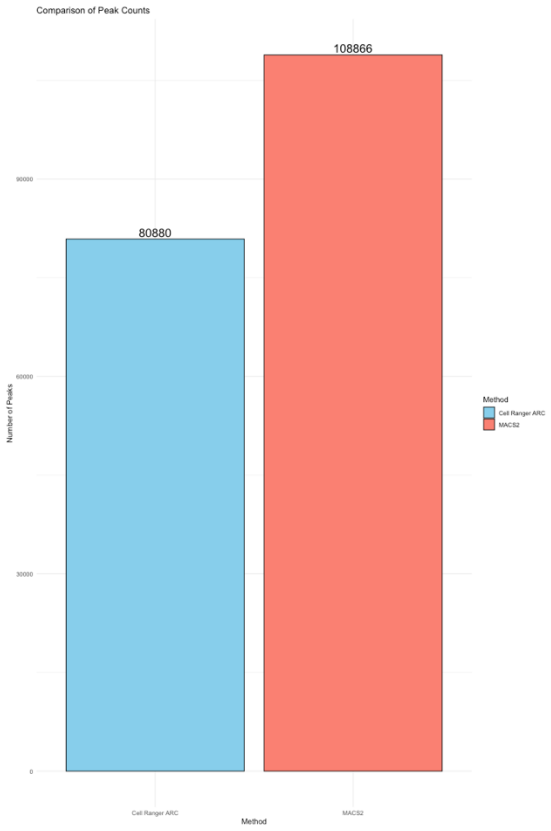
Group Assignment: Group 5
Task: Instead of using the counts from Cellaranger-arc, use MACS2. Compare the obtained peaks.

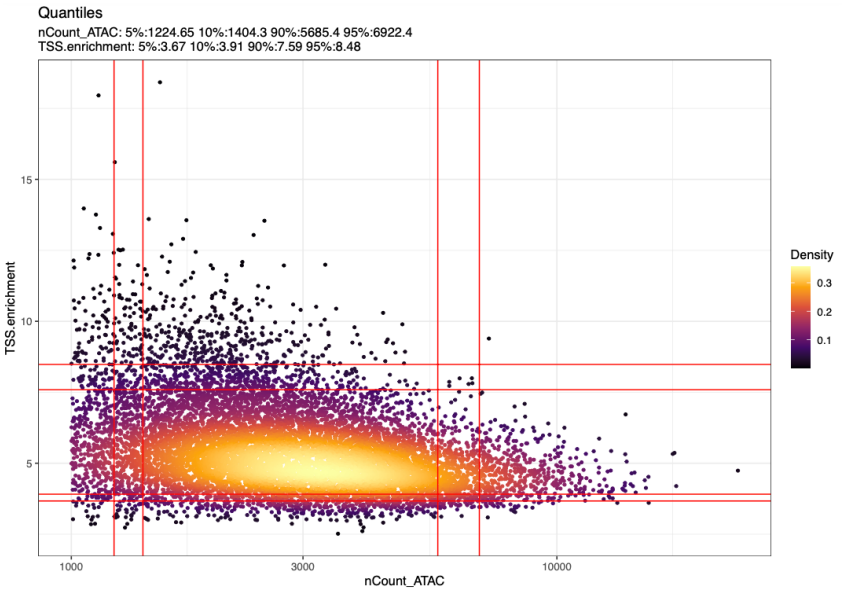
The code used to obtain the following results is found in the Explore_data_Multi.R script uploaded in the following GitHub repository https://github.com/bantaz/BESE394A_course/tree/main/Week_5_Multiome

The barplot shows the number of peaks in each object. MACS2 can be very sensitive in calling peaks, showing more number of peaks when compared with cellranger-arc.

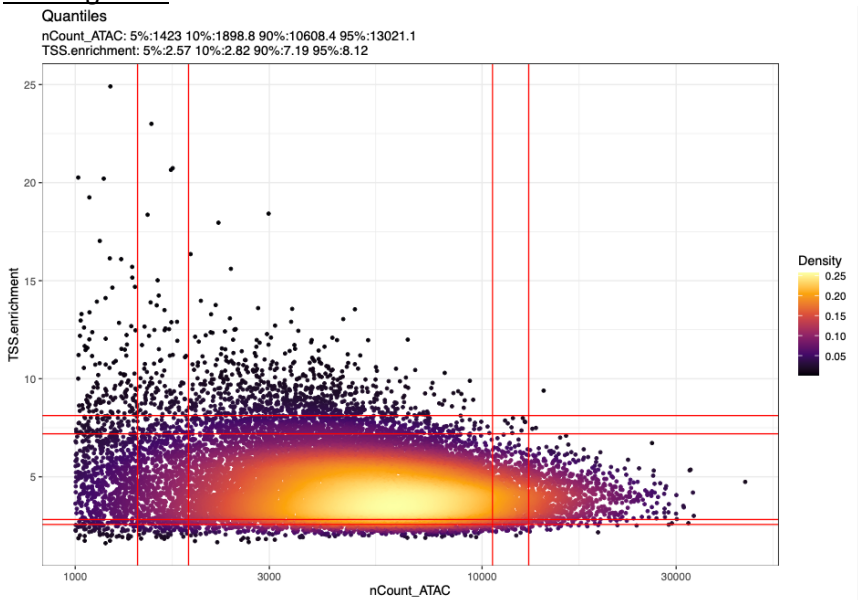


Overall, there are no major difference in terms of QC when using two different methods of peak calling. Nevertheless, the cellranger-arc method shows a broader distribution of ATAC-seq counts per cell and slightly lower TSS enrichment. The MACS2 method shows slightly higher TSS enrichment, suggesting more stringent peak selection, but with a slightly narrower range of ATAC-seq counts per cell.

MACS2



Cellranger-arc



We can visualize MACS2 peak calls alongside the 10x Cellranger peak calls using *CoveragePlot()*. Here, two regions of choice were selected for visualization purpose (chr9-102498973-102499900 and chr1-3229745-3230583). Overall, both methods agree on the presence of a peak within the chosen regions. However, when comparing MACS2 (red line) with cellranger-arc (grey line), we observe narrower region of peak calling in MACS2, suggesting it might be more sensitive and stringent in its peak calling compared to cellranger-arc.