

# Genomics of farm animals/ Sequencing demonstration

## Laboratory examples



**Modul no. 1: Animal genetics**

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# Sequencing procedure

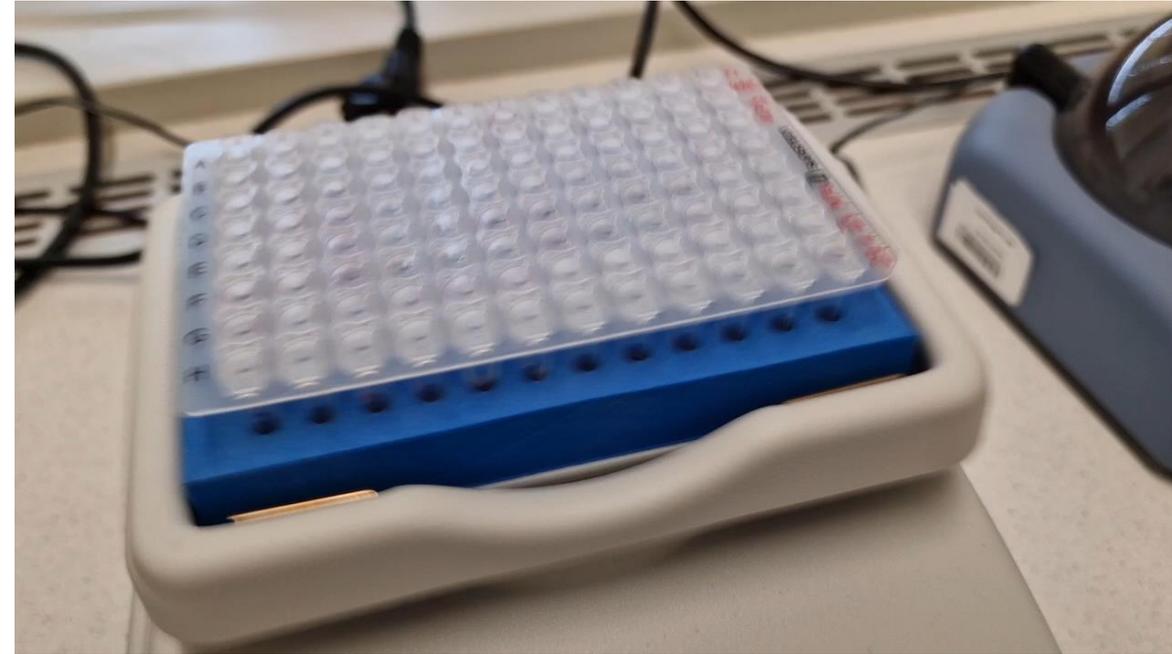
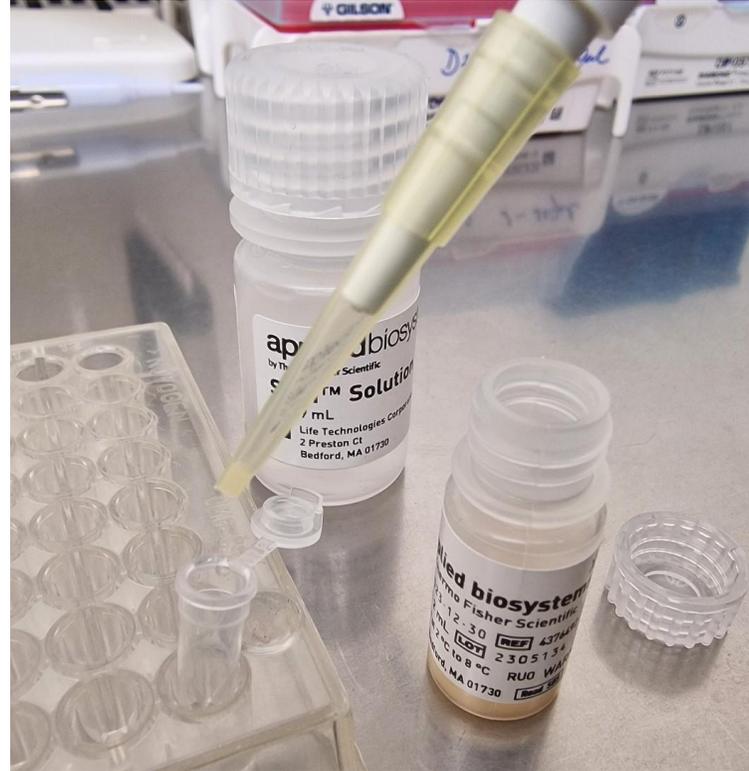
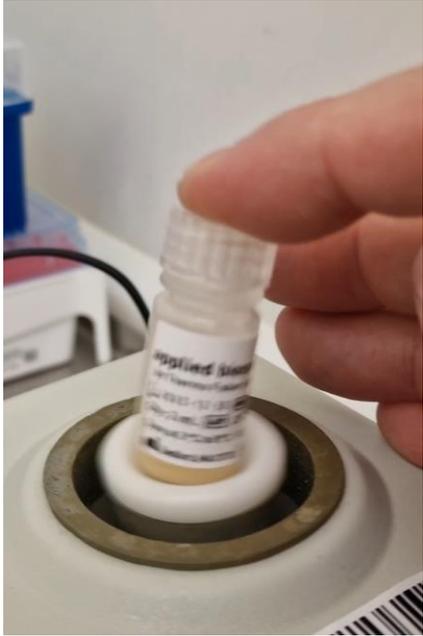
1. Sample preparation :
  - a) cloned DNA (vector+examined DNA-insert)
  - b) PCR product
    - 1.1. Sample cleaning (cleaning in solution or gel isolation)
    - 1.2. Determination of DNA template concentration
2. Sequencing reaction - cyclical  
primer (universal from vector or direct PCR), only 1!  
polymerase (Taq DNA FS, does not have 5'→3' exonuclease activity),  
dNTP,  
labelled ddNTP,  
buffer (+Mg<sup>2+</sup>)
3. Sequencing mixture purification (EtOH+NaAc, columns, absorption) – elimination of free ddNTP
4. Capillary electrophoresis on the sequencer
5. (Automatic) evaluation - sequence determination

