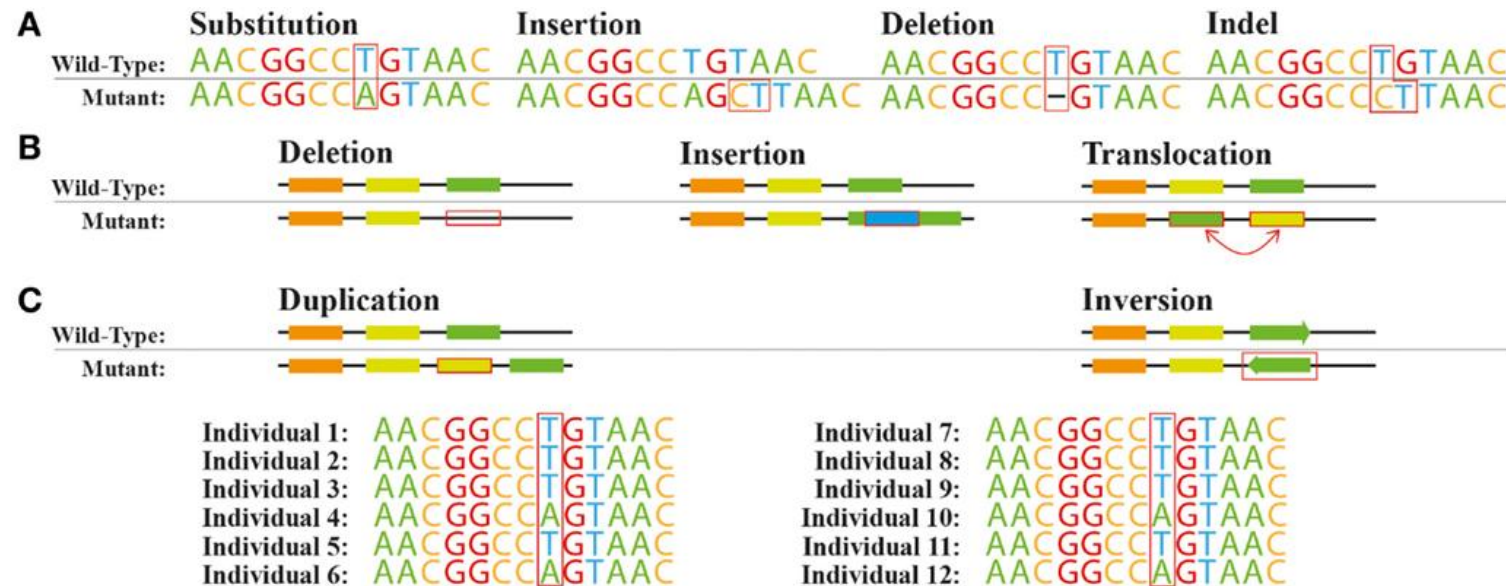


Molecular and evolutionary aspects of genetic variability



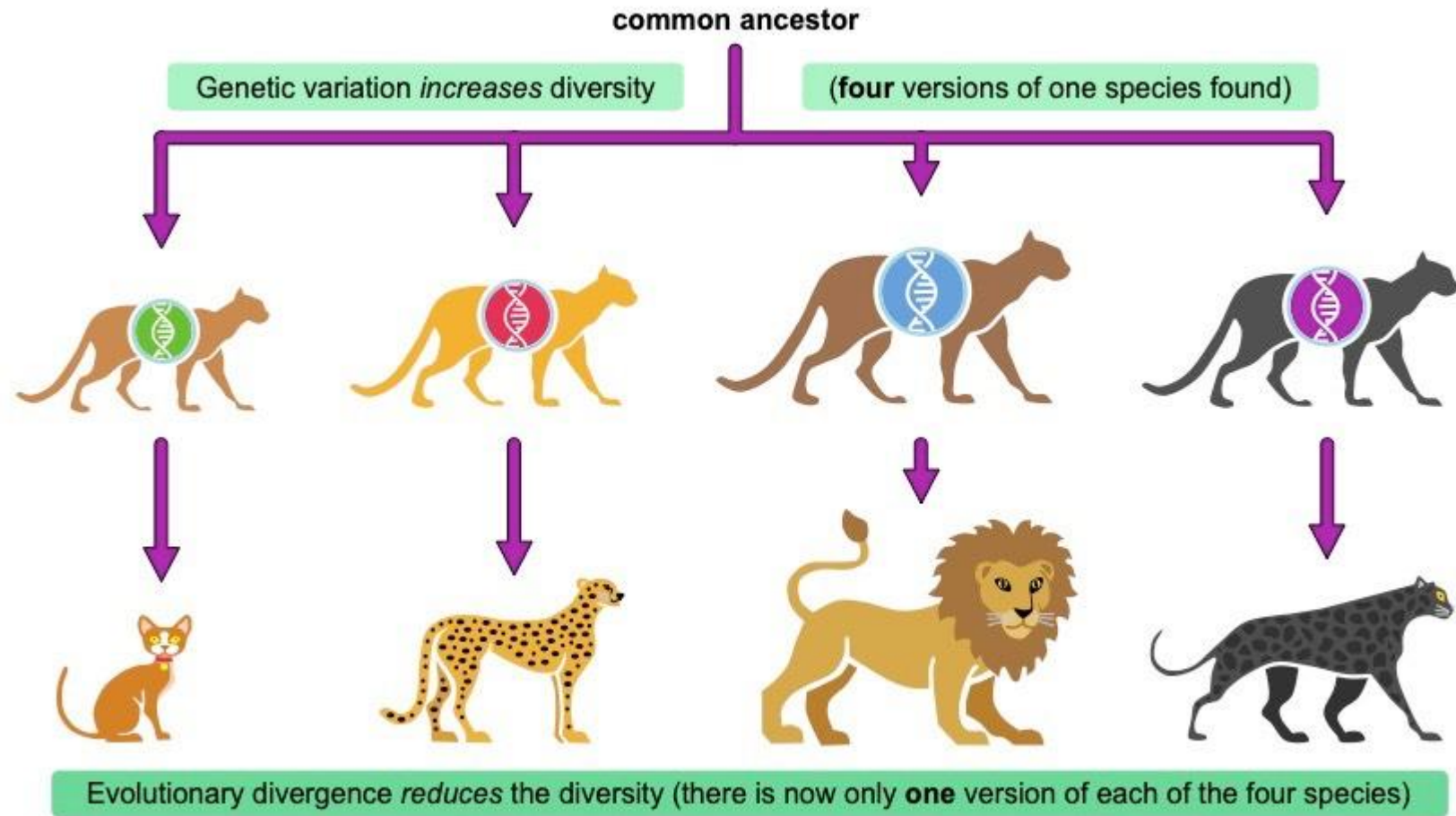
Peter DOVC

University of Ljubljana, Biotechnical Faculty

What is genetic variability?

- Genetic variability, the diversity in genetic makeup among individuals within a population, is the **fundamental raw material** for evolution, driven by molecular processes such as **mutations, gene flow, and sexual reproduction**.
