

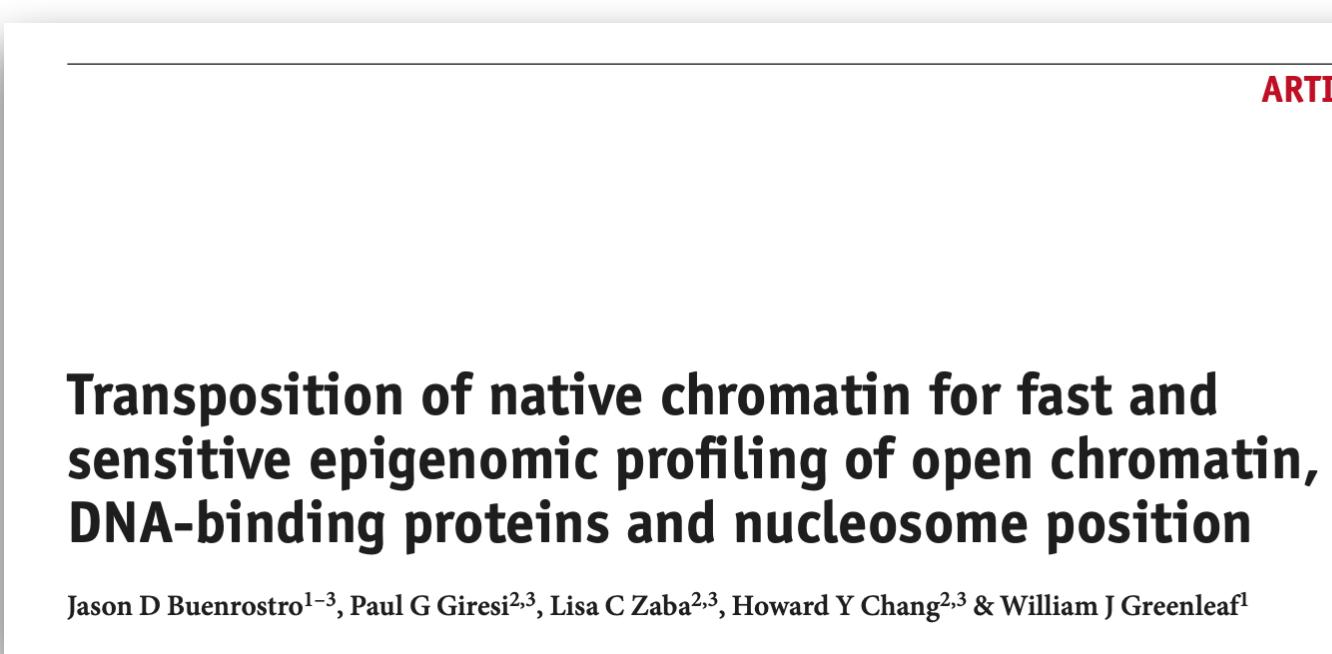
# **ATAC-seq**

**Quality