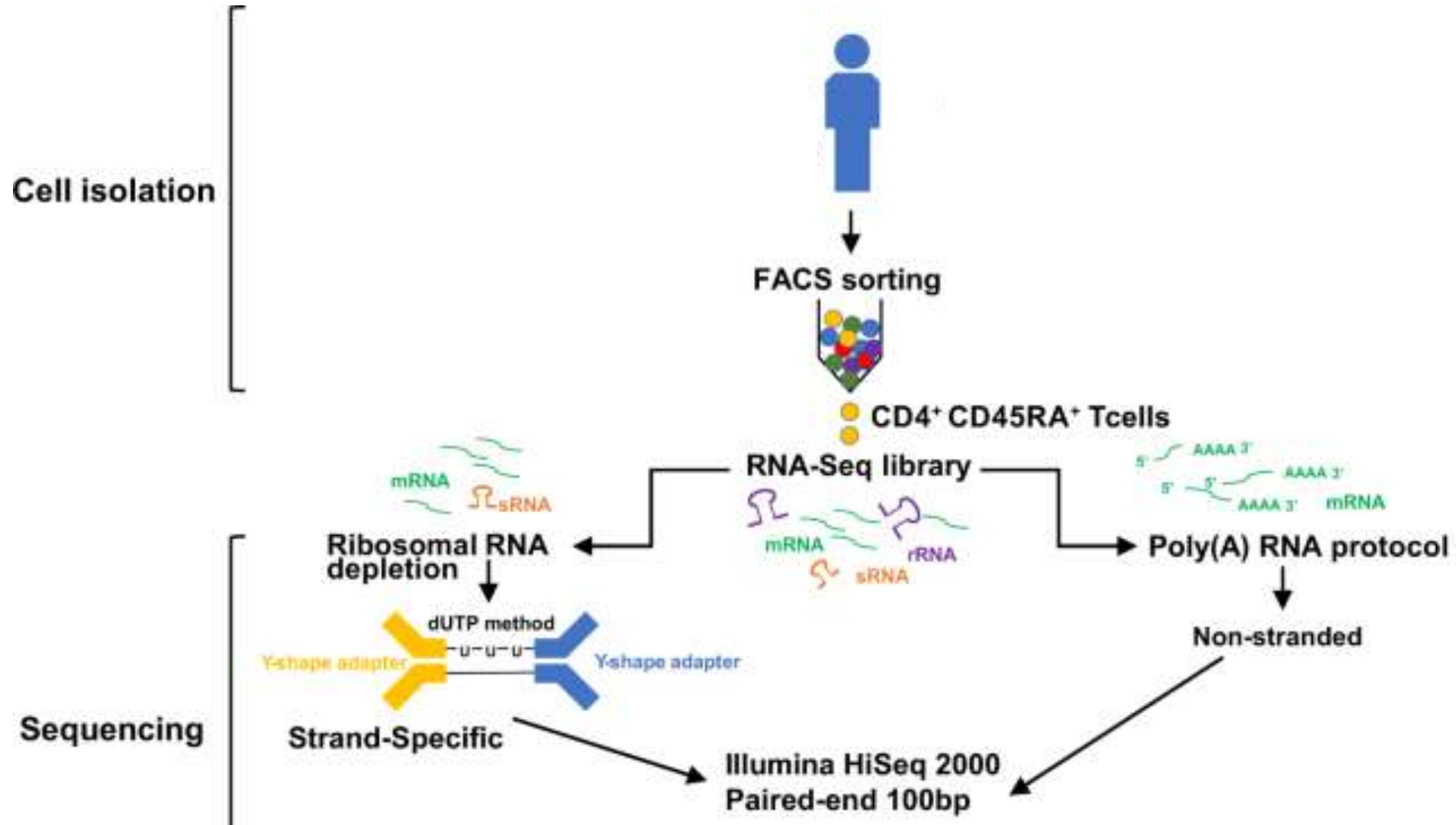
ChIP-seq data analysis pipeline



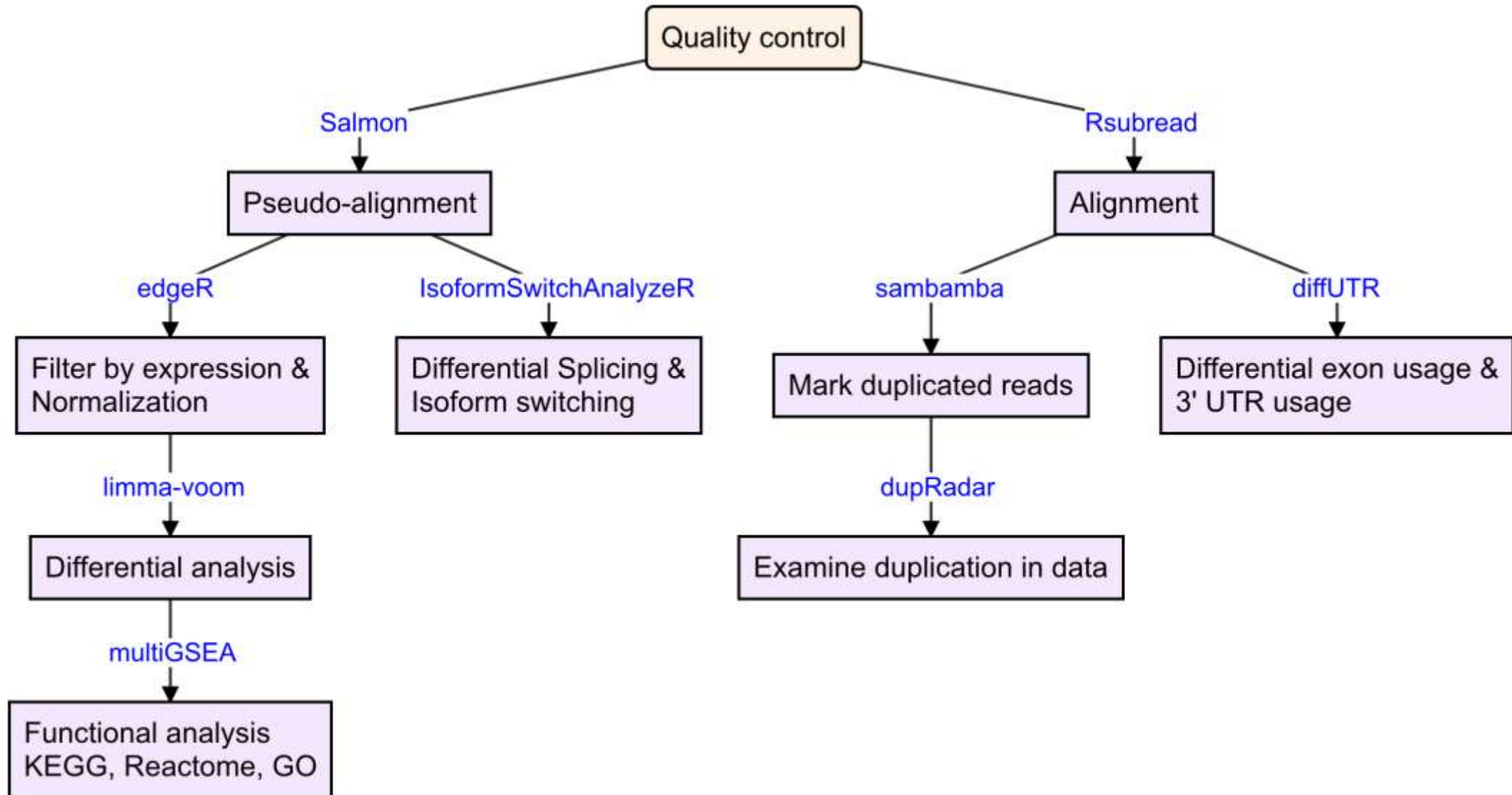
Simplified illustration of transcriptional regulation