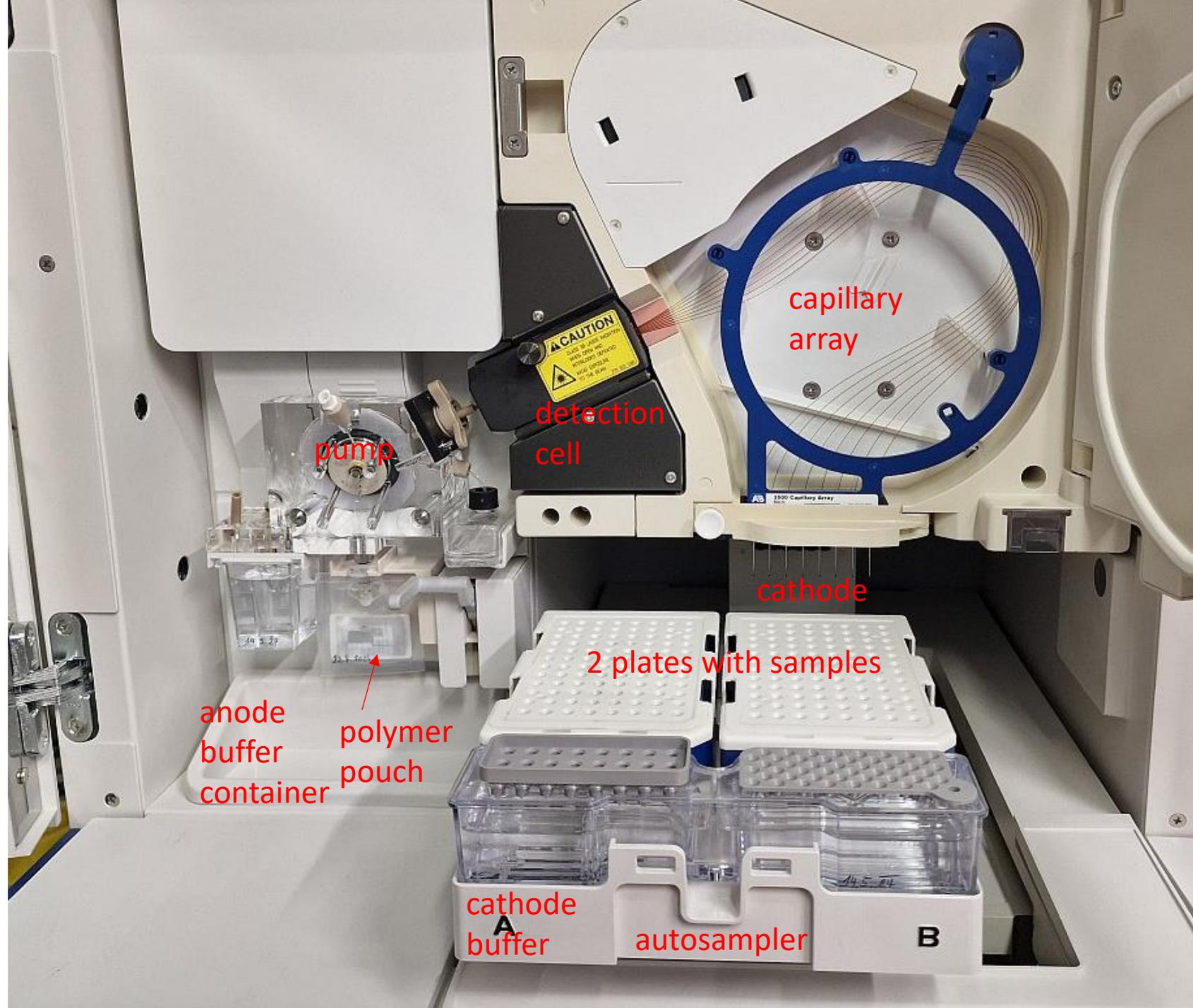


# Sequencing mixture purification

Capture of free nucleotides and terminators by porous reagent emulsion (30 min shaking)

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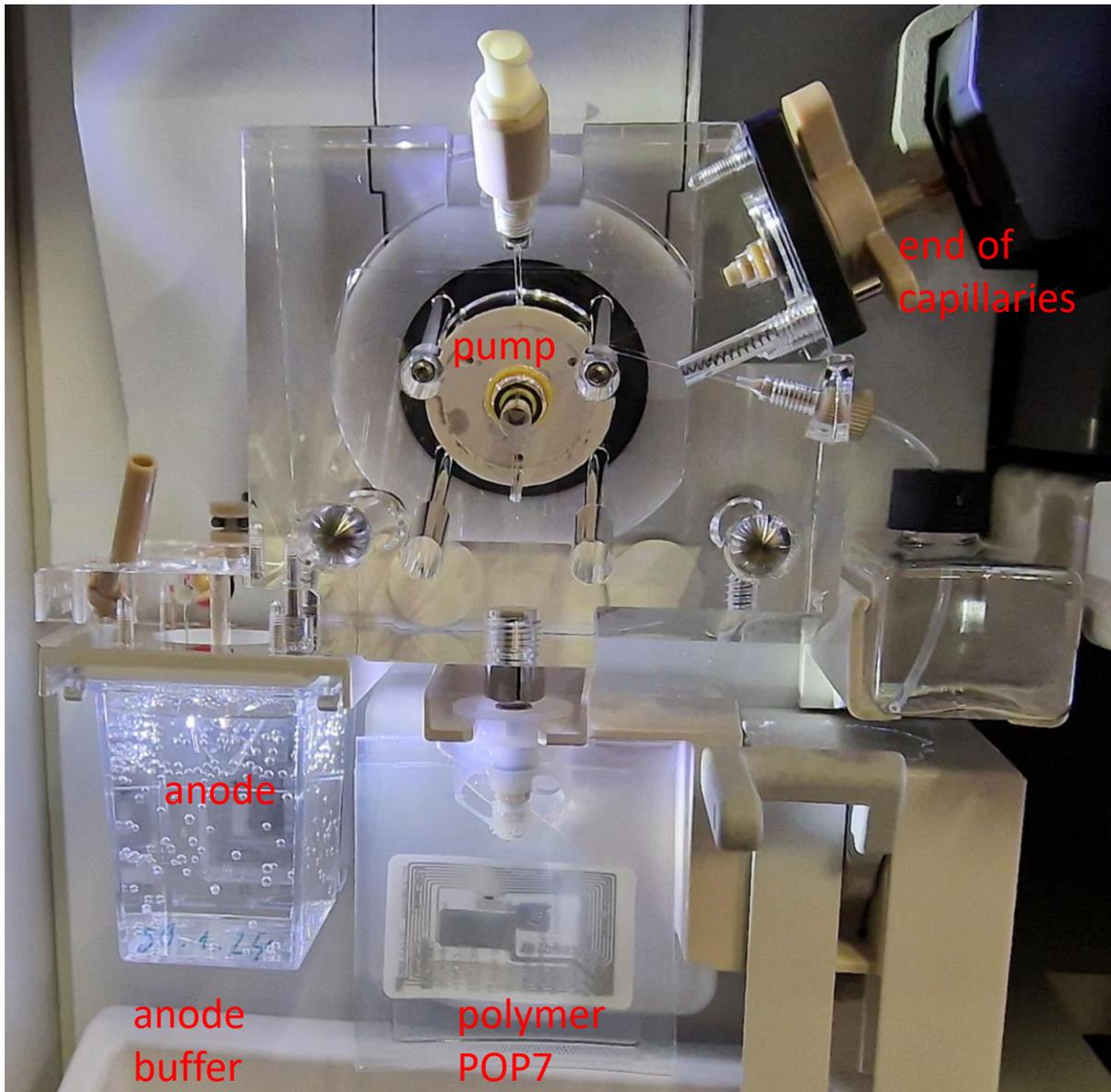




