Exercise 6

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Exercise 1. SNP calling with SAM tools and Galaxy.

- Access source files for today.
- Pileup the mapped reads in the BAM file

```
NGS:SAM Tools>Mpileup

    BAM file: The BAM file you generated
    Using reference genome: hg19
    Genotype Likelihood Computation: Perform a genotype likelihood computation
    Perform INDEL calling: Do not perform indel calling
    Set advanced options: Advanced

    List of regions or sites on which to operate: chr20.bed

    Execute
```

- Mpileup creates a BCF (binary VCF) file which contains the list of variations in a compressed format.
- Convert BCF to VCF
  - Download the BCF file
  - In the samtools directory

```
bcftools view DOWNLOADED_FILE.BCF > Mpileup_chr20.vcf
```

Homework 1. No homework as of today!