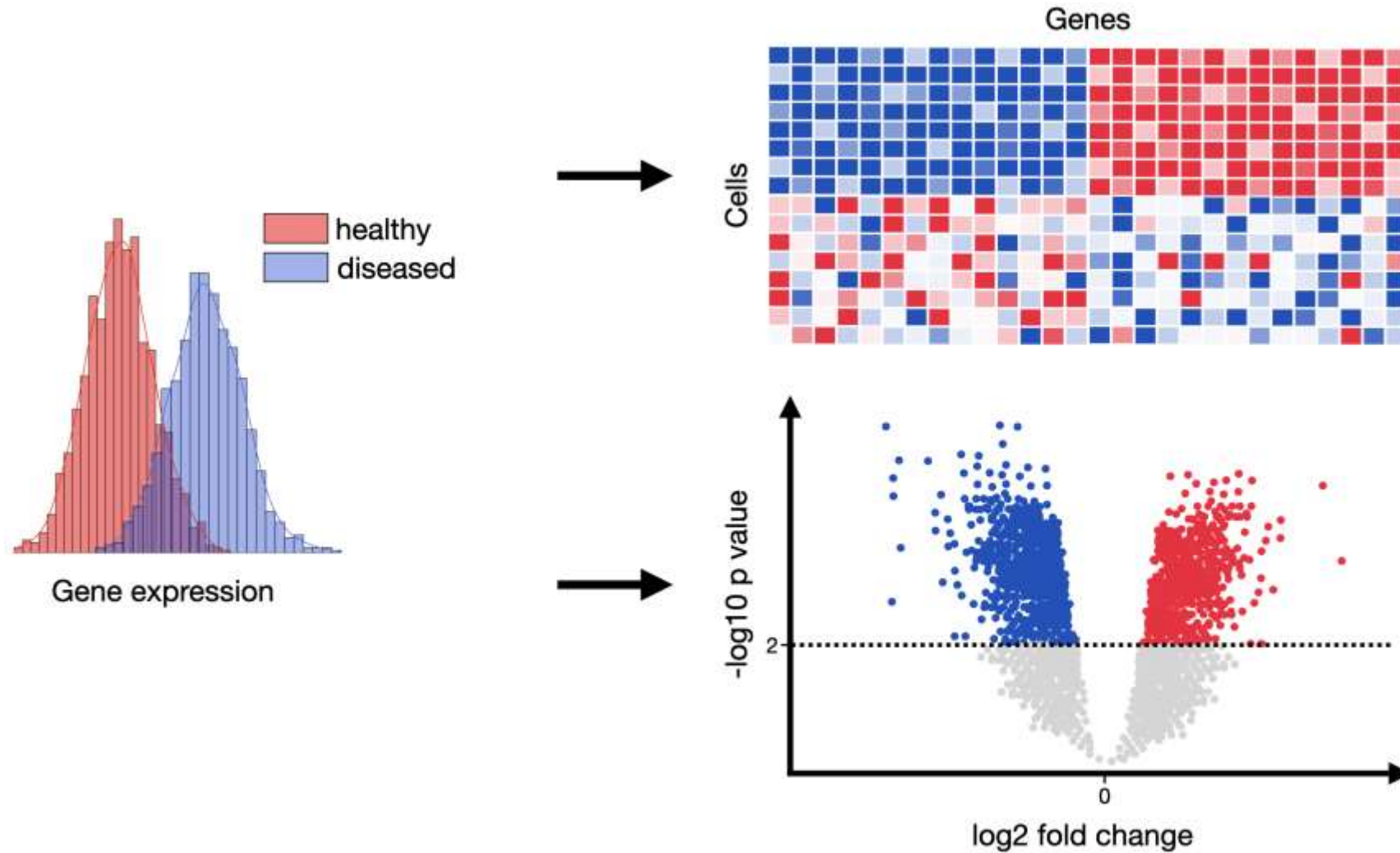
Gene expression



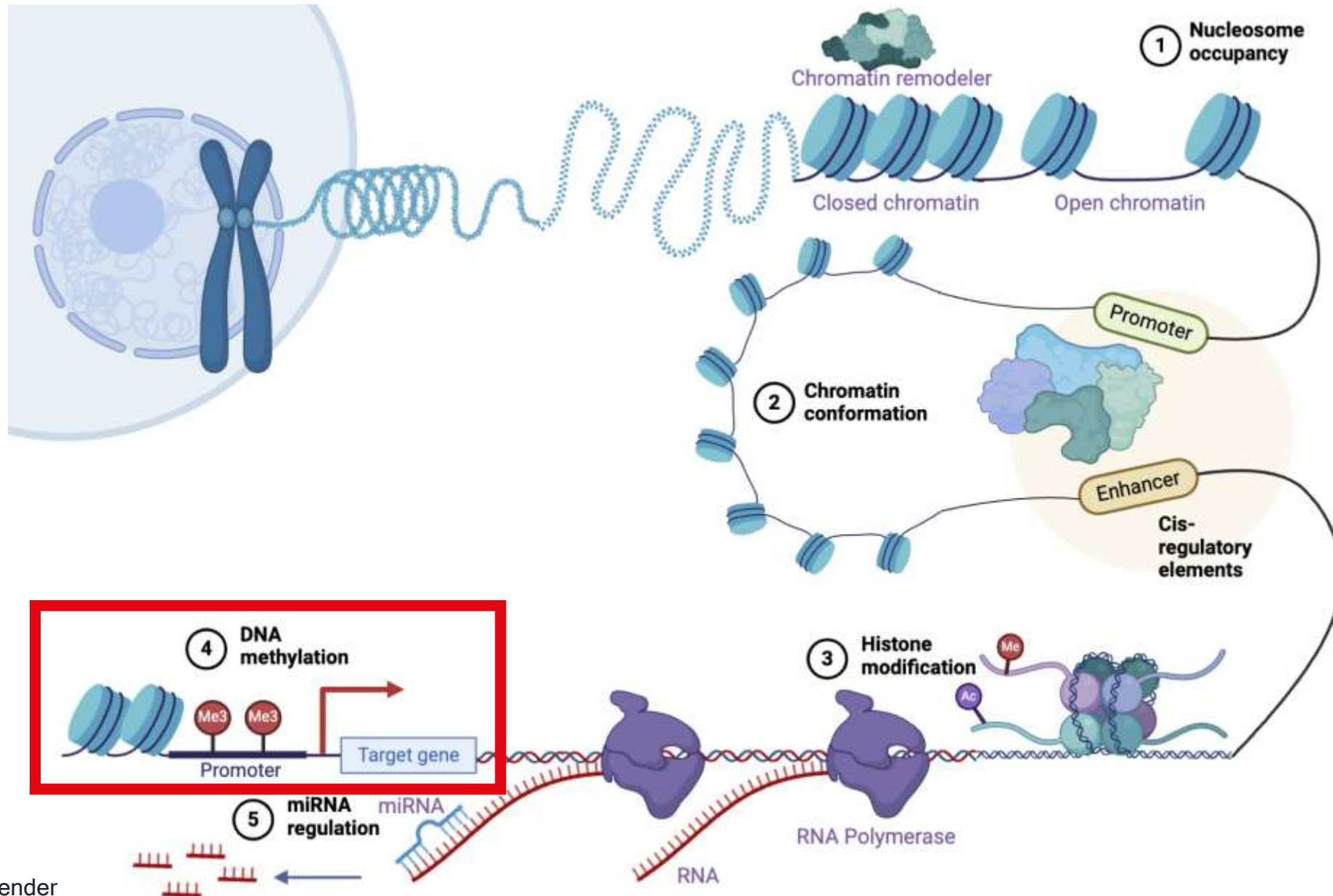
RNA-seq data analysis pipeline



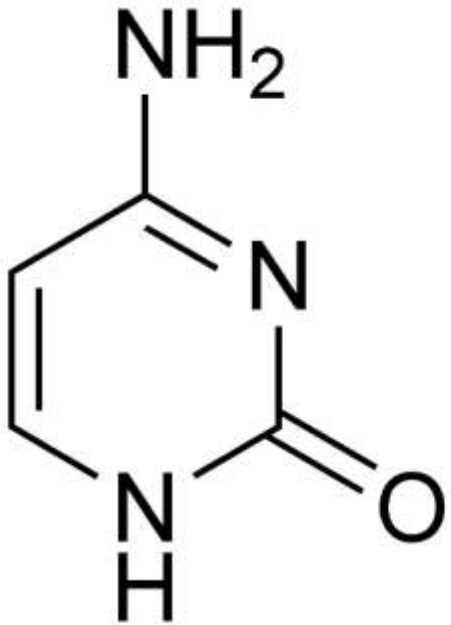
Differences in gene expression



