



Swiss Institute of
Bioinformatics

BIOLOGY-INFORMED MULTIOMICS DATA INTEGRATION AND
VISUALIZATION

Multi-omics data

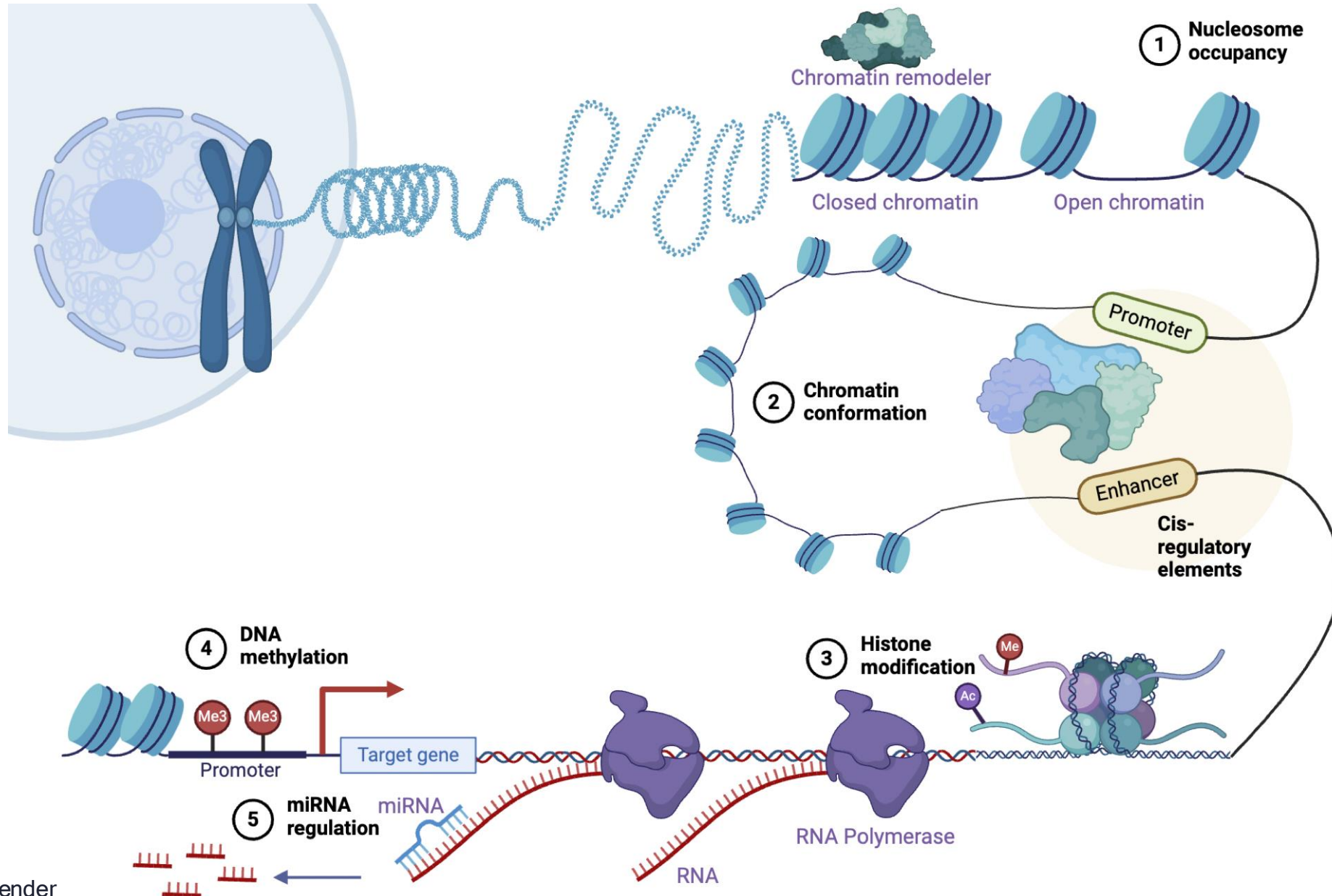
Deepak Tanwar

June 16-17, 2025

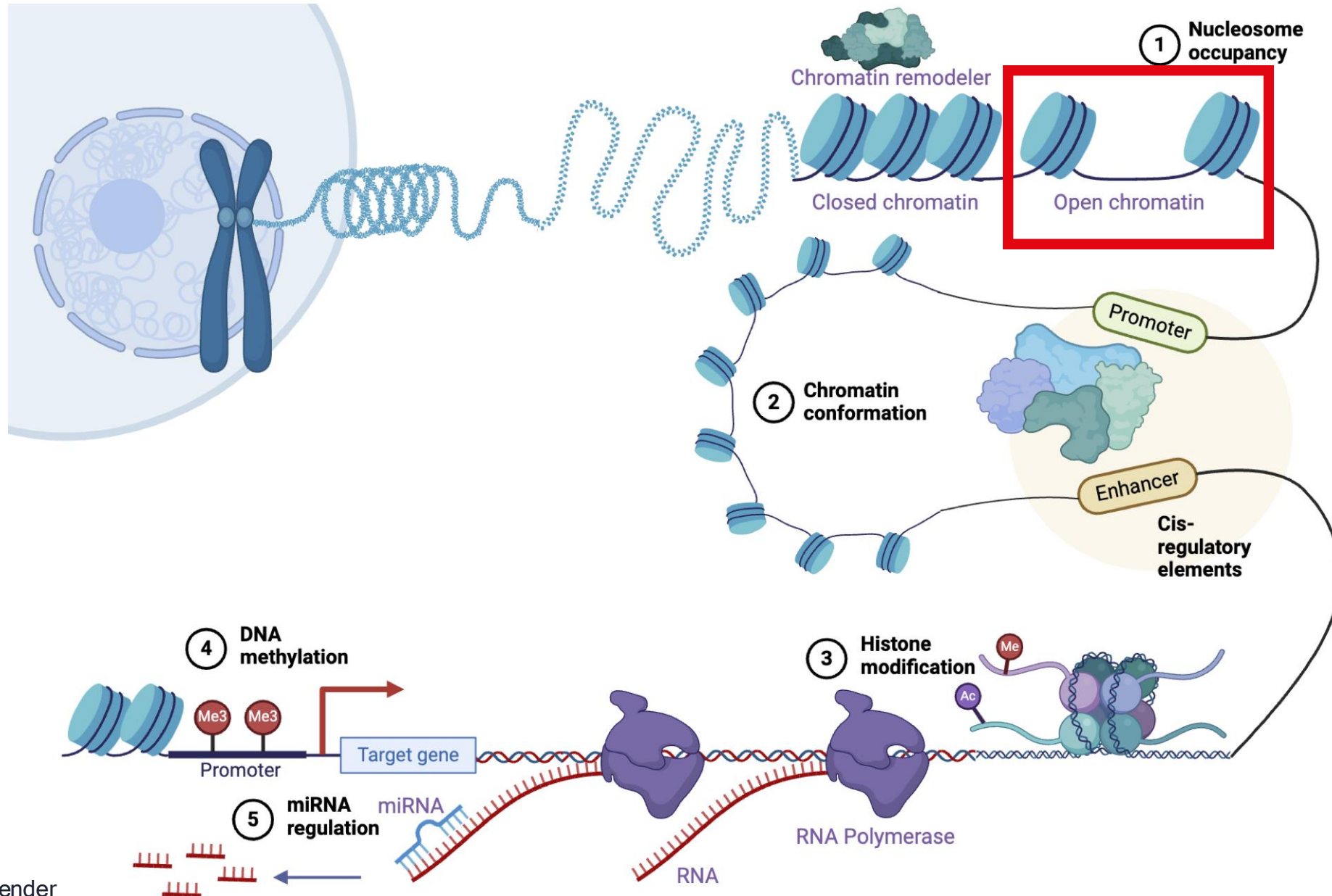
Learning outcomes

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

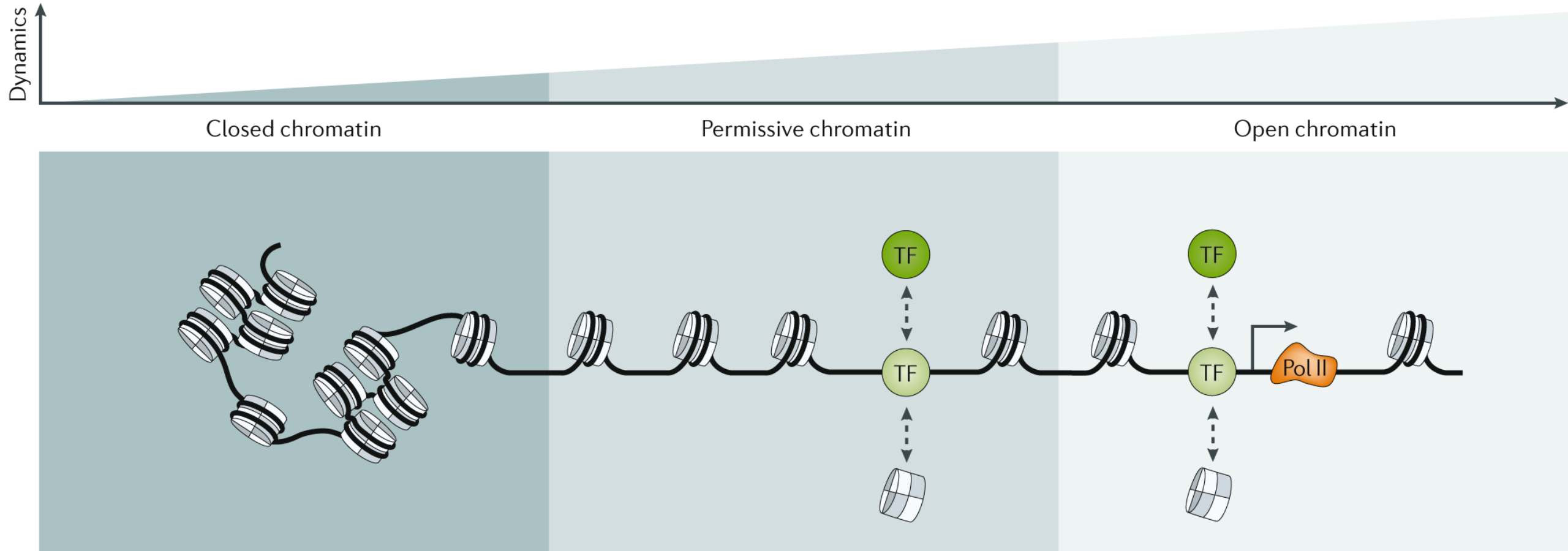
Simplified illustration of transcriptional regulation