control and differential peak analysis in R**

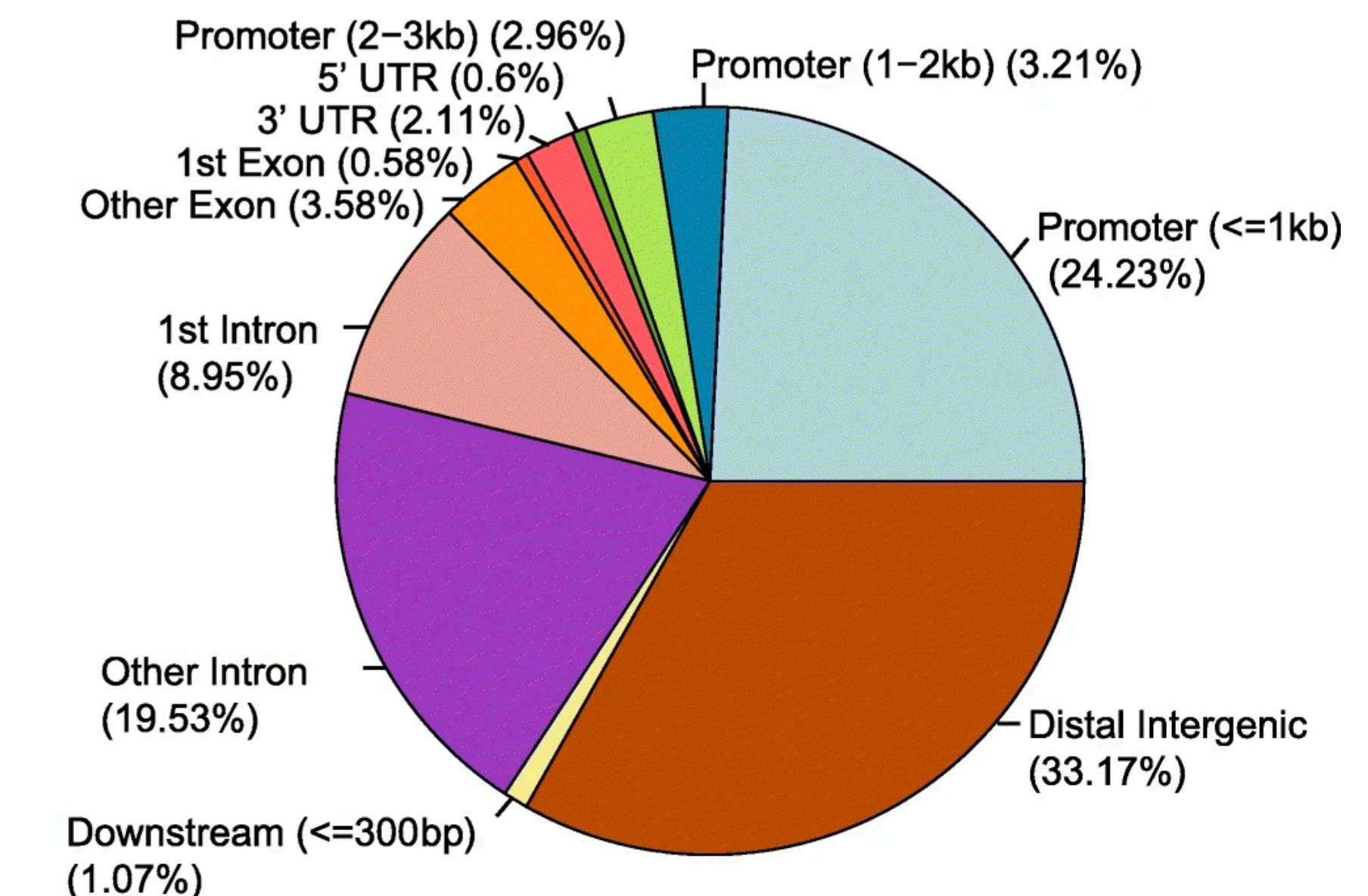
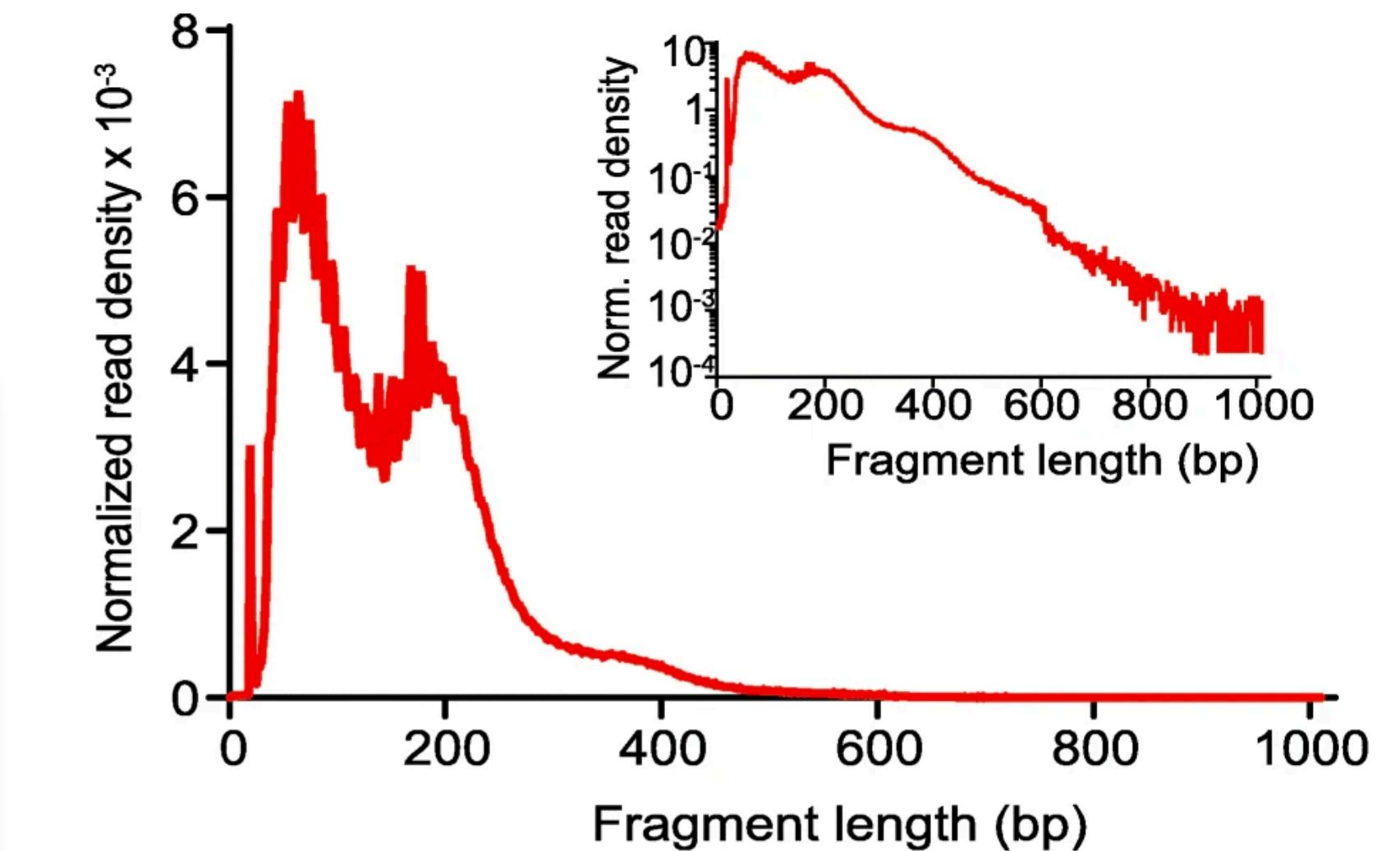