- **Variations in DNA**, and consequently in RNA, and protein sequences, along with **alterations in gene expression** and **epigenetic modifications**, are caused by evolutionary forces like **natural selection** and **genetic drift**, and can ultimately lead to the development of new species and adaptations.

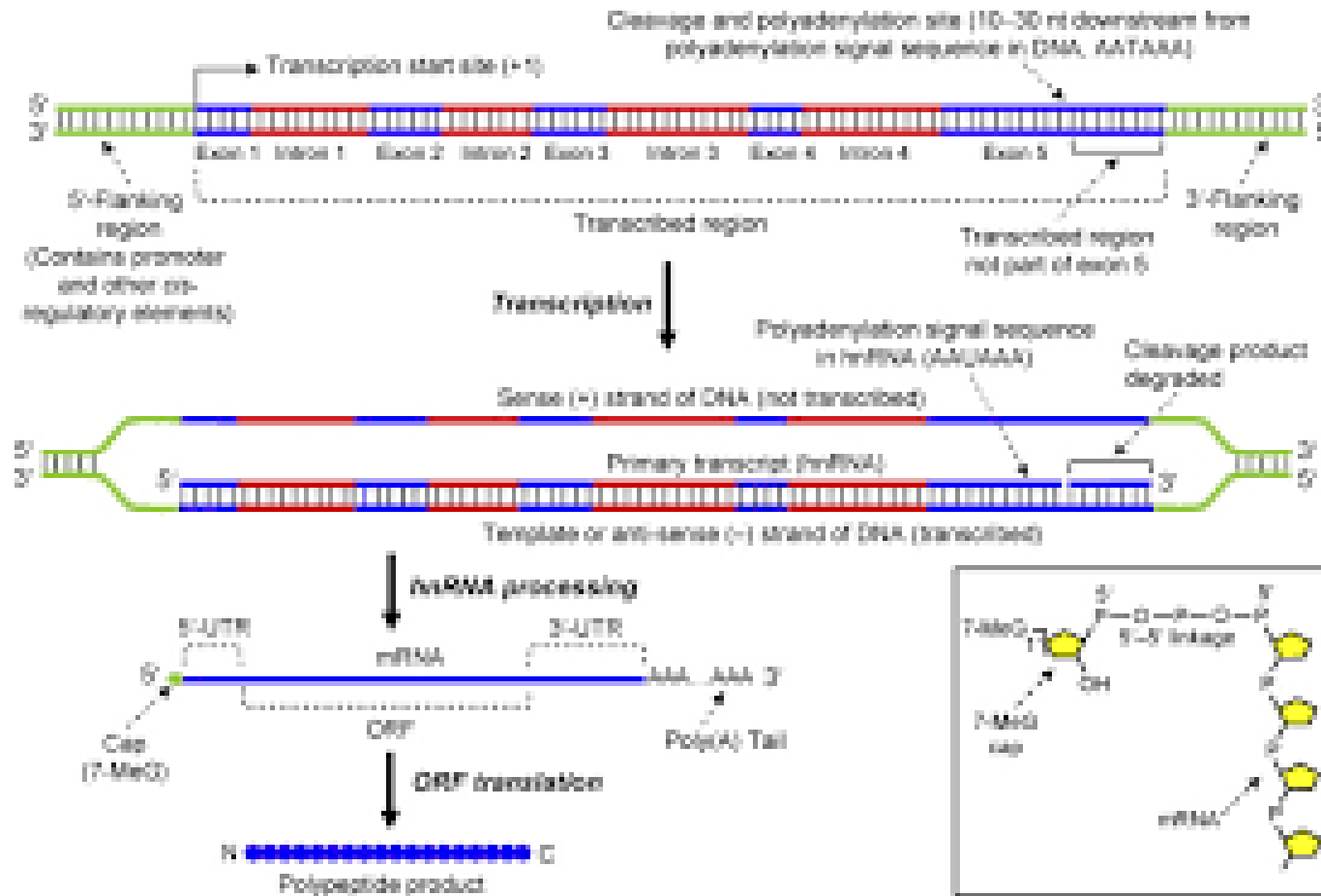
Genetic variation and diversity



Eukaryotic gene structure

- Sense and anti-sense strand
- Exon-intron structure
- Intron splicing signals, intron phase and alternative splicing
- Evolution of introns
- 5'- UTRs (Cap structure G7-met)
- 3'- UTRs (polyadenylation signal)