Simplified illustration of transcriptional regulation



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

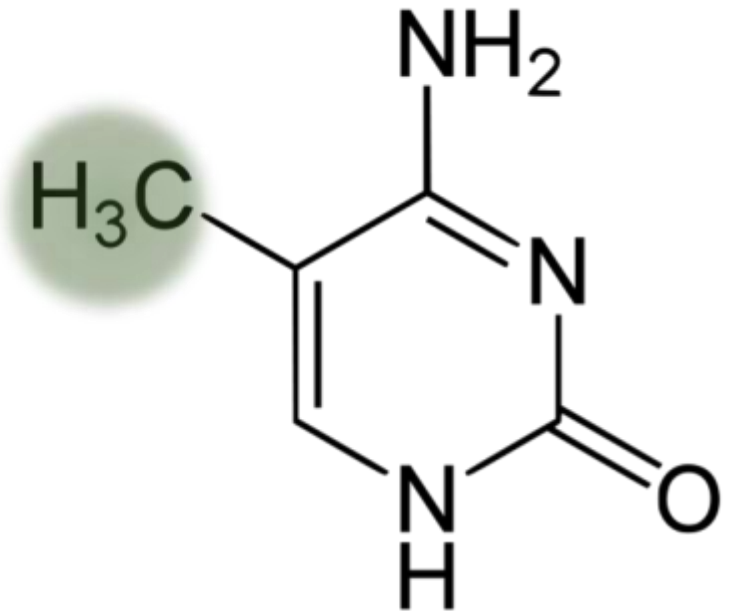


Cytosine

