

DNA SEQUENCING

Techniques:

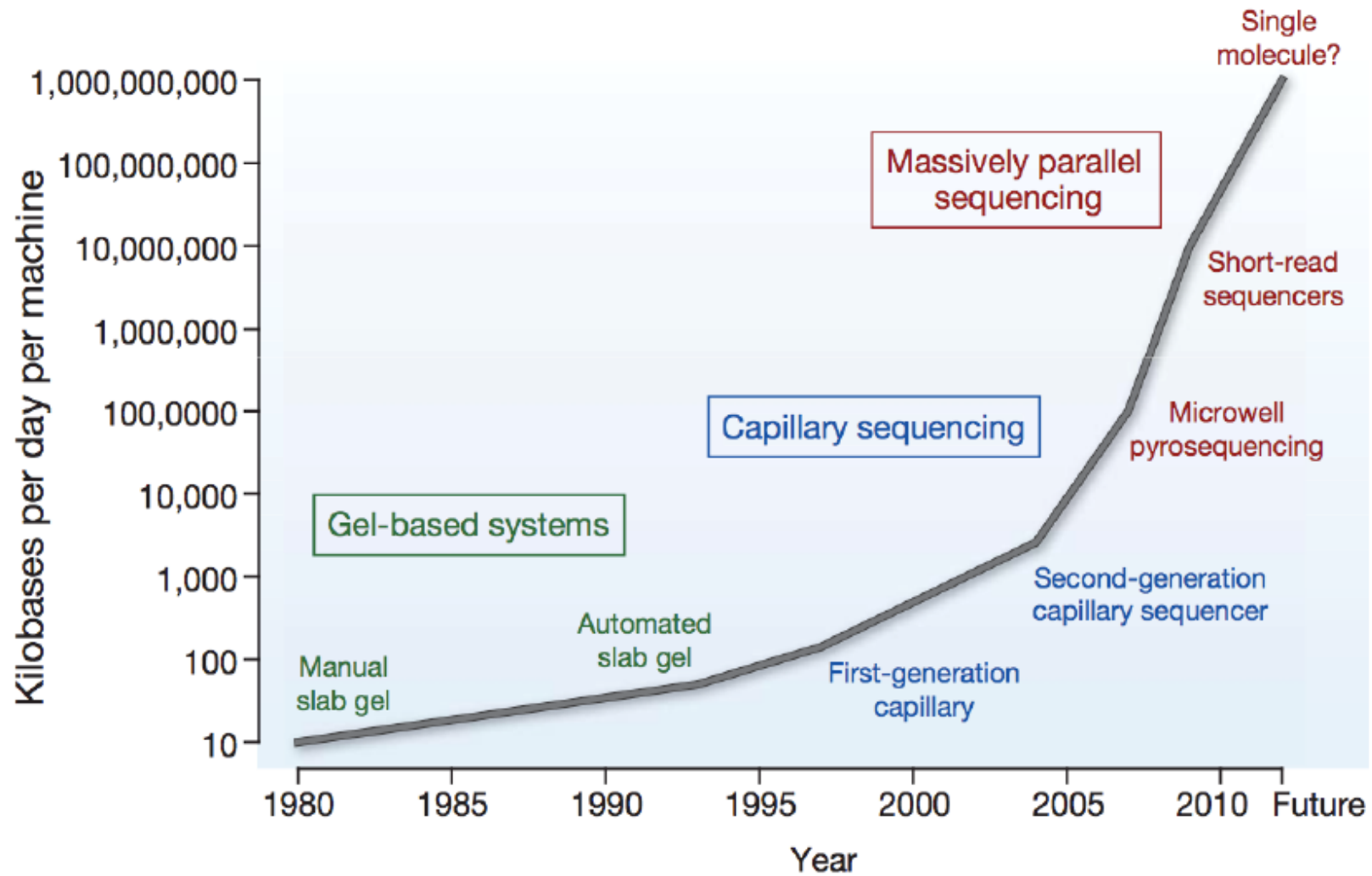
1. Maxam e Gilbert: first method

2. Sanger Sequencing:
basis for all sequencing techniques

3. Massive Parallel Sequencing

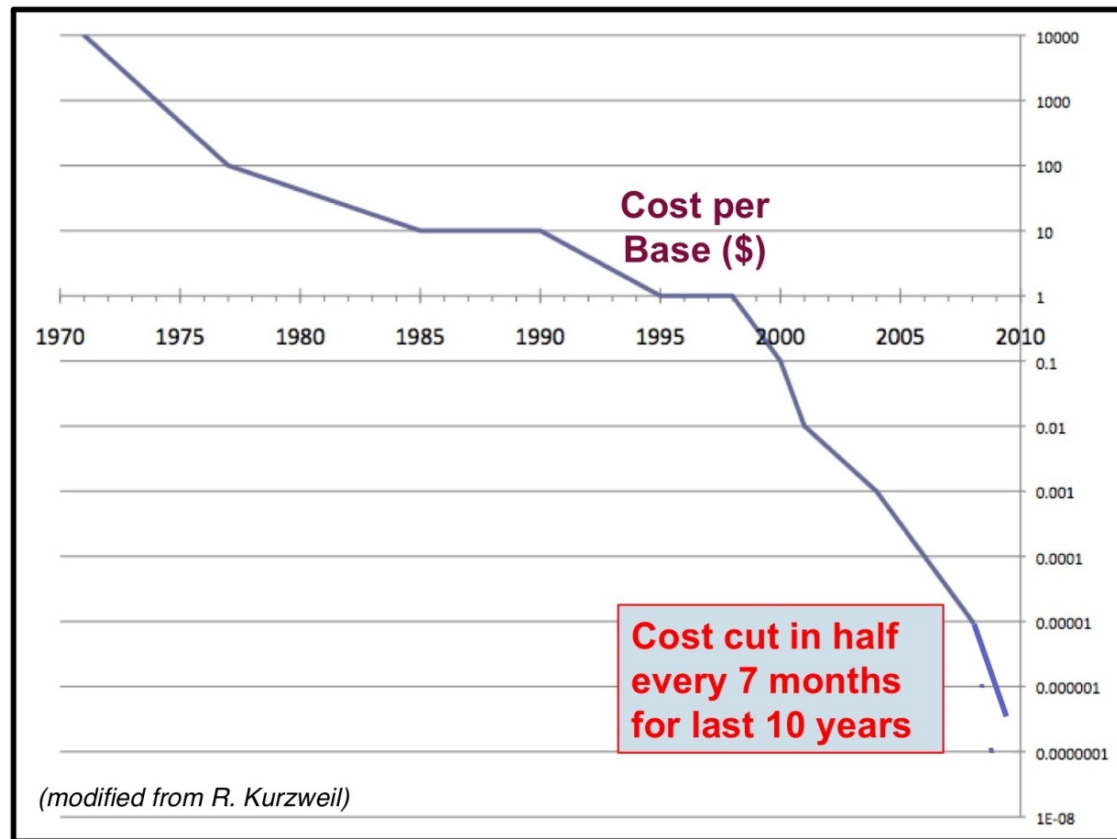
DNA sequencing includes several methods and technologies that are used for determining the order of the nucleotide bases—adenine, guanine, cytosine, and thymine—in a molecule of DNA.

The History of DNA Sequencing Technology



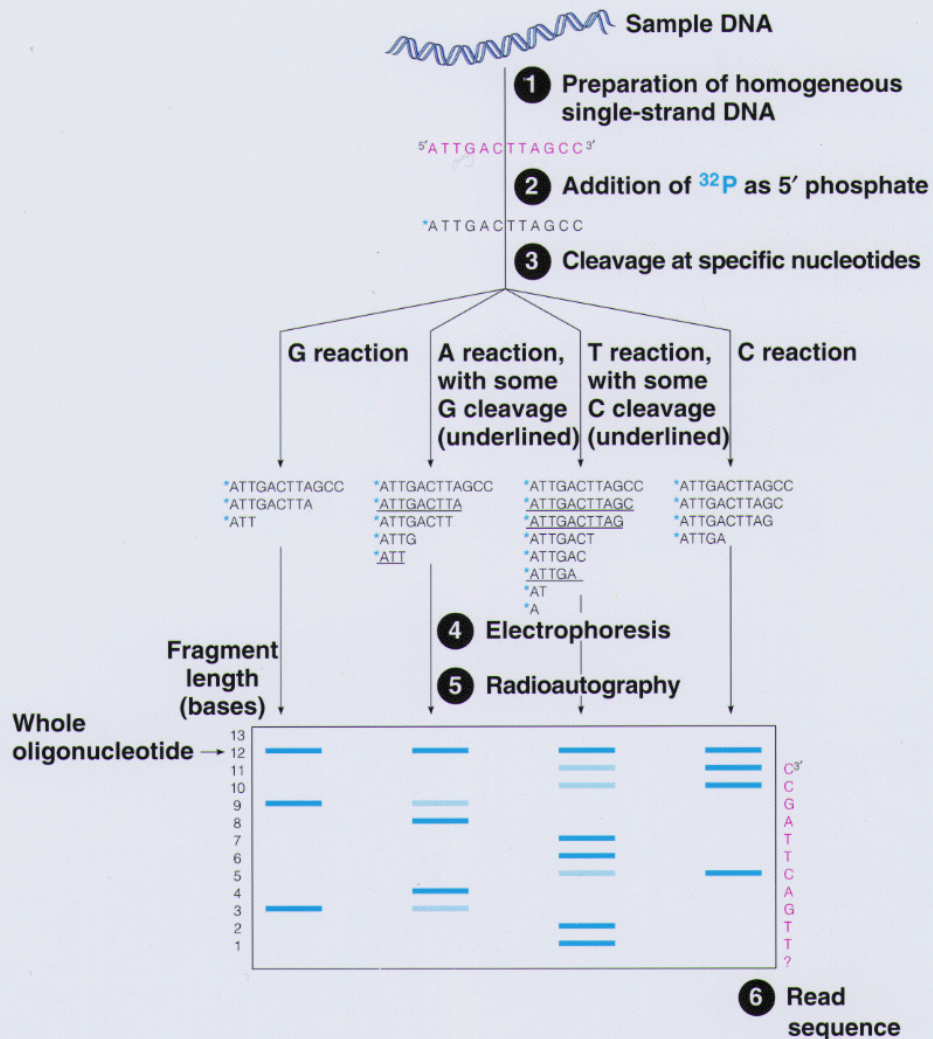
Quickly reduced Cost

Decreasing Cost of DNA Sequencing

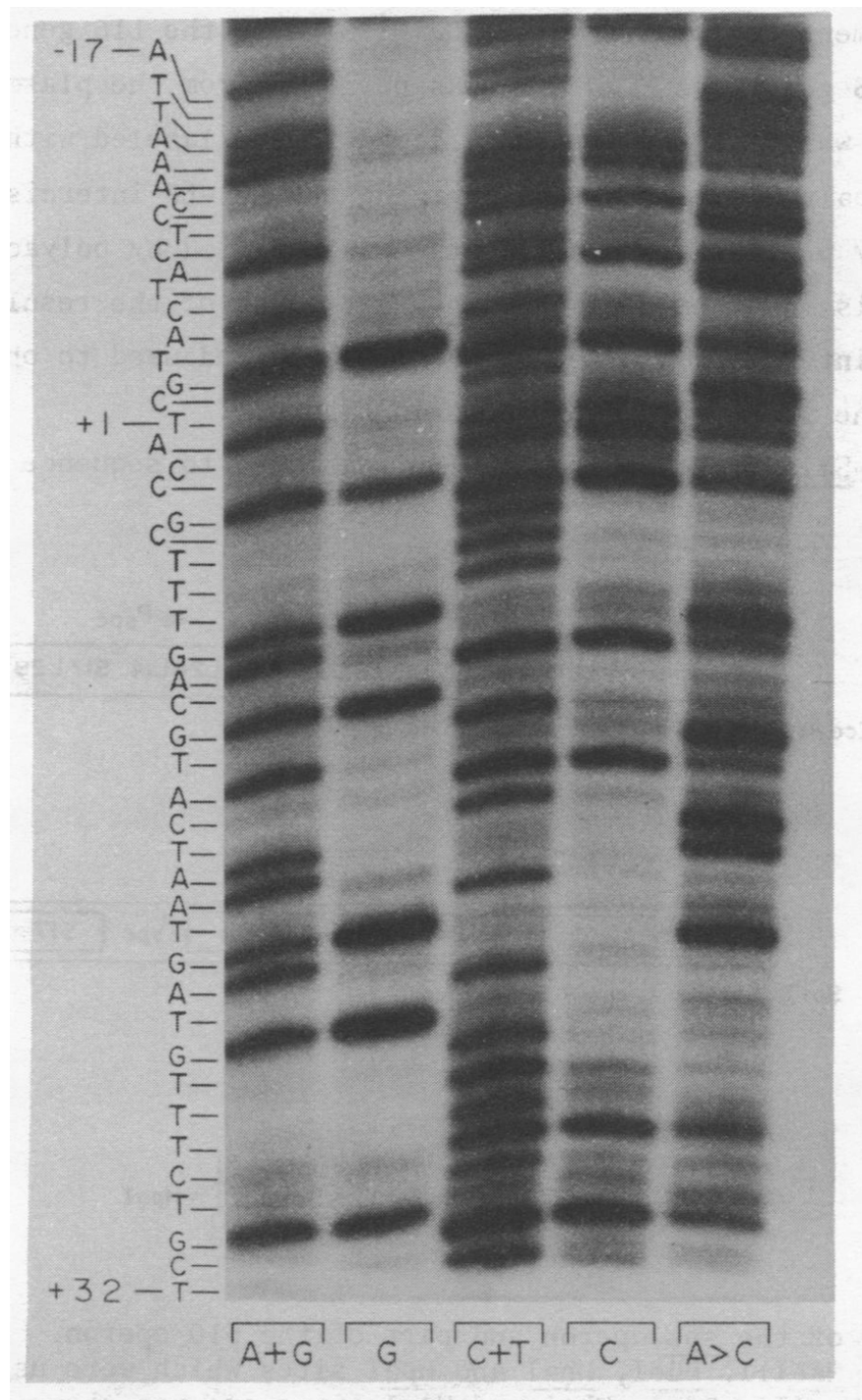


1. Maxam-Gilbert Method chemical sequencing

Figure 4A.4 Sequencing an oligonucleotide by the Maxam-Gilbert method



- Denature a double-stranded DNA to single-stranded by increasing temperature.
- Radioactively label one 5' end of the DNA fragment to be sequenced by a kinase reaction using gamma- ^{32}P -ATP.
- Cleave DNA strand at specific positions using chemical reactions.
 - Reaction 1: Guanines (and to some extent the adenines) are methylated by dimethyl sulfate
 - Reaction 2: Purines (A>>G) are depurinated using formic acid,
 - Reaction 3: Pyrimidines (T>>C) are hydrolysed using hydrazine.
 - Reaction 4: Hydrazine + salt (sodium chloride) inhibits the reaction of thymine for the C-only reaction.
- NOTE: concentration of chemicals is chosen to only cause 1 modification in a molecule of interest
- The modified DNAs may then be cleaved by hot piperidine
- Now in four reaction tubes, we will have several differently sized DNA strands that carry ^{32}P at 5'end
- Fragments are electrophoresed in high-resolution acrylamide gels for size separation.
- These gels are placed under X-ray film, which then yields a series of dark bands which show the location of radiolabeled DNA molecules. The fragments are ordered by size and so we can deduce the sequence of the DNA molecule.



