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What is HTS?

General presentation on the technology

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Plant Analytics

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Laboratories**

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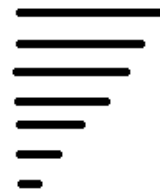
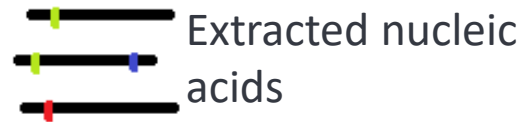
Terms related to HTS

- High throughput sequencing (HTS) = Next generation sequencing (NGS) = deep sequencing
- Different platforms: Illumina dye sequencing, PacBio's SMRT, Ion Torrent, Oxford Nanopore, SOLiD...
- Different techniques: amplicon sequencing (eg. metabarcoding), shotgun sequencing (eg. whole genome sequencing, siRNA sequencing)



Sanger sequencing vs HTS

- Sanger sequencing:
- Targeted
- Nucleic acids are prepared for sequencing by PCR-reaction that produces different length products ending with labeled nucleotides
- Sequencer separates the products by length and detects the labeled nucleotides
- One consensus sequence is produced



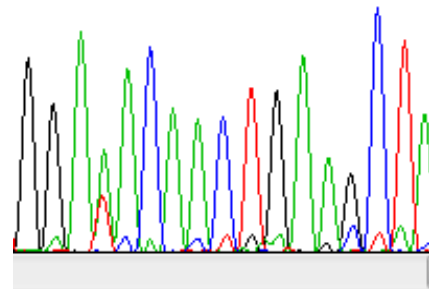
Preparation for sequencing



200 210
GG A A C A A C T G A A S C T A

Output

GGAAACAAC**T**GAAGCTA
GGAAACAAC**C**CTA
GGAT**T**ACAAC**T**GAAGCTA

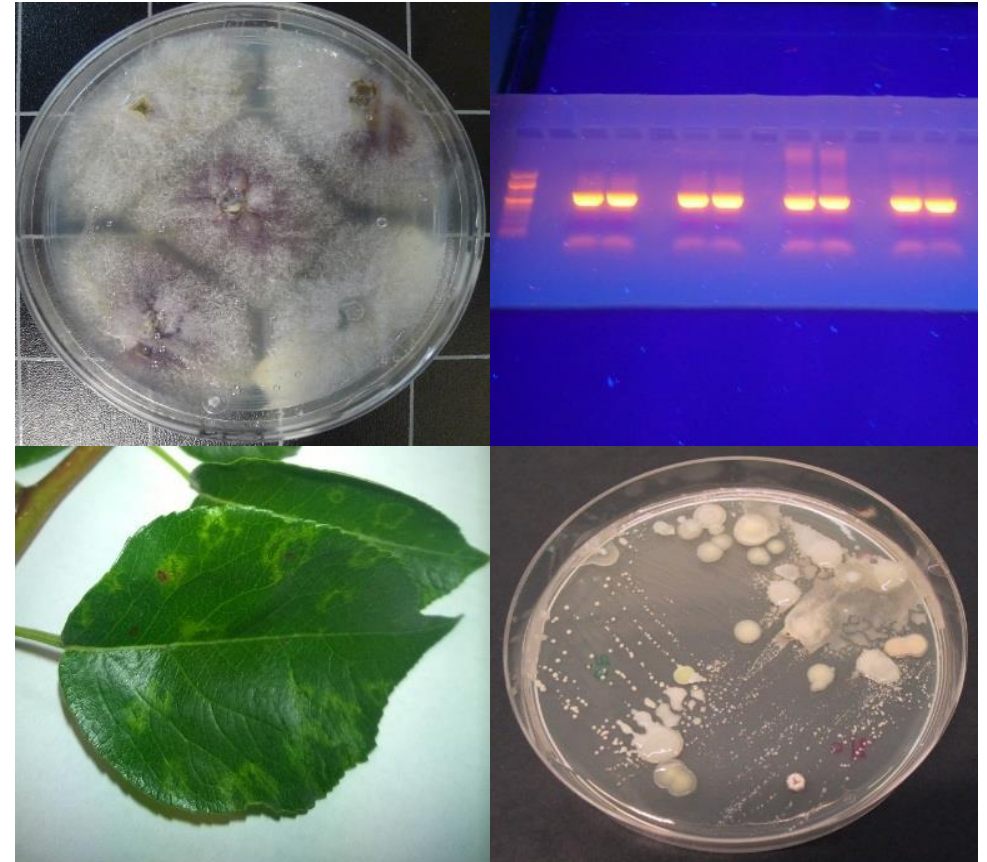


- HTS
- Targeted or non-targeted
- Nucleic acids are prepared for sequencing by library preparation to obtain right amount of right size nucleic acids with flanking adapters (depending on the platform)
- Sequencers detect the nucleic acid incorporation event during elongation or read the strand directly (depending on the platform)
- Individual sequences for each nucleic acid in the sample is produced



HTS procedure starts with (sampling and) nucleic acid extraction

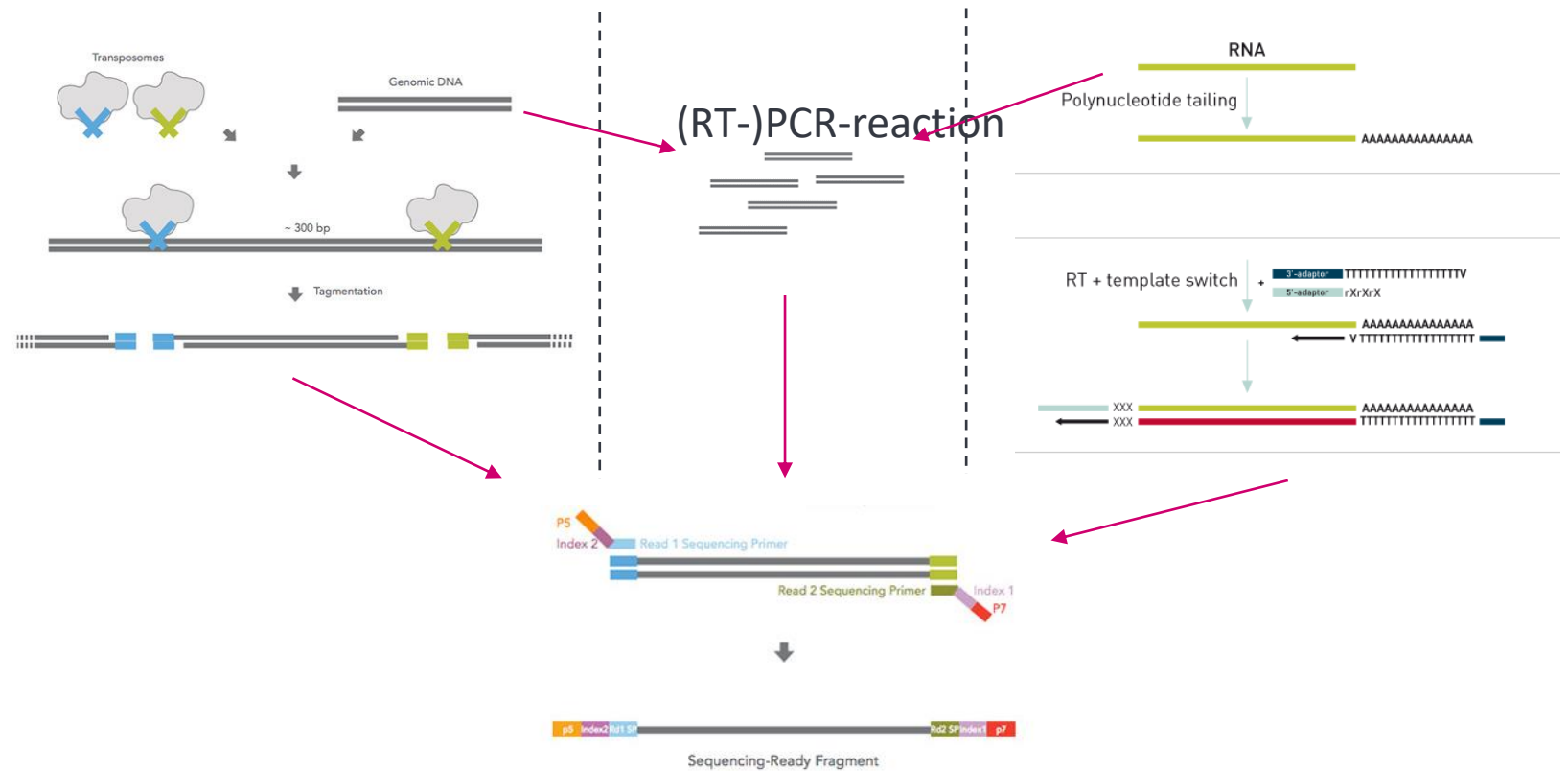
- matrix with multiple organisms, e.g.
 - plant tissue containing microorganisms
 - environmental samples
 - spore traps
- isolated organisms e.g. microbial colonies on artificial media
- The nucleic acids can be
 - genomic DNA or RNA
 - total DNA or RNA
 - small RNAs
 - double-stranded RNAs