# Genetic analyzer (sequencer)

# Anode area of sequencer

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Erasmus+ project 2021-1-SK01-KA220-HED-000032068



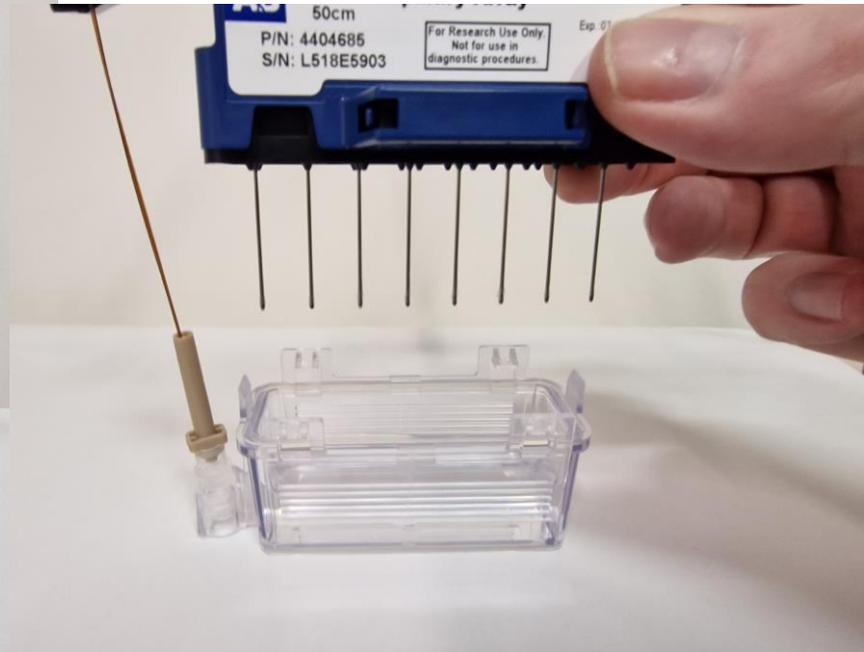
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# Capillary Array

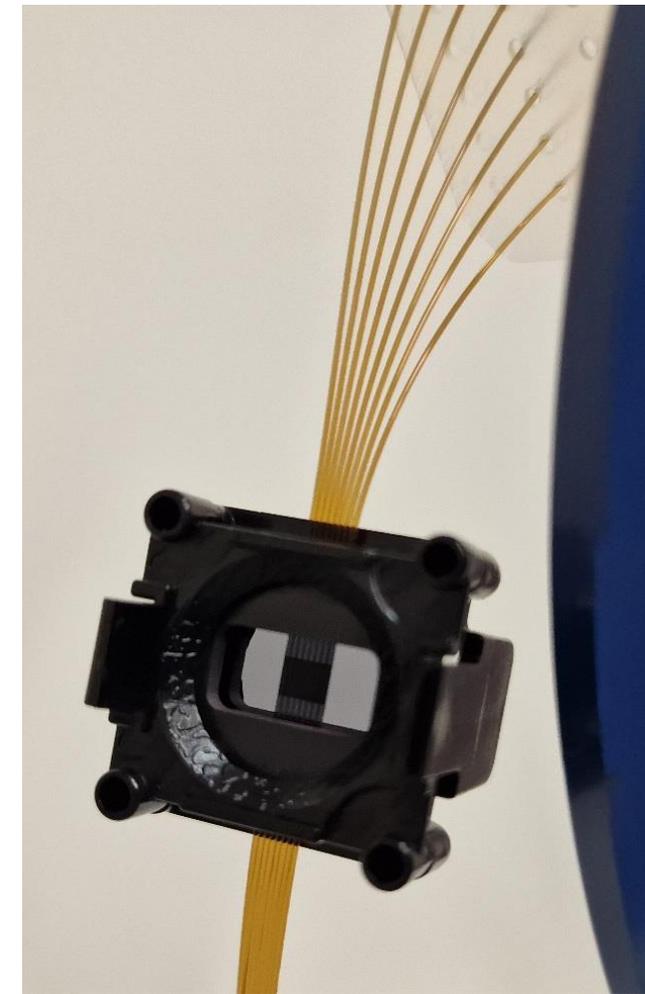
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8 capillaries