Genome structure and organization



Regulation of gene expression through functional sequence elements

- Promoters
- Enhancers
- LCR (Locus Control Regions)
- Epigenetic modifications of the genome (DNA methylation, histone code)

Molecular basis of mutation

- Point mutations
- Recombinations

Other mechanisms generating genetic diversity

- Gene flow
- Origin of new genes from coding sequences
 - Gene duplication
 - 2R hypothesis
 - Unequal crossing over
 - Chromosomal duplication
 - Exon shuffling
 - Gene fusion and fission
- Origin of new genes from noncoding sequences (*de novo*)

Factors affecting allele frequency in the population

- Mutation
- Migration (gene flow)
- Natural selection
- Genetic drift
- Inbreeding

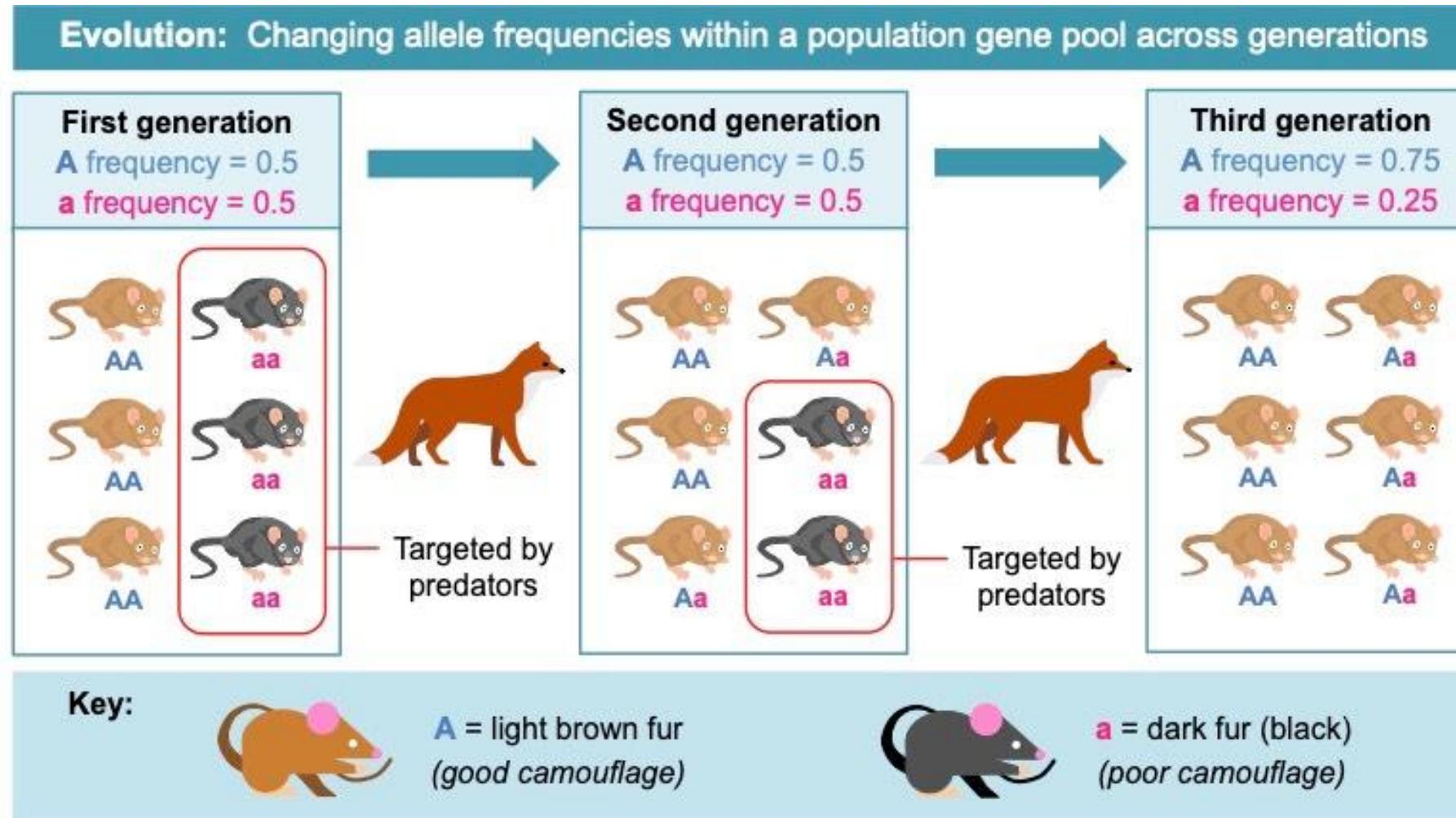
Example of natural selection



Figure 19-10
Introduction to Genetic Analysis, Ninth Edition
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Figure 19-11
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Example of natural selection