Simplified illustration of transcriptional regulation

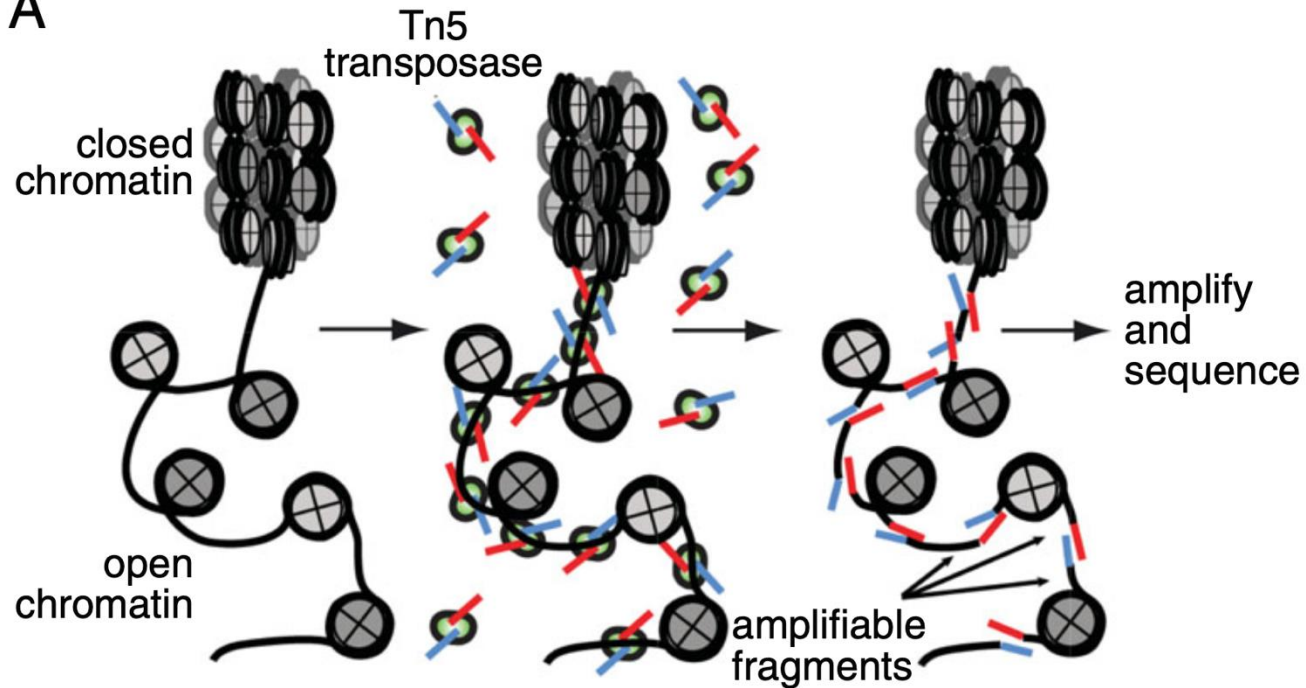


Chromatin accessibility

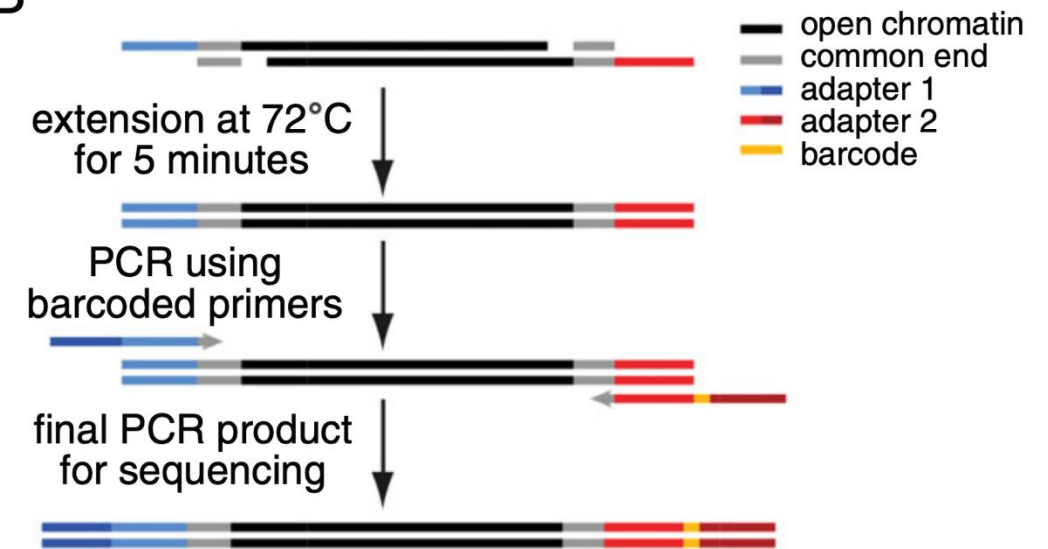


Library preparation for ATAC-seq

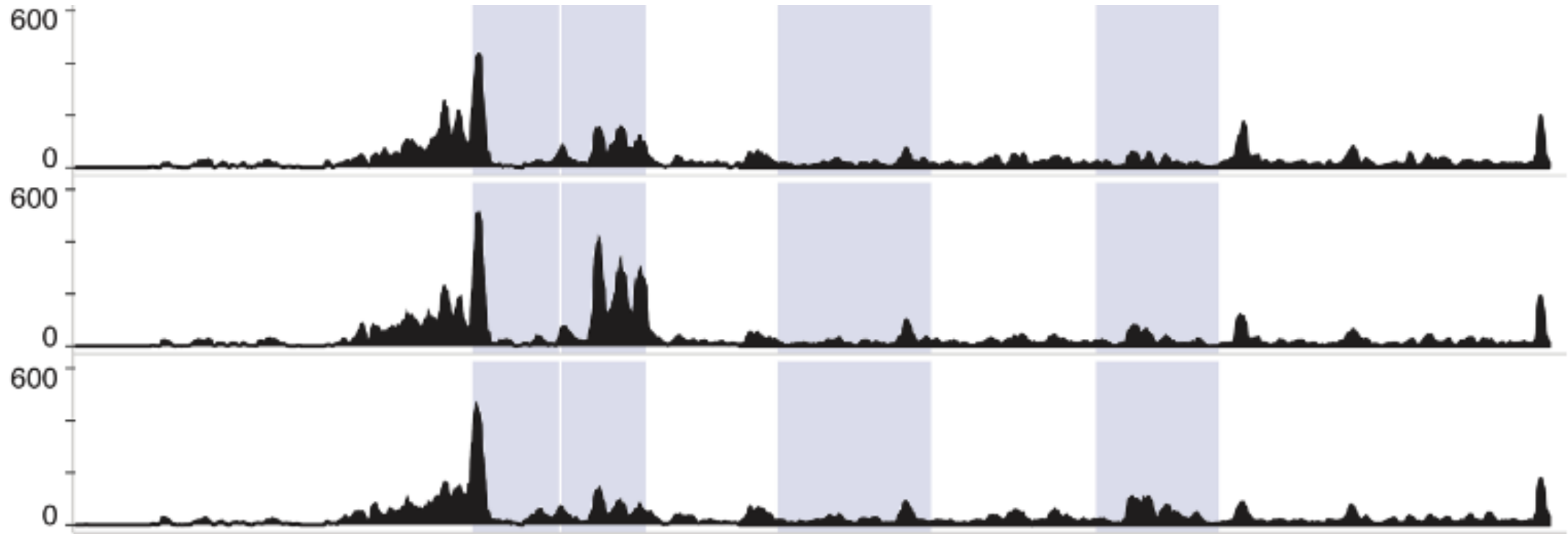