1. Maxam-Gilbert Method chemical sequencing

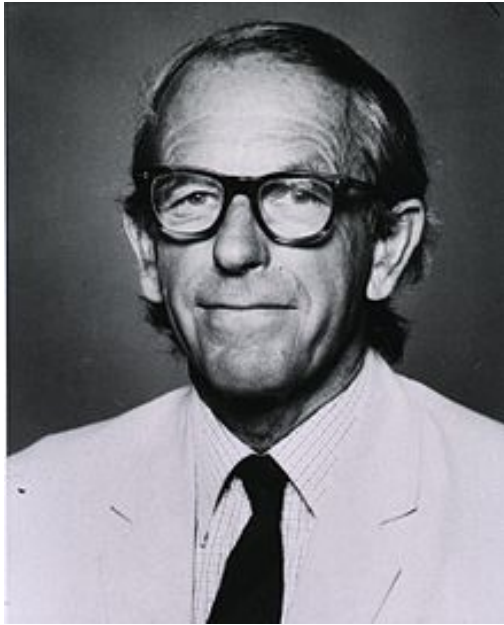
Pros

Maxam-Gilbert sequencing was at one point more popular than the Sanger method. Purified DNA could be used directly, while the Sanger method required that each read start be cloned for production of single-stranded DNA.

Cons

Cons included difficulties scaling up, and the handling of X-rays and radiolabeling, which were harmful to technicians.

2. Sequenziamento di DNA mediante il metodo di Sanger



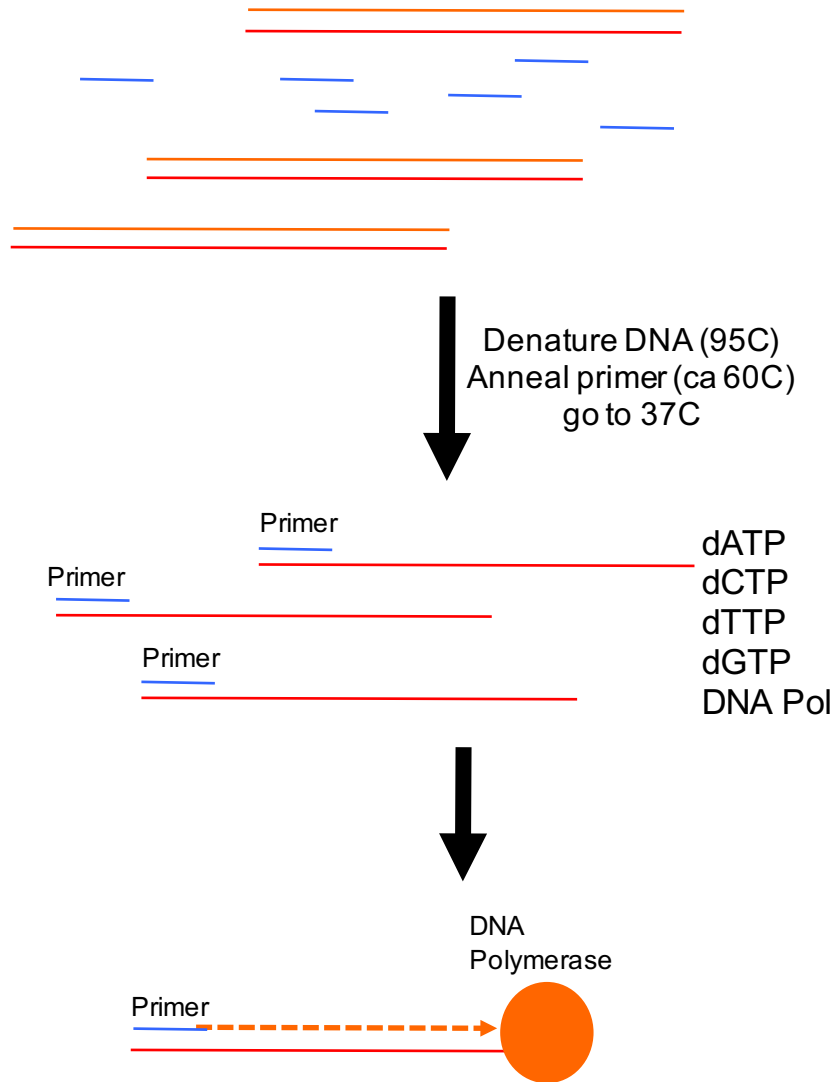
Sequenziamento con
il metodo dei **dideossinucleotidi**

F. Sanger 13 agosto 1918 – 19 novembre 2013

Due premi Nobel. Uno per il sequenziamento dell'insulina ed uno per il sequenziamento del genoma del fago ϕ -X174



General concept in a Sanger sequencing reaction: The synthesis of a new strand of DNA from a ss template DNA



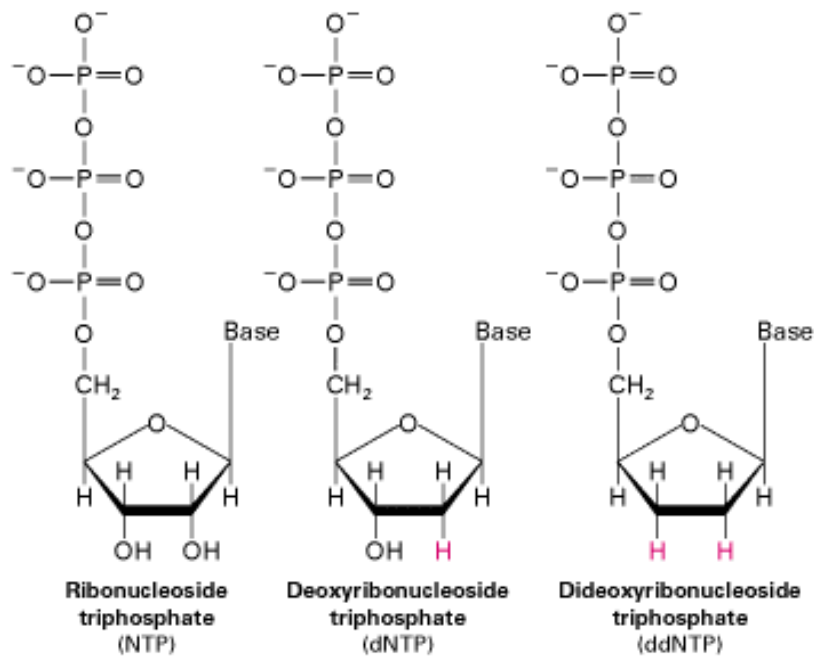
- 1 Primer = oligonucleotide
- Large number of Identical dsDNA molecules that contains primer target site

add dATP, dTTP, dCTP, dGTP
and DNA polymerase

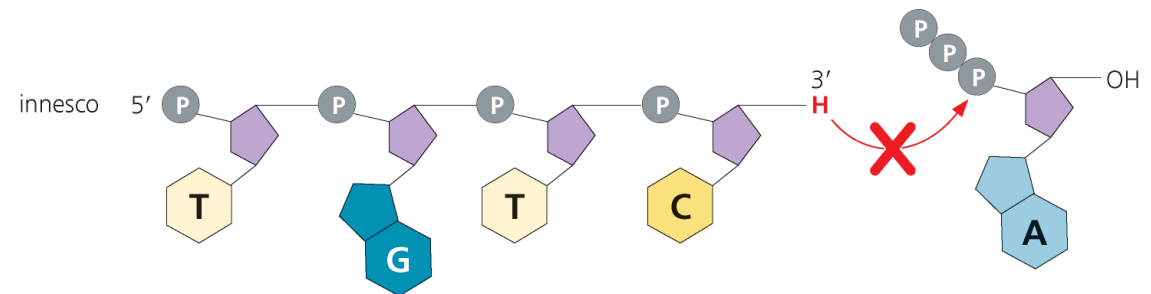
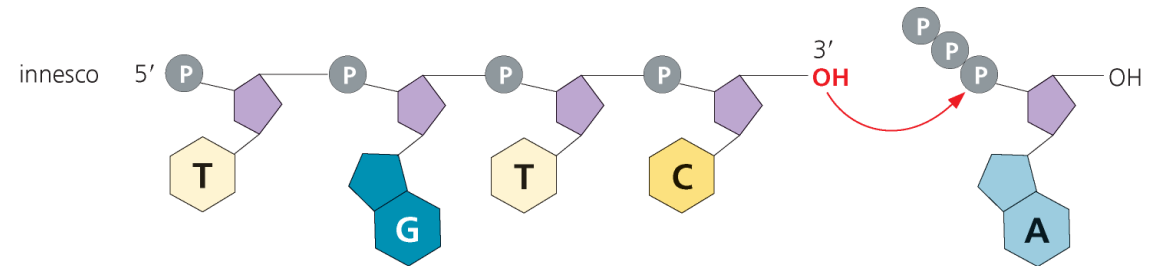
Polymerase elongates template DNA

PROBLEM: HOW CAN WE READ THE NEWLY SYNTHESIZED DNA SEQUENCE??

A great trick: using di-deoxyribonucleoside triphosphates to terminate the synthesis of DNA molecules



deoxyadenine triphosphate



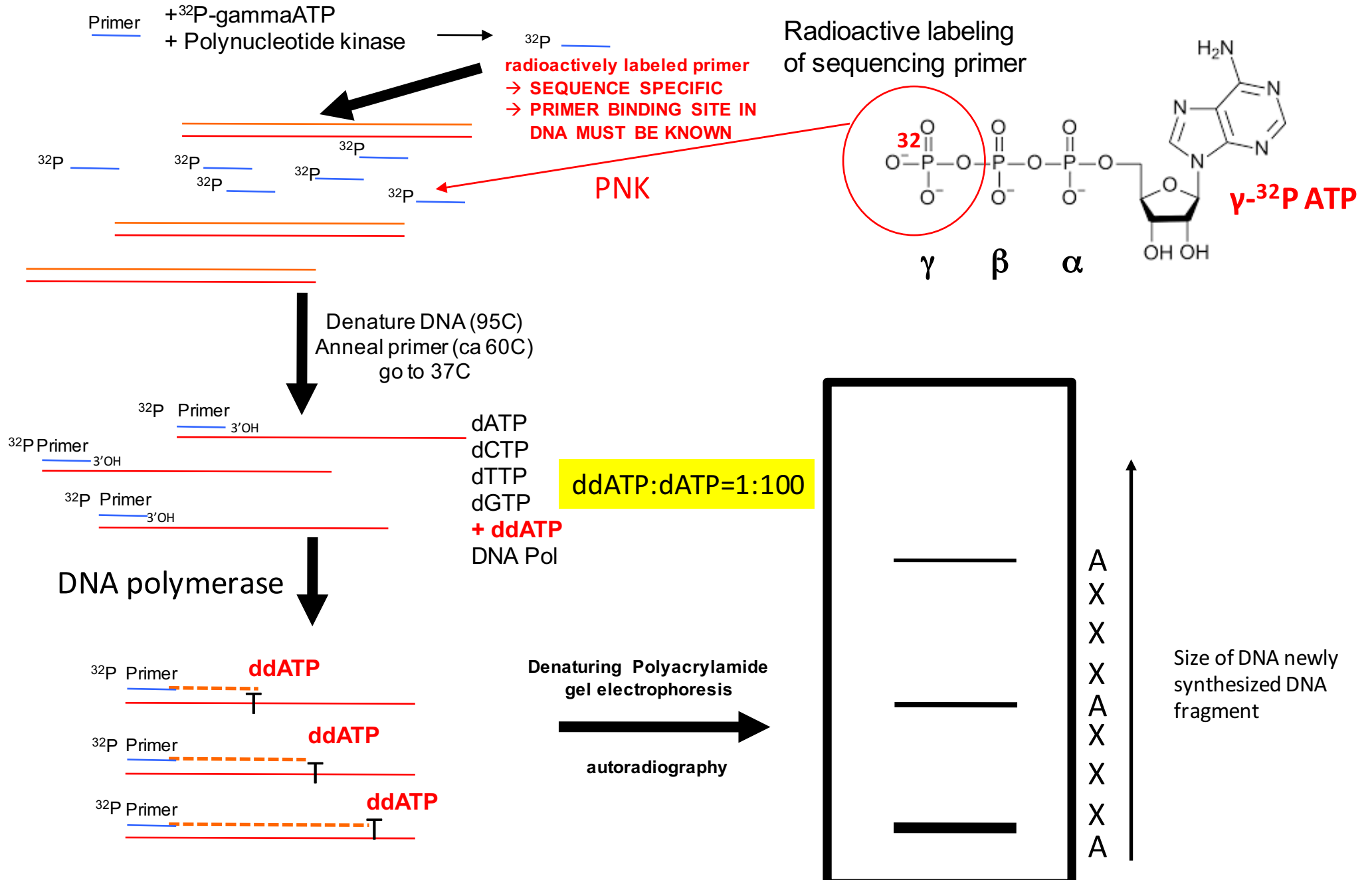
di-deoxyadenine triphosphate

Concept: mixing a low amount of ddATPs into a high amount of dATP (ca 1:100):
A pool of DNA molecules will be generated in which DNA molecules terminate at all possible A sites.

ddNTP enable me to terminate sequencing at a defined position in the newly synthesized DNA molecule

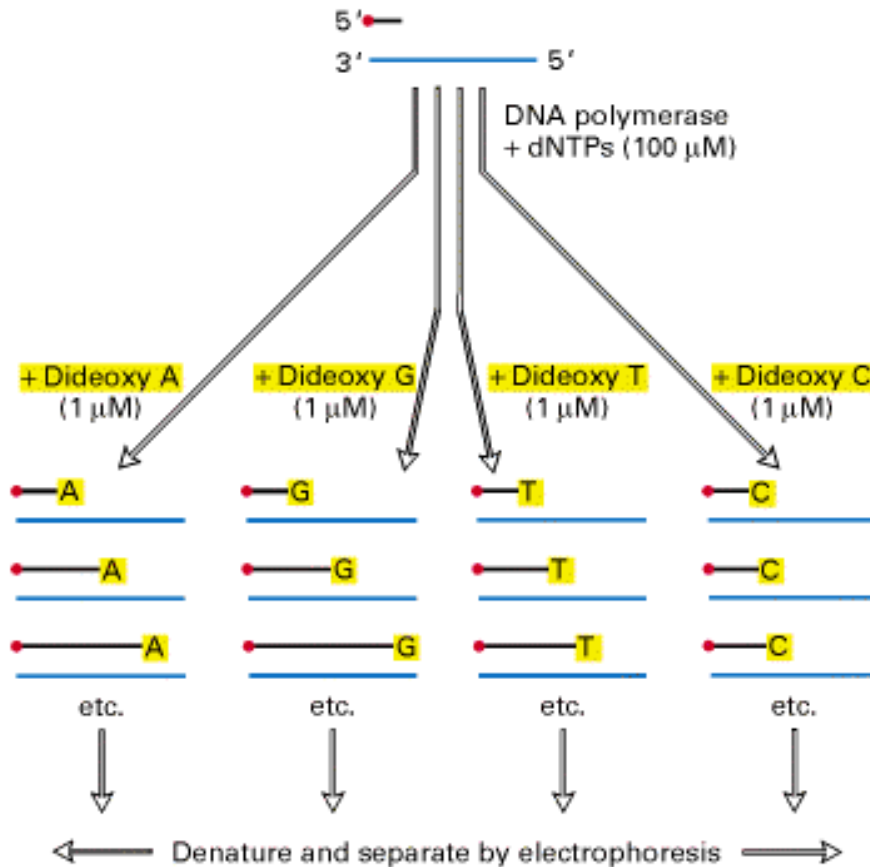
PROBLEM: How can detect sequencing products??

