NGS – variant analysis

Sequencing and alignment

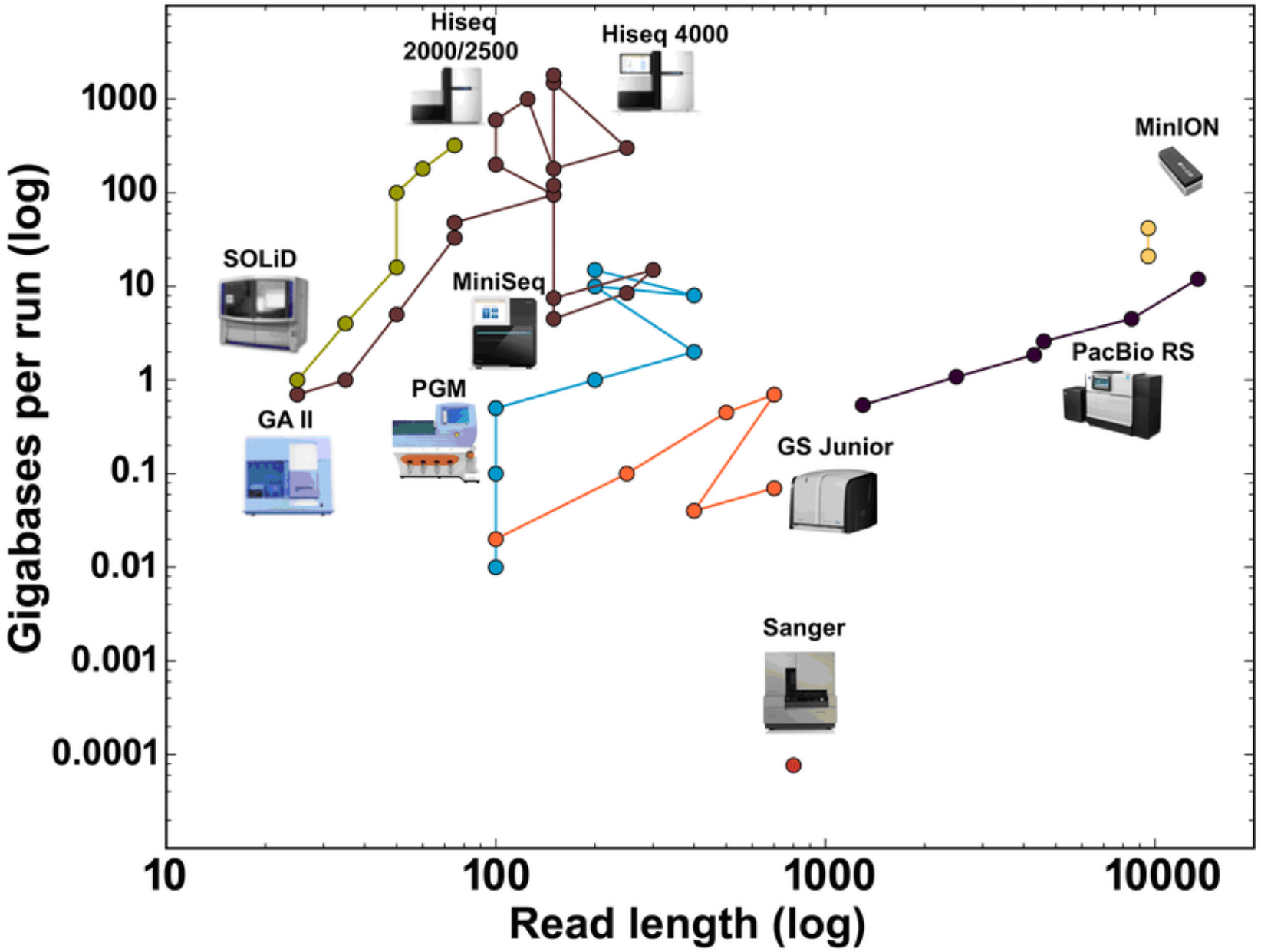


Image from: G. Silva (2016)

Illumina sequencing

- Sequencing-by-synthesis: 2nd generation sequencing
- Massive throughput: up to $500x10^9$ bases/run
- Most used platform today

illumina®

Illumina sequencing

- 50 – 300 bp
- Paired-end (or single-end)

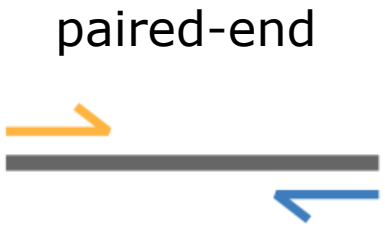


Image from: Illumina (2020)