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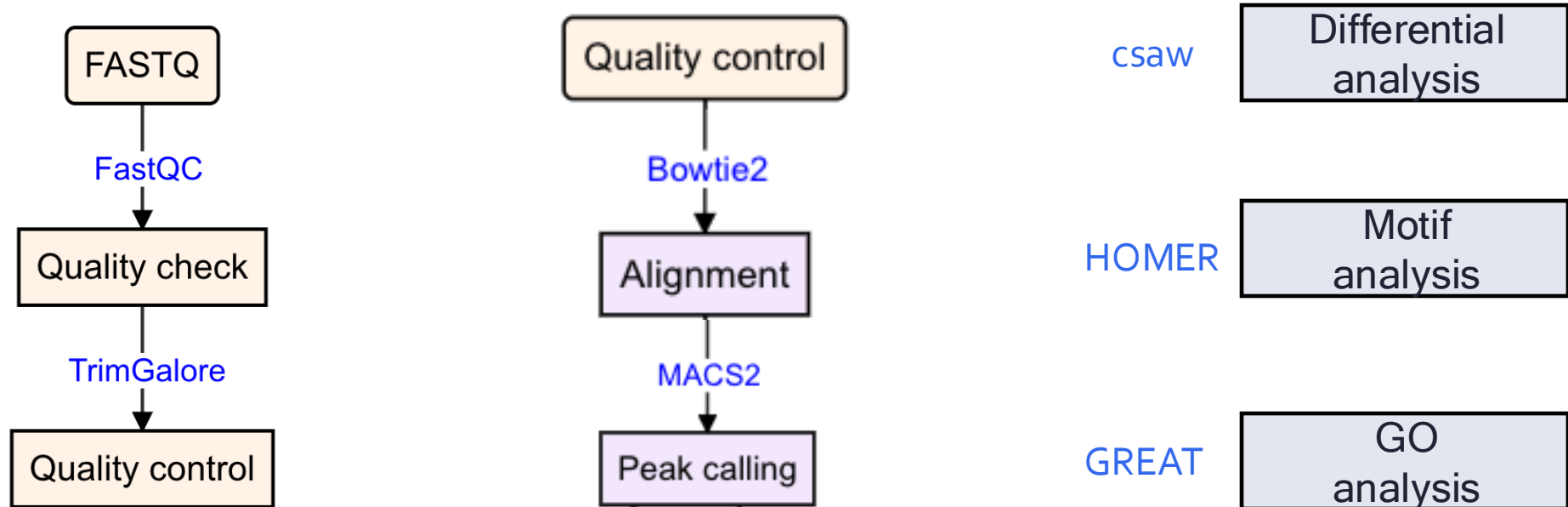
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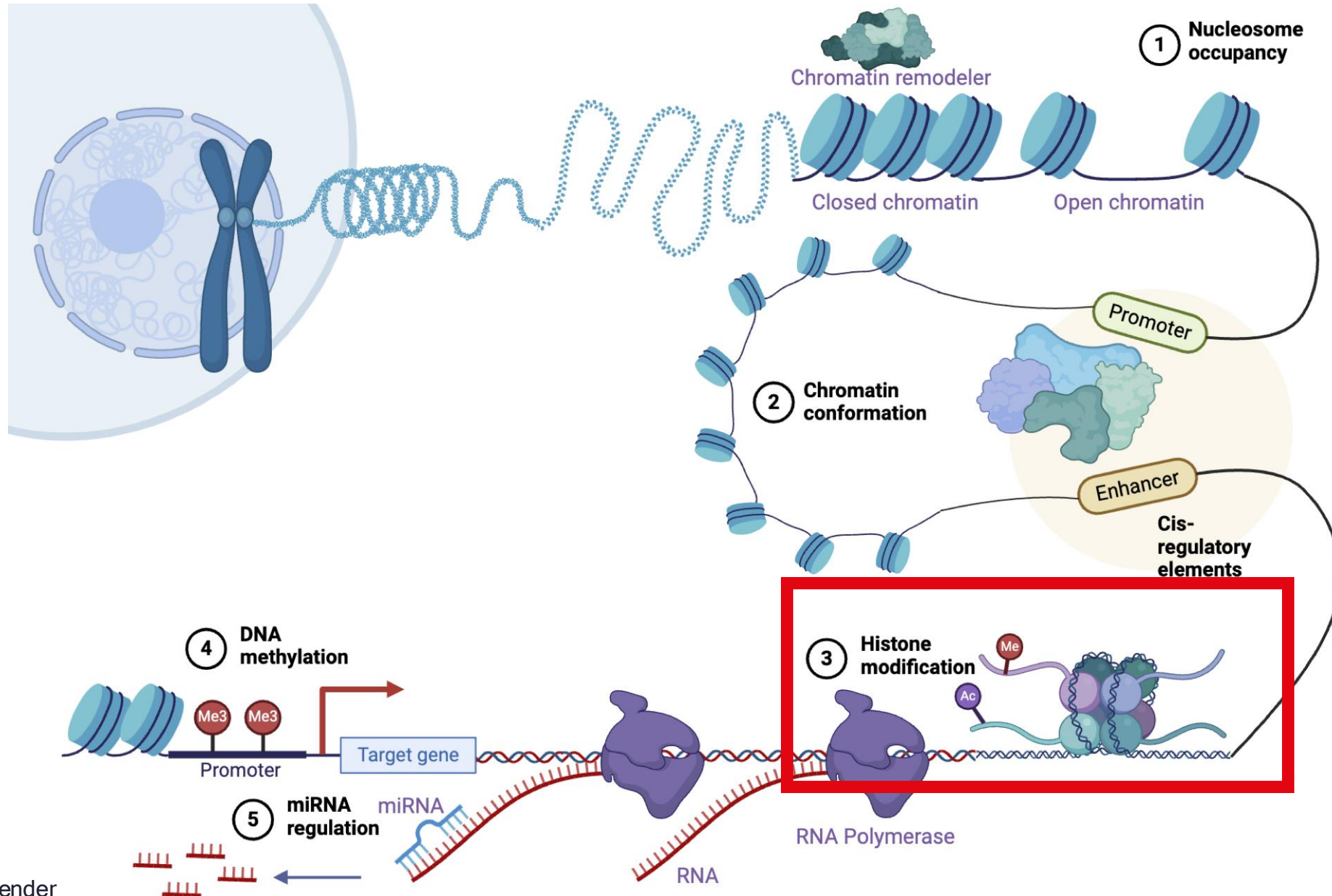
Example snapshot of chromatin accessibility