The neutral theory of evolution

- Synonymous and nonsynonymous substitutions

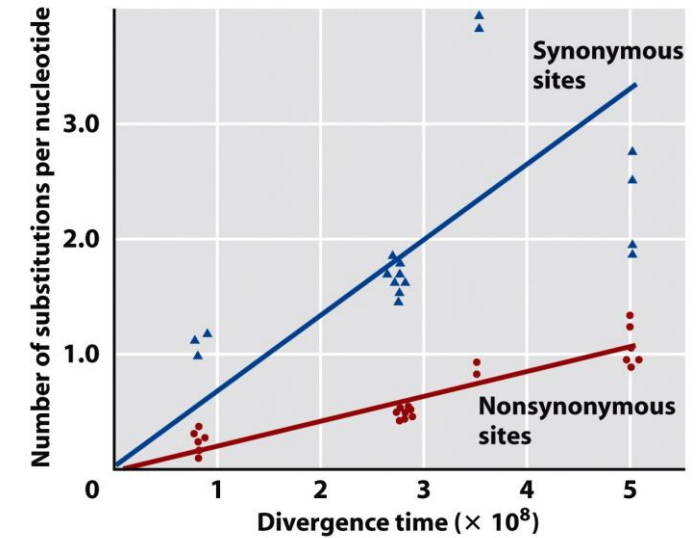
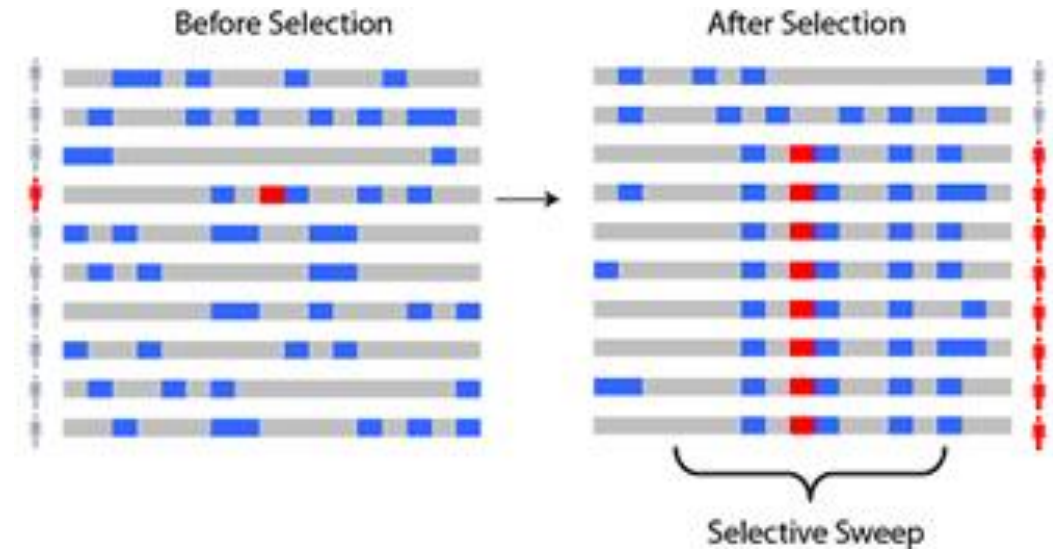


Figure 19-8
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- Signatures of positive selection