Illumina libray prep

shear DNA

↓

Ligate adapters

↓

Barcode + p5/p7 sites

↓

PCR: 8-16 cycles

↓

Sequencing

Images from: New England Biolabs Inc. (2020)

fastq

fasta + basequality (fasta + q = fastq)

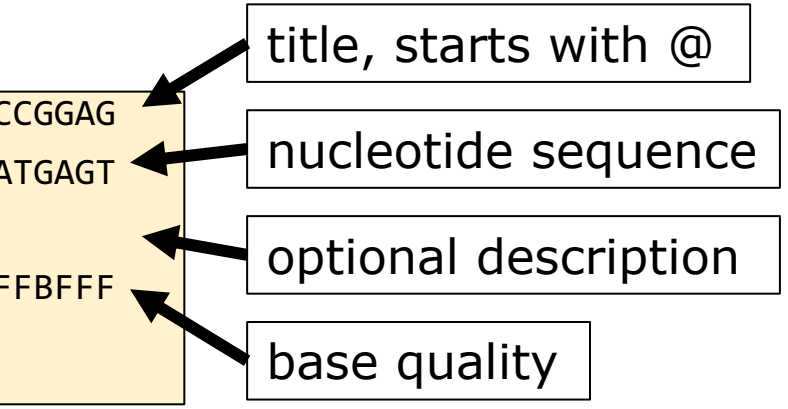
$$BASEQ = -10log_{10}\Pr\{base\ is\ wrong\}$$

$$-10log_{10}(0.01) = 20$$
$$-10log_{10}(0.1) = 10$$
$$-10log_{10}(0.5) = 3$$

fastq

reads.fastq

```
@D00283R:66:CC611ANXX:4:2311:2596:2330 1:N:0:TCCGGAG
ACTCTACGCTCAATAAAGATTTCTGATACGGCTCCTGAAATGCAGAATGAGT
+
B/<<<B<FFFFFFFFFFBBFFFBFFFFBFFFF/FFFFFFFF/BFFFFFBFFF
```



Base quality (phred)