DNA methyl-transferases

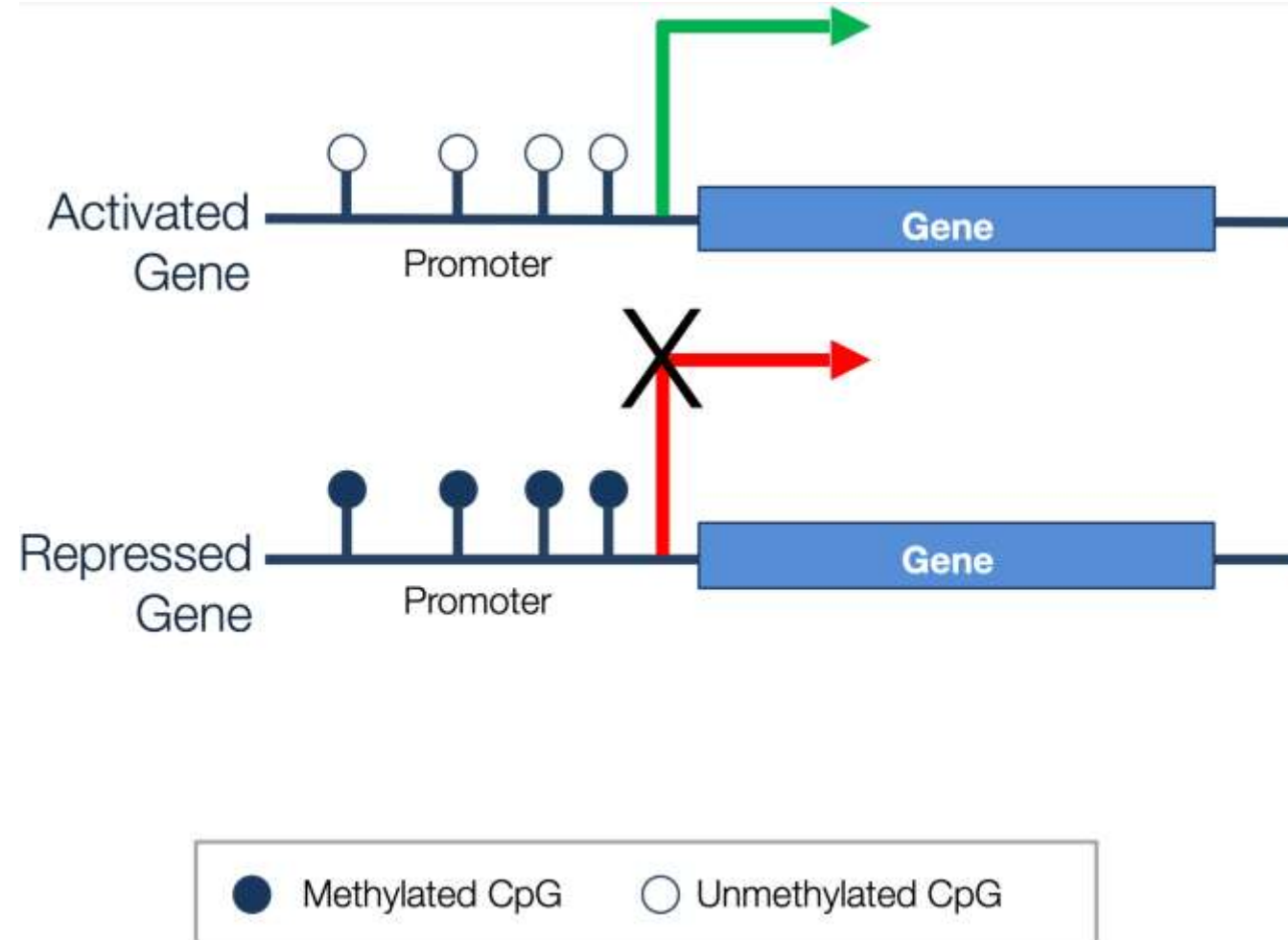


DNA-demethylase(s)
TET enzymes
Passive demethylation

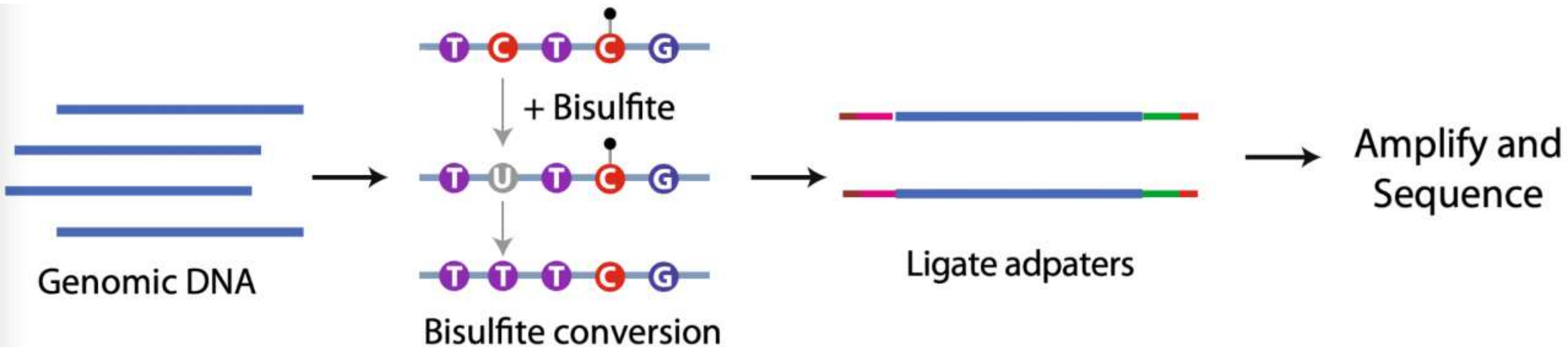


5-methyl Cytosine

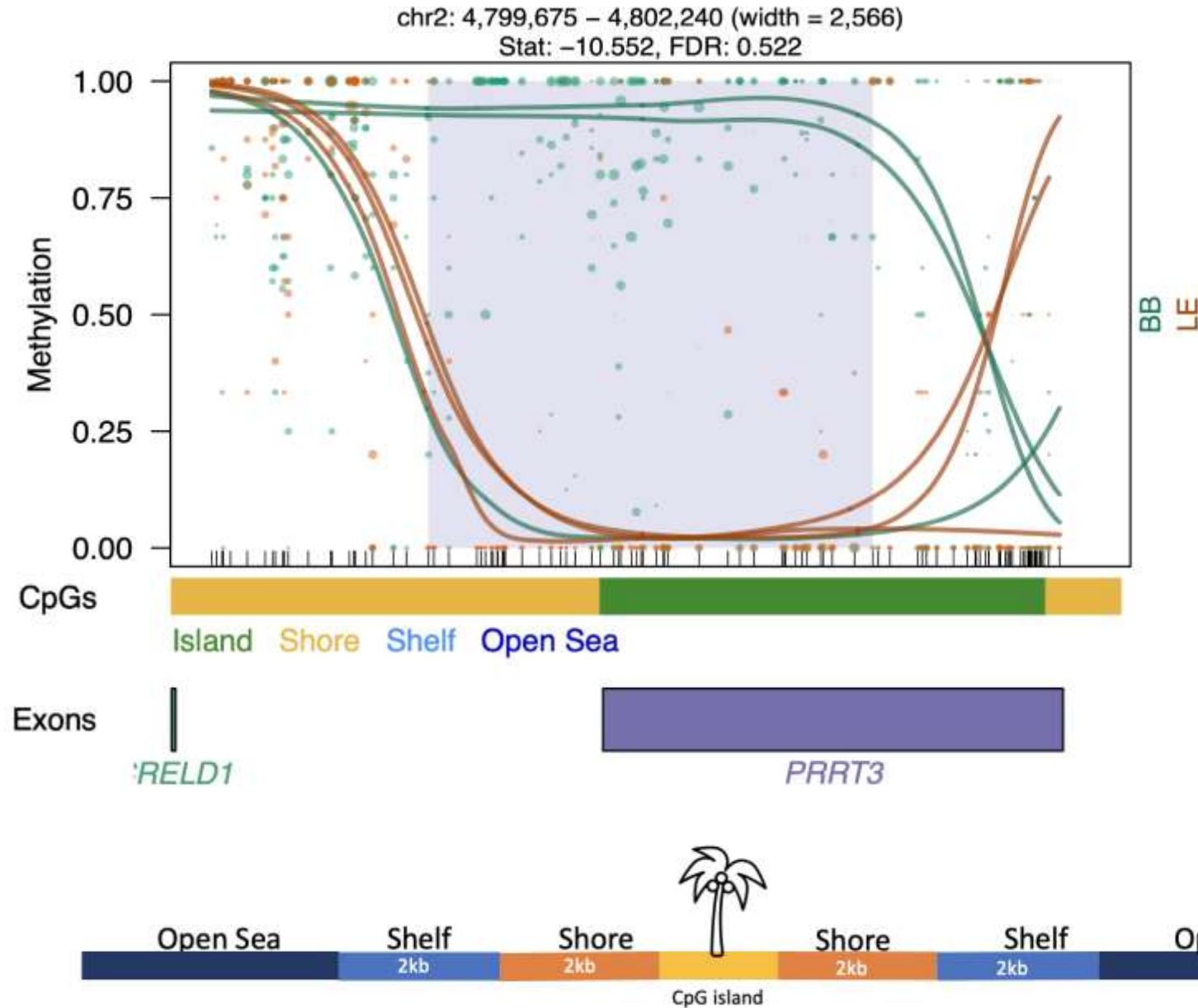