General concept in a sequencing reaction: The synthesis of a new strand of DNA from a ss template DNA

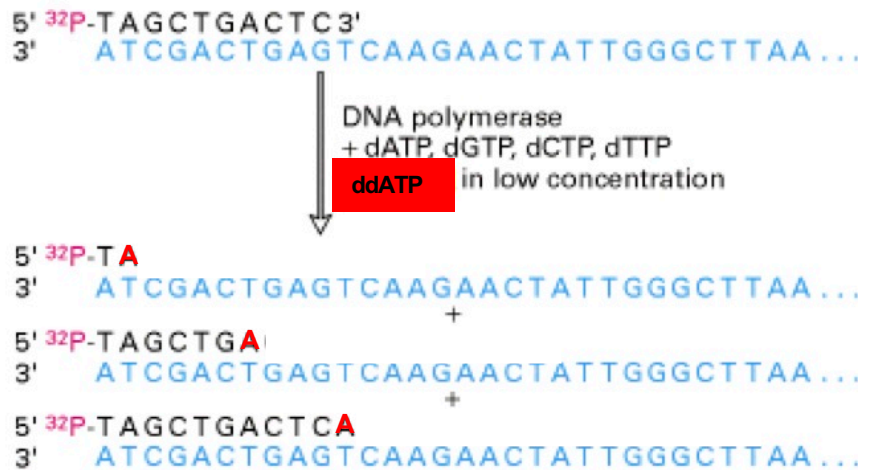
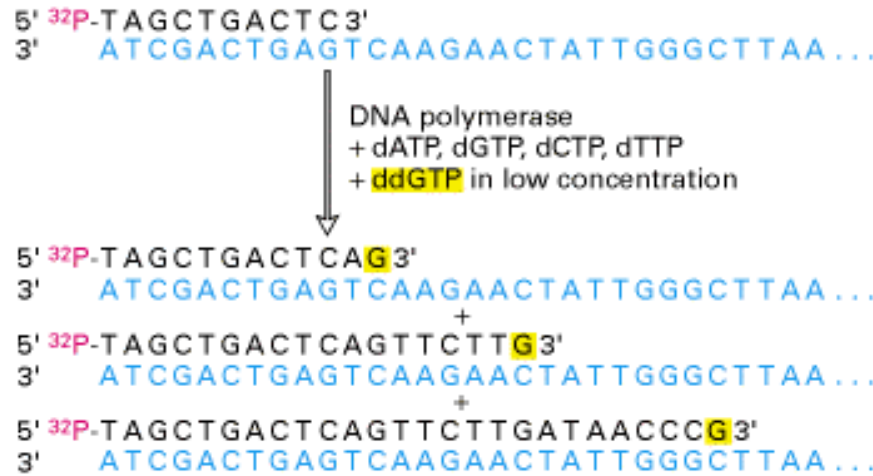


Classic Sanger sequencing of a DNA fragment requires **4 parallel sequencing reactions**

(a)



(b)



Tube3: dNTP mix with ddCTP

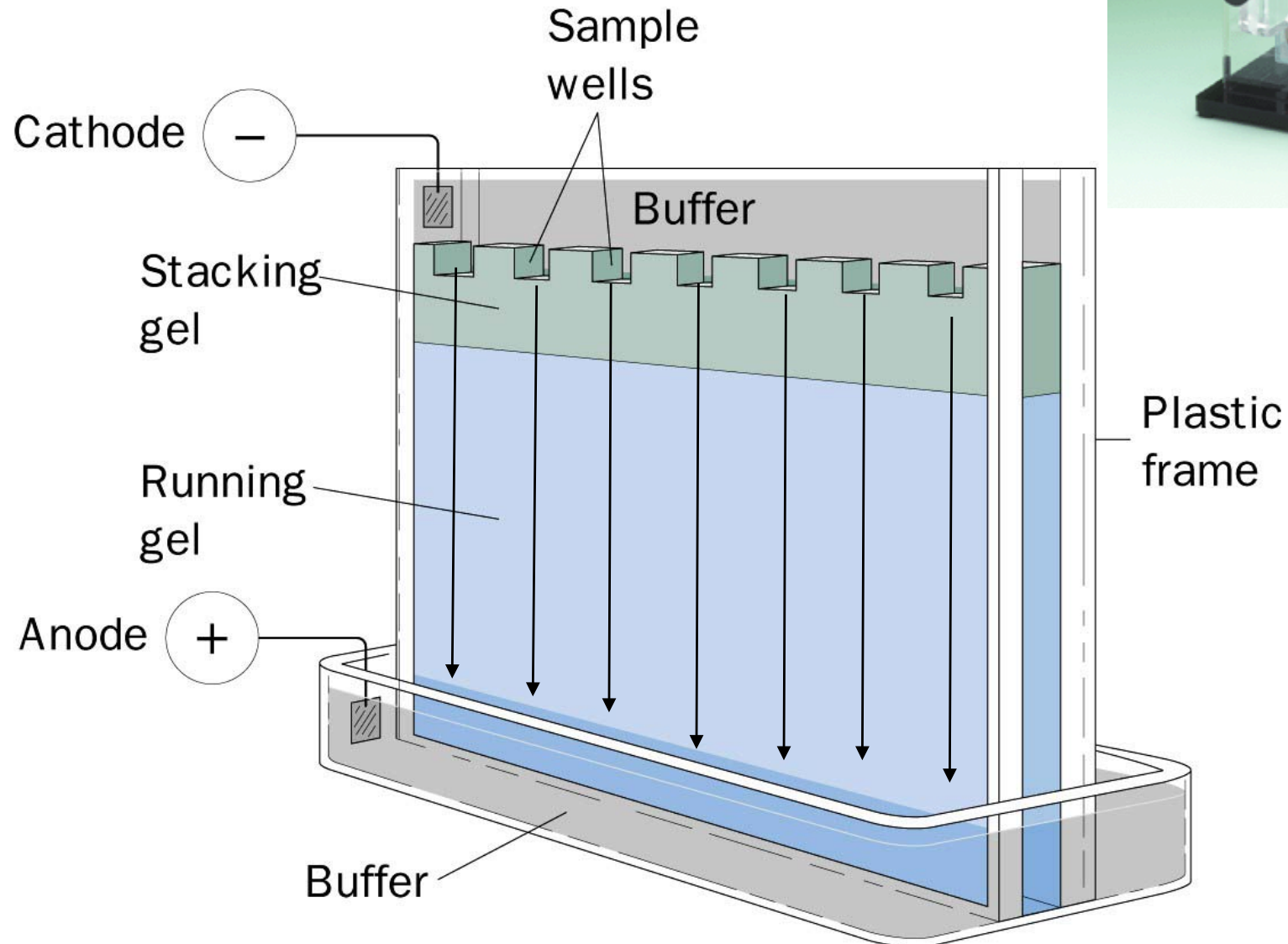
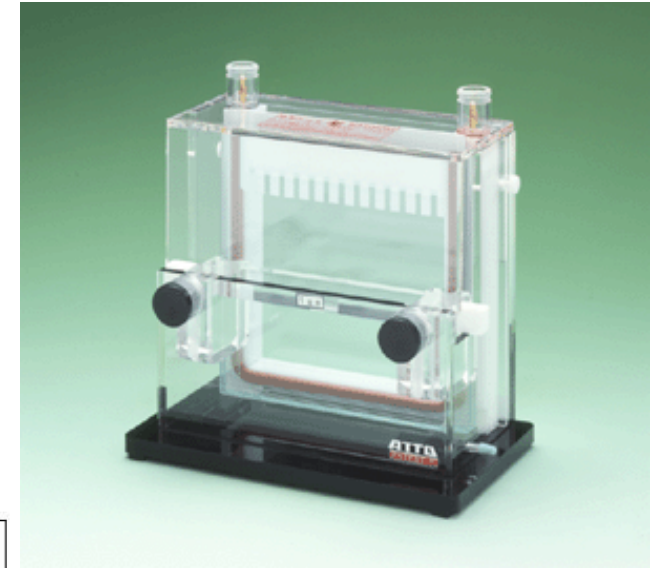
Tube4: dNTP mix with ddTTP

Le due basilari tecniche elettroforetiche per la separazione di frammenti di DNA (e di RNA).

- **Elettroforesi su gel di poliacrilammide (PAGE):**
- il gel è ottenuto per polimerizzazione in soluzione acquosa tamponata di acrilammide con una piccola percentuale di bisacrilammide tra due vetri con intercapedine di 0,5–2 mm mantenuti verticalmente. Il gel è costituito da una rete tridimensionale covalente del polimero ed è sostanzialmente un gel irreversibile.

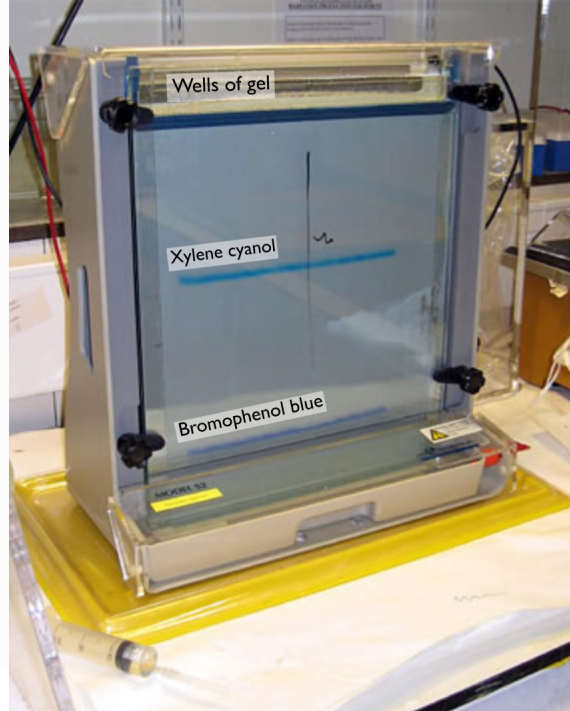
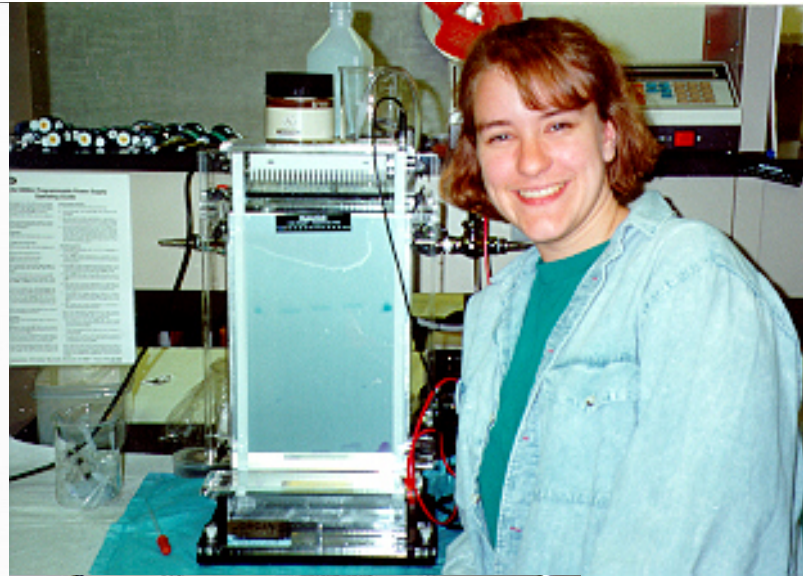
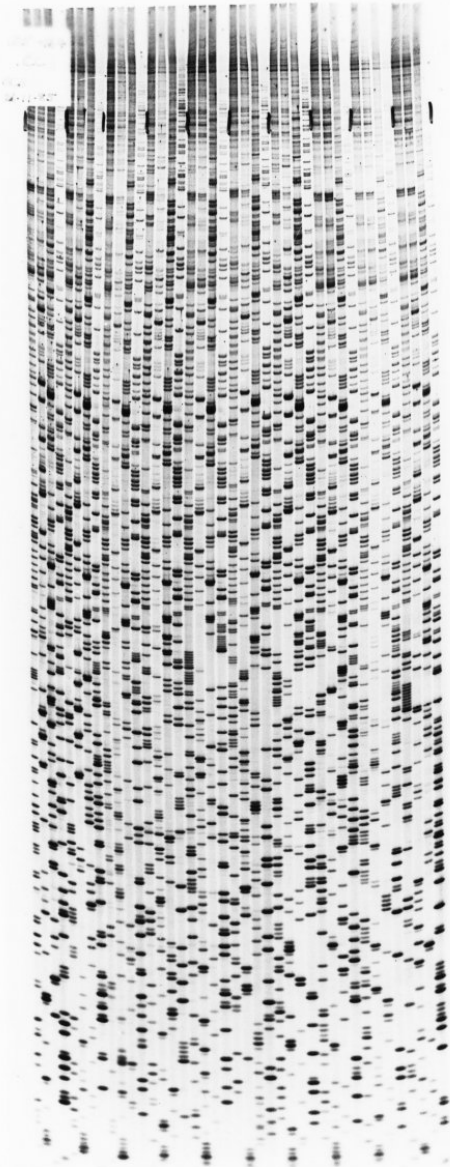
PolyAcrylamide Gel Electrophoresis

il gel è ottenuto per polimerizzazione in soluzione acquosa tamponata di acrilammide con una piccola percentuale di bisacrilammide tra due vetri con intercapedine di 0,5–2 mm mantenuti verticalmente. Il gel è costituito da una rete tridimensionale covalente del polimero ed è sostanzialmente un gel irreversibile.