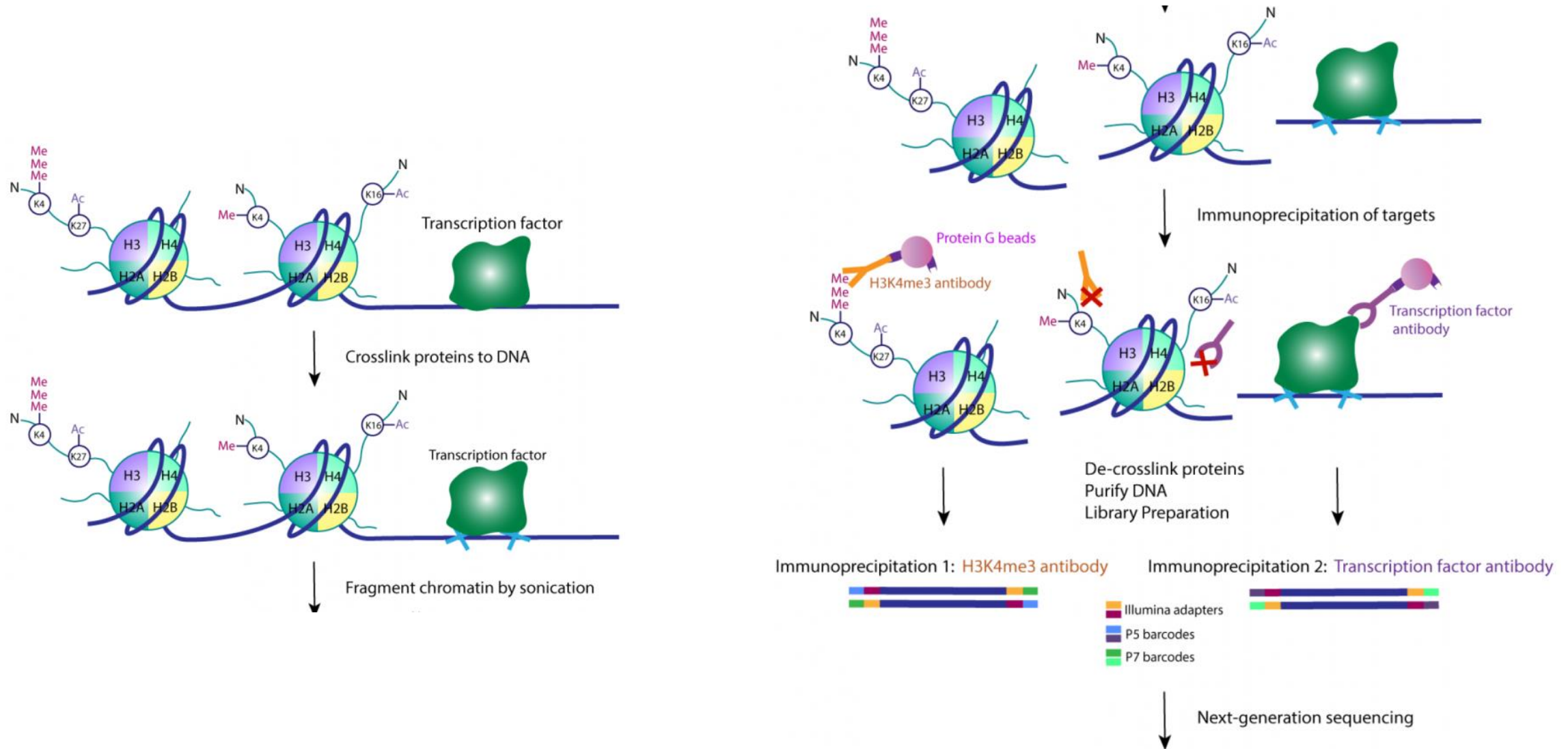
ATAC-seq data analysis pipeline



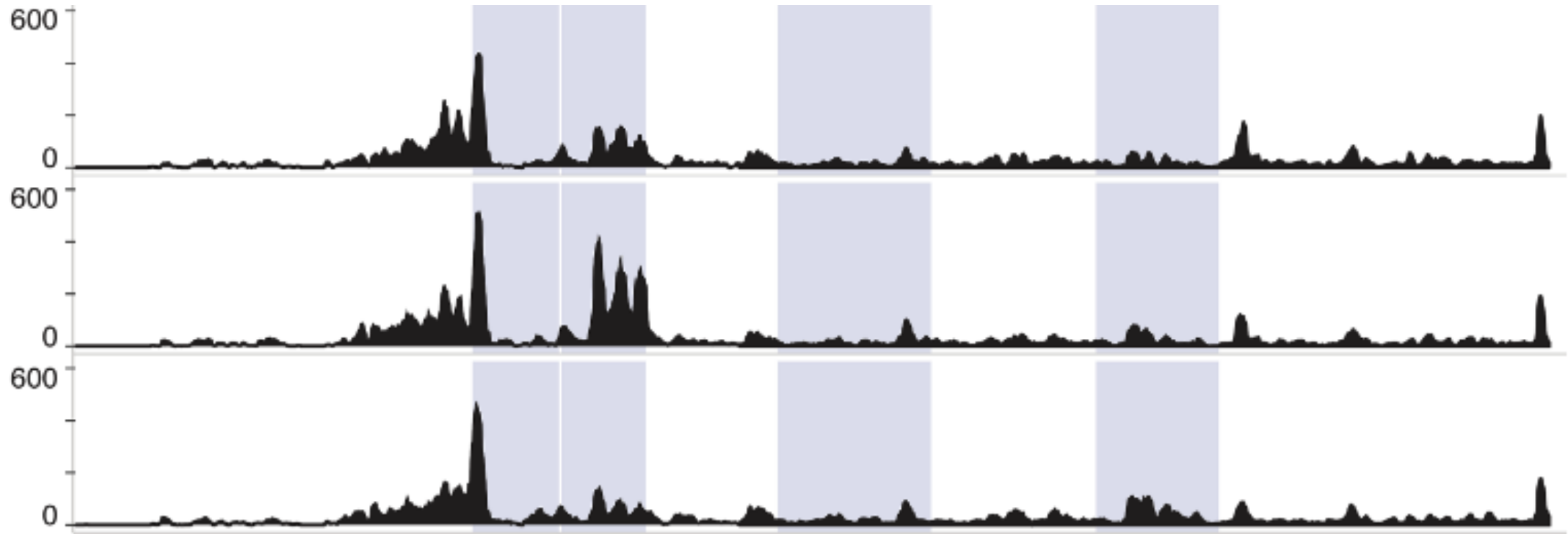
Simplified illustration of transcriptional regulation



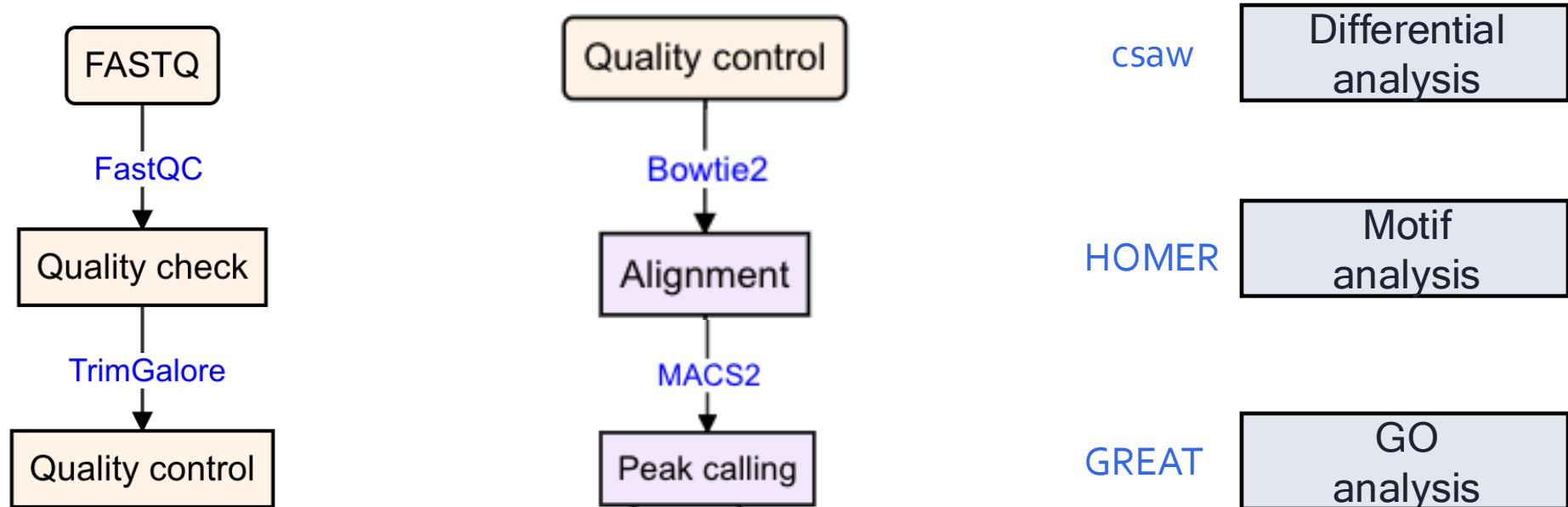
Chromatin Immunoprecipitation sequencing



