# NGS data anlysis course

**Quality control & Data Preprocessing** 

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## 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 . . .

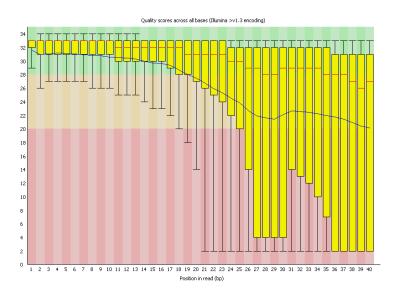
www.bioinformatics.babraham.ac.uk/projects/fastqc

#### • Cutadapt:

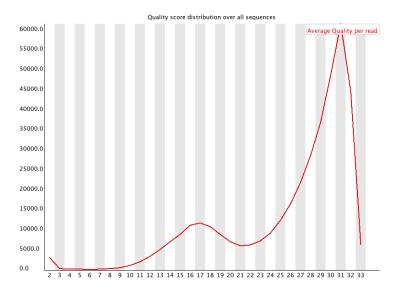
- adapter trimming
- filter reads by length (short, long)
- filter reads by quality

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

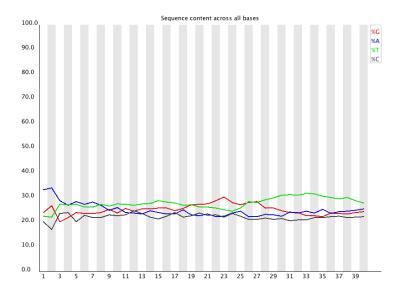
# Per Base Sequence Quality



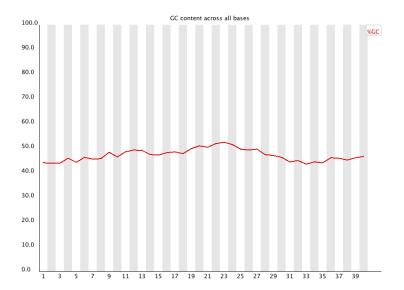
# **Per Sequence Quality**



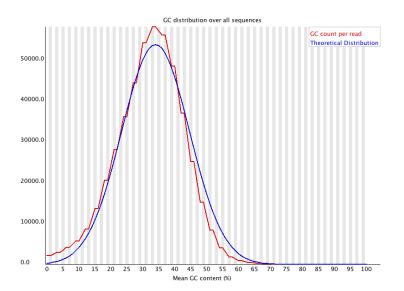
# **Per Base Sequence Content**



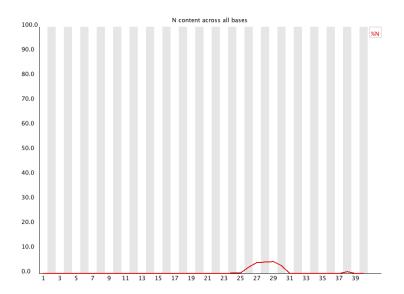
### Per Base GC Content



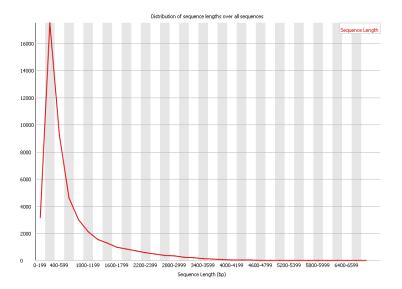
# **Per Sequence Nucleotide Content**



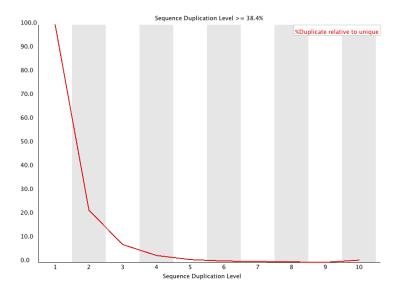
### Per Base N Content



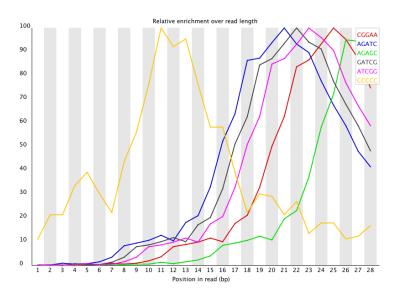
# **Sequence Length Distribution**



# **Duplicate Sequences Distribution**



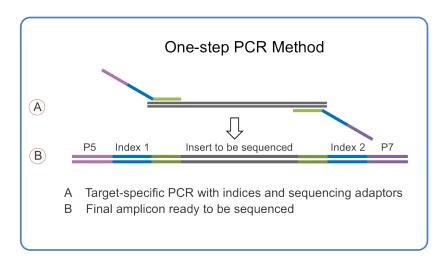
# Overrepresenteda Kmers



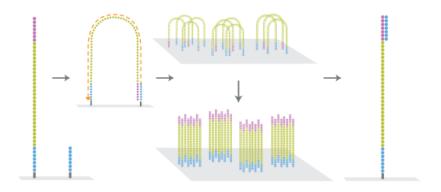
# More FastQ examples and documentation

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

## Sequencing process: PCR primers



# **Sequencing process: PCR primers**



## **NGS** adaptors and Cutadapt