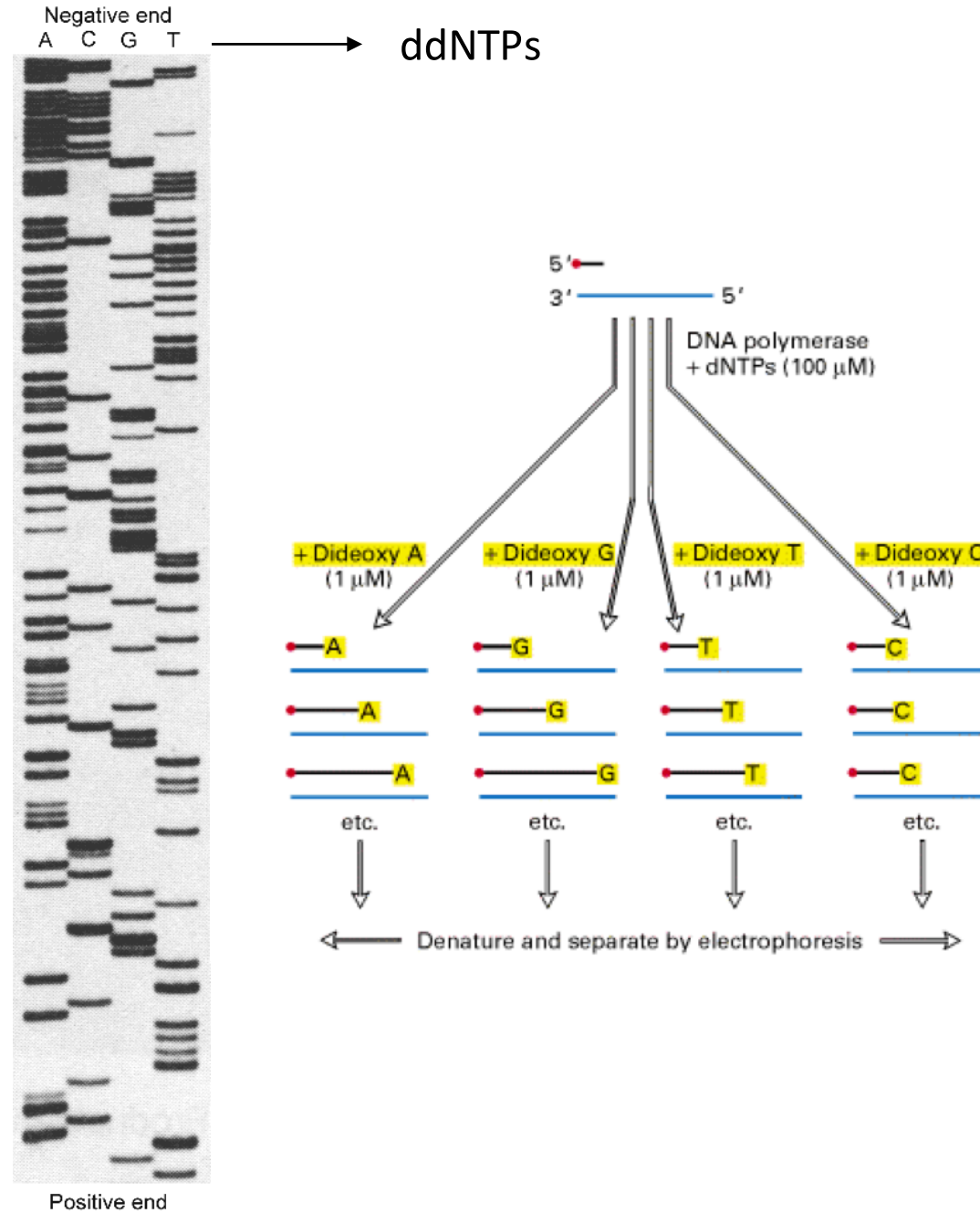
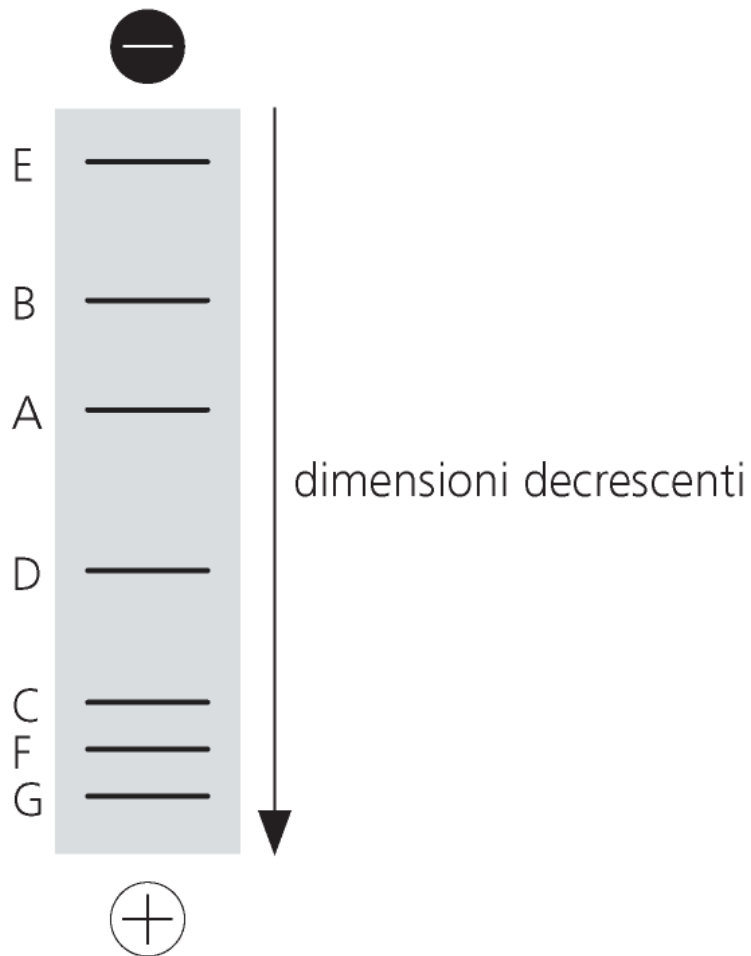
PAGE

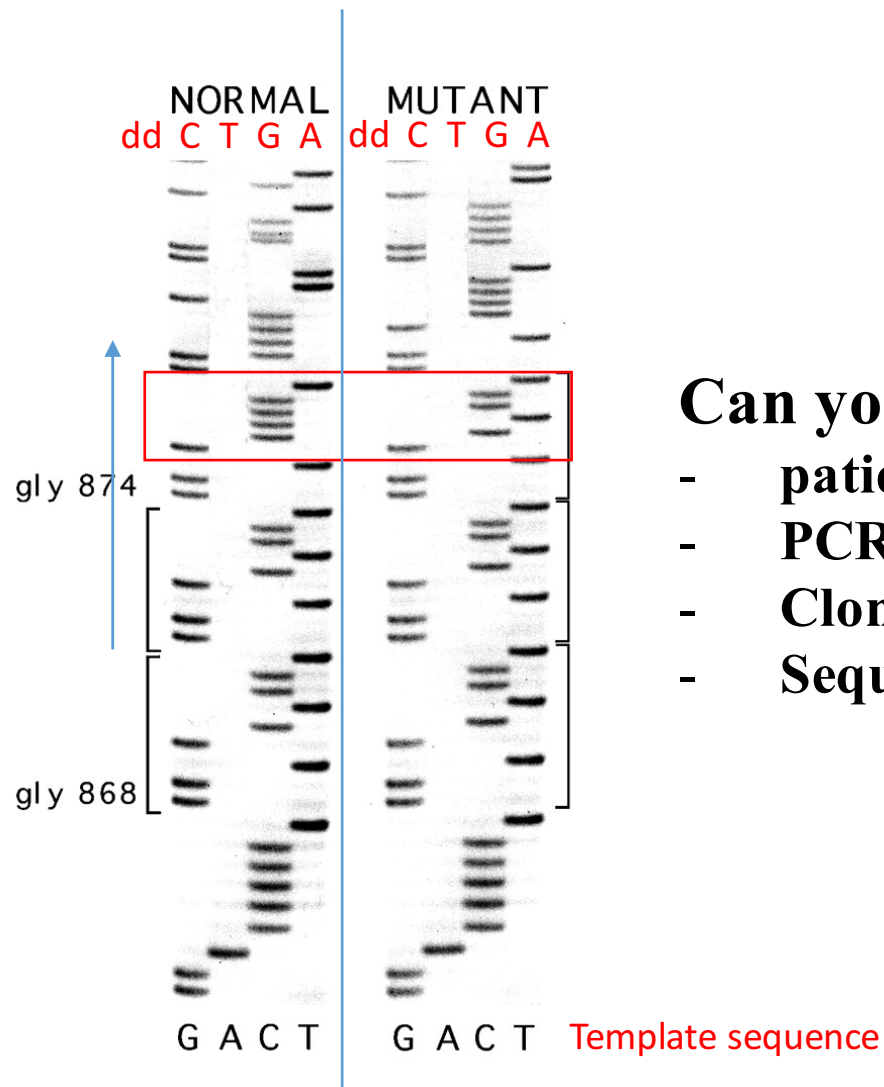
**Read length:
500 – 700 nucleotdi**



Standard in lab
until ca. 1995

Primer is radioactively labelled!!
 All fragments produced by DNA Polymerase
 can be visualized by autoradiography





Can you read the DNA sequence?

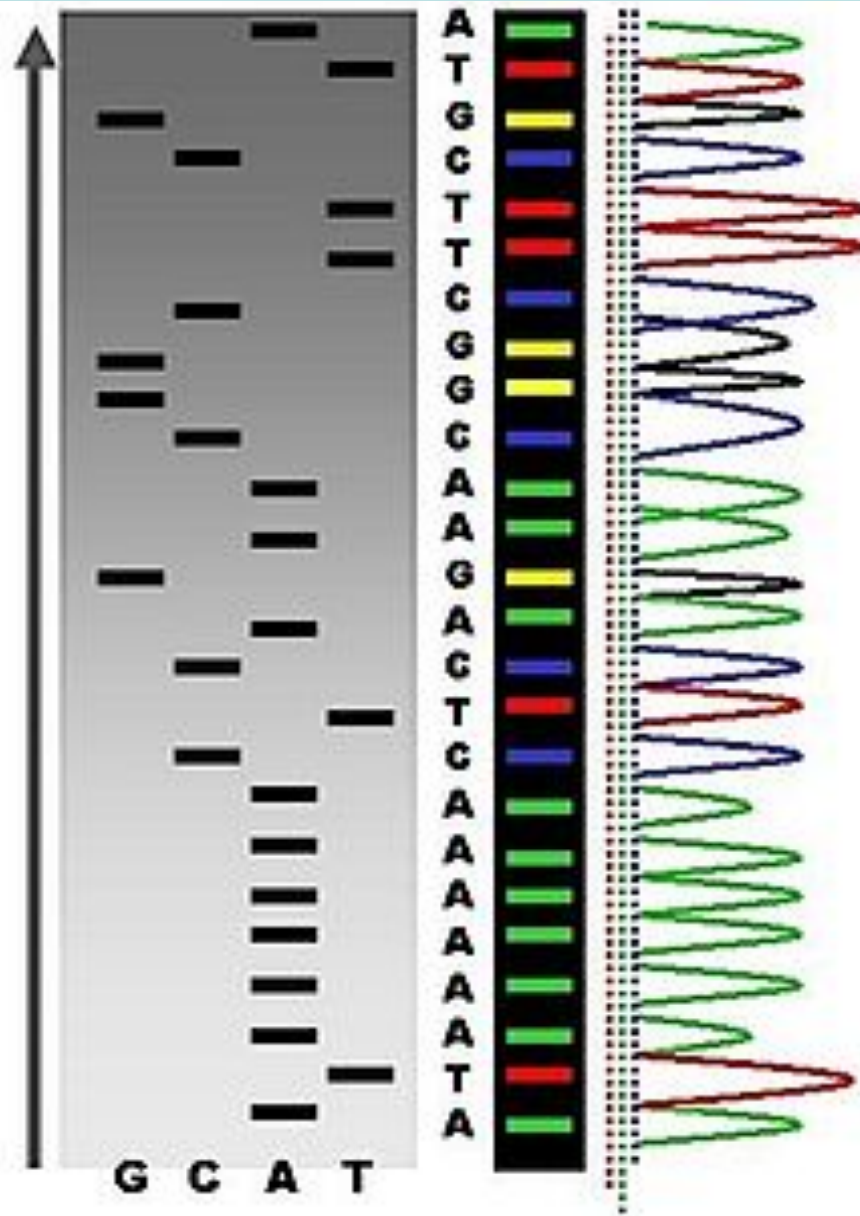
- patient/healthy individual
- PCR of gene-region of interest
- Clone in plasmid, mini/midi
- Sequence PCR fragment

NORMAL: GGT GCT CCT GGT GCT CCT GGT **GCC CCT** GGC CCC GTT GGC CCT GCT
 AMMINO ACID SEQUNCE: G A P G A P G A P G P V G P A

MUTANT: GGT GCT CCT GGT GCT CCT GGT **GCT CCT** GGT **GCC CCT GGC CCC GTT**
 AMMINO ACID SEQUNCE: G A P G A P G A P G **A P G P V**

2.1. Automated sequencing based on Sanger technique

Dye-terminator Sanger sequencing



**Classic
radioactive**

**Dye-terminator
Sanger sequencing**

Dye-terminator Sanger sequencing

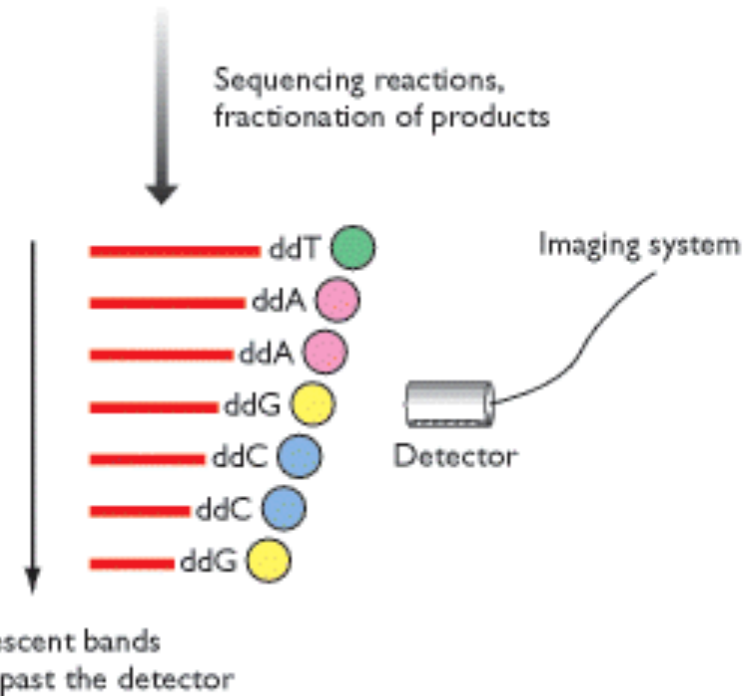
Tre diversi modi di marcare i frammenti di Sanger:

1) I frammenti di Sanger sono resi radioattivi per incorporazione di α -dNTP marcato

Questo metodo richiede quattro reazioni di polimerizzazione separate e quattro corsie elettroforetiche.