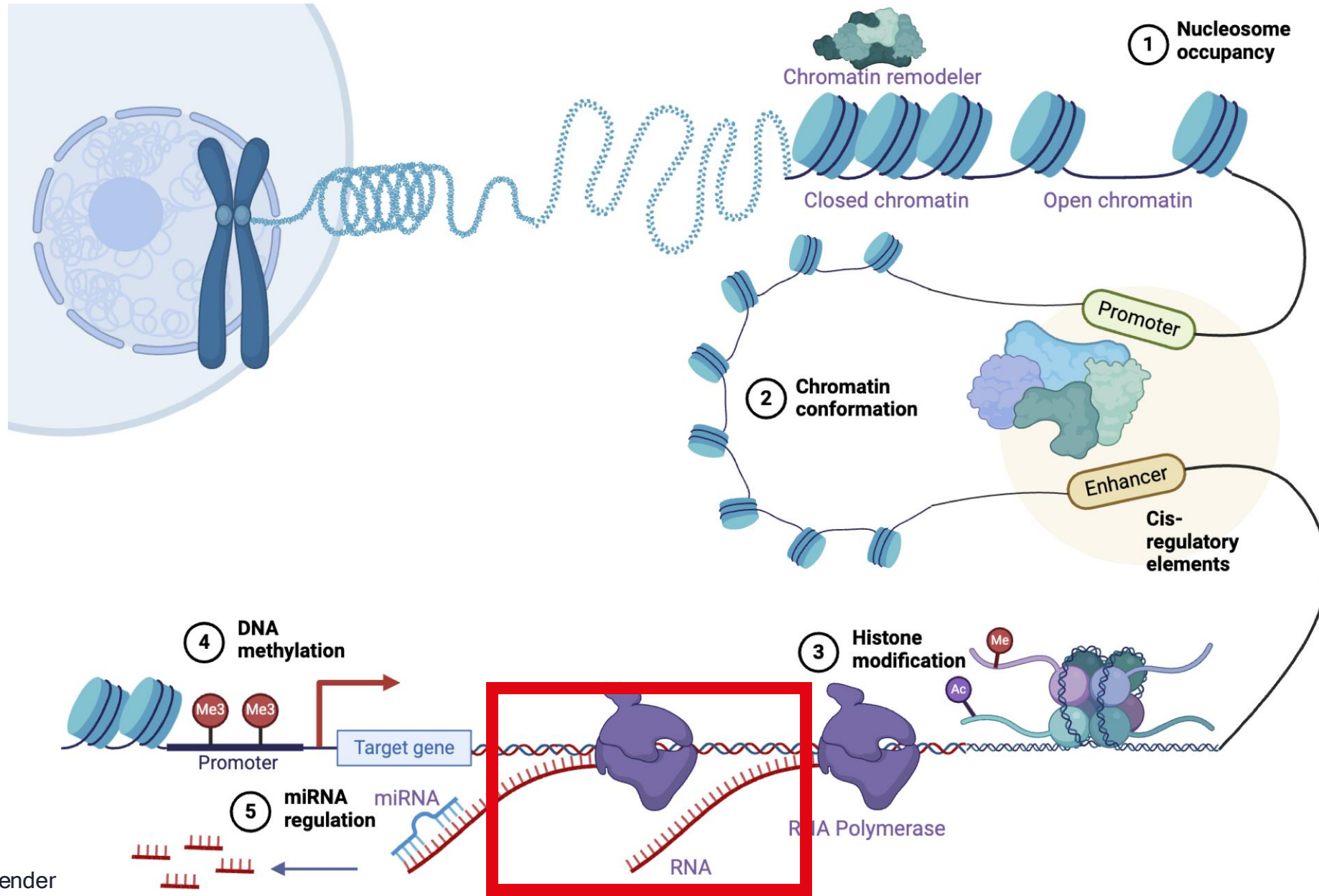
Example snapshot of enrichment



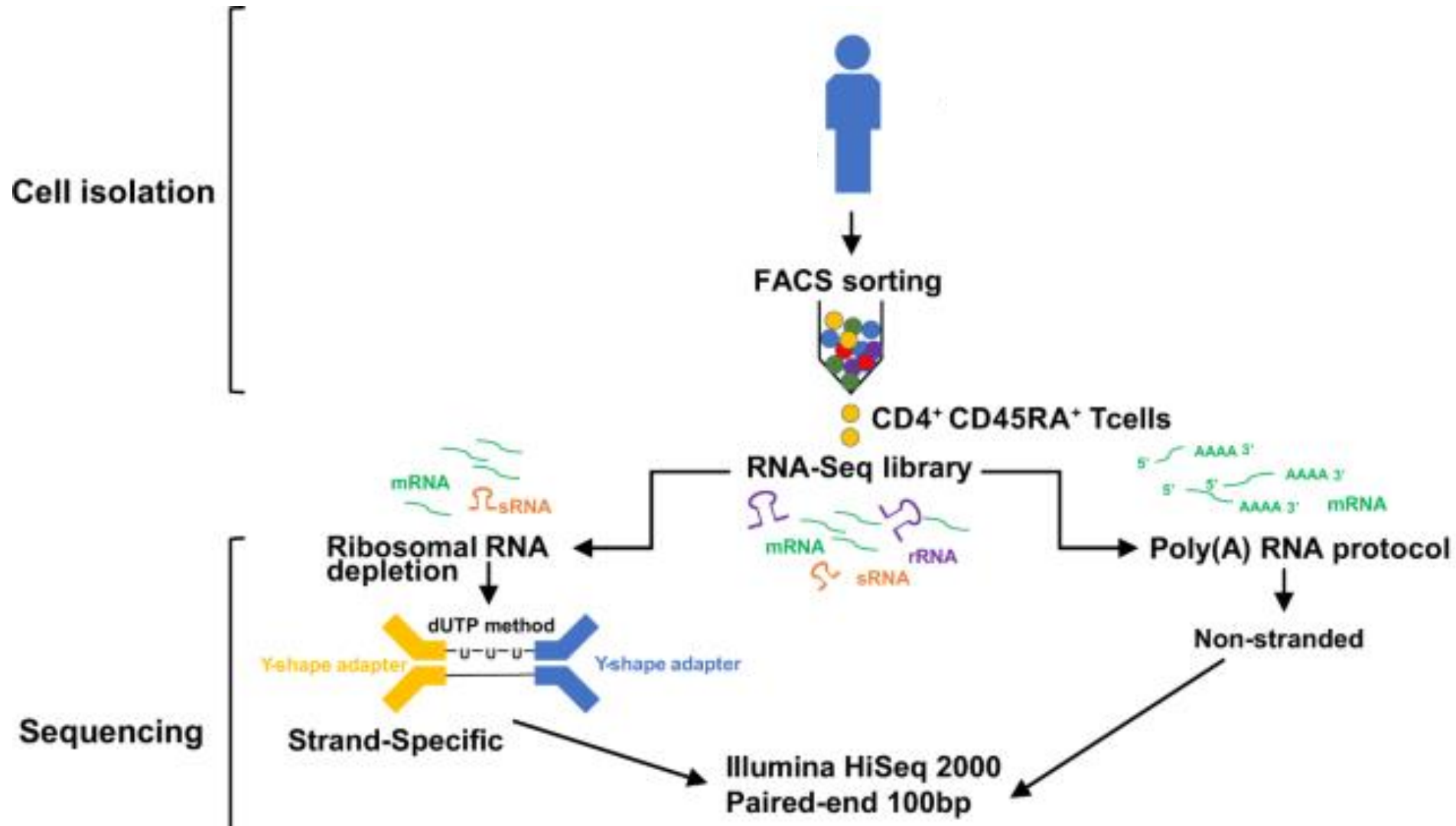
ChIP-seq data analysis pipeline



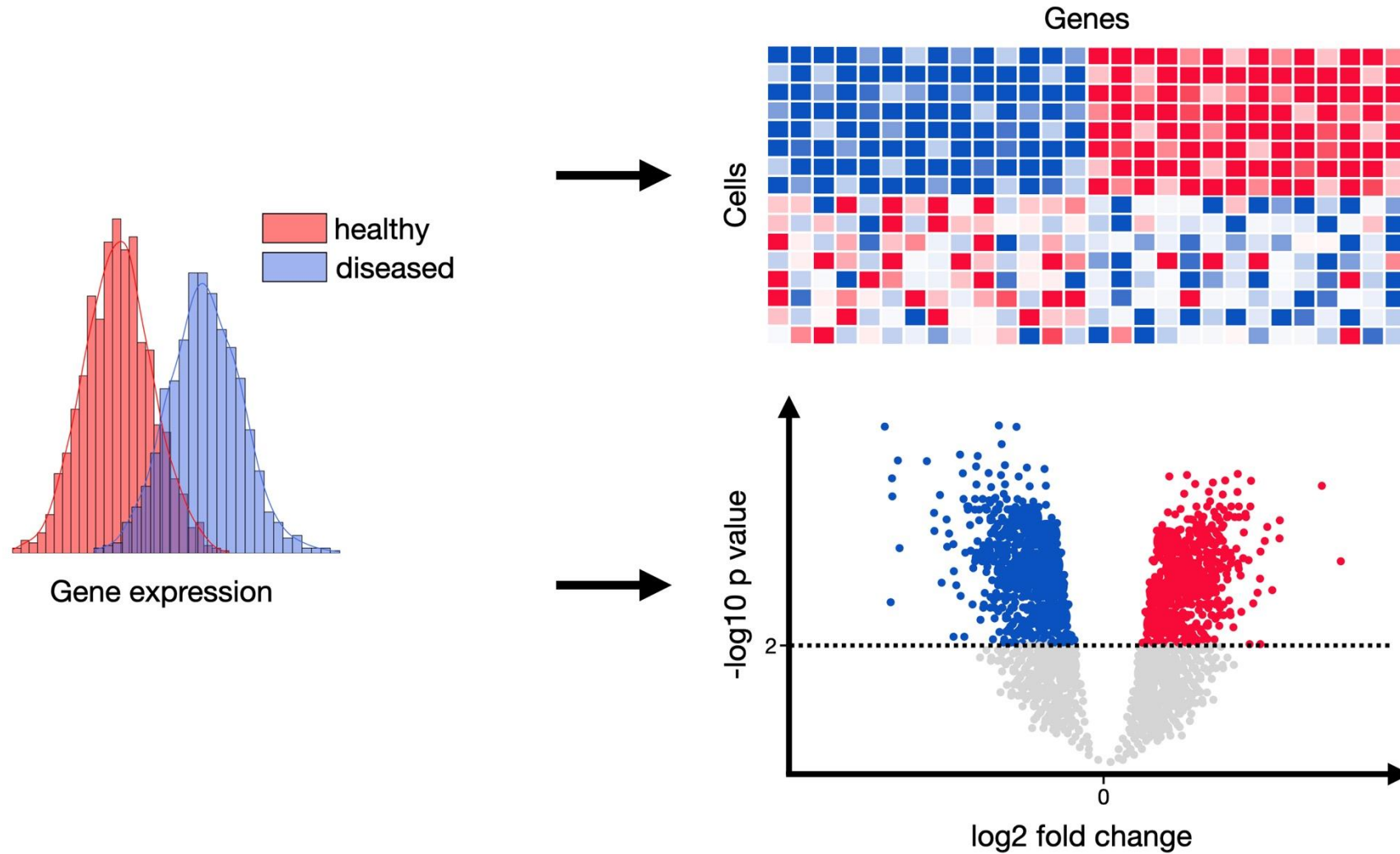
Simplified illustration of transcriptional regulation