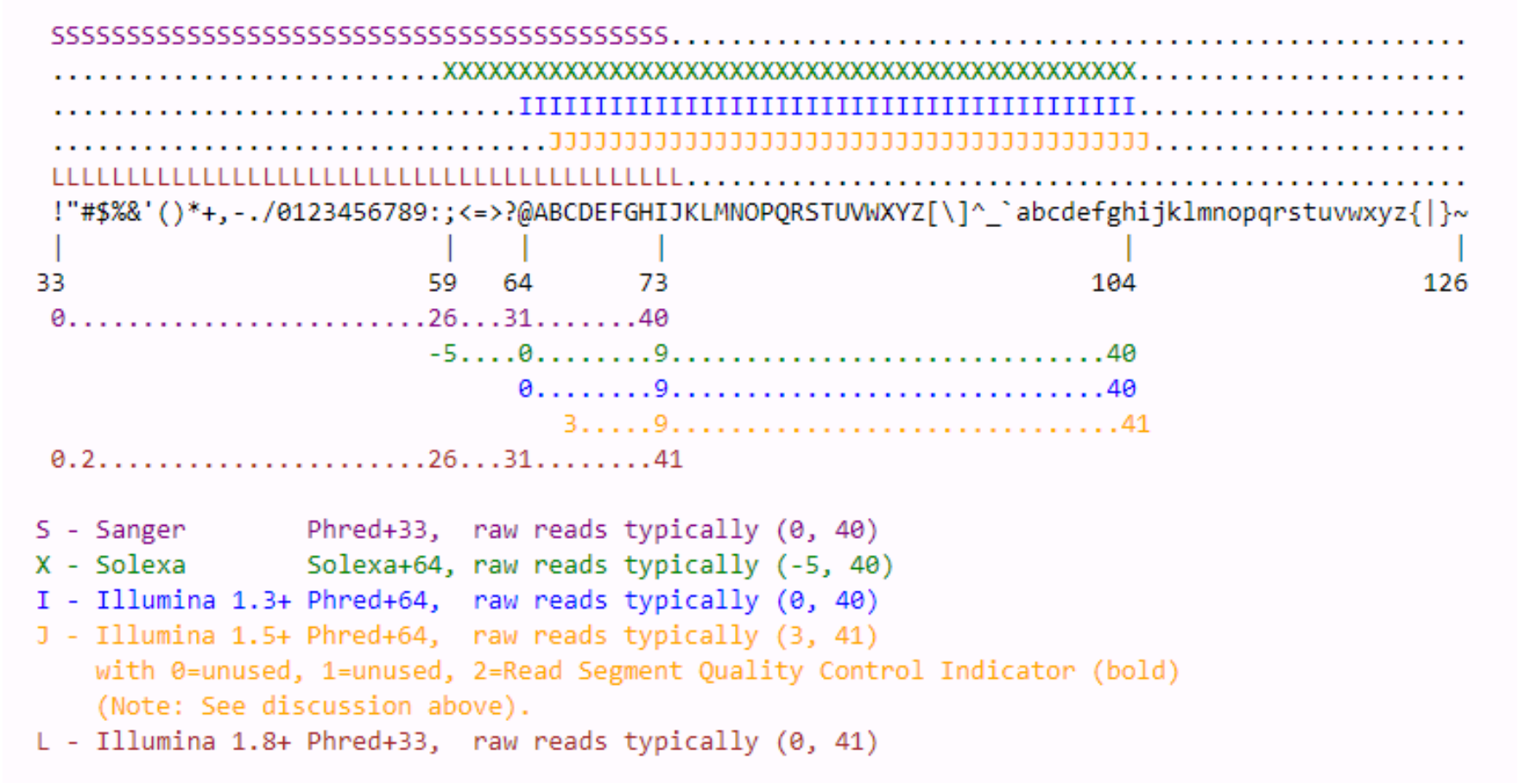
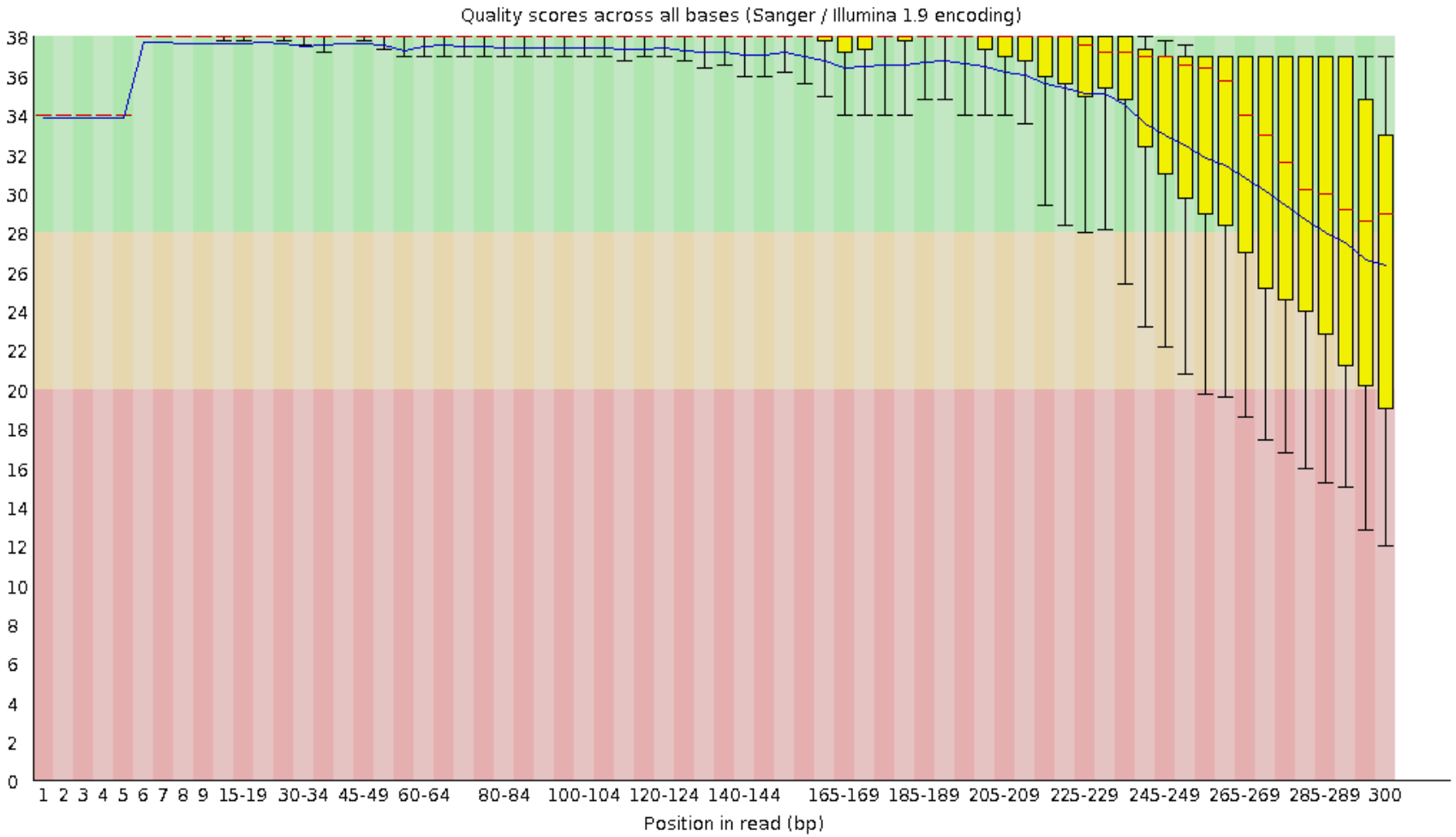