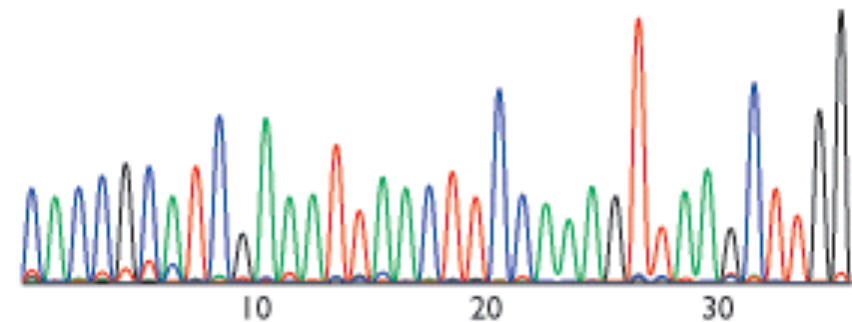
2) Ciascun ddNTP è reso fluorescente con un fluoroforo diverso. Questo metodo consente anche di effettuare tutte le reazioni in un'unica provetta ed unica corsie elettroforetica..

ddA (pink circle) ddC (blue circle) ddNTPs – each with a different fluorescent label
ddT (green circle) ddG (yellow circle)

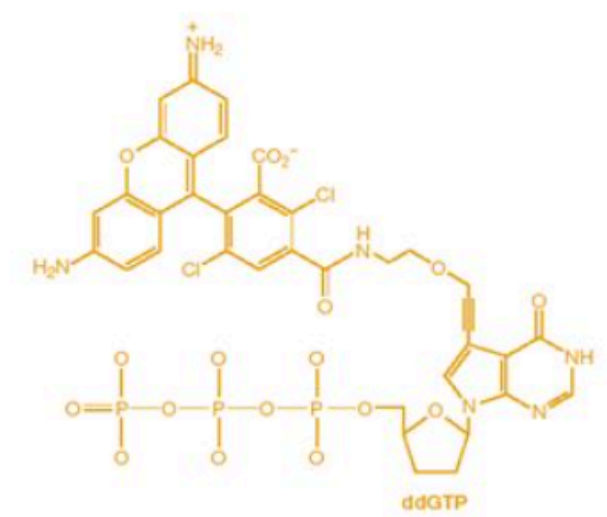
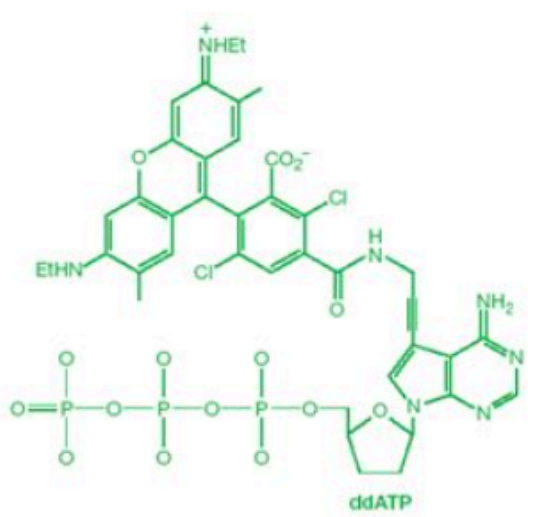
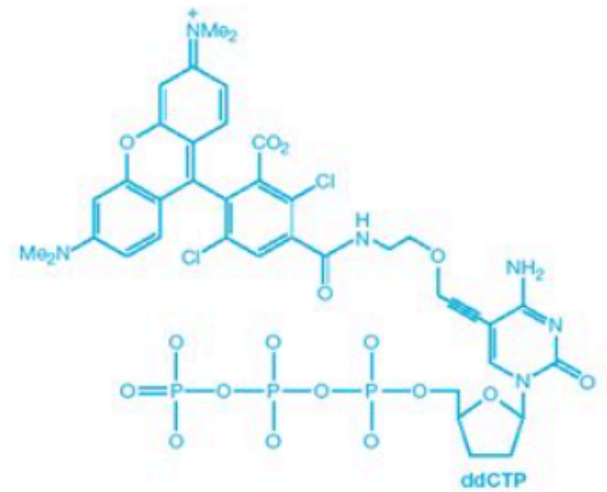
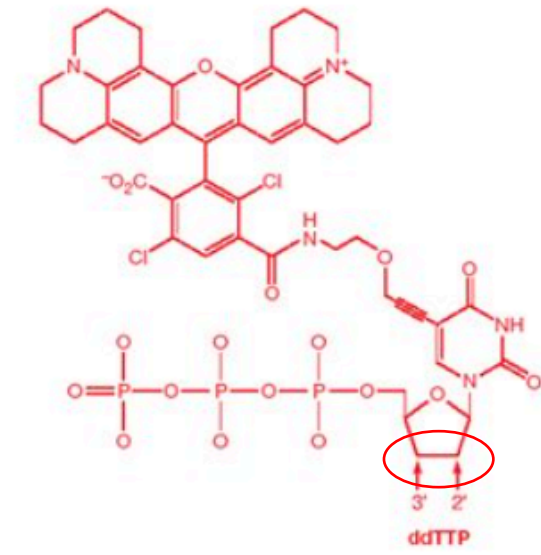
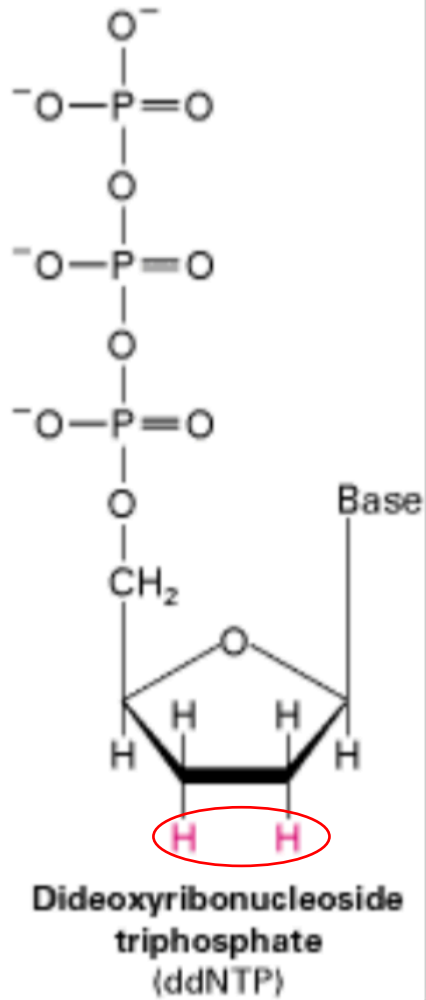


(B)

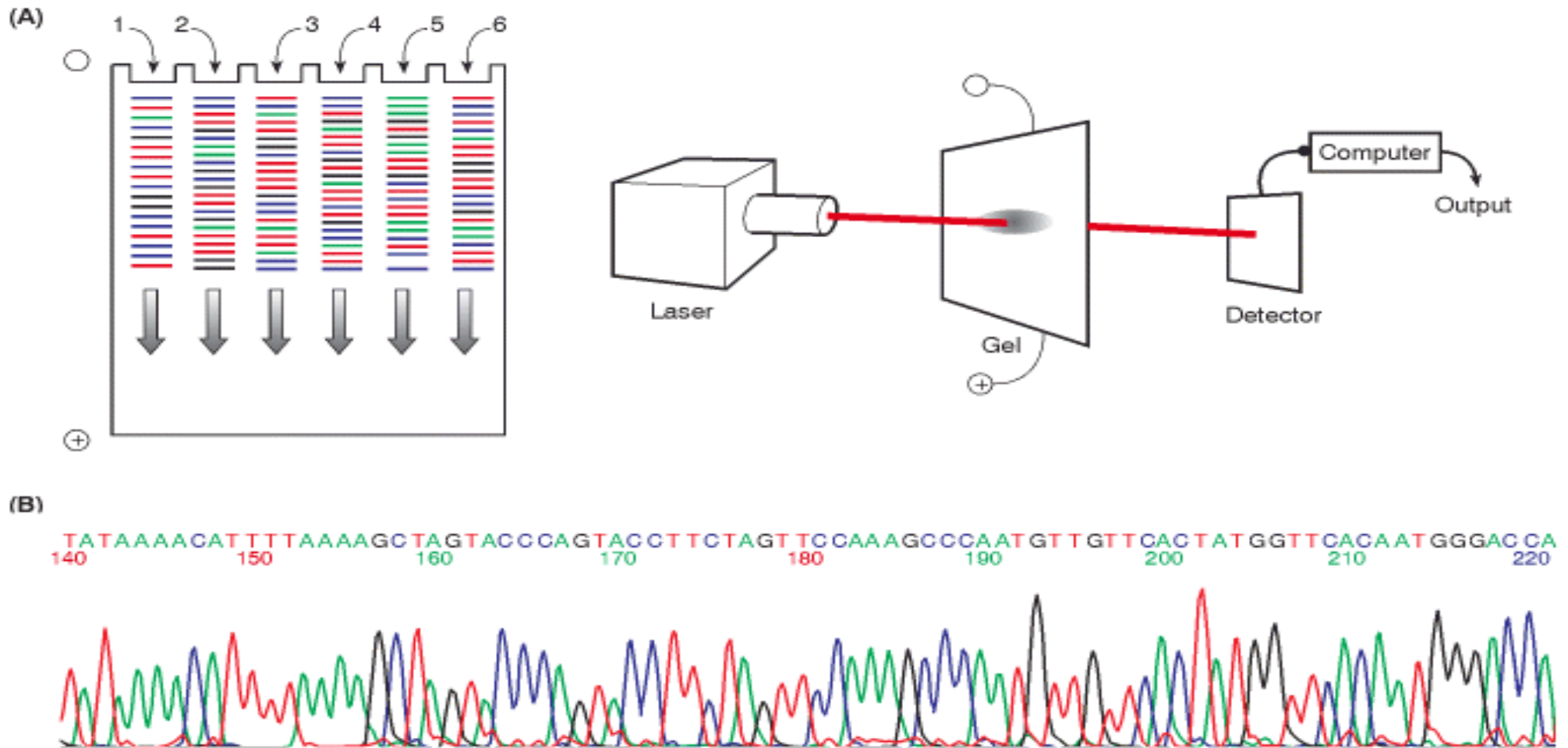
CACCGCATCGAAATTAAC TTCCAAAGTTAAGCTTGG



Dye-terminator ddNTPs



Labeling of each dideoxy-type enables performing sequencing of 4 nucleotide types in only one lane