platinum electrodes



window for fluorescent signal detection



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# Sequencing procedure

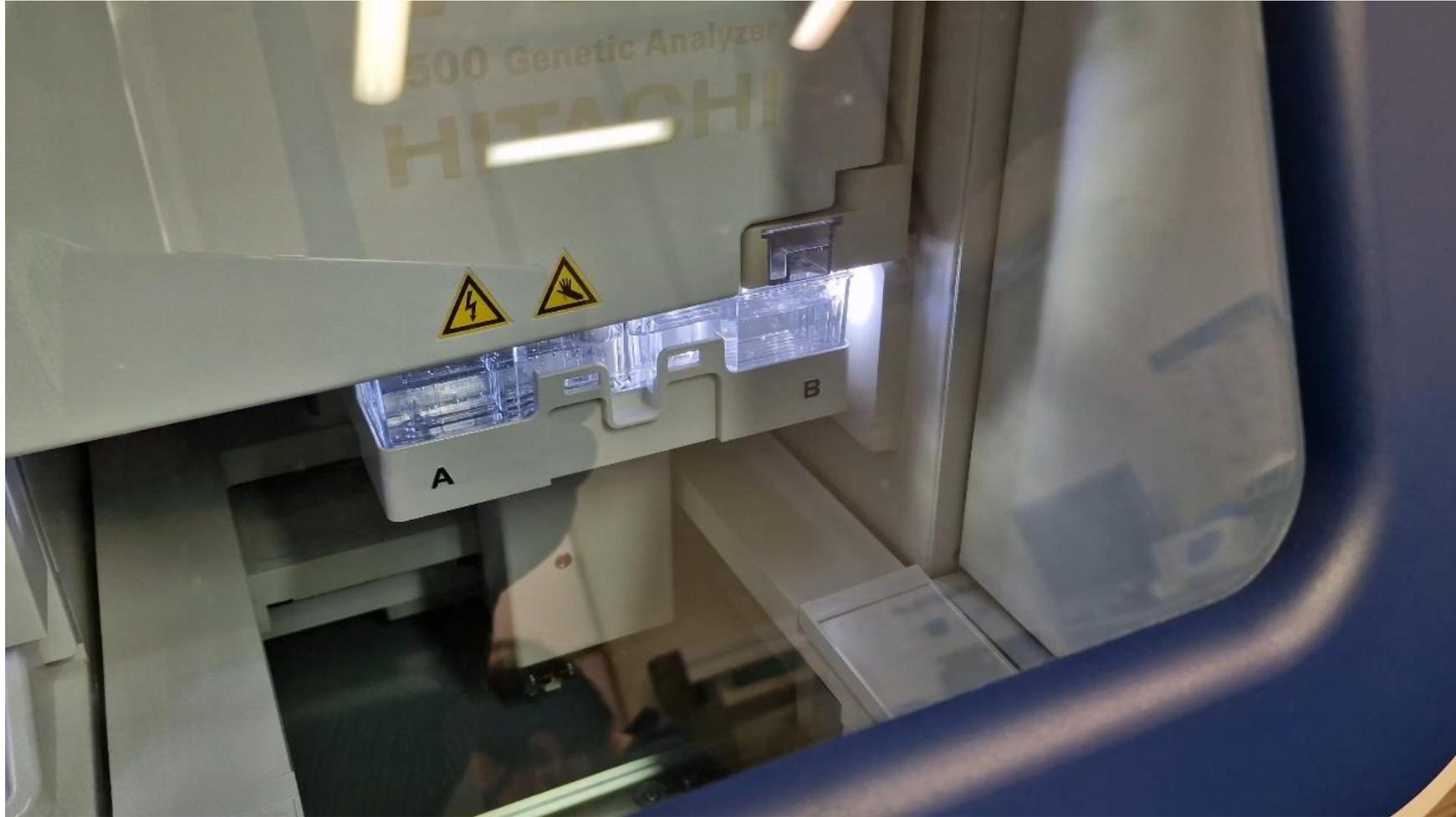
Insertion of anode buffer



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# Sequencing procedure

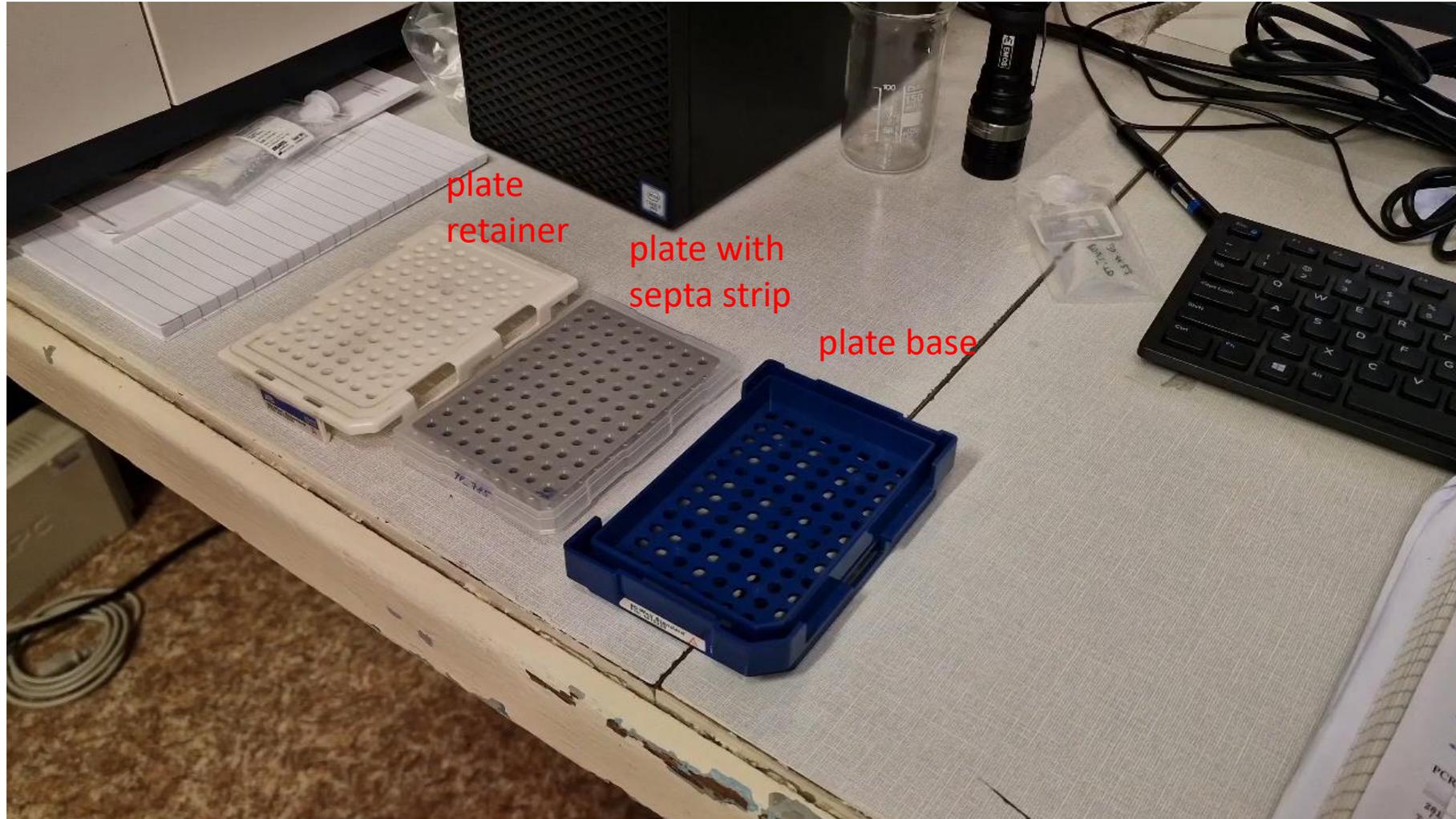
Preparing the sequencer for loading samples



