

m6A pipeline

m6A and input FASTQ files



quality check

trimming

merge references

hg38 reference

HIV reference

reference indexing

alignment

sorting and indexing

post-alignment QC

realign 5' LTR from HIV

m6A peak calling

differential peak calling

m5C pipeline

m5C FASTQ files



trimming

reverse complement reads

quality check

merge references

hg38 reference

HIV reference

reference indexing

alignment

realign 5' LTR from HIV

m5C peak calling

differential peak calling