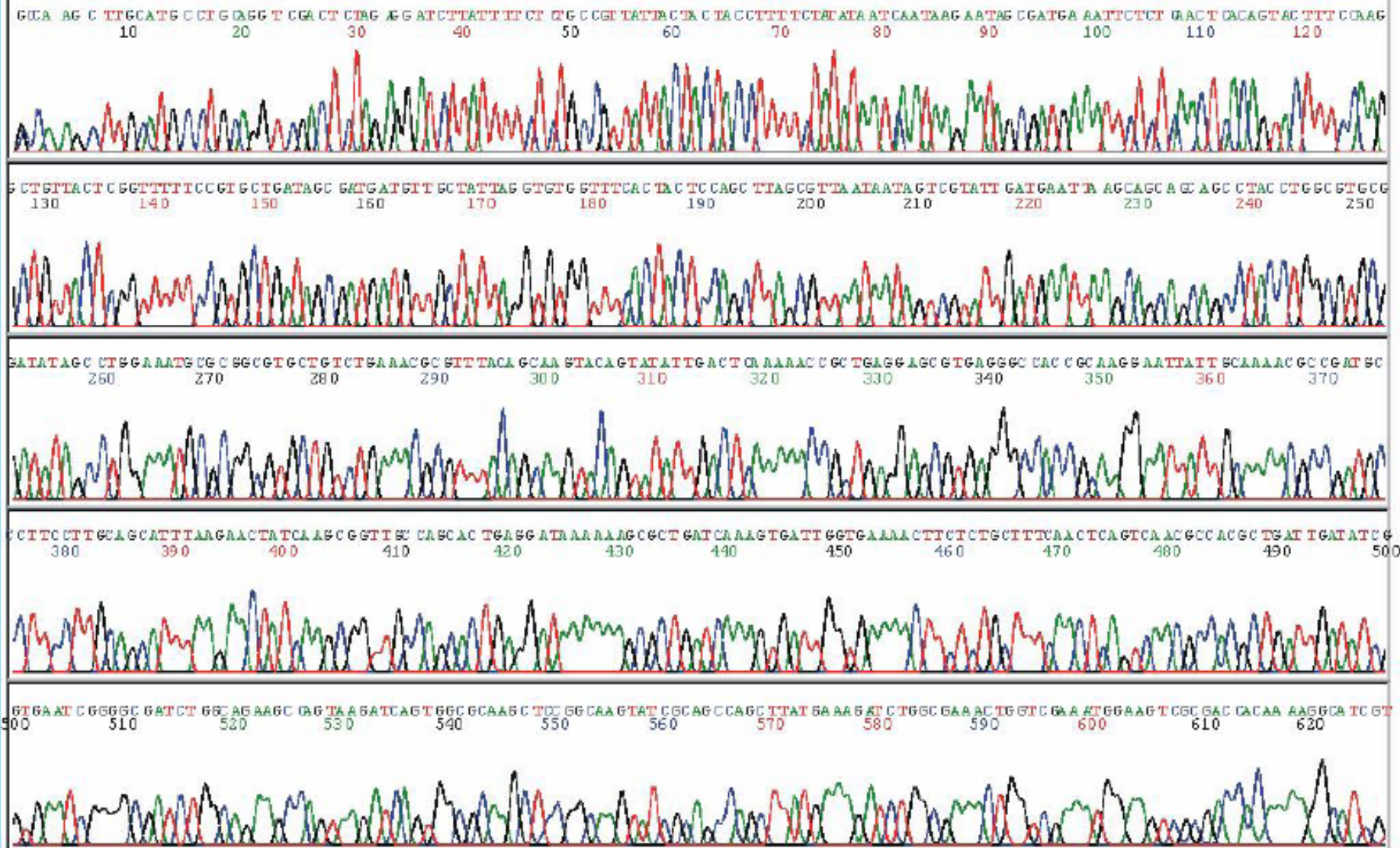




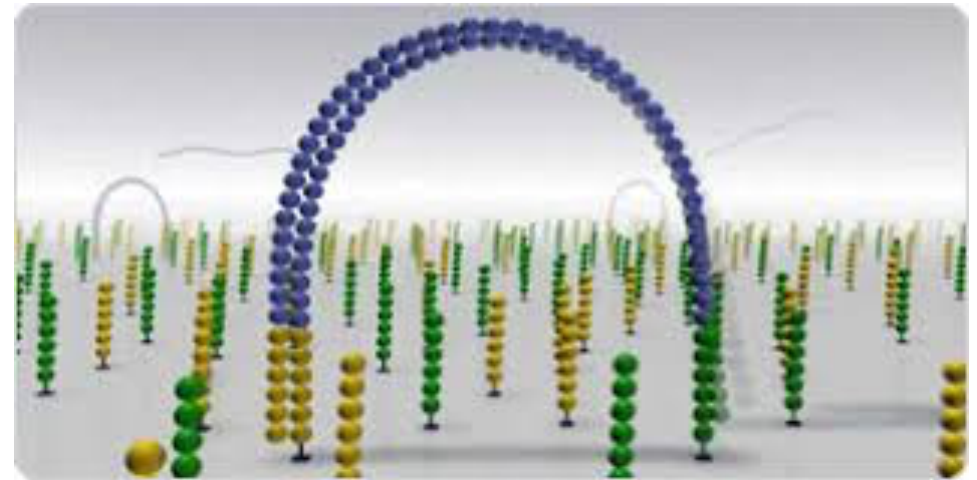
Model 3700 d00462_A05_Tas6up_033.ab1
Version 3.6
Basecaller-POP 5opt.bcpTas6up
BC 1.1.b.2 Cap 33

Signal G:172 A:243 T:195 C:173
DT3700POPS(BD)v3.mob
BLU
Points 2767 to 13845 PK1 Loc: 2767

Page 1 of 2
Tue, Sep 12, 2000 2:37 PM
Tue, Sep 12, 2000 1:21 AM
Spacing: 15.52(15.52)



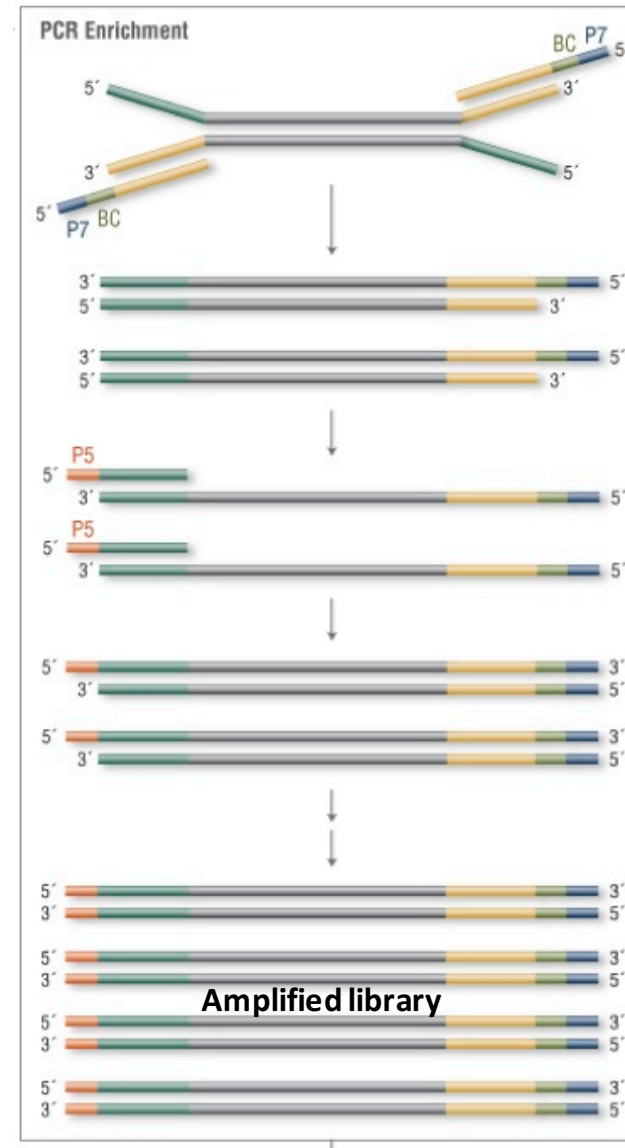
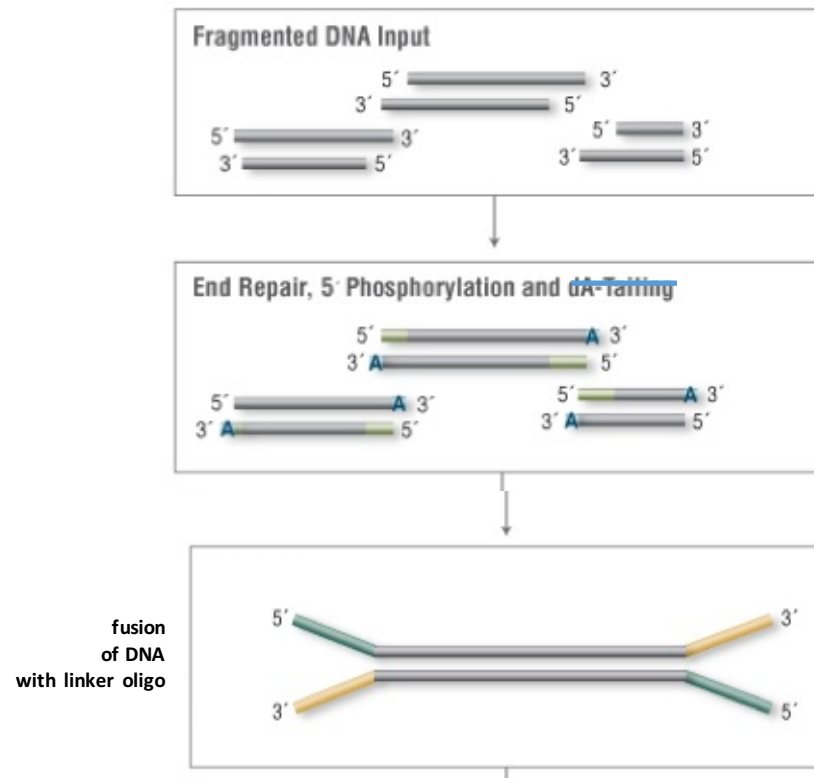
3. Massive parallel sequencing



Next generation sequencing of pools of DNAs

Use DNA to generate DNA libraries:

- Genomic DNA (fragmented)
- Other libraries (cDNA, CHIP,...)



Linkers serve as uniform primer binding sites. This allows the amplification of the entire DNA library using only 2 types of oligonucleotides

BC: barcode.
Each biological sample has common P7 oligos (blue and yellow) and P5 oligos (red/green); however for each biological sample a defined BC sequence is chosen.
This links the sequencing result to the biological sample
→ Many samples can be sequenced at the same time
→ (libraries are prepared separately)

READY FOR MASSIVE PARALLEL SEQUENCING

ChIP seq: Analysis of epigenetic information on the single nucleotide level → GENERATION OF GENOME WIDE EPIGENETIC MAPS

Illumina Massively Parallel Sequencing

<https://www.illumina.com/company/video-hub/pfZp5Vgsbw0.html>

HiSeq 2000

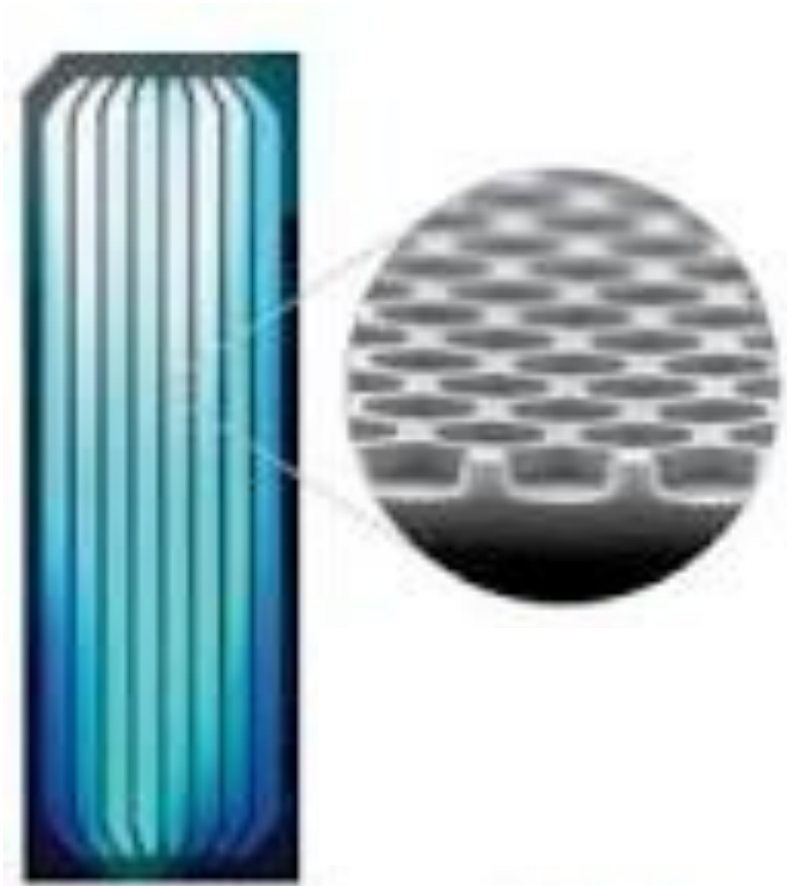


The heart of the Illumina Massive Parallel Sequencer is the “FLOW-CELL”. A surface with millions of small wells that allow thousands of Sanger-sequencing reaction in parallel = “massive parallel sequencing”. In each well a SINGLE MOLECULE of DNA is amplified and sequenced

Illumina offers the most potent massive sequencing instruments – leader on the market

<https://www.youtube.com/watch?v=pfZp5Vgsbw0>

CLUSTER AMPLIFICATION:



Flow cell contains surface with millions of wells

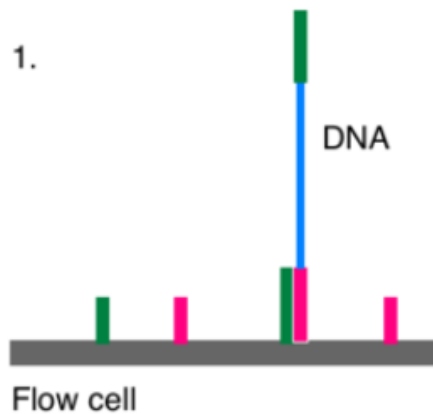
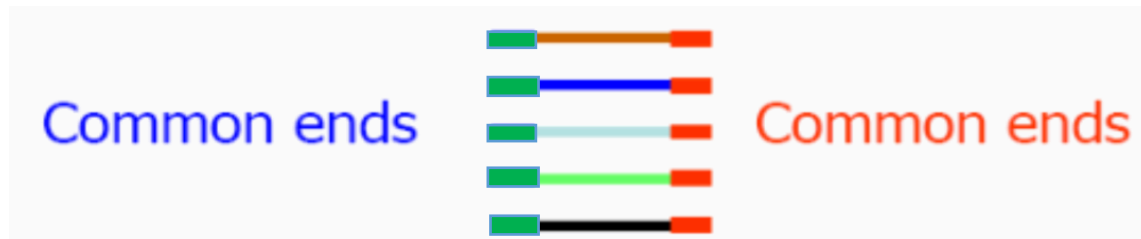
→ Each well contains beads mounted with 2 species of oligonucleotides that hybridize with adaptor oligos of DNA library

→ DNA library will be loaded onto the flow cell in a determined concentration:

ONLY ONE MOLECULE OF DNA WILL BE PROCESSED FOR SEQUENCING IN A SINGLE WELL

CLUSTER AMPLIFICATION:

- making DNA library (~300bp fragments)
- ligation of adapters **A** and **B** to the fragments



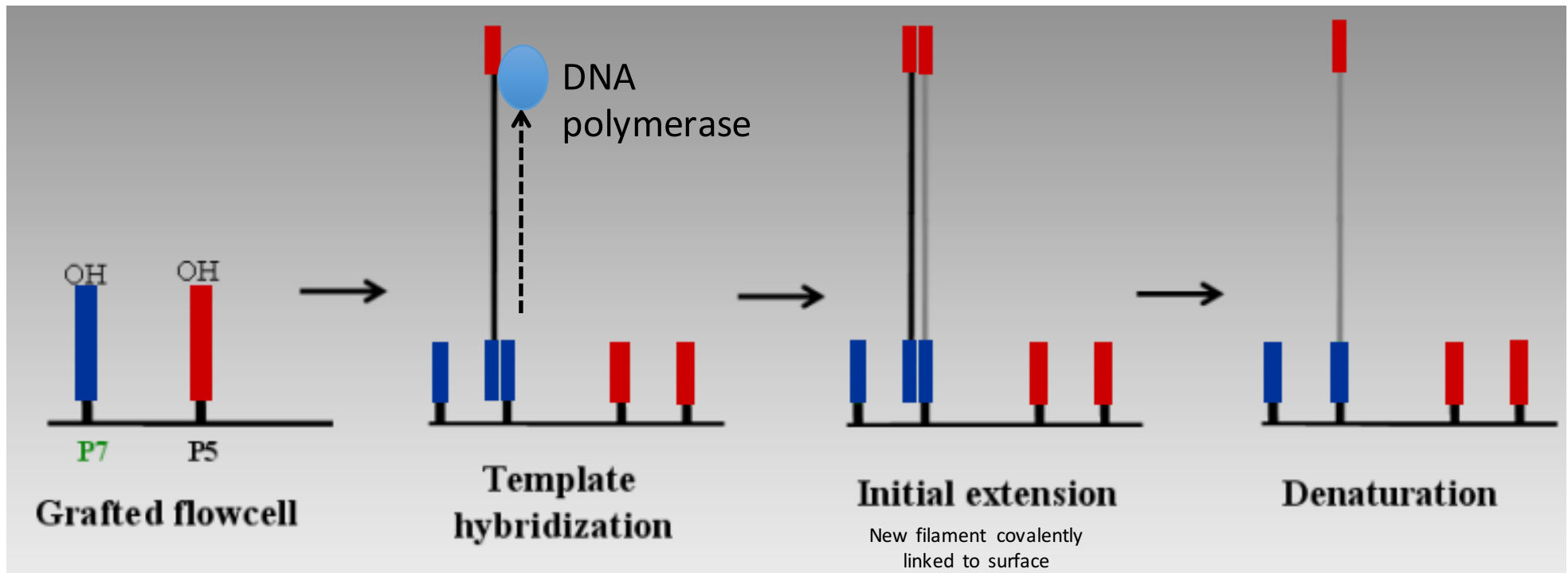
1 well in a flow-cell with billions of wells