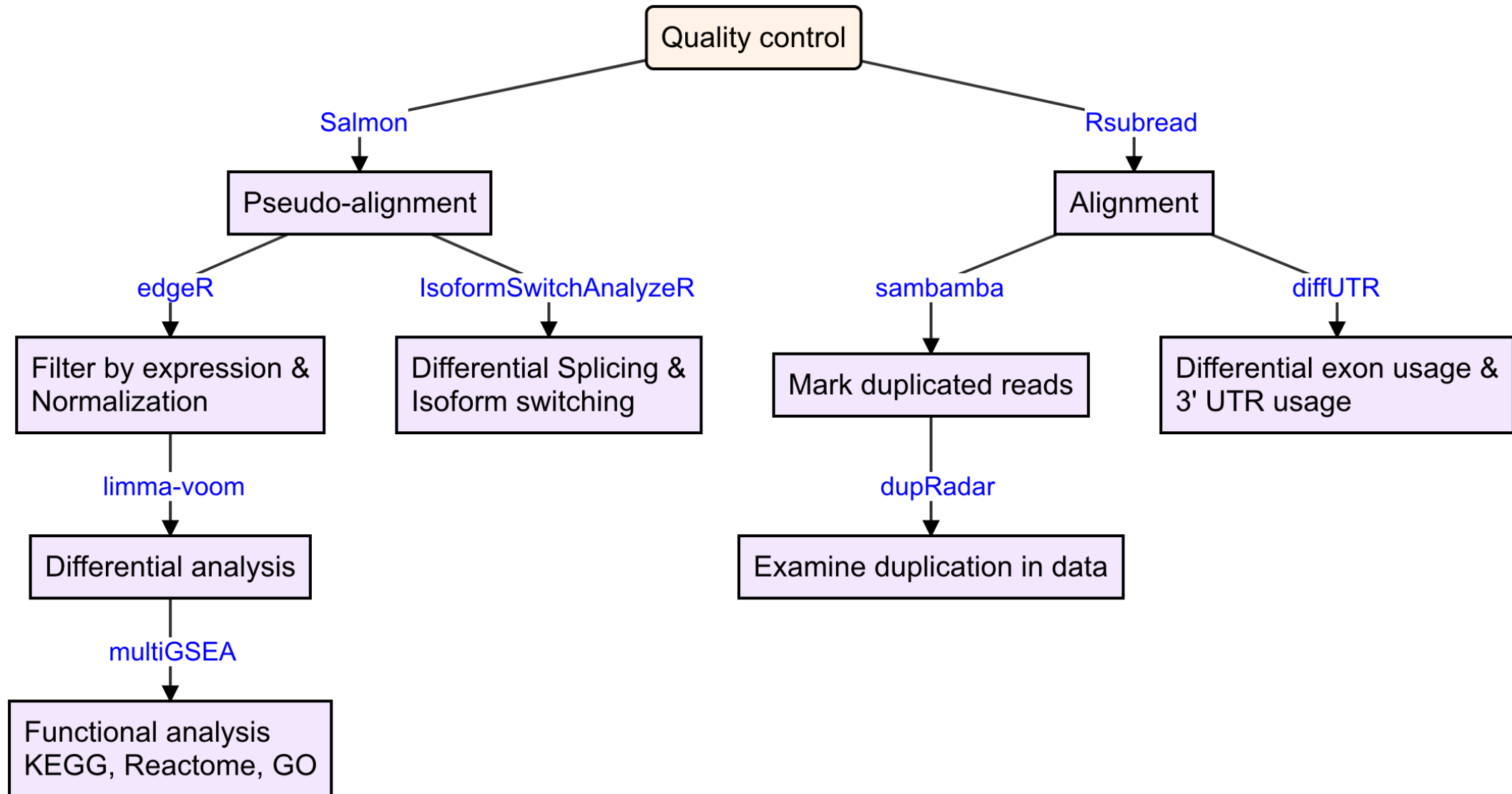
Gene expression



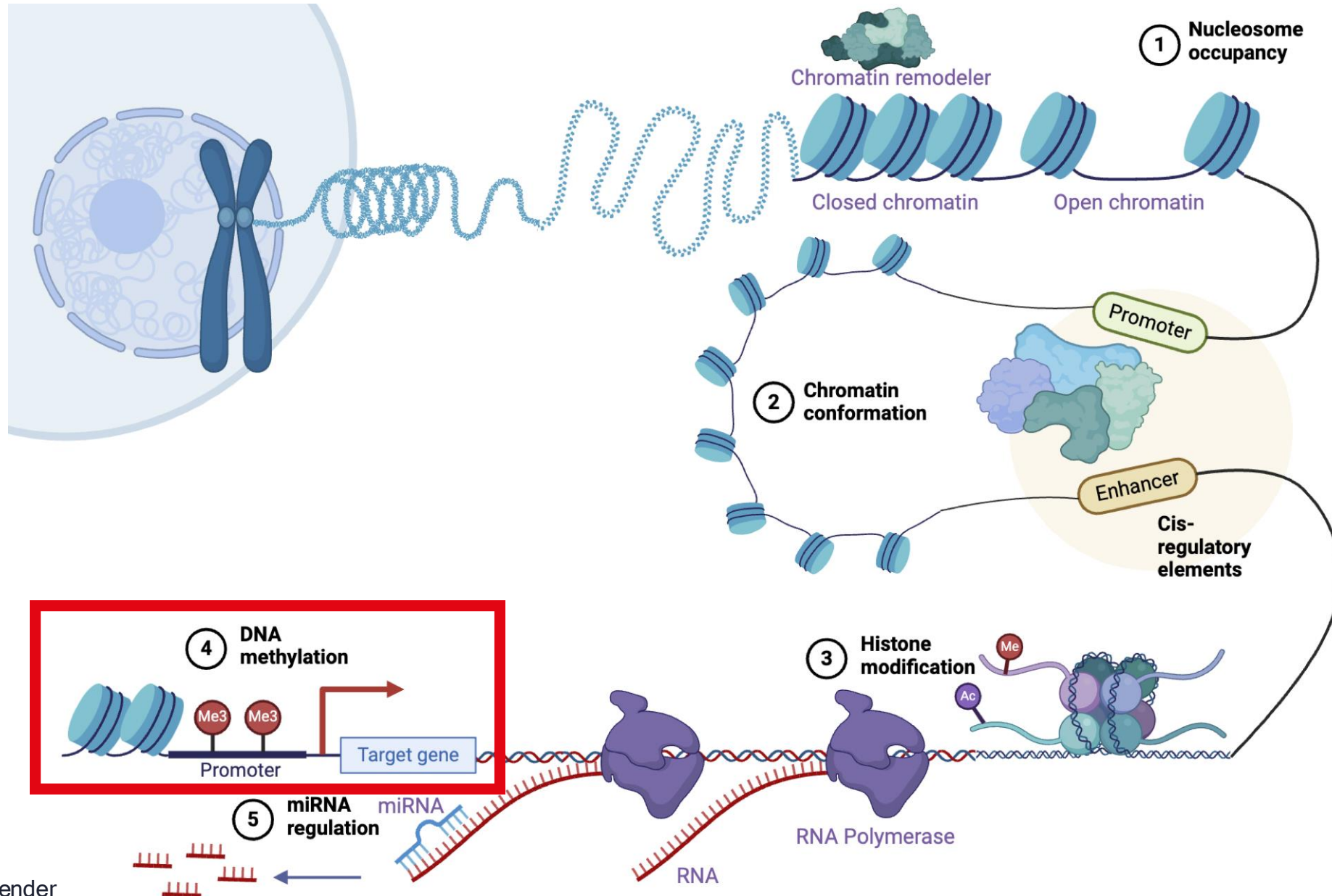
Differences in gene expression



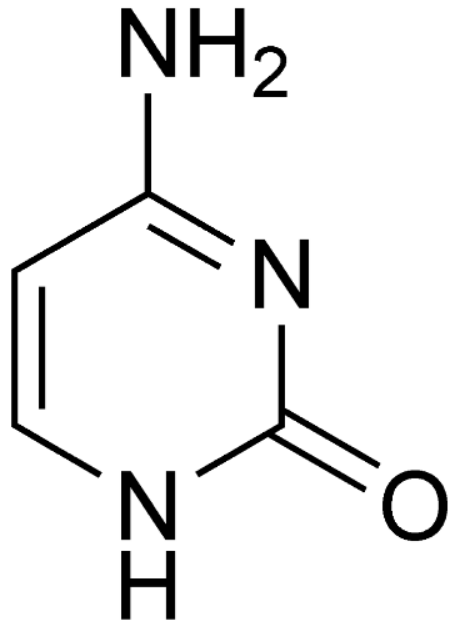
RNA-seq data analysis pipeline



Simplified illustration of transcriptional regulation



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