Role of DNA methylation in transcriptional regulation



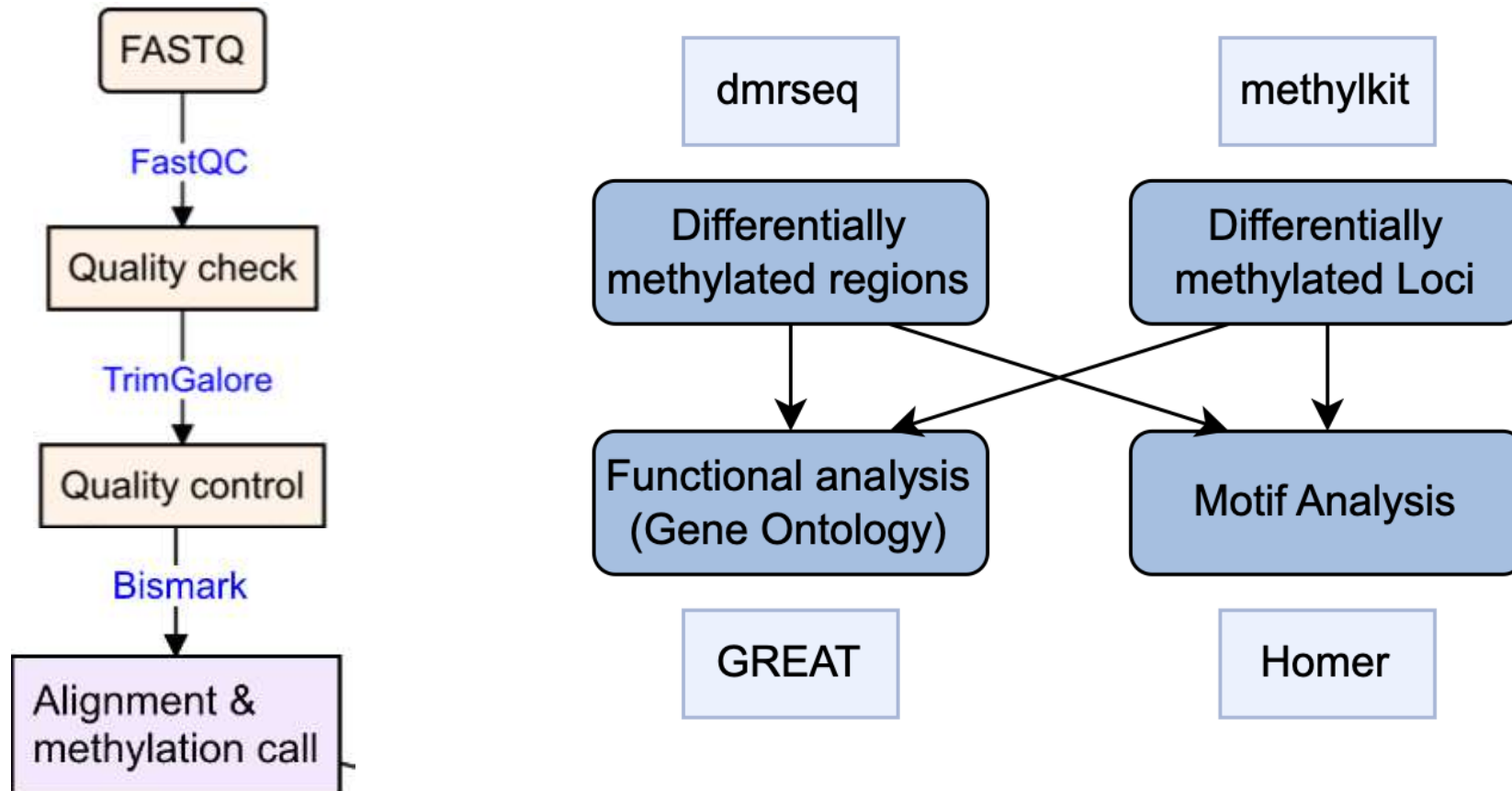
Gold standard to study DNA methylation patterns across the genome: WGBS