1 well, covered with millions of 2 types of oligos

- **complementary** primers are ligated to the surface
- pairing with ChIP ed ssDNA at random position in the well of the flow cell

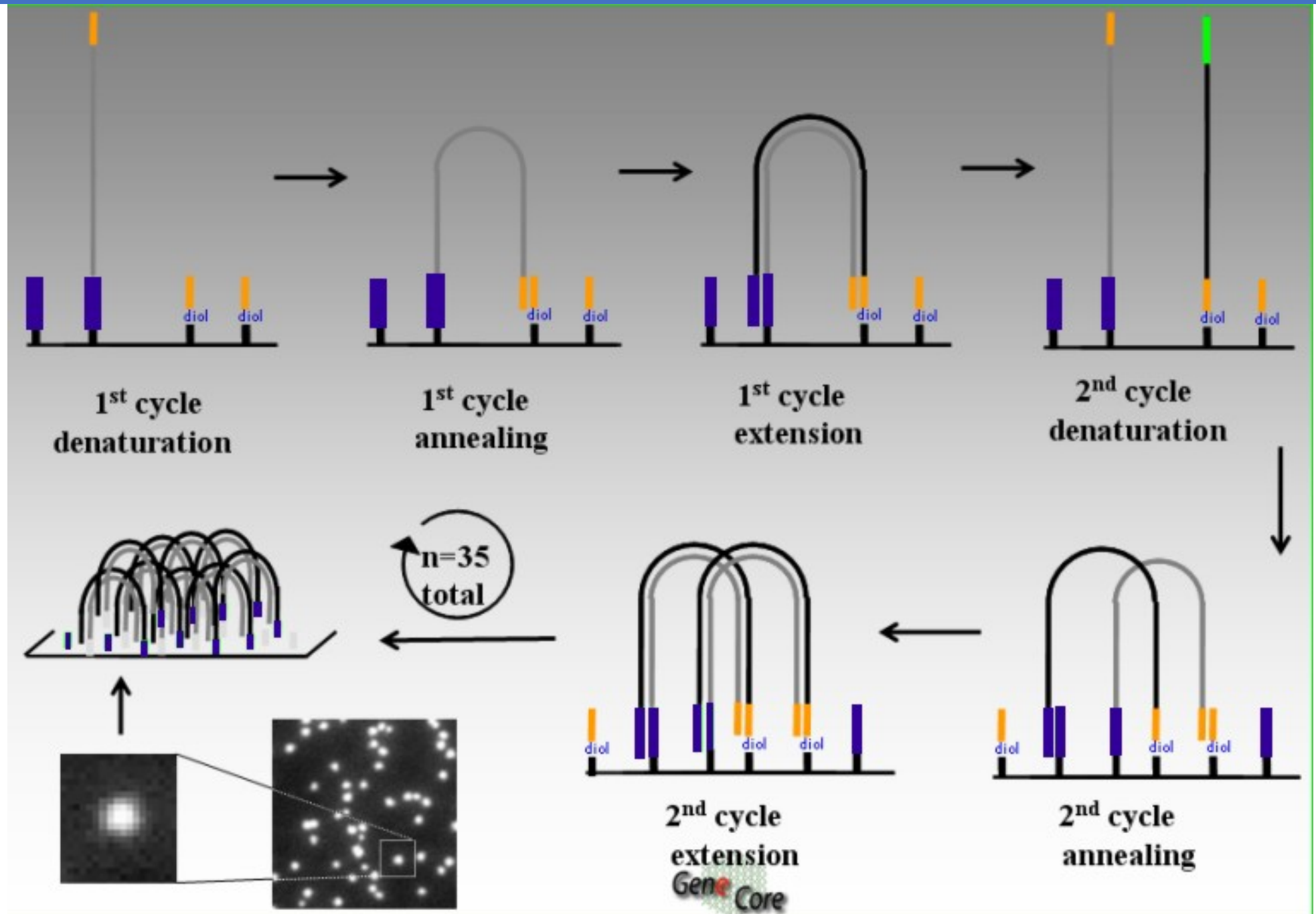
CLUSTER AMPLIFICATION:

Bridge amplification: takes place on surface of beads (each bead is mounted with 2 species of oligos; each oligo can hybridize to a DNA library fragment):
initiation



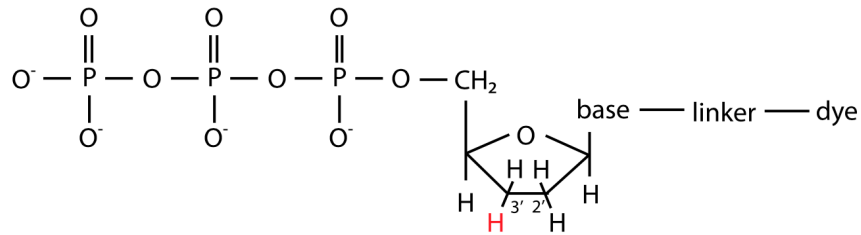
On the surface: complementary oligos

CLUSTER AMPLIFICATION:

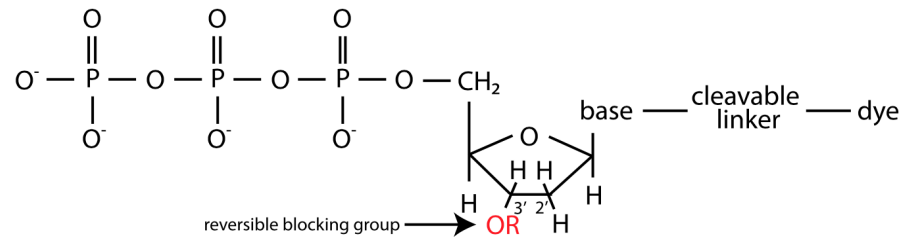


REVERSIBLE CHAIN TERMINATORS:

Sanger fluorescent dideoxynucleotide (ddNTP)



3'-O-blocked reversible terminator



Instead of promoting irreversible primer extension like the Sanger dye terminator method, the reversible chain terminators method uses a cyclic method that consists of nucleotide incorporation, fluorescence imaging and cleavage.

The figure shows a modified nucleotide with a **cleavable dye** and **reversible blocking group**. Once the **blocking group** is removed, a **3'OH** is formed and a new nucleotide may come in.

NOTE: no classic dNTPs are used for sequencing!!!!

Procedure

The steps for such a process can be outlined as follows:

1. Have four dNTP's, each with a different fluorescent marking. These markings should not interfere with base pairing or phosphodiester bond formation.
2. Each dNTP should terminate DNA elongation temporarily with a blocking group on the 3' carbon of the sugar moiety.
3. Upon each cycle, have just one dNTP bind to the elongating strand and emit a fluorescent dye color.
4. Depending on the color emitted, record the particular nucleotide.
5. Cleave the blocking group and fluorescent dye with a palladium-catalyst.
6. Restore a 3' hydroxyl so that the growing strand can now elongate.
7. Repeat from step 1.

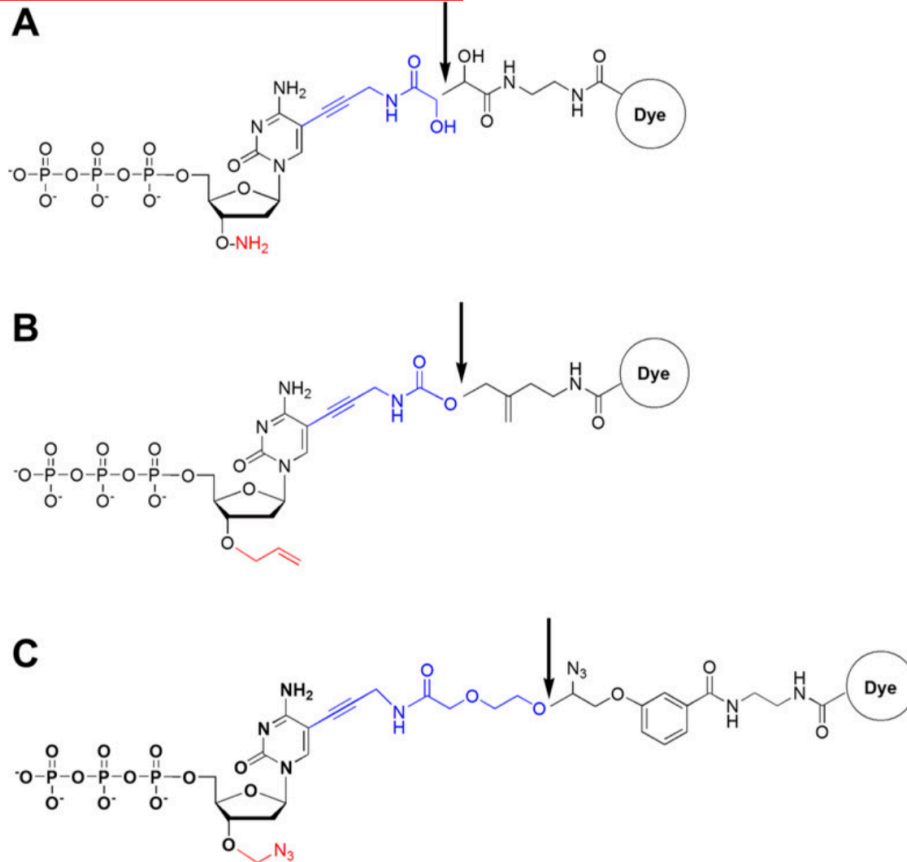
Cons

There are some limitations to this method which include:

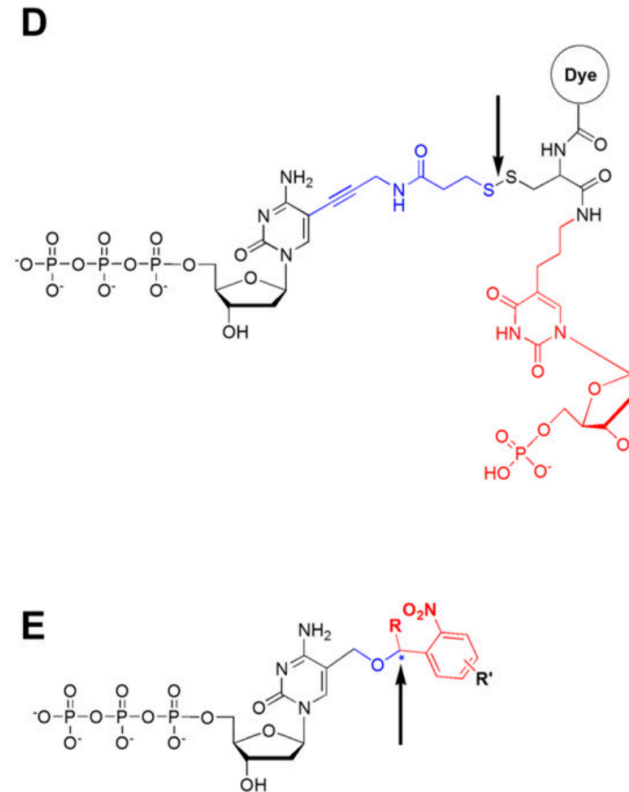
- Incomplete cleavage of blocking groups.
- Difficulties incorporating fluorescent nucleotides.

CLUSTER AMPLIFICATION:

3'-blocked reversible terminators



3'-unblocked reversible terminators

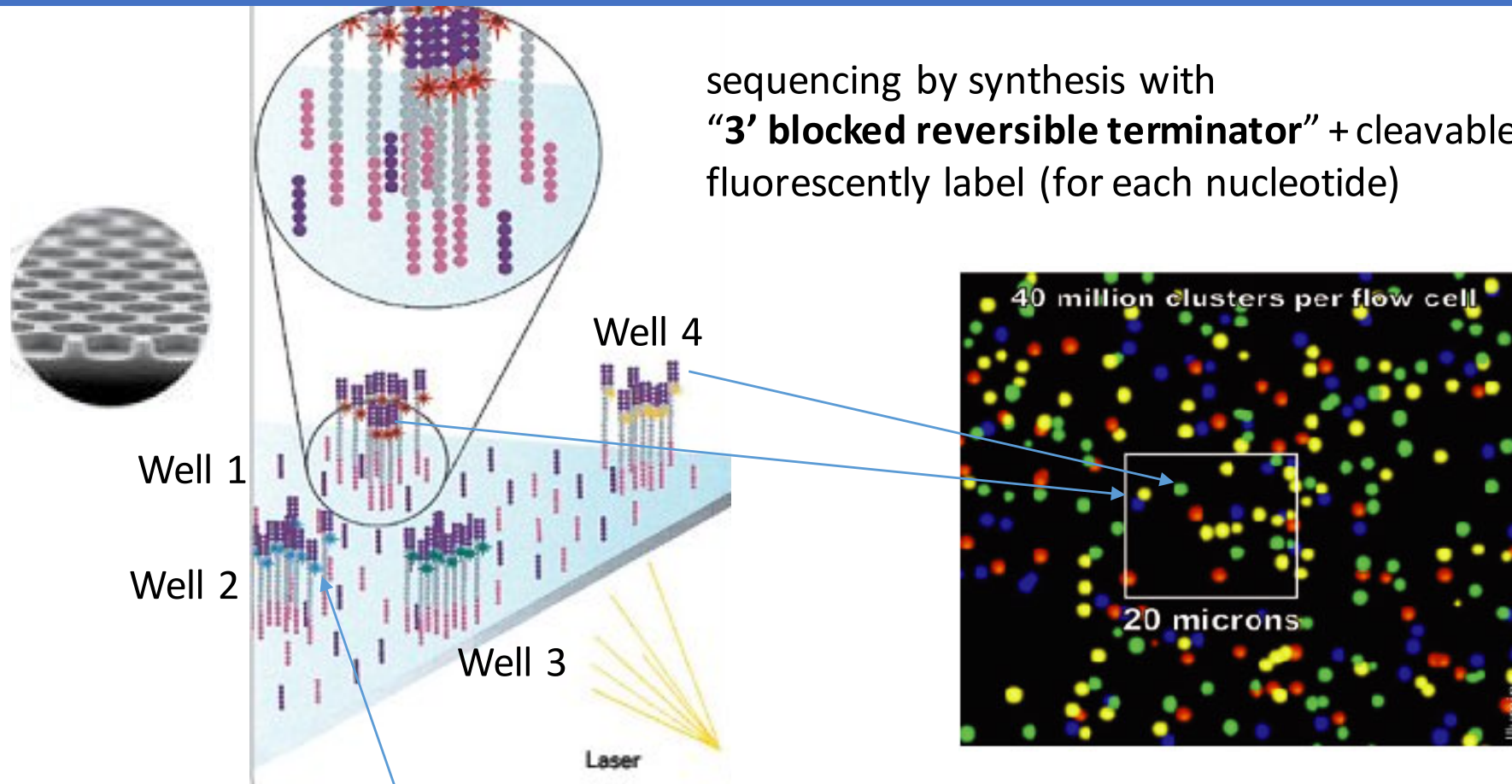


Three different 3'-blocked reversible terminators were shown on the left (A–C) and two 3'-unblocked reversible terminators were shown on the right (D–E).