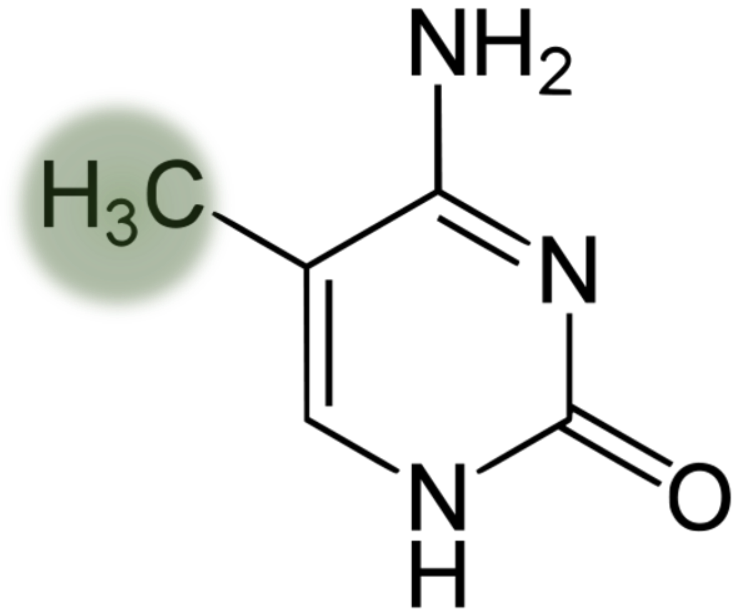


Cytosine

DNA methyl-transferases

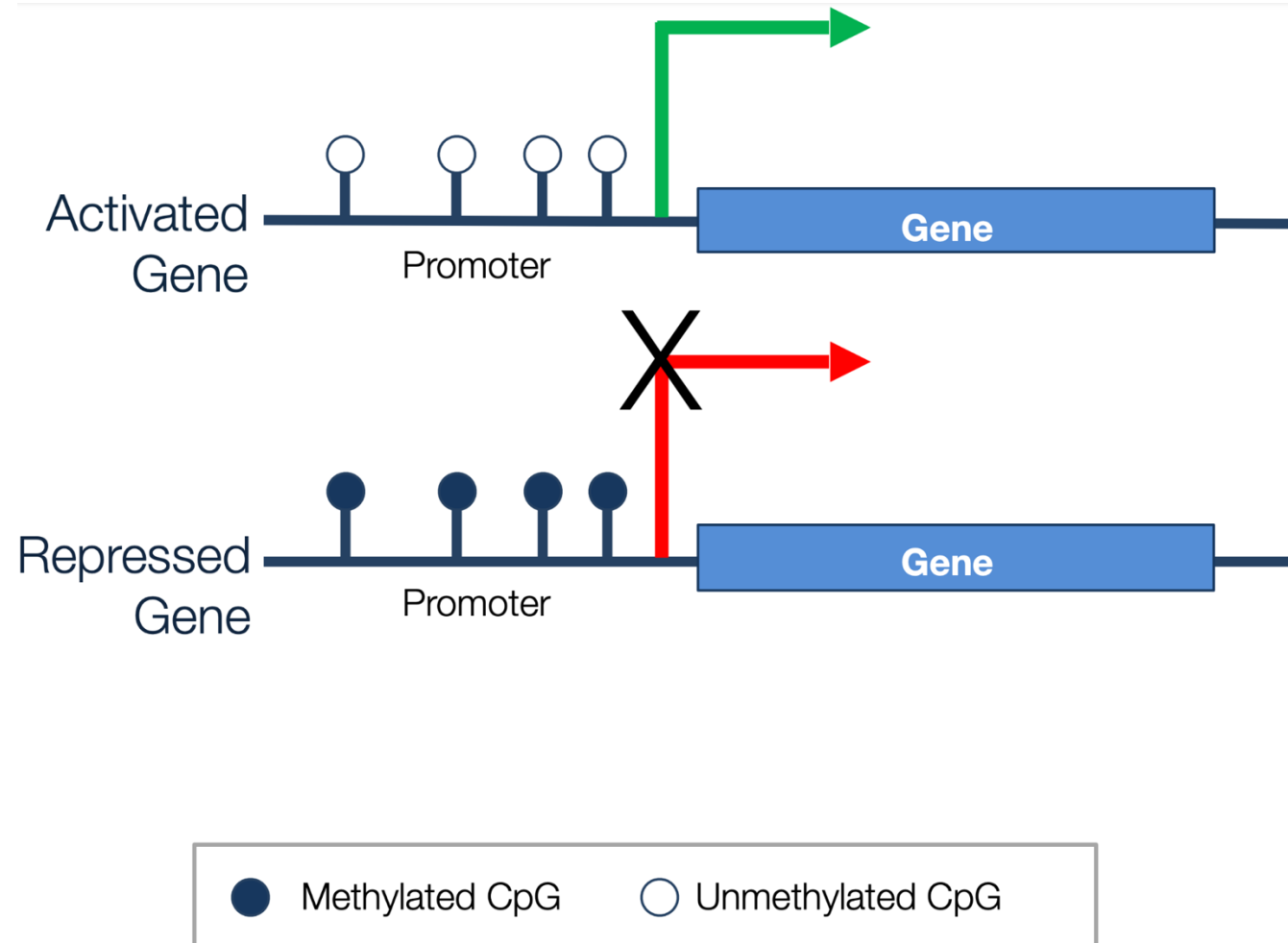


DNA-demethylase(s)
TET enymes
Passive demethylation

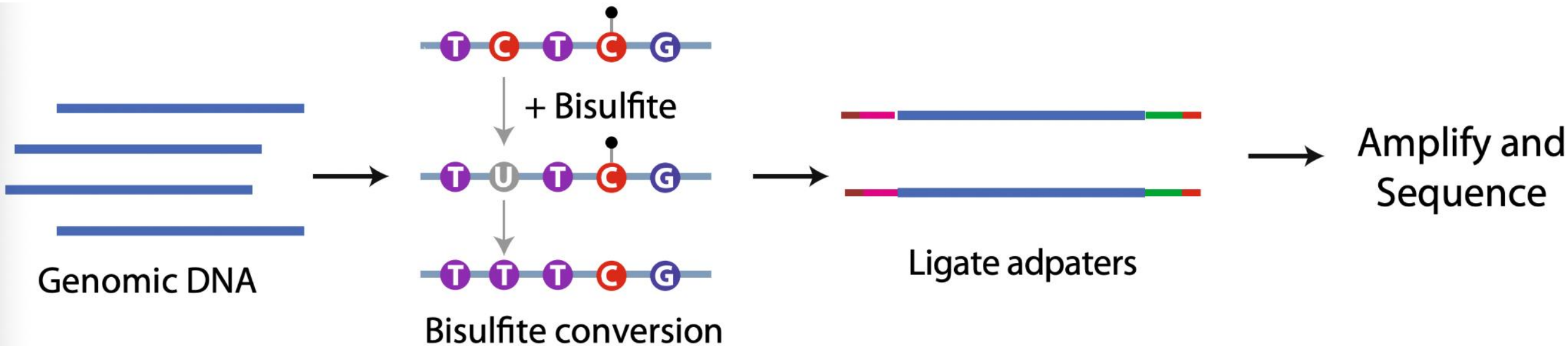


5-methyl Cytosine

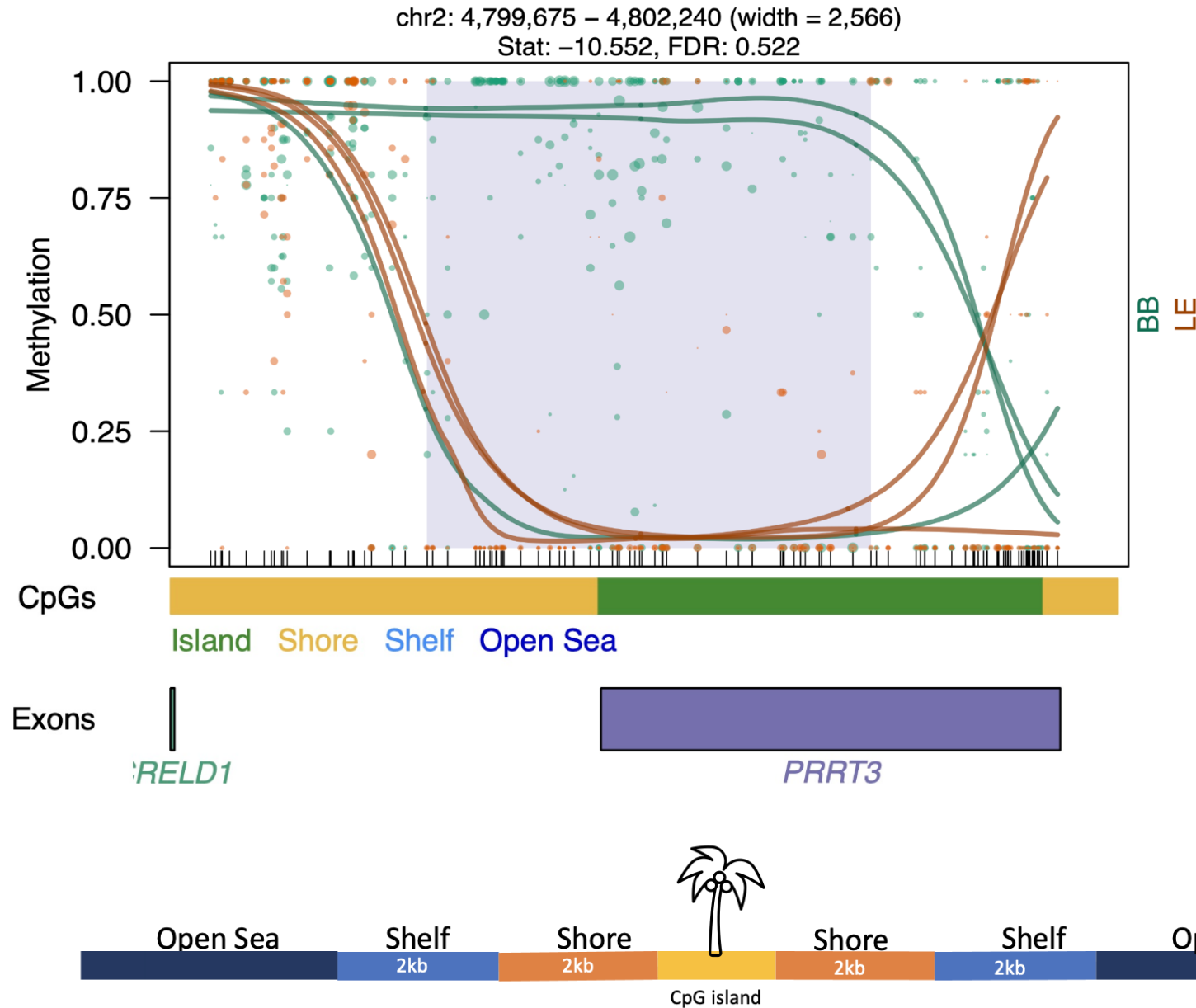
Role of DNA methylation in transcriptional regulation