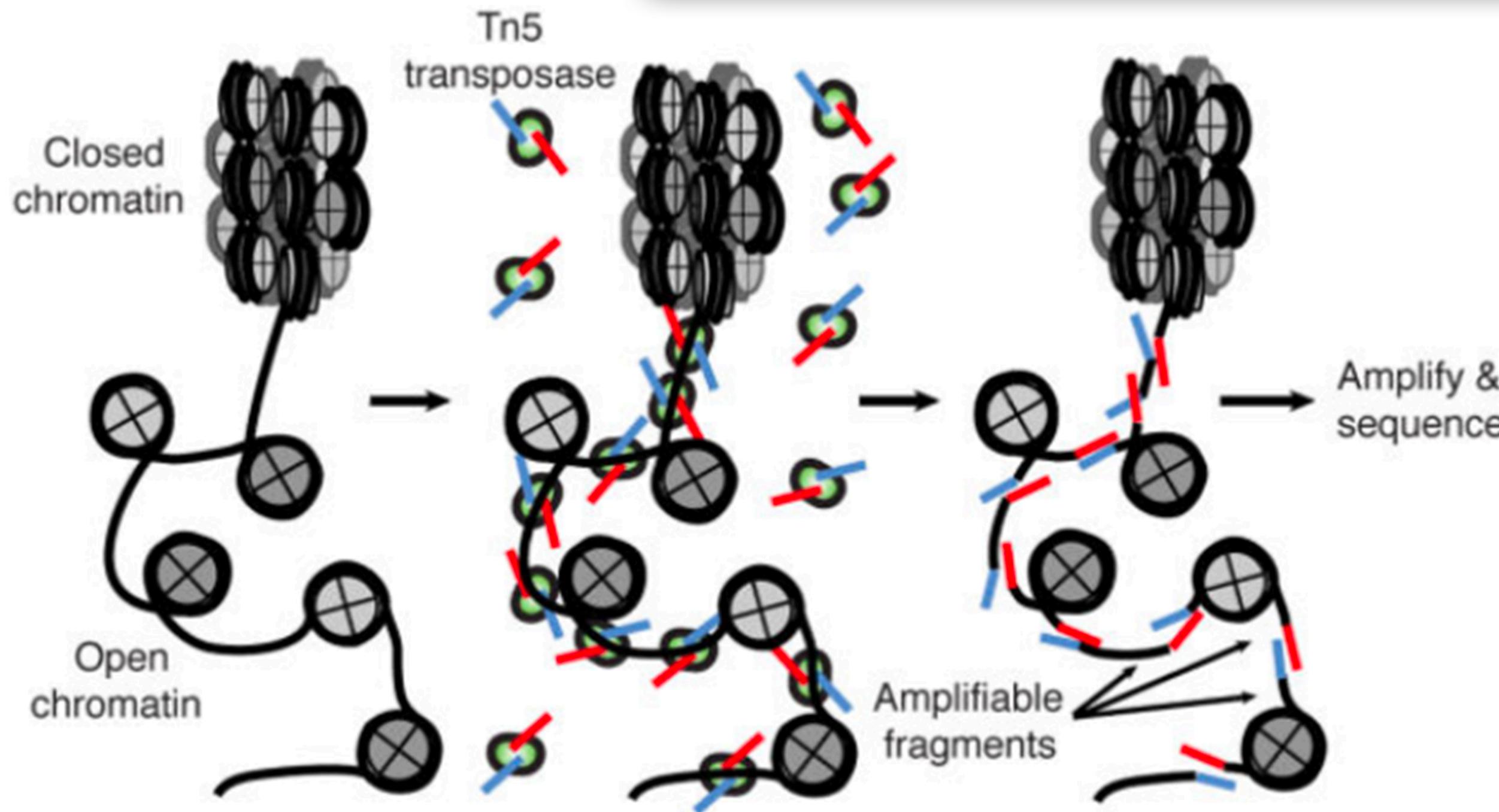
**Sam Buckberry**