Library preparation

- The library preparation produces a sufficient amount of nucleic acids of appropriate size that are flanked with adapters (oligonucleotide sequences) required for sequencing
- Note, direct RNA sequencing also possible

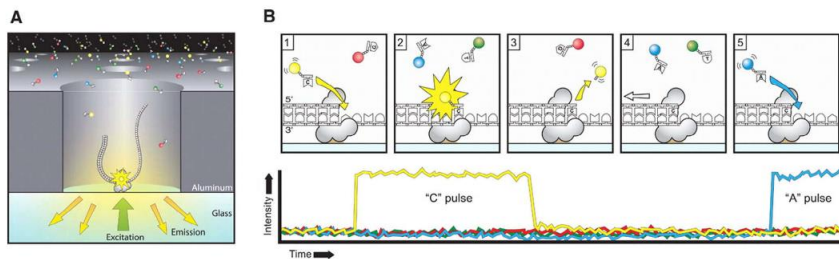




Sequencing

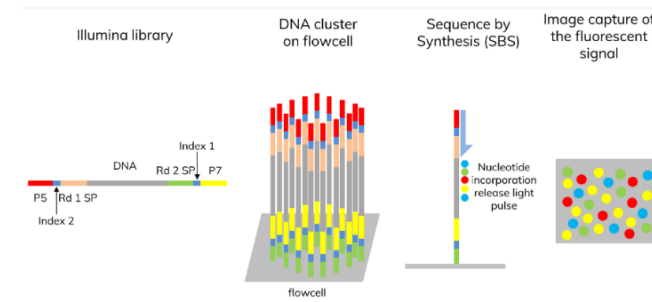
- This step produces the sequences and corresponding quality scores usually in FASTQ format

PacBio Single molecule real-time sequencing measuring kinetic changes caused by nucleotide incorporation



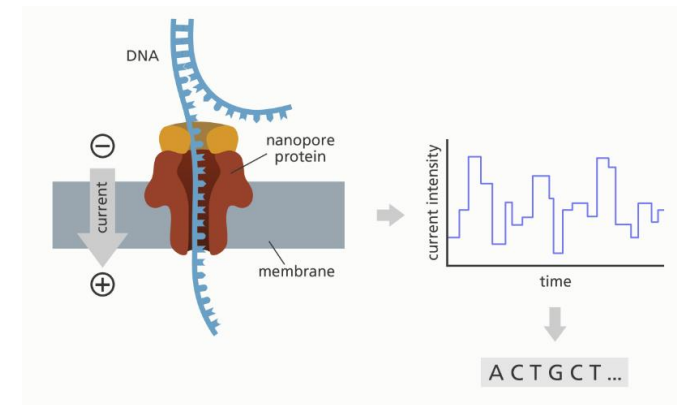
<https://www.cd-genomics.com/pacbio-smrt-system-single-molecule-real-time-sequencing.html>

Illumina dye sequencing capturing fluorescent signals caused by incorporation of labeled nucleotides



<https://www.mdpi.com/2075-4418/13/3/373>

Nanopore sequencing monitoring changes to an electrical current as nucleic acids pass through a protein nanopore