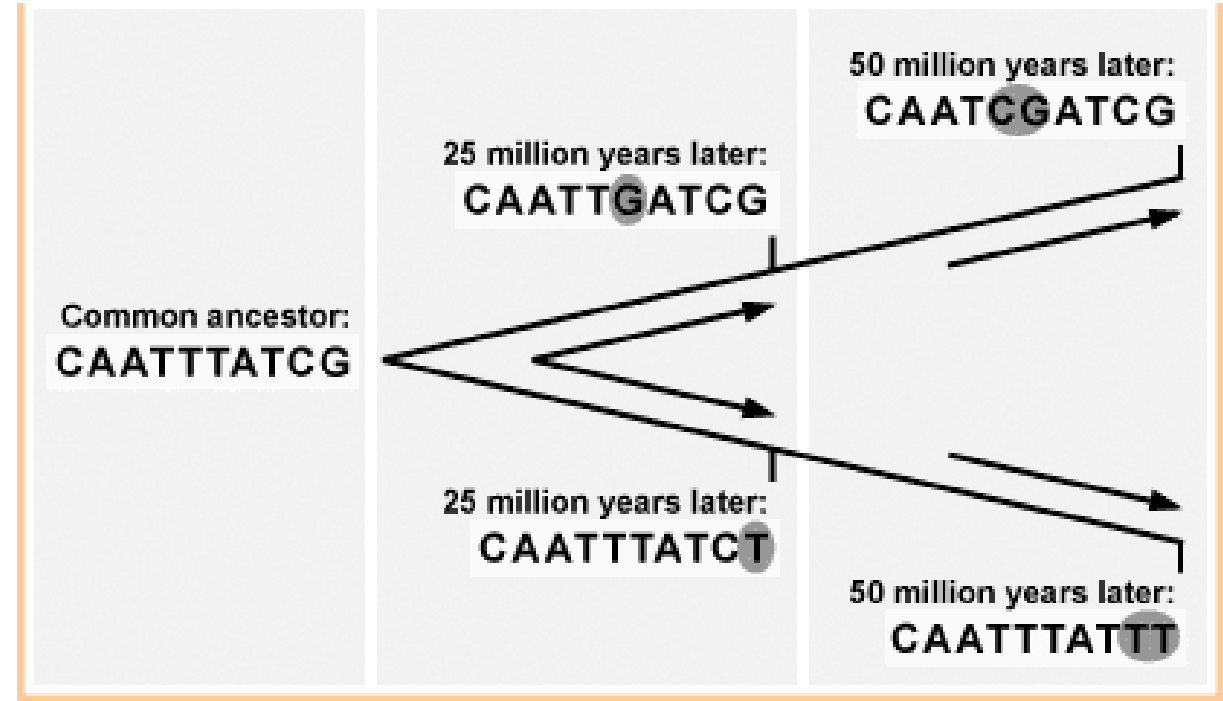


Molecular clock hypothesis

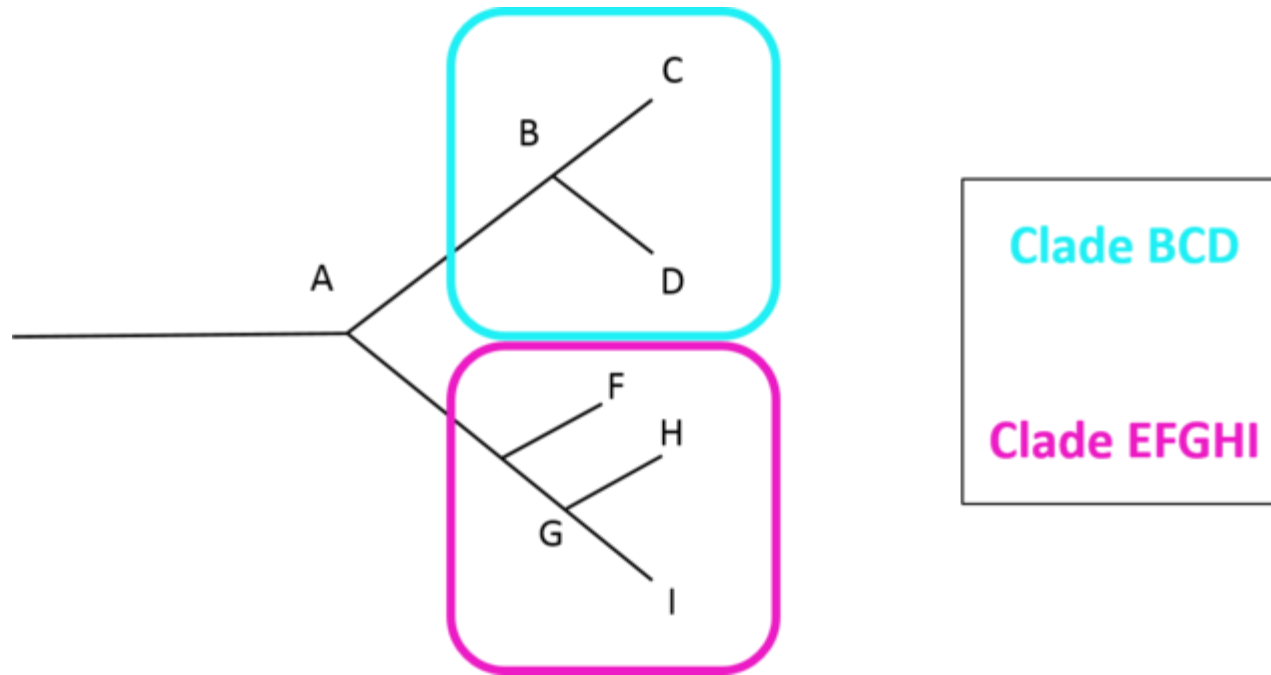
All the mutations occur in the same rate in all the taxa of a tree

The rate of mutations is the same for all positions along the sequence

The molecular clock hypothesis is most suitable for closely related taxa



Molecular phylogenetics



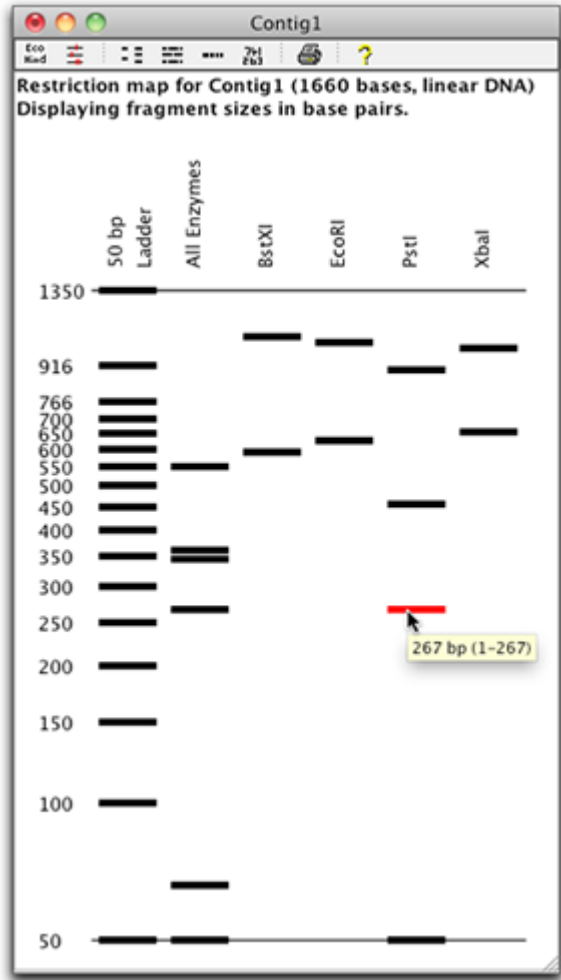
Genetic markers (their background, character - affecting evaluation, detection technology)

- Different types of variation
- Dominant and co-dominant markers
- Direct detection, hybridisation

Genomic technologies

- Restriction analysis
- Short tandem repeats (microsatellites)
- Sanger sequencing
- Pyrosequencing
- SNP genotyping
- NGS (Roche 454, Illumina Solexa, ABI SOLiD)
- Tiling Arrays
- Optical mapping

