1. sed -n '145, 1000000p' hs_ref_GRCh38.p2_chr1.fa > sample.fa

2. python addsnps.py sample.fa sample_1perSNP.fa .01

3. art_illumina -i sample_1perSNP.fa -l 100 -f 5 -ss HS25 -o sample_1perSNP

4. bwa mem -R '@RG\tID:Seq01p\tSM:Seq01\tPL:ILLUMINA\tPI:330' sample.fa sample_1perSNP.fq > sample_1perGATK.sam

5. samtools view -b -S sample_1perGATK.sam > sample_1perGATK.bam

6. samtools sort sample_1perGATK.bam sortedGATK

7. samtools index sortedGATK.bam

8. java -jar /usr/local/bioinf/gatk/picard.jar CreateSequenceDictionary R=sample.fa O= sample.dict

9. samtools index sample.fa

10. java -jar /usr/local/bioinf/gatk/GenomeAnalysisTK.jar -T HaplotypeCaller -R /usr/home/a/125/tug85760/ass14/new/sample.fa -I /usr/home/a/125/tug85760/ass14/new/sortedGATK.bam -o gatk.vcf