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# Sequencing procedure

## Plate assembly preparation



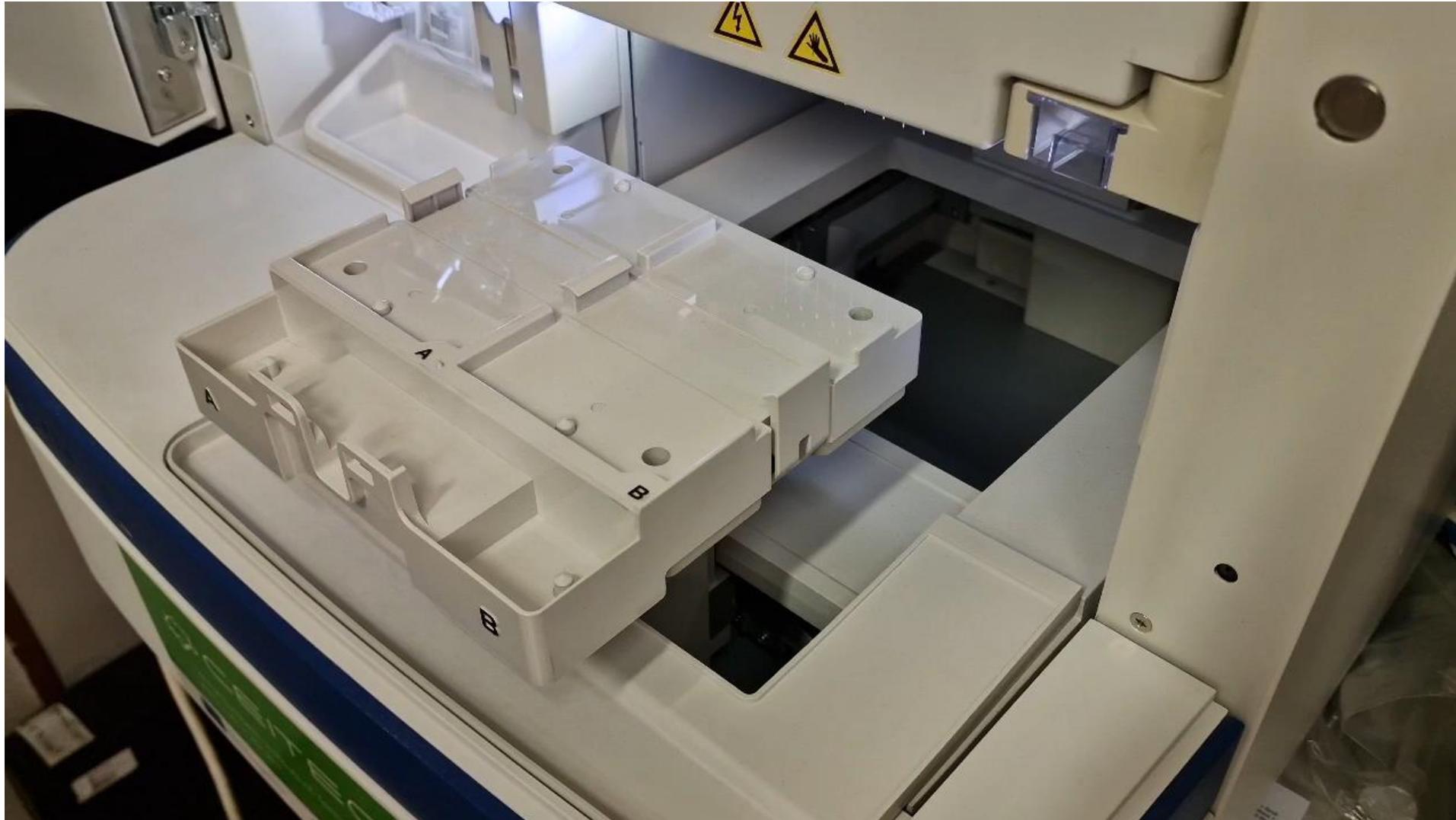
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# Sequencing procedure