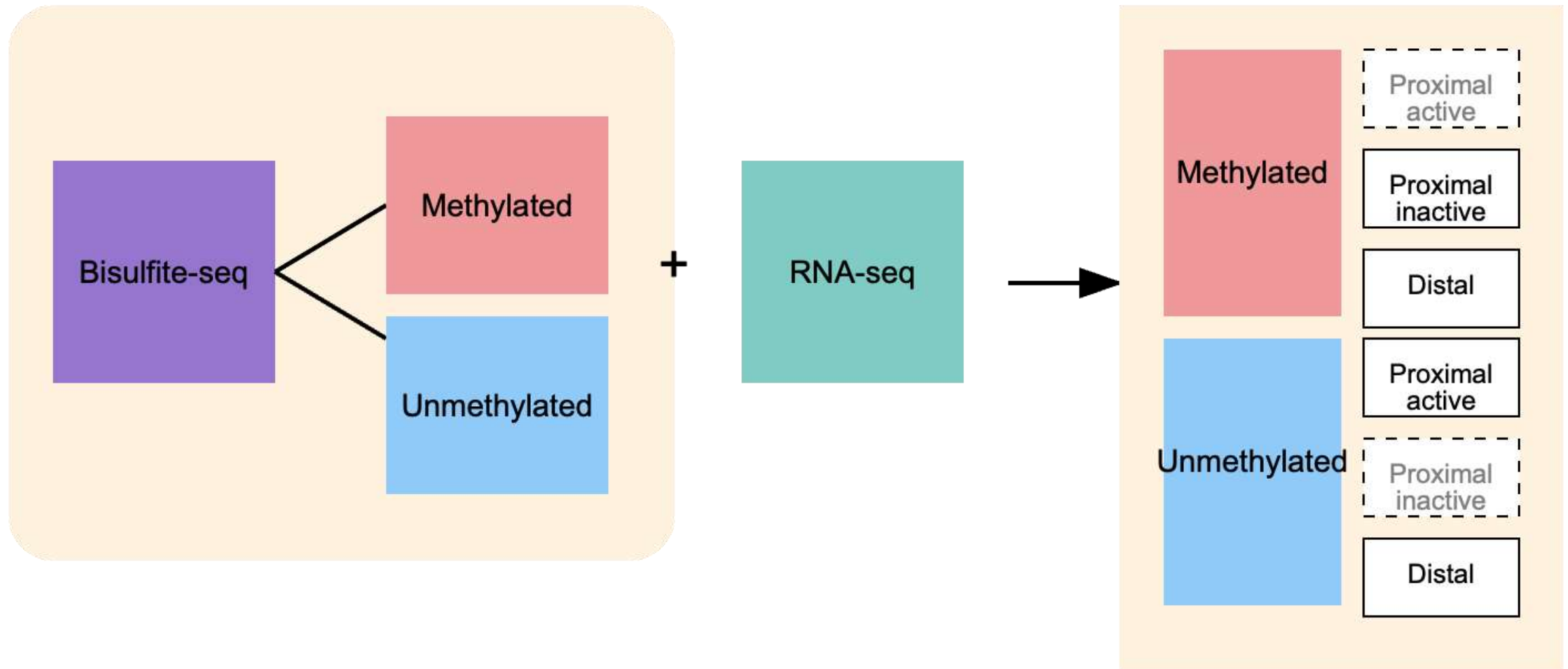
Example plot for DNA methylation



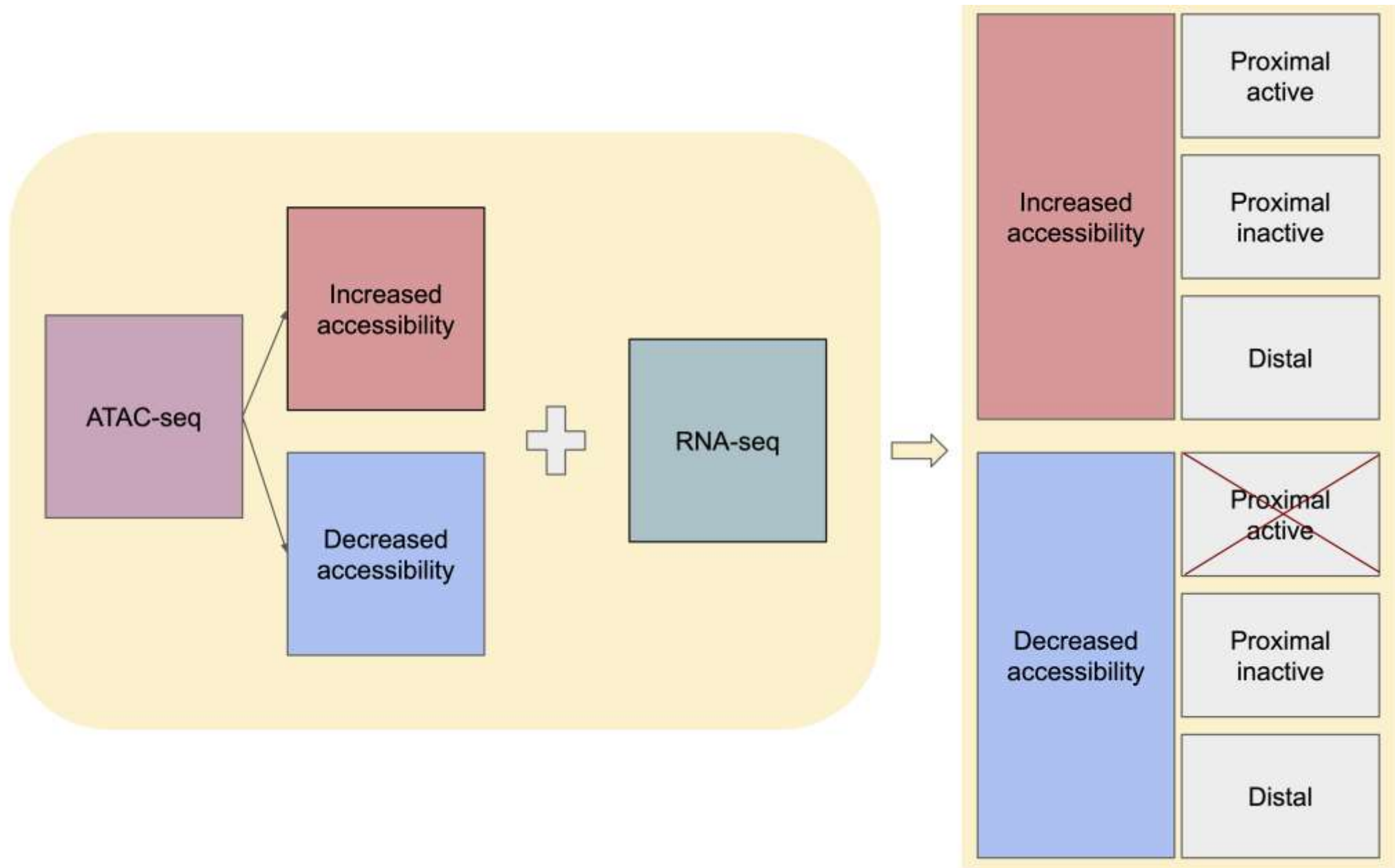
DNAme data analysis pipeline



Integration of RNA-seq and WGBS

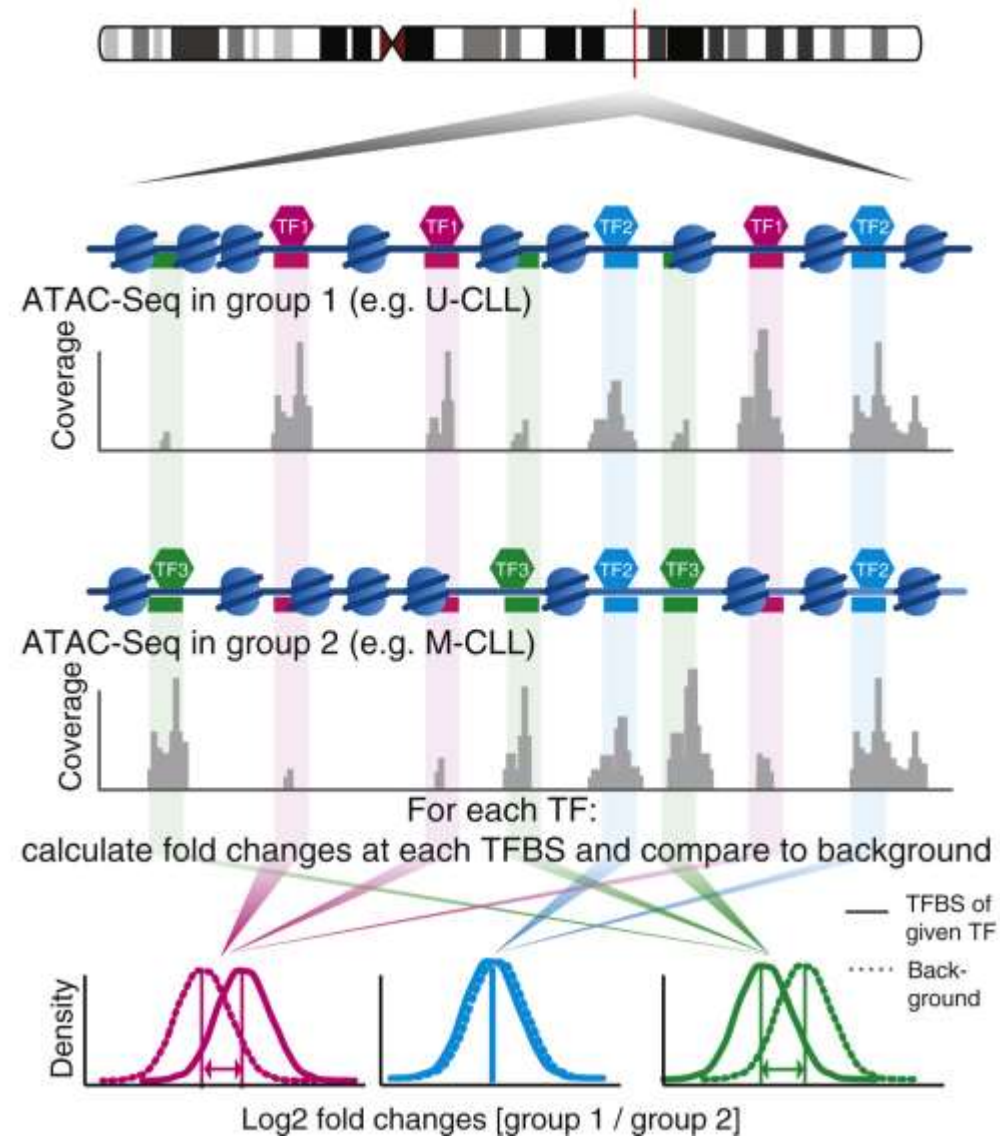


Integration of RNA-seq and ATAC-seq

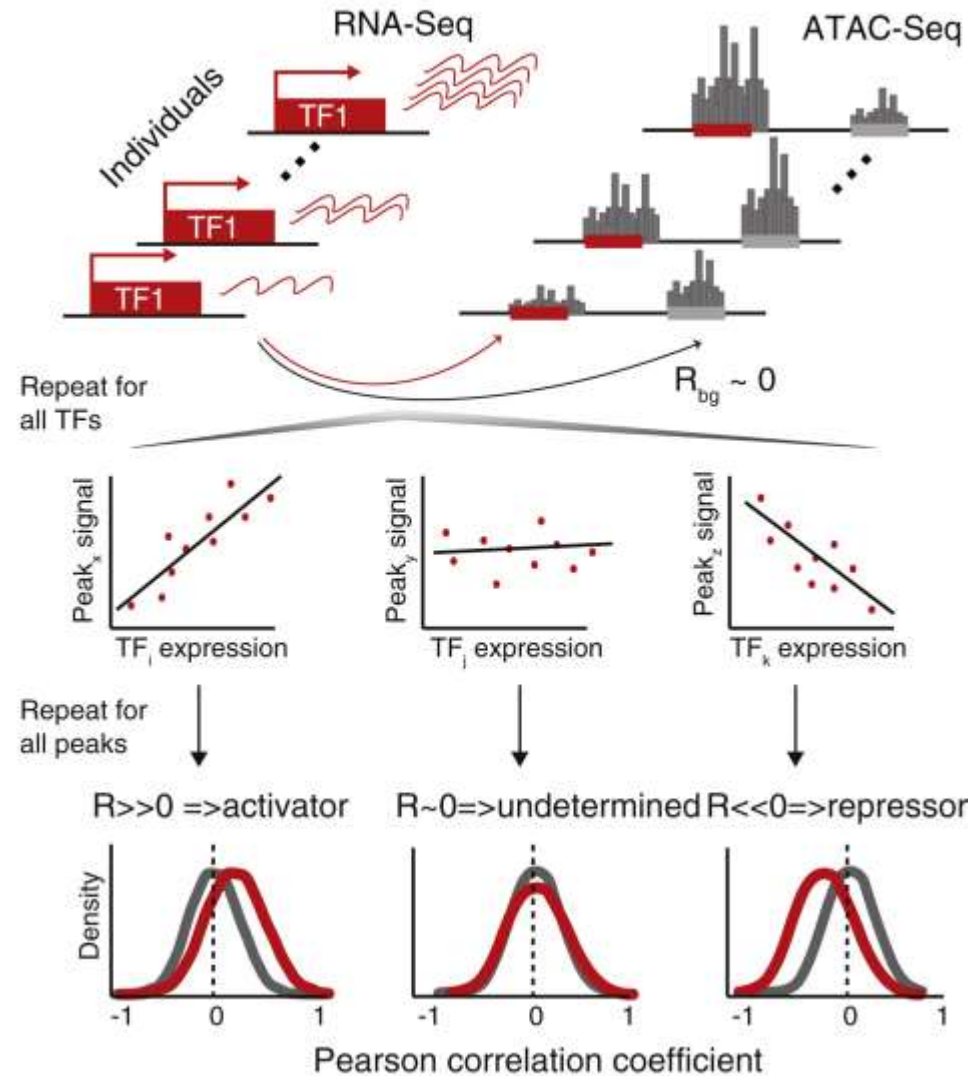


Integration of RNA-seq and ATAC-seq: diffTF

A Schematic of diffTF - basic mode



B Schematic of diffTF - classification mode



Multi-omics integration overview

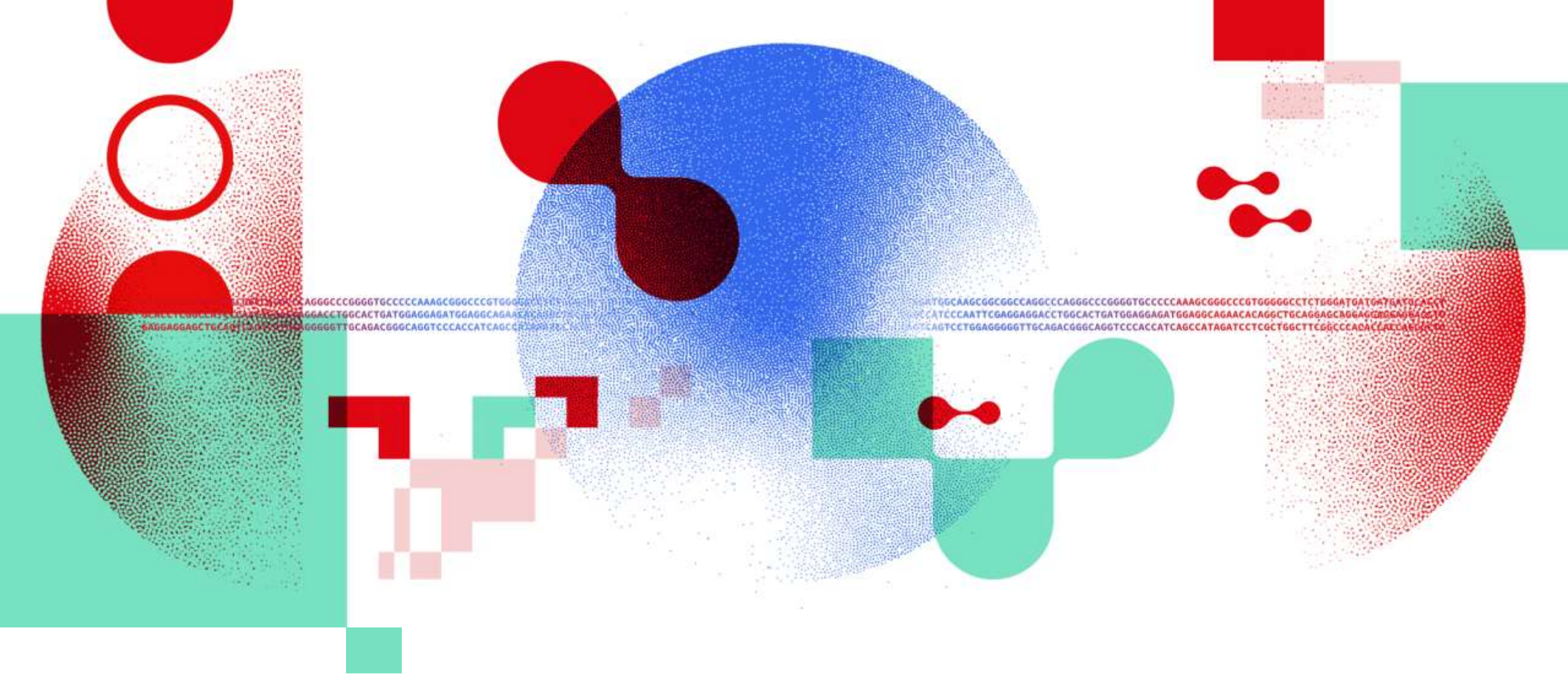
Feature	Systematic Approaches	Ad-hoc Approaches
Definition	Algorithmic frameworks for integrating multiple omics datasets using statistical or machine learning models.	Custom, hypothesis-driven integration of 1–2 omics datasets based on specific biological questions.
Tools	<ul style="list-style-type: none">- mixOmics, DIABLO- MOFA- MINT- sGCCA	<ul style="list-style-type: none">- diffTF- Custom R/Python scripts
Supervision	Supervised, unsupervised, or semi-supervised	Typically unsupervised or guided by prior biological knowledge
Omics Types	Multiple omics datasets (≥ 2), can be diverse (transcriptomics, epigenomics, proteomics, etc.)	Usually 2 omics types (e.g., RNA-seq + ATAC-seq)
Advantages	<ul style="list-style-type: none">- Scalable and reproducible- Handles complex data- Reveals hidden patterns- Supports biomarker discovery	<ul style="list-style-type: none">- 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

DATA SCIENTISTS FOR LIFE

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