1. Use file reads.fastq
2. Map it with bowtie with 2 mismatch and with 0 mismatches saving them into two different SAM files: reads0.sam and reads2.sam (run bowtie without any input to see available options)
3. Collect statistics what percentage of reads map in one and another case.
4. Convert both SAMs into BAMs.
5. From UCSC browser get coordinates of Fgf21 gene of mouse genome (version mm10).
6. Use bedtools (option “coverage”, no arguments will give you help) and get number of reads from reads0.bam and reads2.bam that are inside of this gene.
7. Report 2 numbers from 3) and 2 numbers from 6).