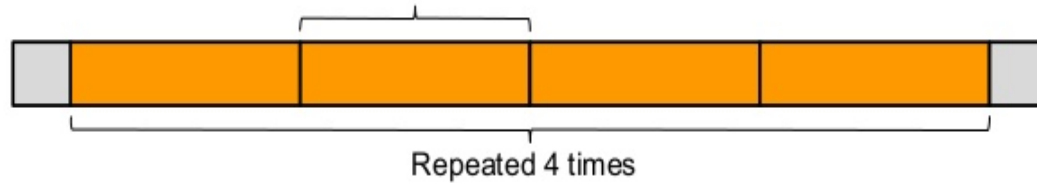
Restriction analysis and STRs



Tandem Repeat elements

Minisatellite: Variable Number Tandem Repeats (VNTR)

Repeat unit size = hundreds base pairs



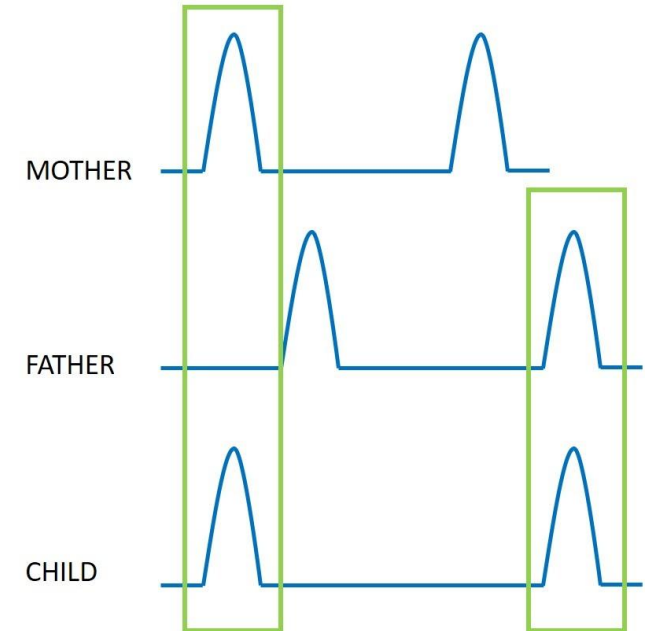
Microsatellite: Short Tandem Repeats (STR) – Simple Sequence Repeats (SSR)