<https://www.yourgenome.org/facts/what-is-oxford-nanopore-technology-ont-sequencing/>



Analysis of raw reads (including quality control)

- Bioinformatic analysis that may include:
 - Elimination of low quality reads
 - Demultiplexing for pooled samples
 - Primer/adaptor/index removal
 - Duplicated or background reads removal
 - Pairing and merging reads
 - Artefacts removal

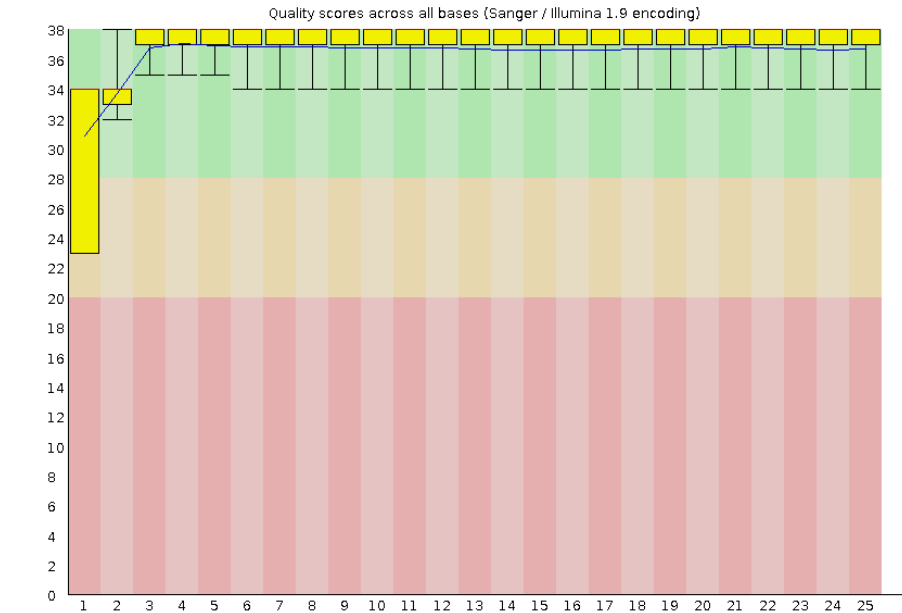


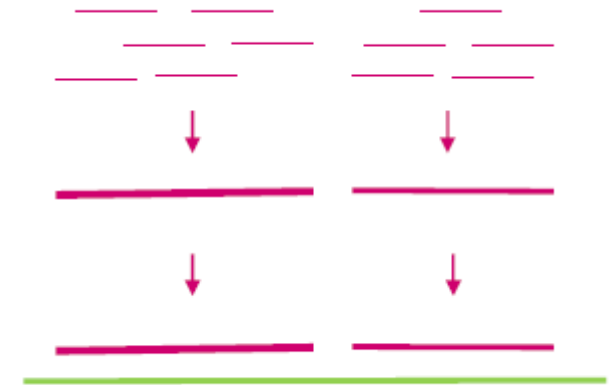
Table 1: Quality Scores and Base Calling Accuracy

Phred Quality Score	Probability of Incorrect Base Call	Base Call Accuracy
10	1 in 10	90%
20	1 in 100	99%
30	1 in 1,000	99.9%
40	1 in 10,000	99.99%
50	1 in 100,000	99.999%



Identification of targets

- Bioinformatic step including optional steps
 - Direct annotation of individual reads
 - De novo assembly of (short) reads to create longer contigs
 - Clustering of amplicon sequences based on similarity
 - Mapping of reads on reference sequence
- Leading to annotation of the sequences, e.g.
 - Taxonomic classification
 - Functional annotation
 - Variant calling





Analysis of controls

- Bioinformatic step in which the controls used in the experiment are checked against predefined quality metrics and thresholds to
 - Evaluate contamination
 - Evaluate whether targets are found as expected
 - Find possible sequencing errors
 - Evaluate whether the results need to be confirmed



Applications in plant health

- Identification of pests causing novel diseases
- Development of specific tests (generating sequence data)
- Surveillance programmes
- Detection of pests in propagation material and nuclear stocks
- Post-entry quarantine testing
- Other routine testing



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Thank you

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