
Download FASTQ files from ENCODE
Merge single-end FASTQ files by biological replicate
Merge paired-end FASTQ files by biological replicate
Trim single-end data with trimmomatic
Trim paired-end data with trimmomatic
Align trimmed single-end reads with bowtie2
Align trimmed paired-end reads with bowtie2
Use samtools to merge paired-end reads and filter PCR duplicates
Filter reads by unique kmer
Use macs2 to call peaks
Download the genome .chain file
Use liftOver to find peaks unique to the T2T reference genome
Unique Peaks