Repeat unit size = 2 - 6 base pairs

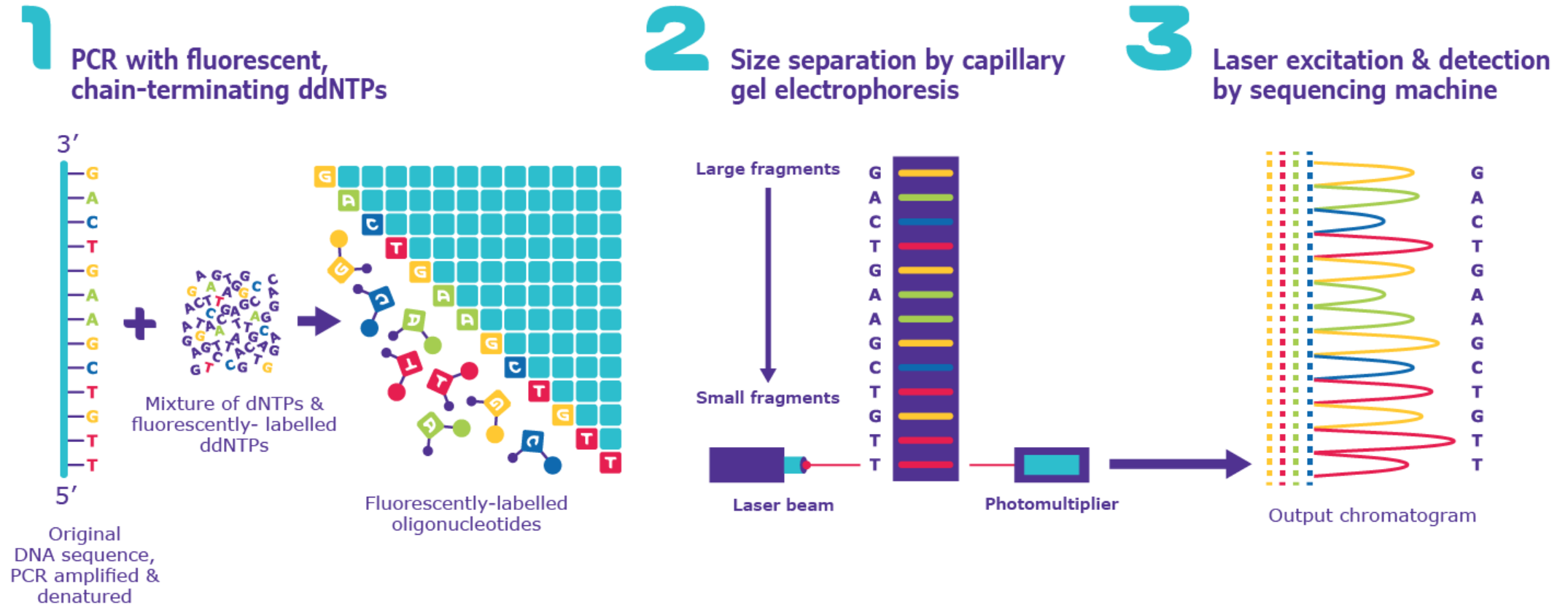


HAGenetics.org

MICROSATELLITES



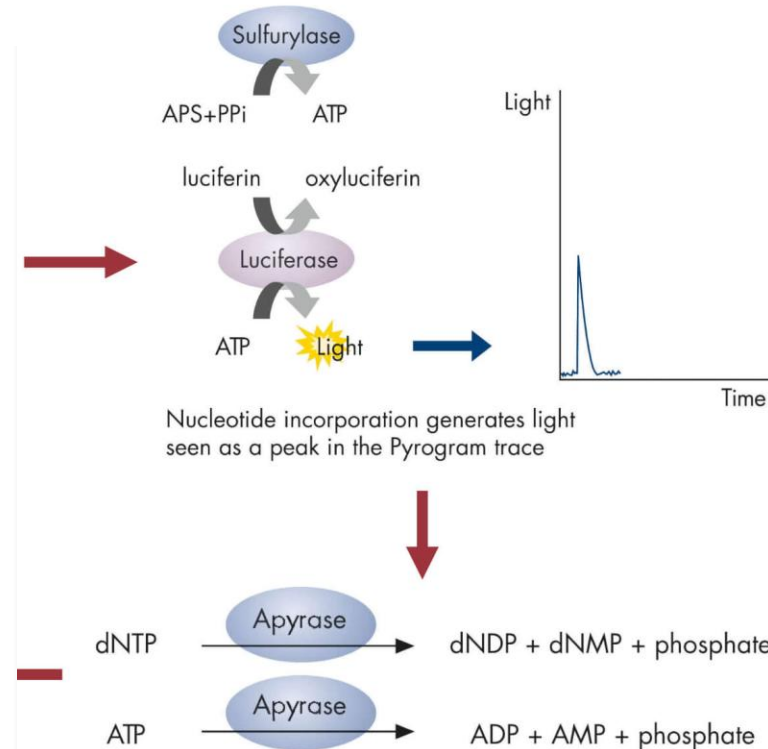
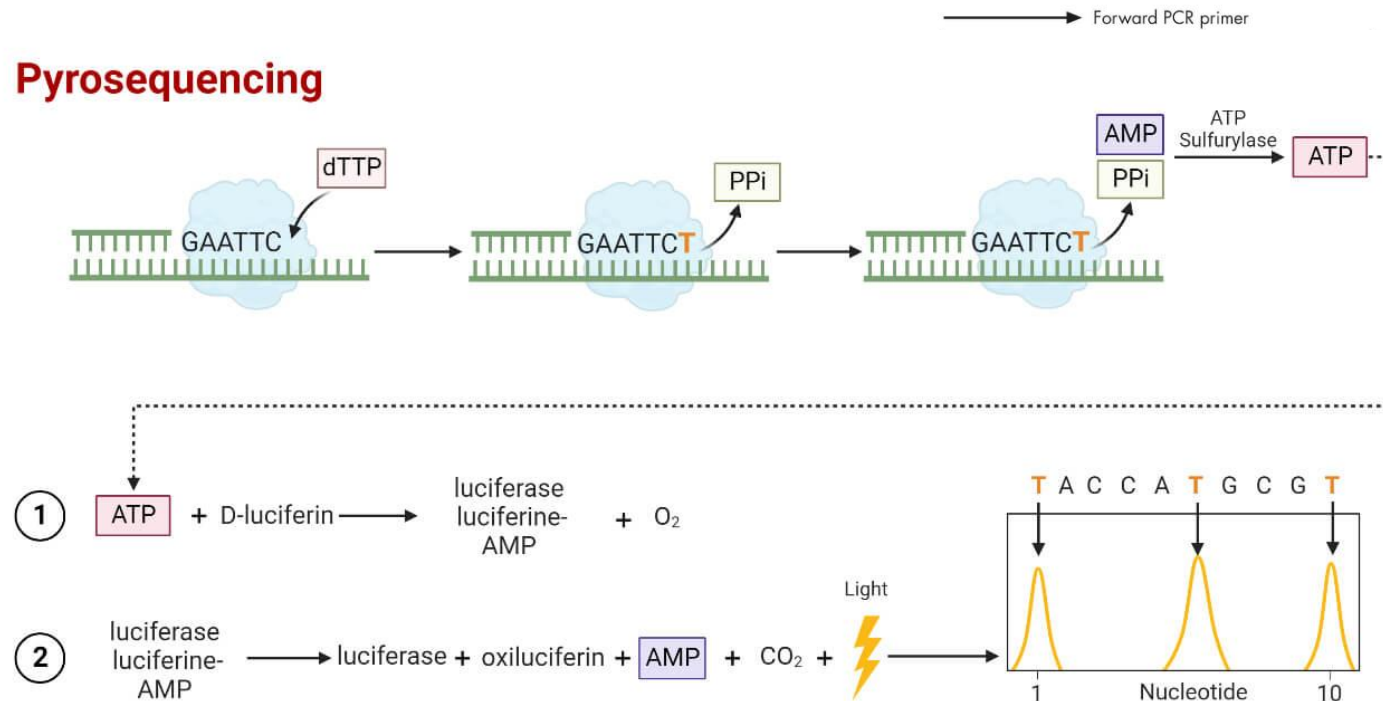
Sanger sequencing



