Quality Control for RAW Data – Practical session

1. Open a terminal window
   The programs used in this tutorial are called from the command line. In order to do that, the first step is to open a Terminal window. To do this go to:

   Applications → Accessories → Terminal 

   A new window will open with a prompt ready for an input. Now change to the directory with the sequence data. Type on the terminal:

   cd $HOME/mda13/QC_Raw/

2. Open FastQC program
   To start the FastQC program, you have to type on the terminal window:

   fastqc &

   The FastQC application will start in a new window.
   You can minimize the terminal window, but **do not close it** while using the FastQC application. Otherwise, FastQC will be also closed.

3. Load a file into FastQC
   From the FastQC program, go to:

   File → Open

   And load from the folder **$home/mda13/QC_Raw** the file called

   mirna.fastq

4. Look at the different FastQC result sections and answer the following questions

Questions:

Sample **mirna.fastq**

1. Do a quality control for the sample **using FastQC.**
   What are the parameters you consider bad quality indicators?
   Write down your conclusions:

2. Trim your sample based on its quality with a **minimum quality threshold of 20.**
   You should use Fastx_toolkit, so type on the terminal:
   fastq_quality_trimmer -t 20 -i mirna.fastq -o mirna_t20.fastq

   And now you do the quality control for the new file *mirna_t20.fastq* from FastQC.
   What are the main changes?
   Write down your conclusions:

3. Trim the sample based on its quality with a **minimum quality threshold of 28.**
   You should use Fastx_toolkit, so type on the terminal:
   fastq_quality_trimmer -t 28 -i mirna.fastq -o mirna_t28.fastq

   And now you do the quality control for the new file *mirna_t28.fastq* from FastQC.
   Is there any quality improvement over the previous filter?
   Write down your conclusions:

4. Trim the sample based on its quality with a **minimum quality threshold of 28**, removing the reads with a **length lower than 30.**
   You should use Fastx_toolkit, so type on the terminal:
   fastq_quality_trimmer -t 28 -l 30 -i mirna.fastq -o mirna_t28l30.fastq

   And now you do the quality control for the new file *mirna_t28l30.fastq* from FastQC.
   Is there any quality improvement over the previous step?
   How many reads have been removed?
   Write down your conclusions:

5. Trim the sample based on its quality with a **minimum quality threshold of 28**, removing the reads with a **length lower than 35.**
   You should use Fastx_toolkit, so type on the terminal:
   fastq_quality_trimmer -t 28 -l 35 -i mirna.fastq -o mirna_t28l35.fastq

   And now you do the quality control for the new file *mirna_t28l35.fastq* from FastQC.
   Is there any quality improvement over the previous step?
   How many reads have been removed?
   Write down your conclusions:

Sample **solid.fastq**

1. Do a quality control for the sample using **FastQC**.
   What are the parameters you consider bad quality indicators?
   Write down your conclusions:

2. **Trim** your sample based on its quality with a **minimum quality** threshold of **20**.
   You should use Fastx_toolkit, so type on the terminal:
   fastq_quality_trimmer -t 20 -i solid.fastq -o solid_t20.fastq

   And now you do the quality control for the new file *solid_t20.fastq* from FastQC.
   What are the main changes?
   Do you consider the trimming to be effective?
   Write down your conclusions:

3. **Trim** the sample based on its quality with a **minimum quality** threshold of **28.**
   You should use Fastx_toolkit, so type on the terminal:
   fastq_quality_trimmer -t 28 -i solid.fastq -o solid_t28.fastq

   And now you do the quality control for the new file *solid_t28.fastq* from FastQC.
   Is there any quality improvement over the previous filter?
   Write down your conclusions:

4. Trim the sample based on its quality with a **minimum quality** threshold of **28**, removing the reads with a **length lower than 47.**
   You should use Fastx_toolkit, so type on the terminal:
   fastq_quality_trimmer -t 28 -l 47 -i solid.fastq -o solid_t28l47.fastq

   And now you do the quality control for the new file *solid_t28l47.fastq* from FastQC.
   Is there any quality improvement over the previous step?
   How many reads have been removed?
   Write down your conclusions:

5. Remove the reads with **less than a 90%** with **quality above 20.**
   You should use Fastx_toolkit, so type on the terminal:
   fastq_quality_filter -q 20 -p 90 -i solid.fastq -o solid_q20p90.fastq

   And now you do the quality control for the new file *solid_q20p90.fastq* from FastQC.
   Has the filter been effective?
   How many reads have been removed?
   Write down your conclusions:

Annex 1: Fastx_toolkit

fastq_quality_trimmer

usage: fastq_quality_trimmer [-h] [-v] [-t N] [-l N] [-z] [-i INFILE] [-o OUTFILE]
Part of FASTX Toolkit 0.0.13 by A. Gordon (gordon@cshl.edu)

```
  [-h]        = This helpful help screen.
  [-t N]      = Quality threshold - nucleotides with lower
                quality will be trimmed (from the end of the sequence).
  [-l N]      = Minimum length - sequences shorter than this (after trimming)
                will be discarded. Default = 0 = no minimum length.
  [-z]        = Compress output with GZIP.
  [-i INFILE]  = FASTQ input file. default is STDIN.
  [-o OUTFILE] = FASTQ output file. default is STDOUT.
  [-v]        = Verbose - report number of sequences.
                If [-o] is specified,  report will be printed to STDOUT.
                If [-o] is not specified (and output goes to STDOUT),
                report will be printed to STDERR.
```

fastq_quality_filter

usage: fastq_quality_filter [-h] [-v] [-q N] [-p N] [-z] [-i INFILE] [-o OUTFILE]
Part of FASTX Toolkit 0.0.13 by A. Gordon (gordon@cshl.edu)

```
  [-h]        = This helpful help screen.
  [-q N]      = Minimum quality score to keep.
  [-p N]      = Minimum percent of bases that must have [-q] quality.
  [-z]        = Compress output with GZIP.
  [-i INFILE]  = FASTA/Q input file. default is STDIN.
  [-o OUTFILE] = FASTA/Q output file. default is STDOUT.
  [-v]        = Verbose - report number of sequences.
                If [-o] is specified,  report will be printed to STDOUT.
                If [-o] is not specified (and output goes to STDOUT),
                report will be printed to STDERR.
```

Examples:

- Trimming of sequences with quality lower than 20:

```
fastq_quality_trimmer -t 20 -i <sample>.fastq -o <sample_out>.fastq
```

- Trimming of sequences with quality lower than 20 and minimum length of 30:

```
fastq_quality_trimmer -t 20 -l 30 -i <sample>.fastq -o <sample_out>.fastq
```

- Trimming of sequences with less than 90% of bases with quality above 20:

```
fastq_quality_filter -q 20 -p 90 -i <sample>.fastq -o <sample_out>.fastq
```