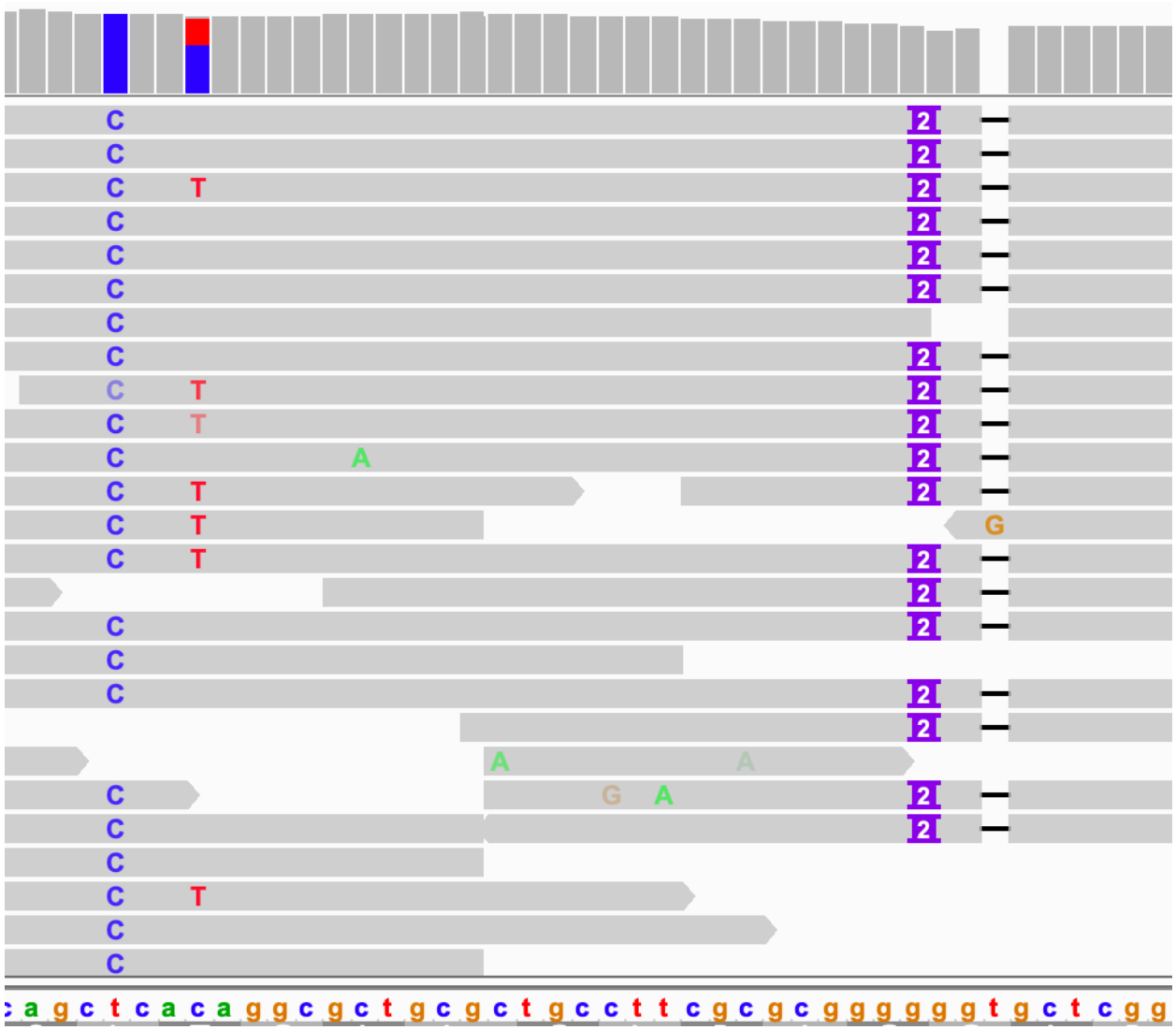