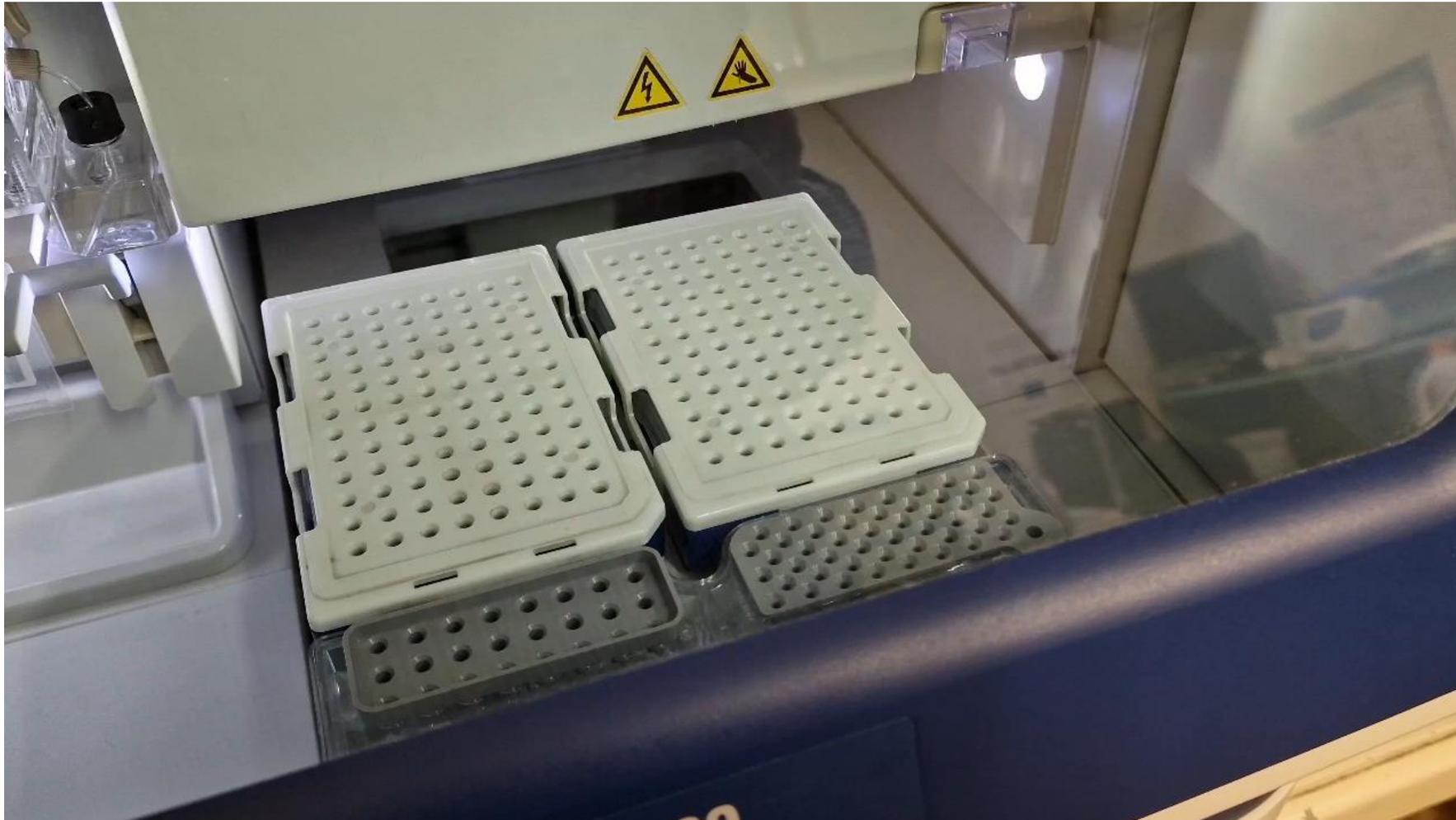
Insertion of the sample plate



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# Sequencing procedure

Samples stored in both plates (2 x 96 samples)



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# Sequencing procedure

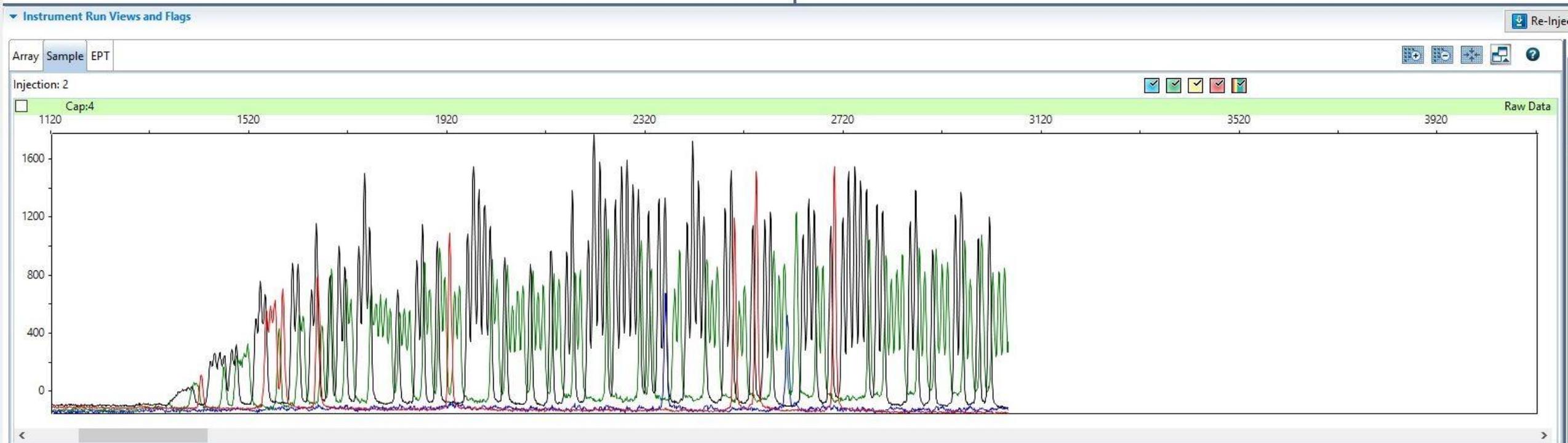
Injection of samples into capillaries: electroinjection