# ATAC-seq analysis methods are maturing

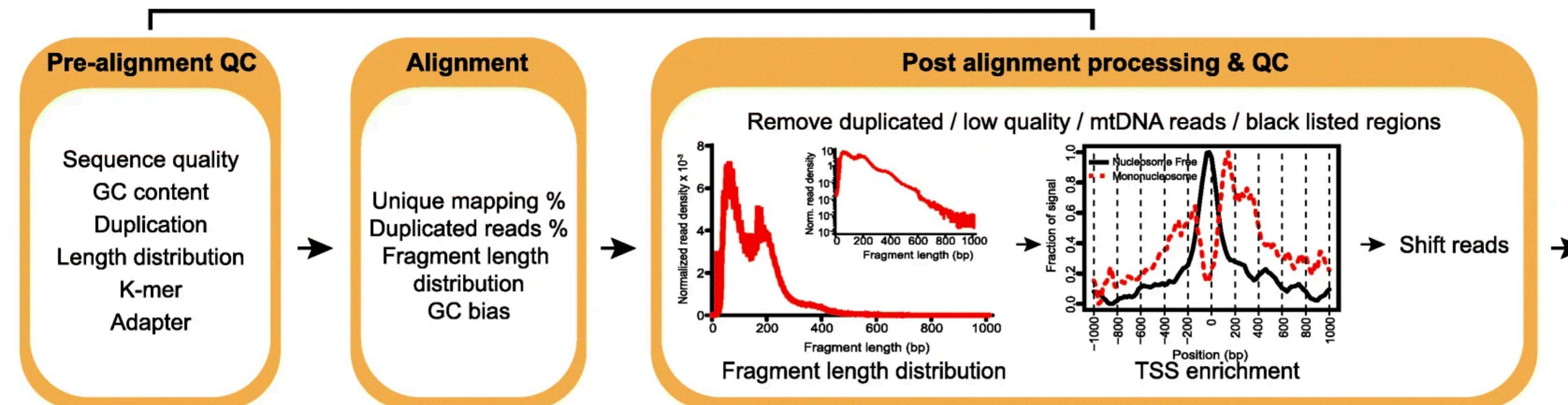
2013



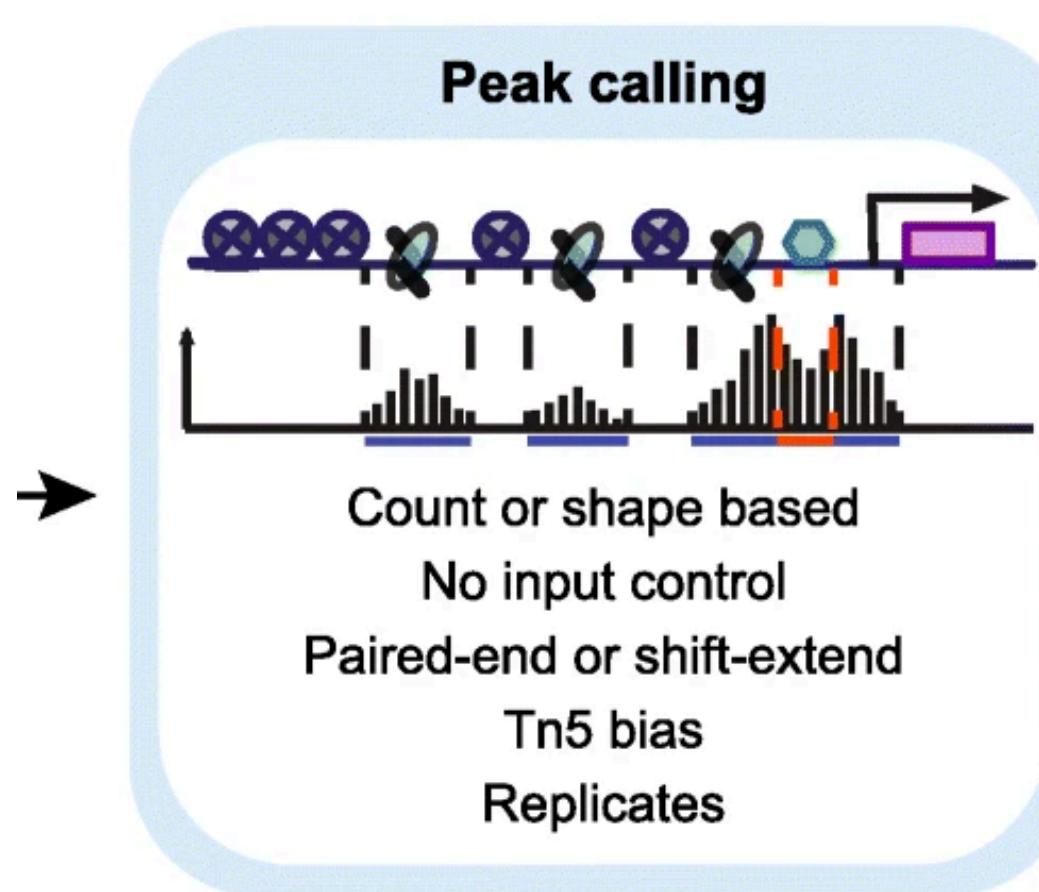
2020



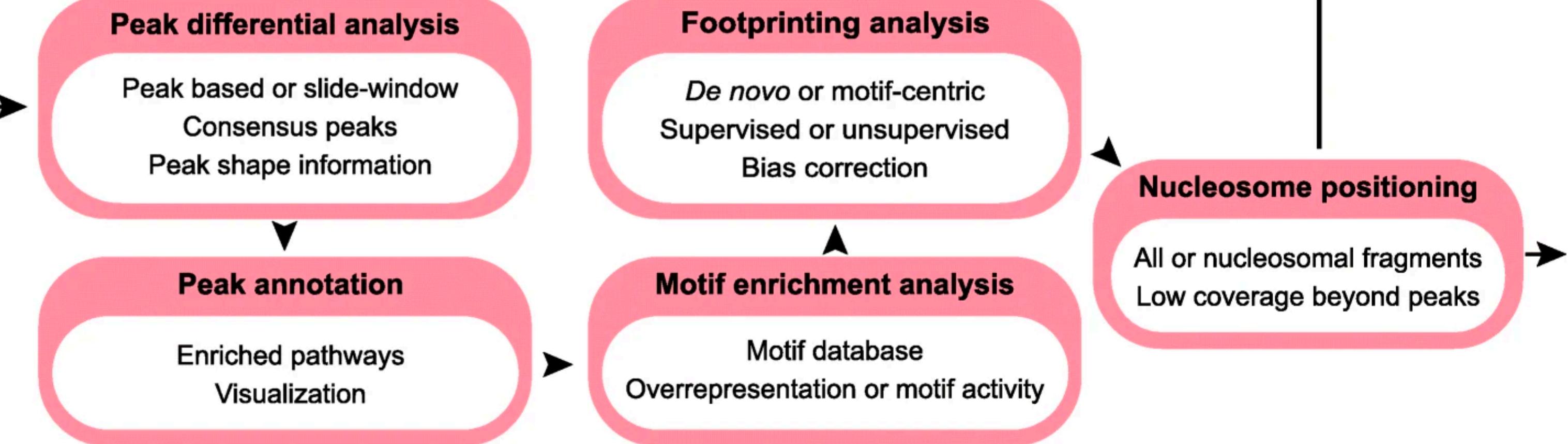
## Pre-analysis



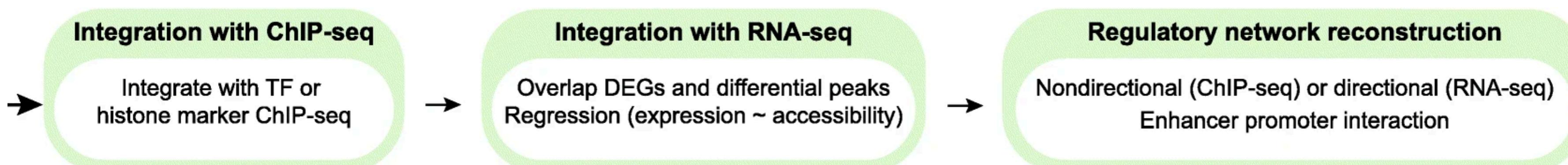