Image from: Wikipedia (https://en.wikipedia.org/wiki/FASTQ_format)

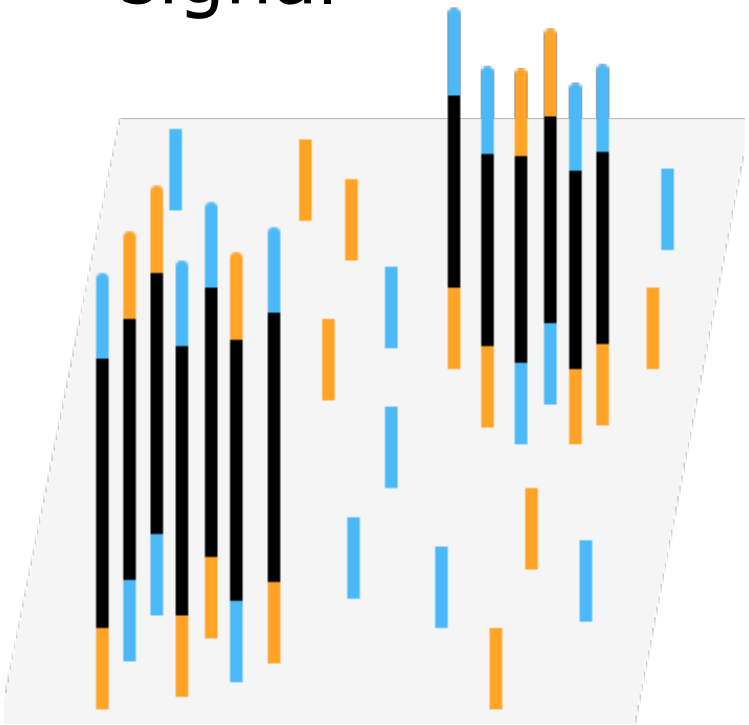
Quiz Question 3

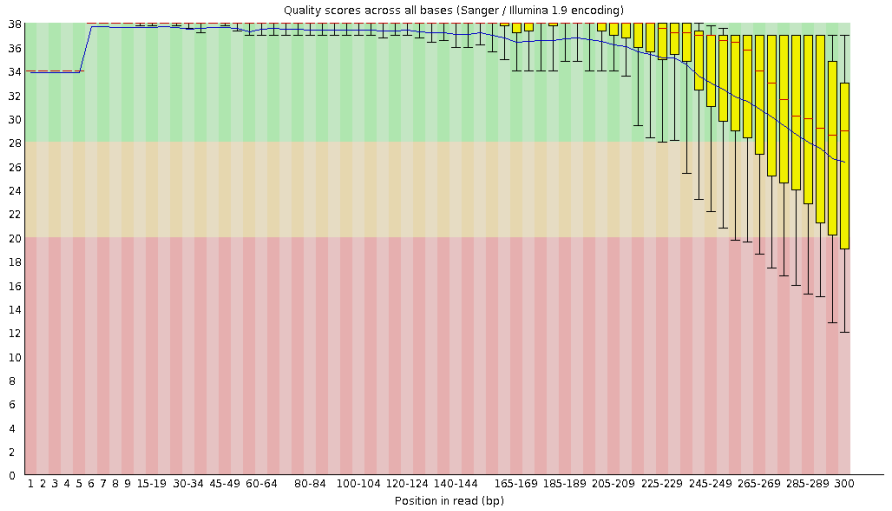

Quality scores across all bases (Sanger / Illumina 1.9 encoding)
38
36
34
32
30
28
26
24
22
20
18
16
14
12
10
8
6
4
2
0
1 2 3 4 5 6 7 8 9 15-19 30-34 45-49 60-64 80-84 100-104 120-124 140-144 165-169 185-189 205-209 225-229 245-249 265-269 285-289 300
Position in read (bp)