The chemical structures in red denote the reversible terminating groups. Arrows indicate the site of cleavage separating the fluorescent groups from the nucleotide, and the chemical structures in blue denote the molecular scars that are attached to the base.

Illumina: massive parallel sequencing:

sequencing by synthesis with
“3’ blocked reversible terminator” + cleavable
fluorescently label (for each nucleotide)



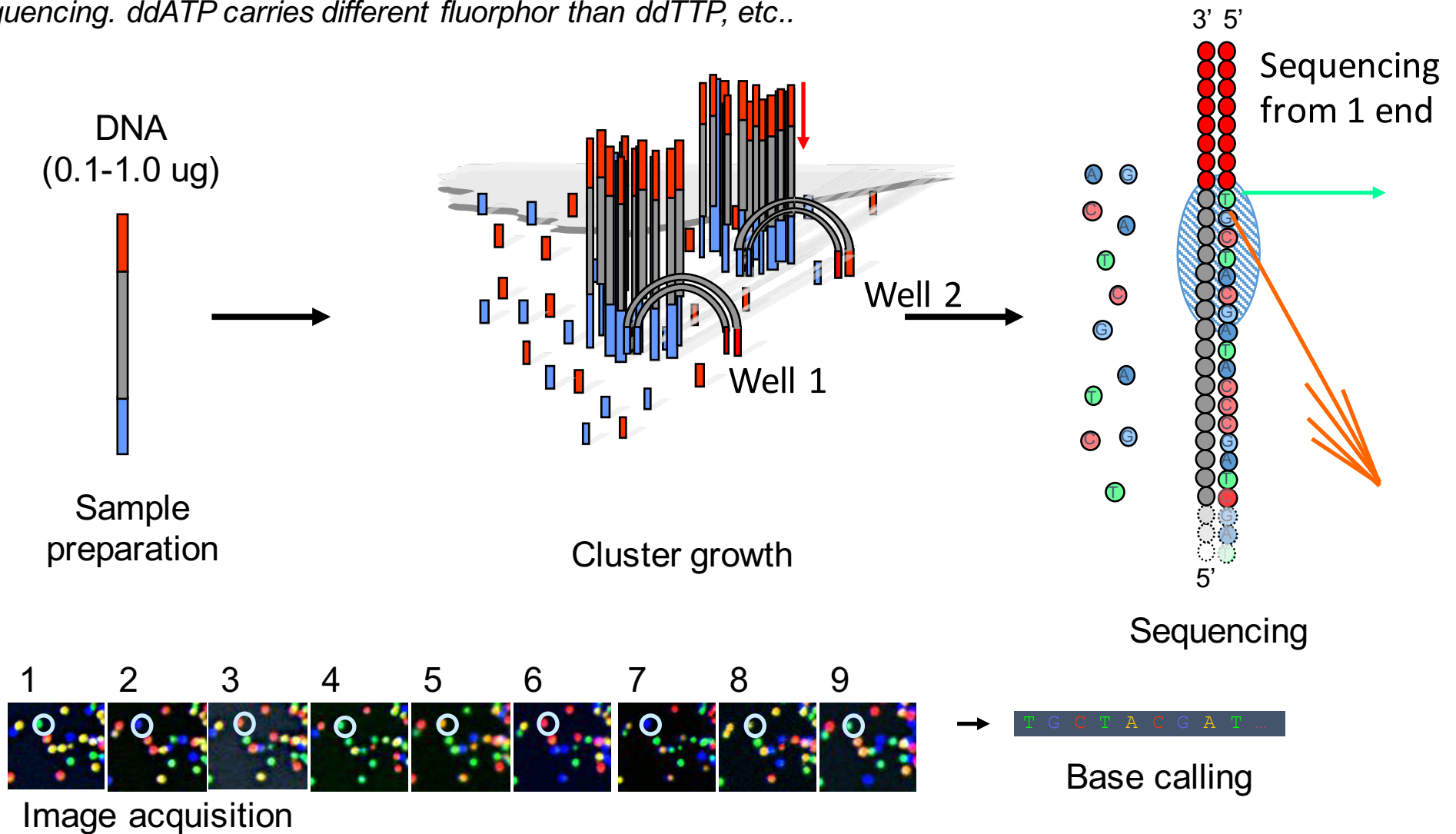
1. Start of synthesis using primer = incorporation of fluorescent 3’blocked reversible terminator: synthesis blocked
2. Scanning of fluorescent signals of all wells of flow-cell with laser (image)
3. Dye cleavage + elimination of reversible blocking group
4. wash step
1. Repeat steps 1-4 ca. 150x

READ LENGTH: ca: 150nt from each primer (2x150nt = 300nt)

Illumina Sequencing Technology

Robust Reversible Terminator Chemistry Foundation

In each round of sequencing a fluorescently labelled ddNTP will be used for sequencing. ddATP carries different fluorophore than ddTTP, etc..



Illumina: paired end sequencing increases information content

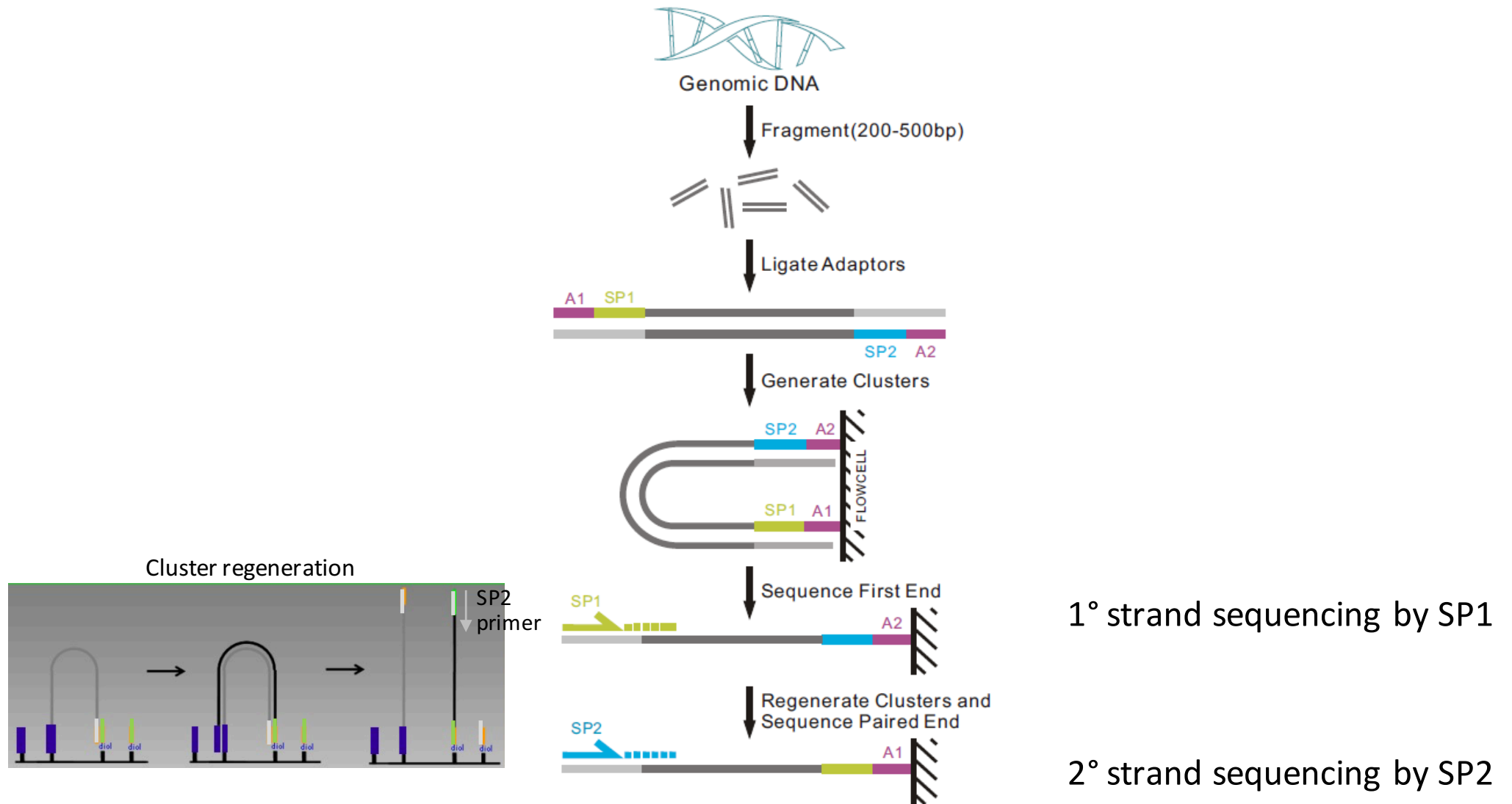


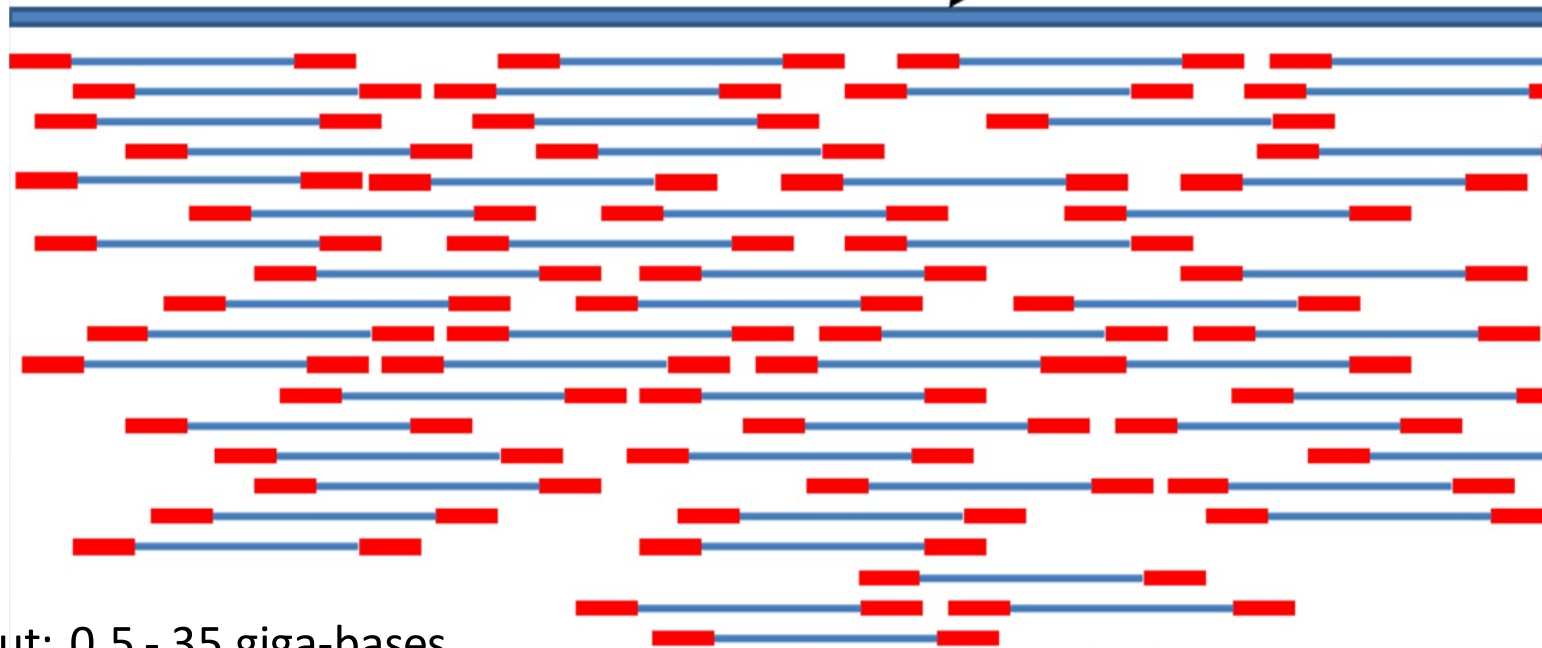
Figure 1-2-1 Pipeline of paired-end sequencing (www.illumina.com)

Data analysis: obtained sequence reads are aligned along genomic DNA sequence → high number of reads necessary to obtain full sequence coverage

Read length: 50 – max. 300 nt

Read does not necessarily cover entire library DNA fragment

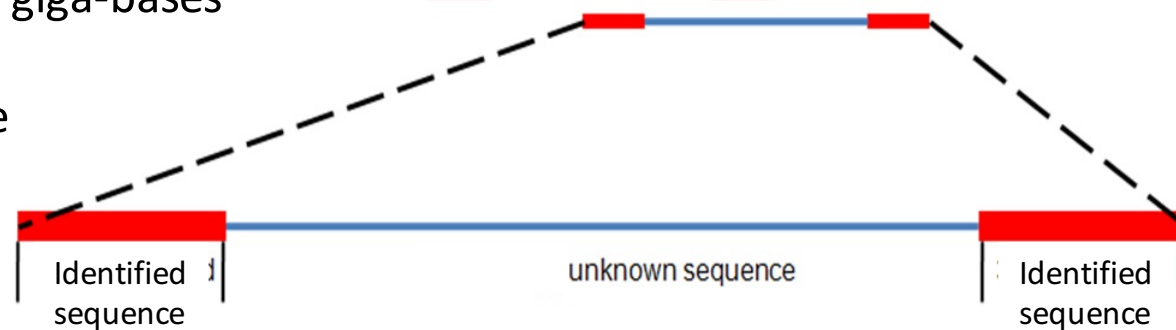
Reference Genome Sequence



Max. output: 0.5 - 35 giga-bases

$= 3.5 \times 10^{10}$

= 10x human genome



Sequence derived from one amplified cluster

PILE – UP ALIGNMENT ACROSS THE REFERENCE GENOME