## Core analysis

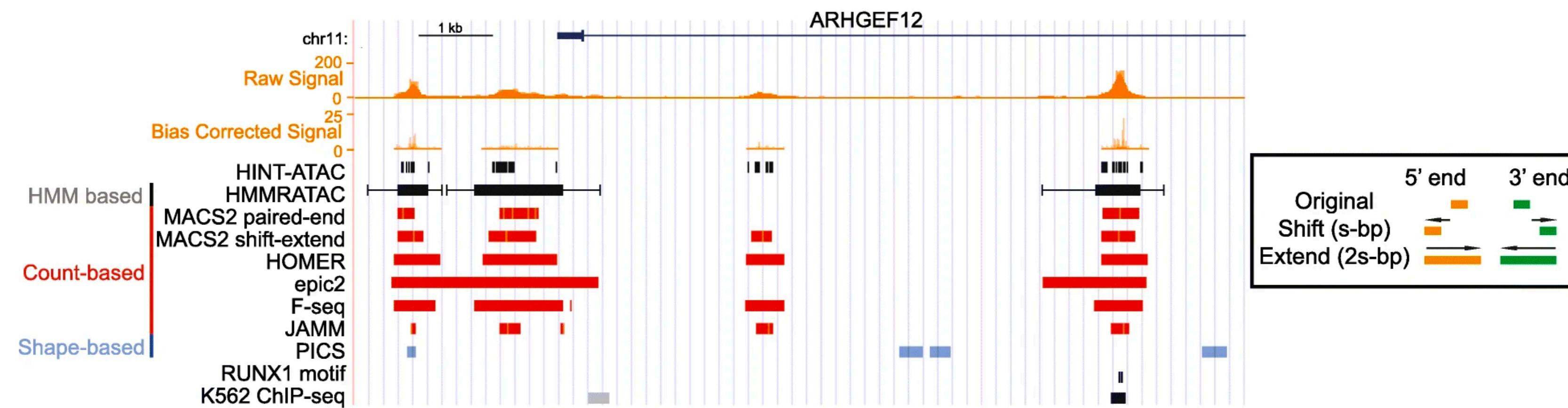
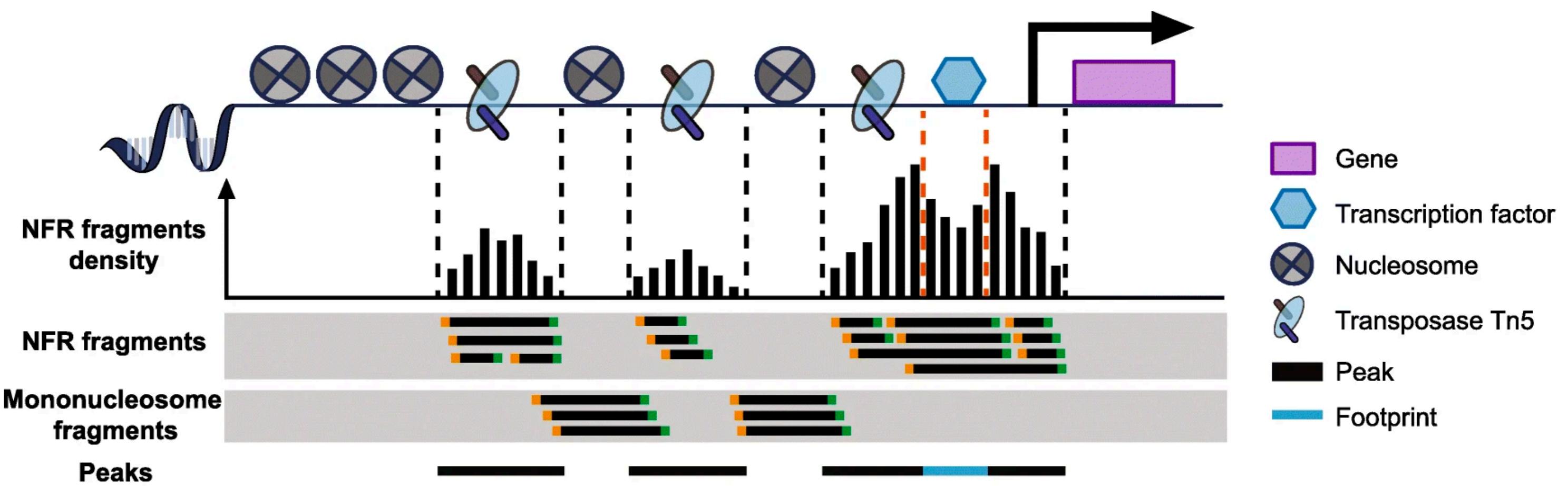


## Advanced analysis



## Integration with multiomics data





# Getting started

1. Open RStudio on your own computer or navigate to <http://35.226.108.244:8787> to use a virtual machine server with RStudio
2. Within RStudio, select File > New project and then click ‘Version control’, then click ‘Git’.
3. In the Repository URL box, enter <https://github.com/SamBuckberry/ATACseq-workshop.git>