Illumina - limitations

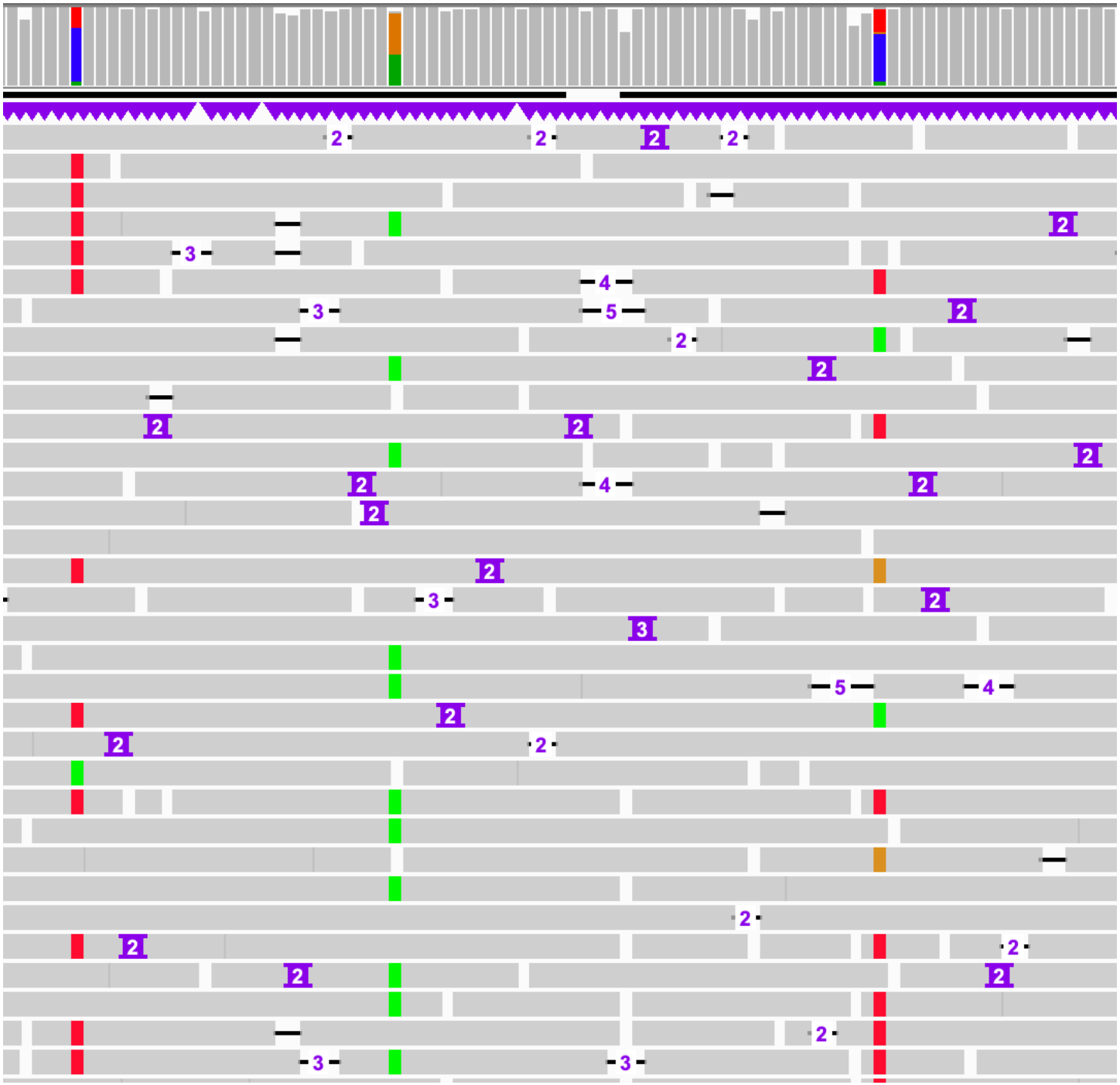
- Bridge amplification
- Lengths are limited by out-of-phase of signal





Long reads (3rd generation)

- Crux: maximizing signal from a single-molecule base read-out
- Single molecule, so no out-of-phase signal
- Two frequently used platforms:
  - PacBio SMRT sequencing
  - Oxford Nanopore Technology



Quiz Question 4

Long reads

- More error -> difficulties for variant analysis
- But:
  - PacBio CCS: high baseQ + no bias
  - Long reads can have higher mapping qualities
  - Long reads improve haplotyping