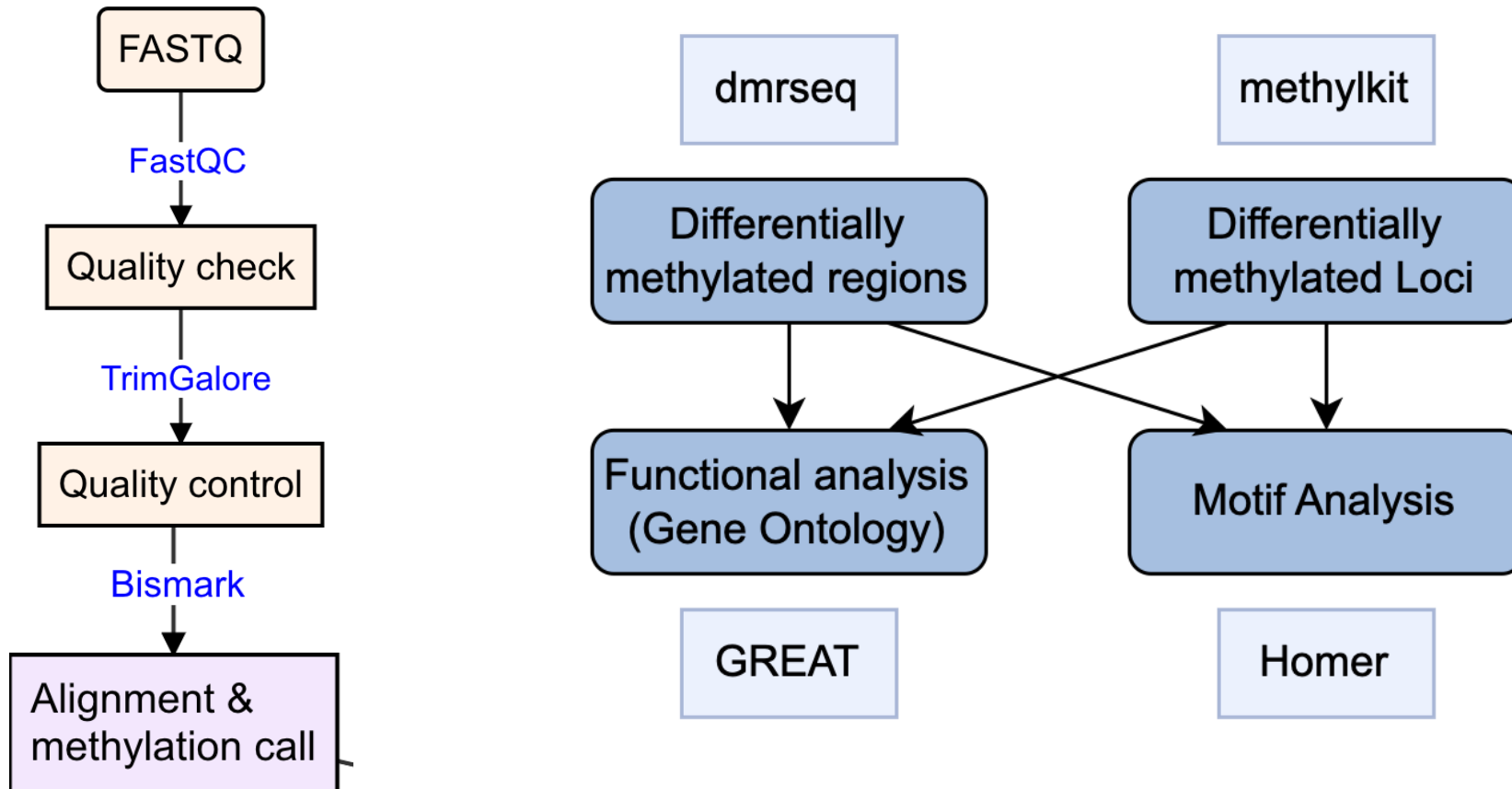
Gold standard to study DNA methylation patterns across the genome: WGBS



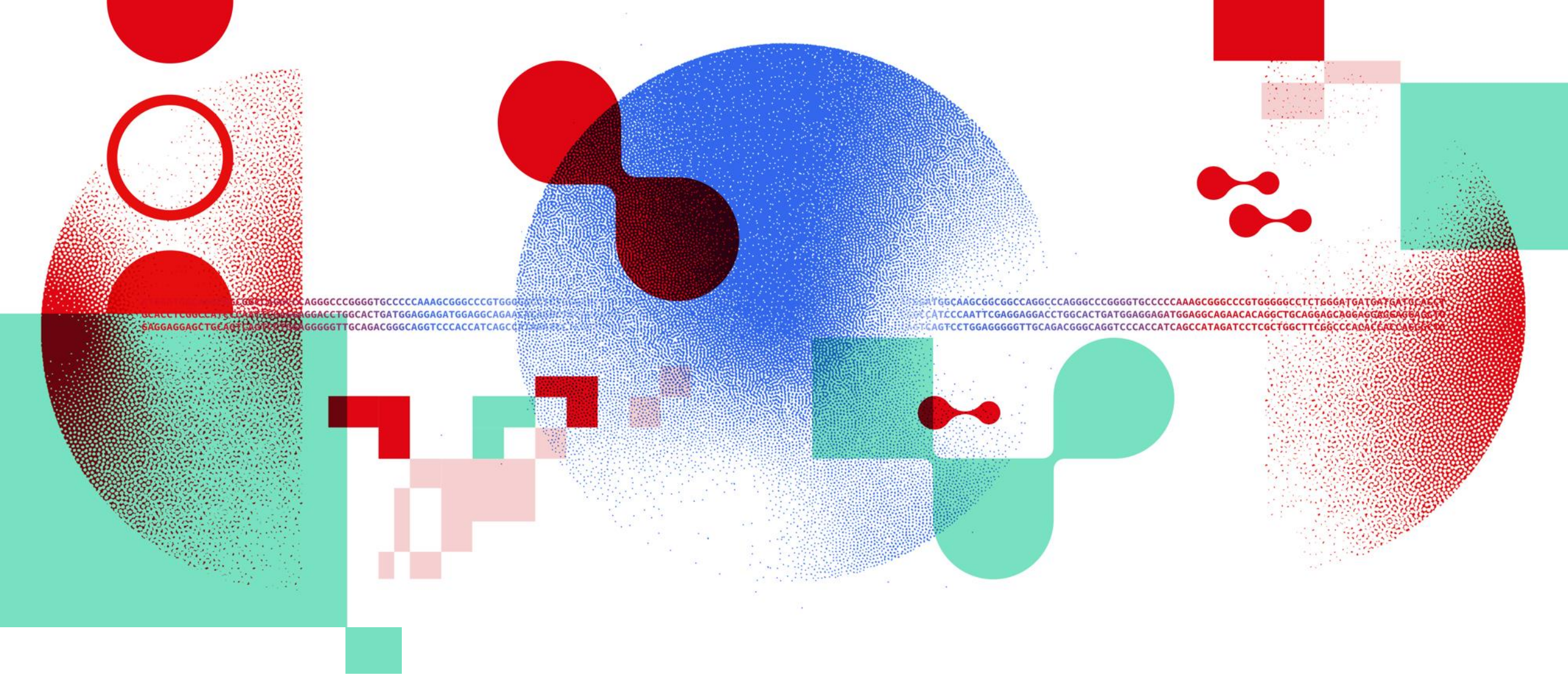
Example plot for DNA methylation



DNAme data analysis pipeline



Quiz: 6-10



Thank you

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