Introduction to Bulk RNAseq data analysis

QC of raw reads with FastQC - Solutions

Contents

Exercise

1. a) Check the location of the current directory using the command `pwd`

   b) If the current directory is not `Course_Materials`, then navigate to the **Course_Materials** directory using the `cd` (**c**hange **d**irectory) command:

```
cd ~/Course_Materials
```

2. a) Use `ls` to list the contents of the directory. There should be directory called **fastq**

   b) Use `ls` to list the contents of the **fastq** directory:

```
ls fastq
```

> SRR7657883.sra_1.fastq.gz SRR7657883.subset_2M.sra_1.fastq.gz
> SRR7657883.sra_2.fastq.gz Test_adapter_contamination.gq.gz.
> SRR7657883.subset_2M.sra_2.fastq.gz

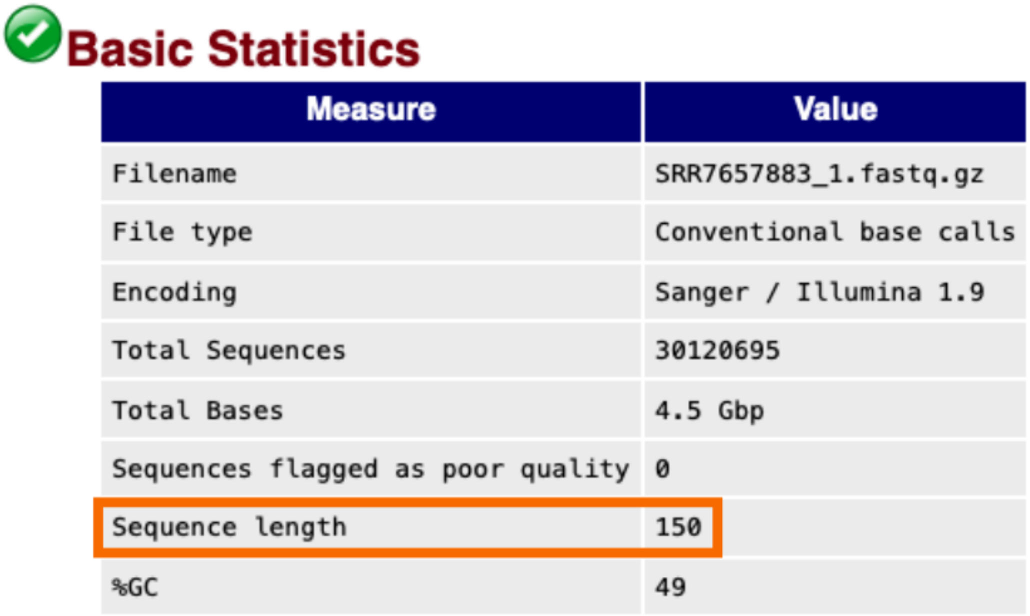
You should see two fastq files called *SRR7657883.sra_1.fastq.gz* and *SRR7657883.sra_1.fastq.gz*. These are the files for read 1 and read 2 of one of the samples we will be working with.

3. Run fastqc on one of the fastq files:

```
fastqc fastq/SRR7657883.sra_1.fastq.gz
```

This creates two files in the *fastq* directory. The first is the QC report in html format and the second is a zip file containing the data summary data used to generate the report. > ⇒ *SRR7657883.sra_1_fastqc.html* > ⇒ *SRR7657883.sra_1_fastqc.zip*

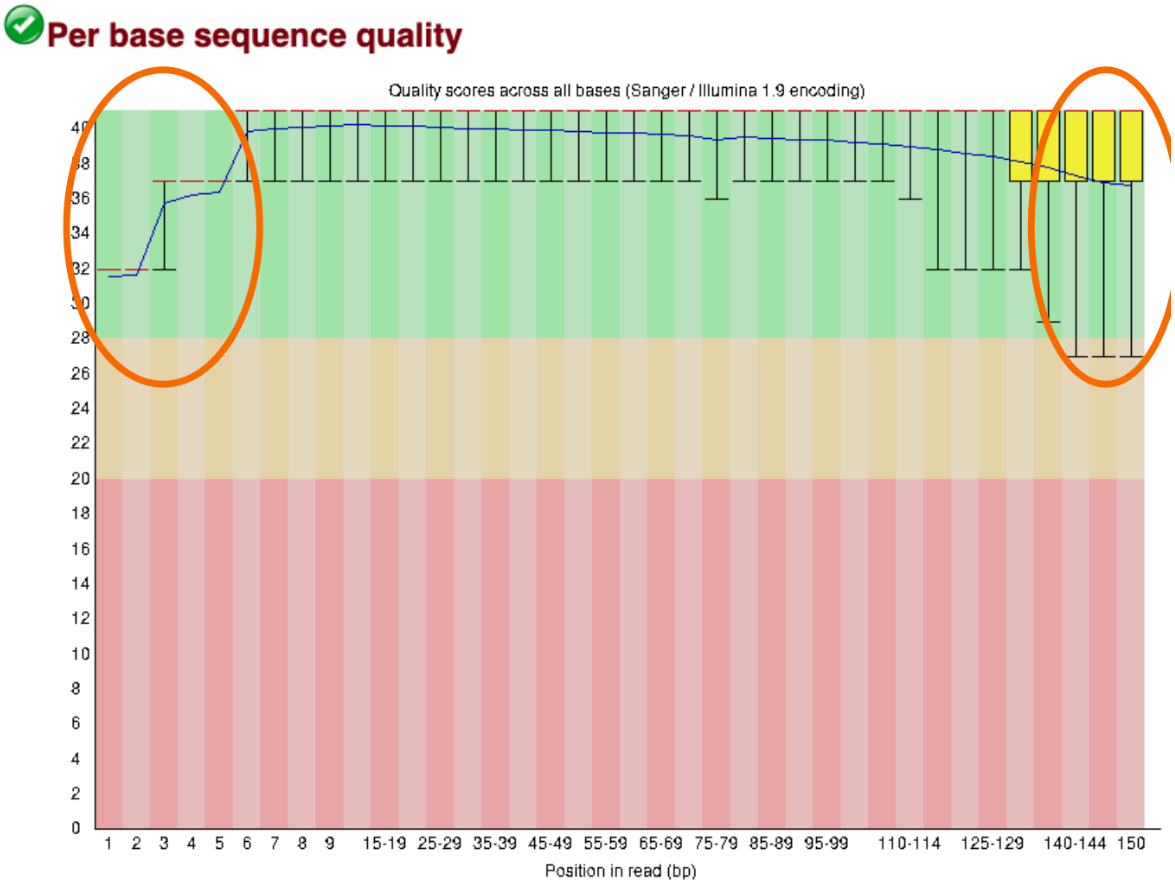
4. Open the html report in a browser and see if you can answer these questions:



Basic Statistics

Measure	Value
Filename	SRR7657883_1.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	30120695
Total Bases	4.5 Gbp
Sequences flagged as poor quality	0
Sequence length	150
%GC	49

A) What is the read length?
150
B) Does the quality score vary through the read length?



Per base sequence quality

Yes, the first few bases and the last few bases are typically of lower quality.
C) How is the data's quality?

Overall, pretty good.