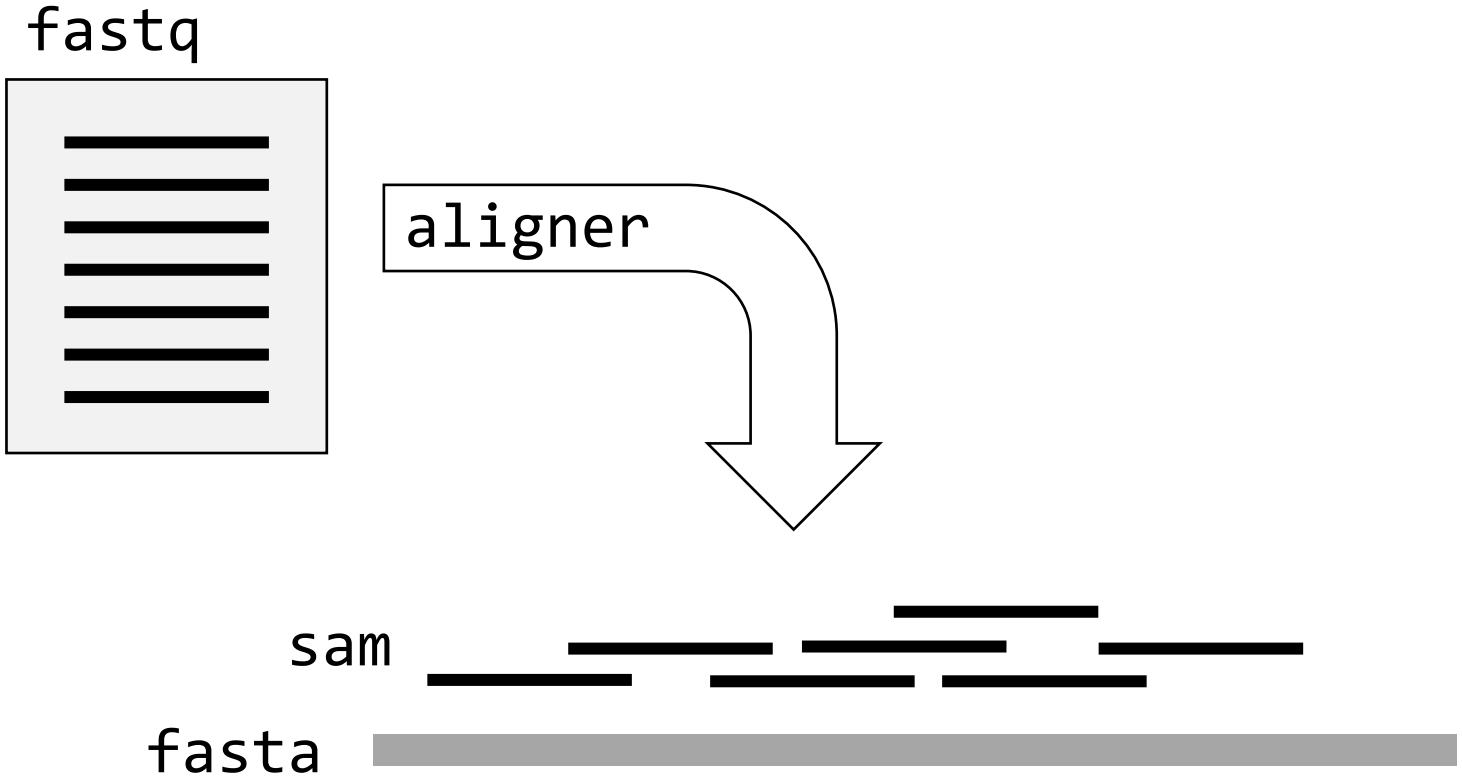
PACBIO®

Oxford NANOPORE Technologies

What to sequence?

- Whole genome/metagenome
- Reduced representation:
  - Bait capture/whole exome sequencing
  - Restriction Enzyme based (e.g. RAD seq)
  - Amplicon sequencing
  - RNA-seq

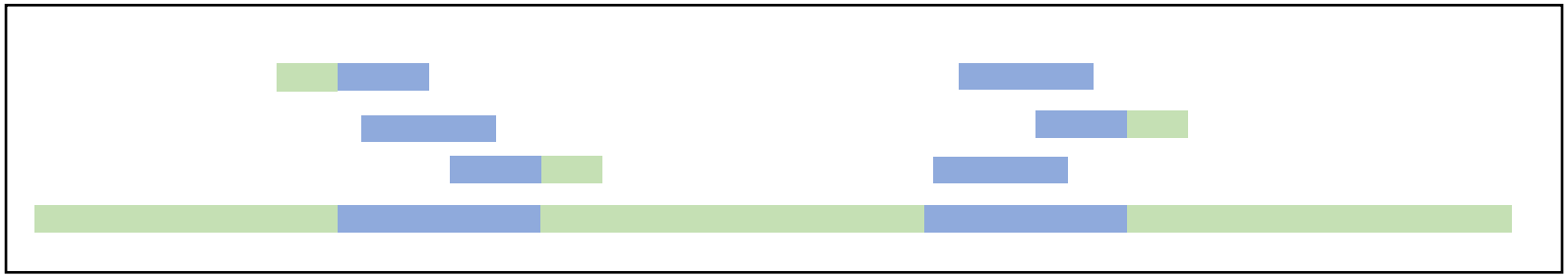
Read alignment (phred)



