NGS data anlysis course

Quality control & Data Preprocessing

Ignacio Medina
David Montaner & Marta Bleda



FastQ Format

- Standard Format for NGS data
- Conversion can be done from sff, fasta + qual, ...
- Extension of the Fasta format
- Text-based formats (easy to use!)
- If not compressed, it can be huge

http://en.wikipedia.org/wiki/FASTQ_format

Quality measurements

Base-calling **error probabilities** are reported by sequencers. Usually in **Phred** (quality) score. Usually coded by ASCII characters

Phred score

$$Q = -10 log_{10} P$$

$$P=10^{\frac{-Q}{10}}$$

http://en.wikipedia.org/wiki/Phred/_quality/_score#Definition

NGS Data Preprocessing Steps

- File parsing: convert to fastq format form sff, fasta + qual
 ...
- Split multiplex samples.
- Quality Control of the raw data.
- Filtering and trimming reads by quality.
- Adapter trimming
- Quality Control of the trimmed and filtered reads

Software

FastQC:

- quality control
- some filtering . . .

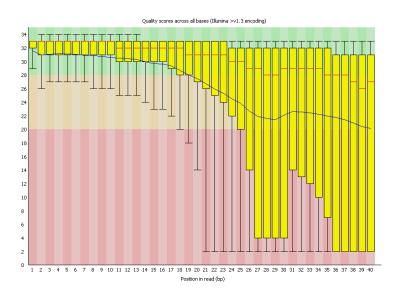
www.bioinformatics.babraham.ac.uk/projects/fastqc

• Cutadapt:

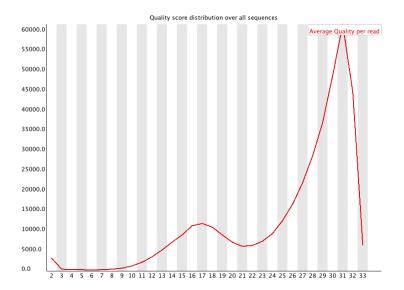
- adapter trimming
- filter reads by length (short, long)
- filter reads by quality

http://code.google.com/p/cutadapt

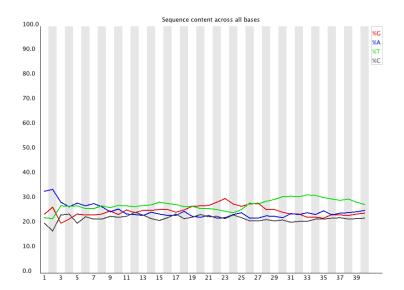
Per Base Sequence Quality



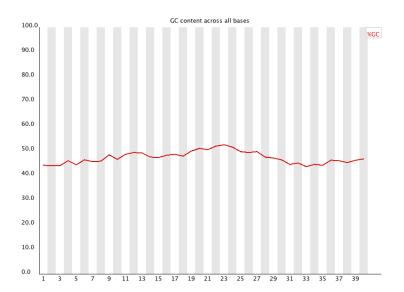
Per Sequence Quality



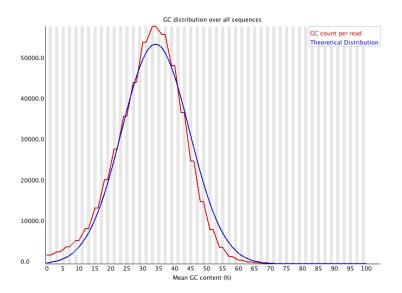
Per Base Sequence Content



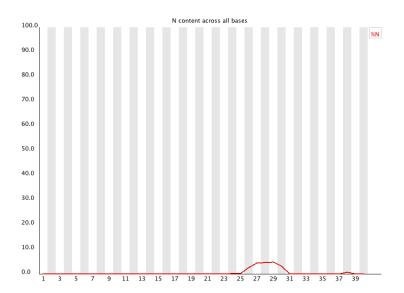
Per Base GC Content



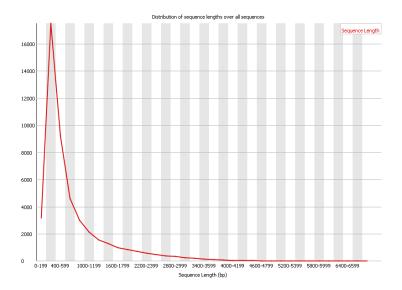
Per Sequence Nucleotide Content



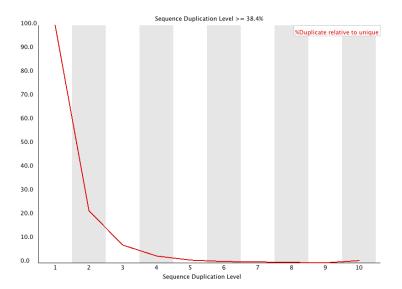
Per Base N Content



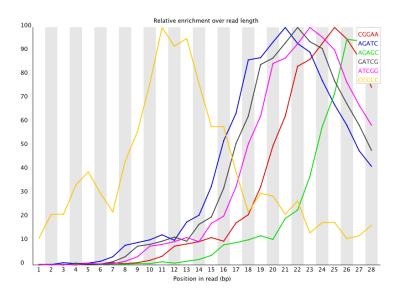
Sequence Length Distribution



Duplicate Sequences Distribution



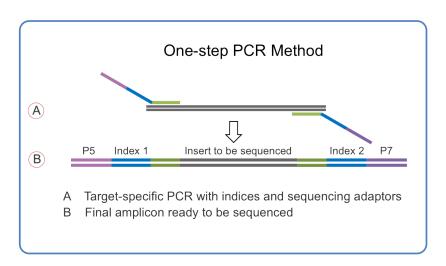
Overrepresenteda Kmers



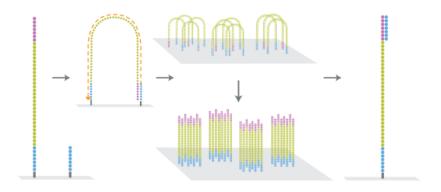
More FastQ examples and documentation

- ... may be found at FastQ home page
 - Example Reports

Sequencing process: PCR primers



Sequencing process: PCR primers



NGS adaptors and Cutadapt

