

```
#make a directory to hold the analysis
```

```
mkdir chipseq
```

```
cd chipseq
```

```
#build the indexes needed by the bowtie2 aligner
```

```
bowtie2-build ../data/hs_ref_GRCh38_chr20.fa chr20
```

```
#use bowtie2 to align the single reads to the chr20 index, for H3K27 and input
```

```
bowtie2 -x chr20 -U ../data/HUES64_rep1.H3K27me3.chr20.fastq.gz -S
```

```
HUES64_rep1.H3K27.sam
```

```
bowtie2 -x chr20 -U ../data/HUES64_rep1.input.chr20.fastq.gz -S HUES64_rep1.input.sam
```

```
#use samtools to create a sorted, indexed bam file for each output file
```

```
samtools view -b HUES64_rep1.H3K27.sam -o HUES64_rep1.H3K27.bam
```

```
samtools sort HUES64_rep1.H3K27.bam -o HUES64_rep1.H3K27_sorted.bam
```

```
samtools index HUES64_rep1.H3K27_sorted.bam
```

```
samtools view -b HUES64_rep1.input.sam -o HUES64_rep1.input.bam
```

```
samtools sort HUES64_rep1.input.bam -o HUES64_rep1.input_sorted.bam
```

```
samtools index HUES64_rep1.input_sorted.bam
```

```
#repeat the process for the second replicates for each sample
```

```
bowtie2 -x chr20 -U ../data/HUES64_rep2.H3K27me3.chr20.fastq.gz -S
```

```
HUES64_rep2.H3K27.sam
```

```
bowtie2 -x chr20 -U ../data/HUES64_rep2.input.chr20.fastq.gz -S HUES64_rep2.input.sam
```

```
samtools view -b HUES64_rep2.H3K27.sam -o HUES64_rep2.H3K27.bam
```

```
samtools sort HUES64_rep2.H3K27.bam -o HUES64_rep2.H3K27_sorted.bam
```

```
samtools index HUES64_rep2.H3K27_sorted.bam
```

```
samtools view -b HUES64_rep2.input.sam -o HUES64_rep2.input.bam
```

```
samtools sort HUES64_rep2.input.bam -o HUES64_rep2.input_sorted.bam
```

```
samtools index HUES64_rep2.input_sorted.bam
```

```
#use MACS2 callpeak to call peaks in the aligned reads. First look at the help
```

```
#so that you can see what options exist
```

```
macs2 callpeak -h
```

```
#now call peaks, using the inputs as controls and the H3K27 as treatments
```

```
macs2 callpeak -t HUES64_rep1.H3K27_sorted.bam HUES64_rep2.H3K27_sorted.bam -c
```

```
HUES64_rep1.input_sorted.bam HUES64_rep2.input_sorted.bam -n HUES64_H3K27
```

#download all of the sorted bam and bai files, as well as HUES64_H3K27_summits.bed,
#and look at chromosome 20 with all of this data in IGV.
#navigate to a MACS2 peak and take a screenshot. You should see a pileup of reads
#in the enriched conditions relative to the controls