Software

- Basic alignment:
  - `bowtie2`
  - `bwa-mem`
- Long reads:
  - `minimap2`

Mapping quality



$$MAPQ = -10log_{10}\Pr\{mapping\ position\ is\ wrong\}$$

$$-10log_{10}(0.01) = 20$$
$$-10log_{10}(0.5) = 3$$

sam

sequence alignment format

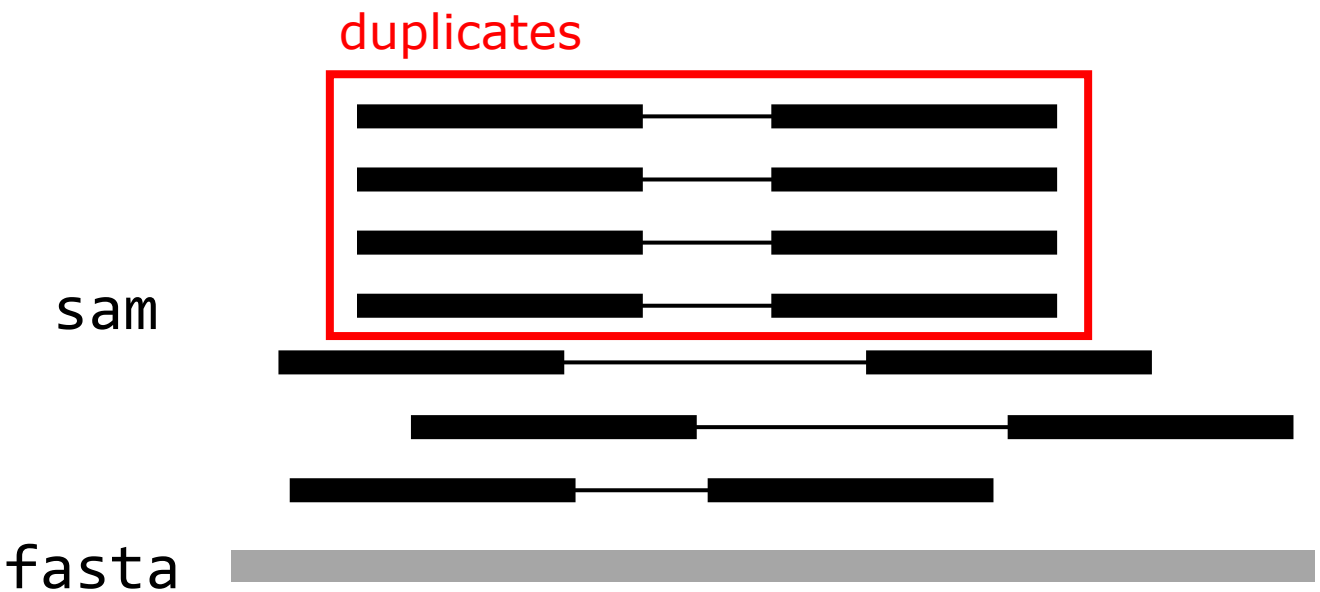
sam header

```
@HD     VN:1.0  SO:coordinate
@SQ     SN:U00096.3     LN:4641652
@PG     ID:bowtie2      PN:bowtie2      VN:2.4.1
CL: "/opt/miniconda3/envs/ngs/bin/bowtie2-align-s \
--wrapper basic-0 \
-x /home/ubuntu/ecoli/ref_genome//ecoli-strK12-MG1655.fasta \
-1 /home/ubuntu/ecoli/trimmed_data/paired_trimmed_SRR519926_1.fastq \
-2 / home/ubuntu/ecoli/trimmed_data/paired_trimmed_SRR519926_2.fastq"
```

SAM column	**example**
read name	SRR519926.5
flag	89
reference	U00096.3
start position	61
mapping quality	42
CIGAR string	214M
reference name mate is mapped	=
start position mate	476
fragment length	515
sequence	CATCACCATTCCCAC
base quality	@>4:4C@89+&9CC@
optional	AS:i:-2
optional	XN:i:0

Quiz Question 5

Marking duplicates



Marking duplicates

- Variant calling: each read is an independent observation of the genome
- Duplicates (can) have the same molecular origin -> not independent
- Removing duplicates probably doesn't have a big effect on variant analysis

Ebbert MTW et al. (2016) Evaluating the necessity of PCR duplicate removal from next-generation sequencing data and a comparison of approaches. BMC Bioinformatics.

Unique Molecular Identifiers

- UMI added before PCR reaction
- Detect PCR duplicates and PCR errors