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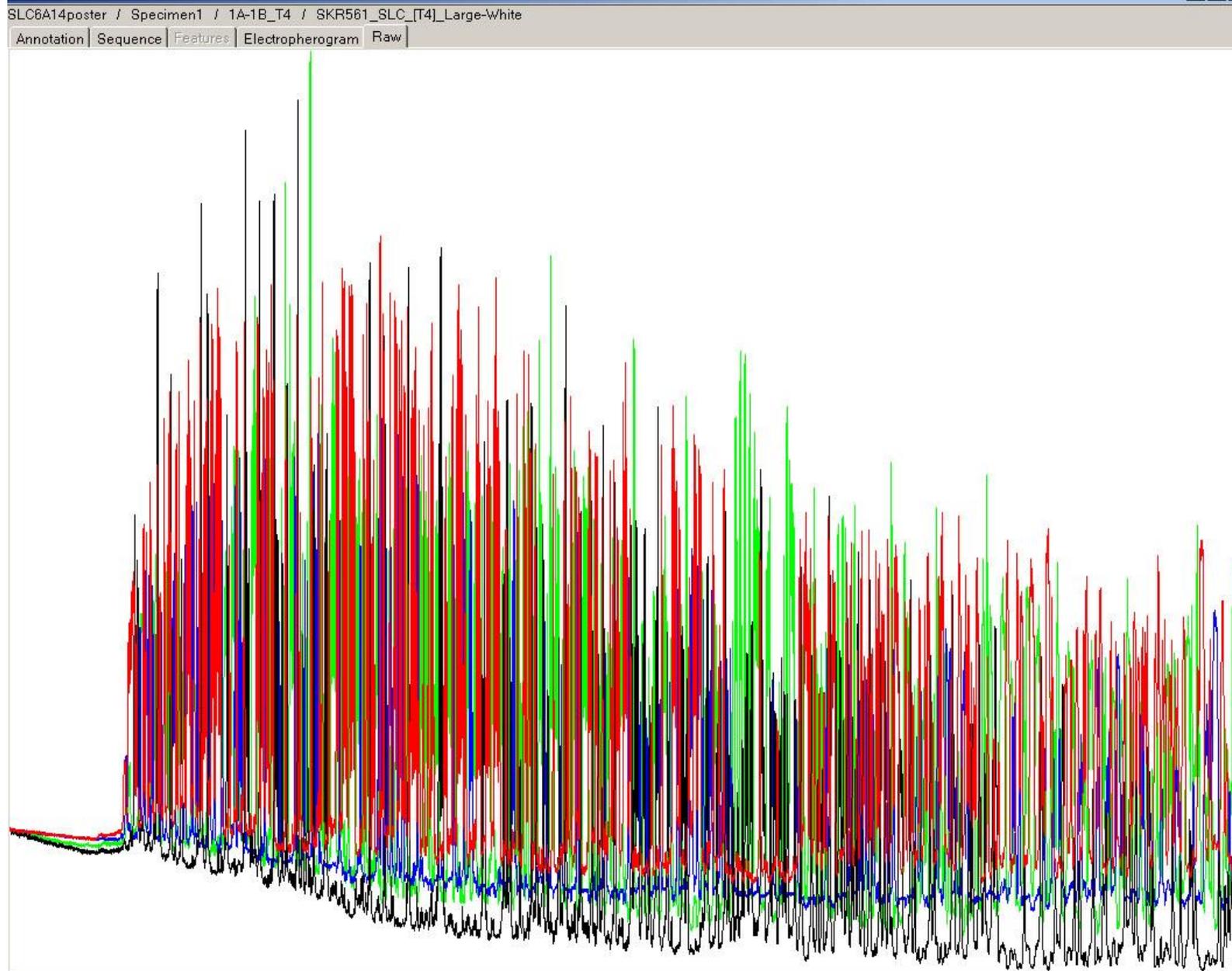
# Sequencing procedure

The reading of the fluorescent signal takes place gradually as the relevant fragments travel to the sensor



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# Raw data



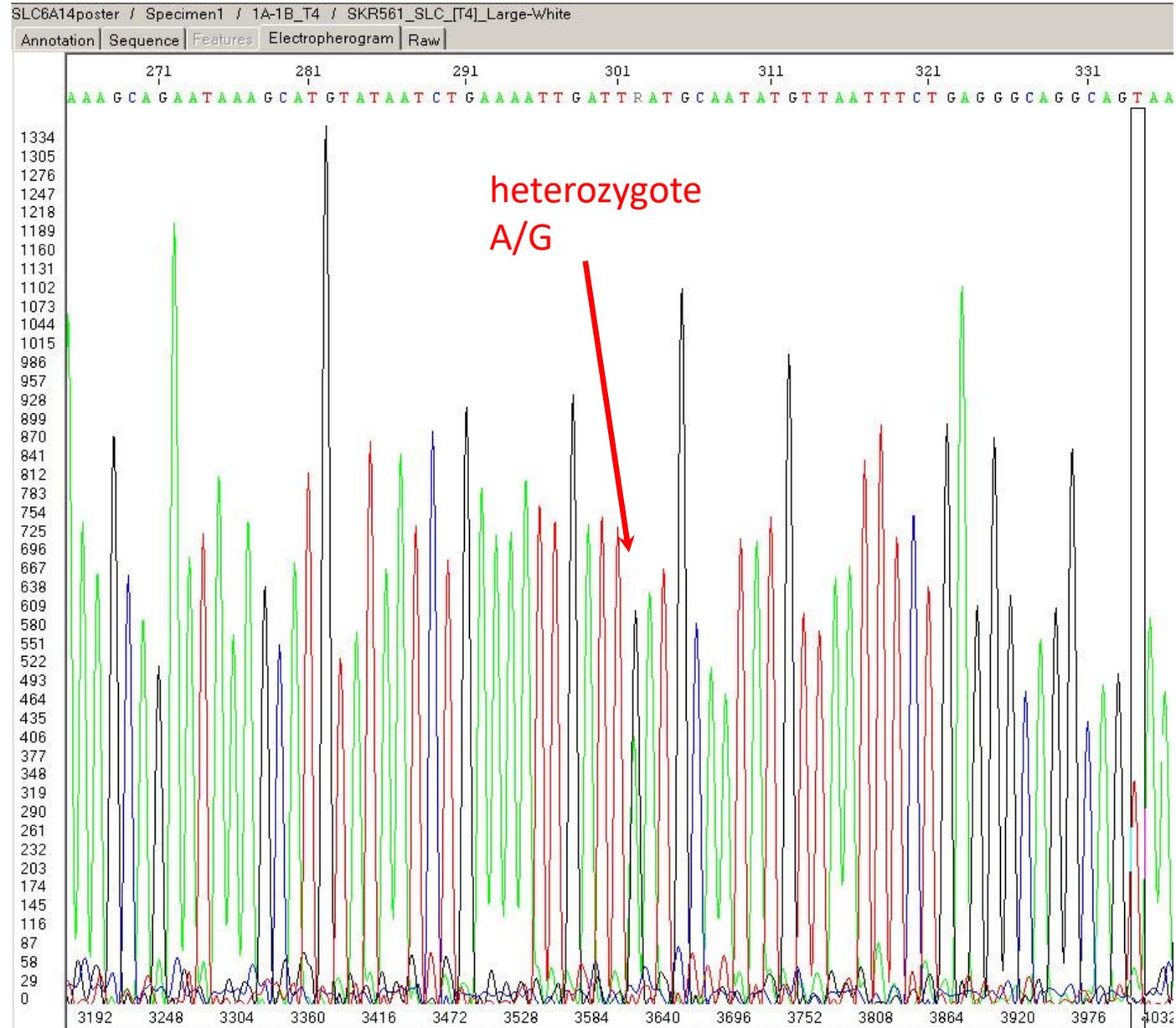
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# Evaluated electrophoretogram (heterozygote)

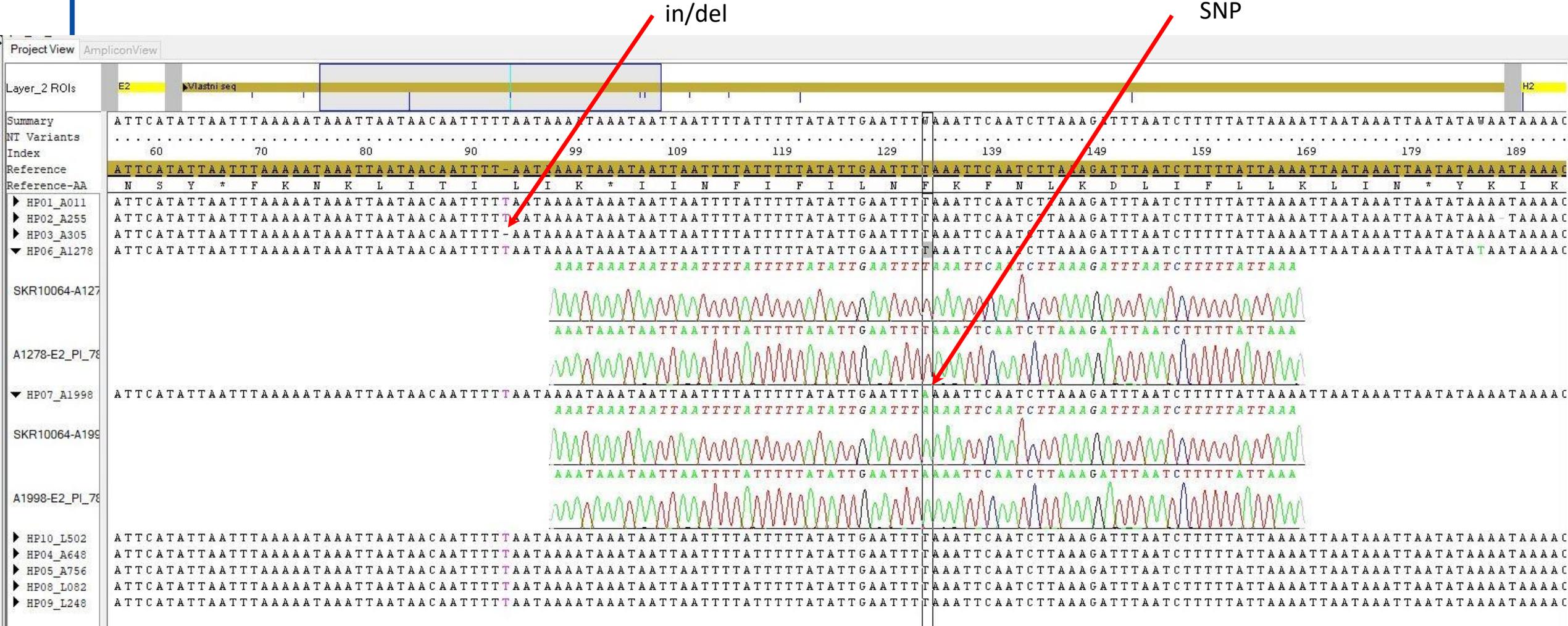
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# Sequence comparison

Seqscape software: example of polymorphisms in mt DNA in honeybee



# Sequence export

Fasta format

```
>F.693.
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GAGCCCCGACATAGCTTTCCCCGAATAAATAATATAAGATTTTGATTACTGCCCCCTCCCTAATATTACTTATTTCT
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>F.694.
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CCCGGC TGGAGGTGGGGATCCTATTTTATATCAACATTTATTT
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>F.696.
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TTACTTTTATCTTTGCCAGTATTAGCTGGAGCTATTACTATACTTTTAAACCGATCGTAATCTTAATACATCATTTTTTTGA
TCCAGCTGGAGGAGGTGATCCTATTTTATACCAACATTTATTT
```

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# Comparison Clustal

<https://www.ebi.ac.uk/jdispatcher/msa/clustalo>

COLOR SCHEME: clustal2

LEGEND: A R N D C Q E G H I L K M F P S T W Y V B X Z

4 sequences

46 50 100 150 200 250 300 350 400 450 500 550 600 650 145

F.696  
F.695  
F.693  
F.694

```
TTCATT AAGATT ACTAATTCGAGCGGAATTAGGAACCCAGGATCTTTAATTGGAGATGATCAAATTTATAATACAATTGT AACAGCCCATGCATTTA ^
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```





## Partners:



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and Humanities



Czech University  
of Life Sciences Prague



# Thank you for your attention!

*This presentation has been supported by the Erasmus+ KA2 Cooperation Partnerships grant no. 2021-1-SK01-KA220-HED-000032068 "Innovation of the structure and content of study programs in the field of animal genetic and food resources management with the use of digitalisation - Inovácia obsahu a štruktúry študijných programov v oblasti manažmentu živočíšnych genetických a potravinových zdrojov s využitím digitalizácie". The European Commission support for the production of this presentation does not constitute an endorsement of the contents which reflects the views only of the authors, and the Commission cannot be held responsible for any use which may be made of the information contained therein.*



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