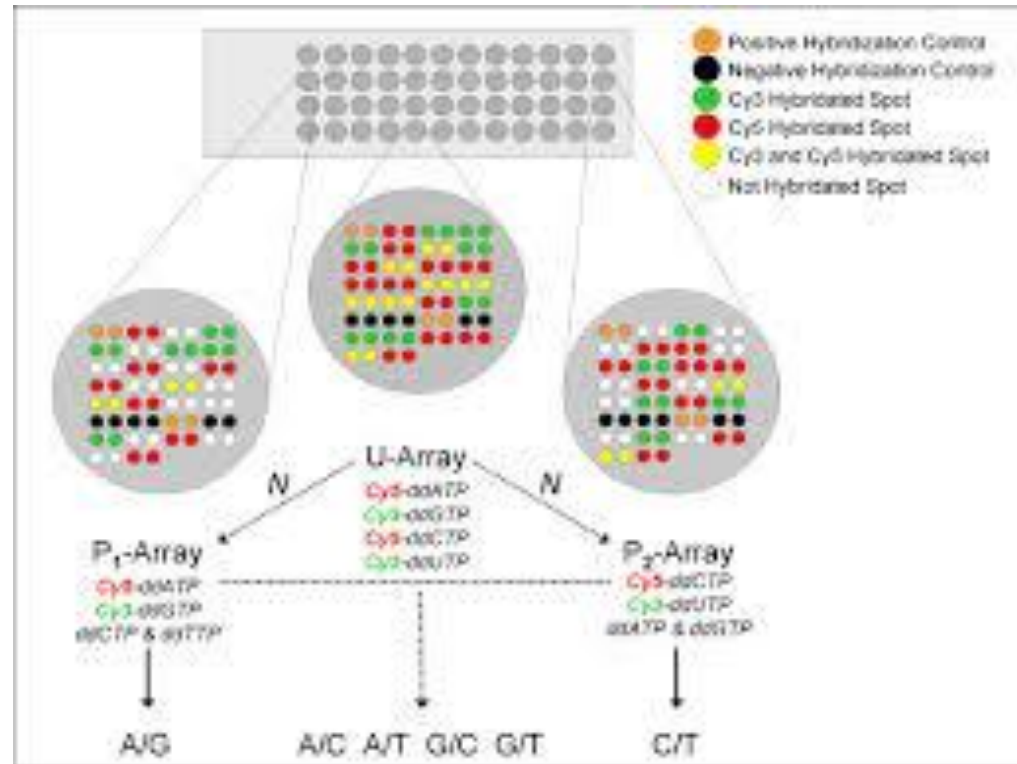
Pyrosequencing

Principle of Pyrosequencing

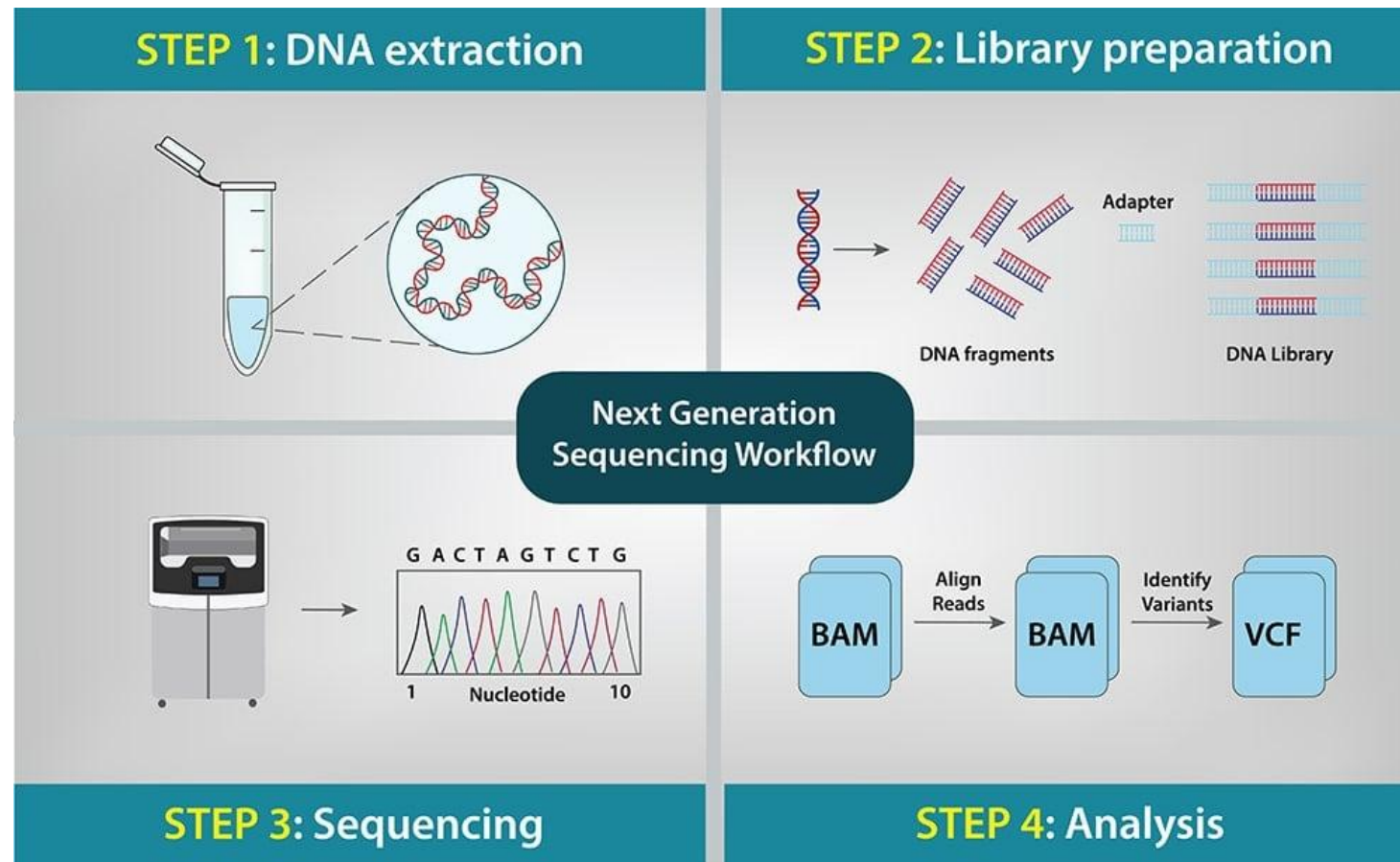
Pyrosequencing



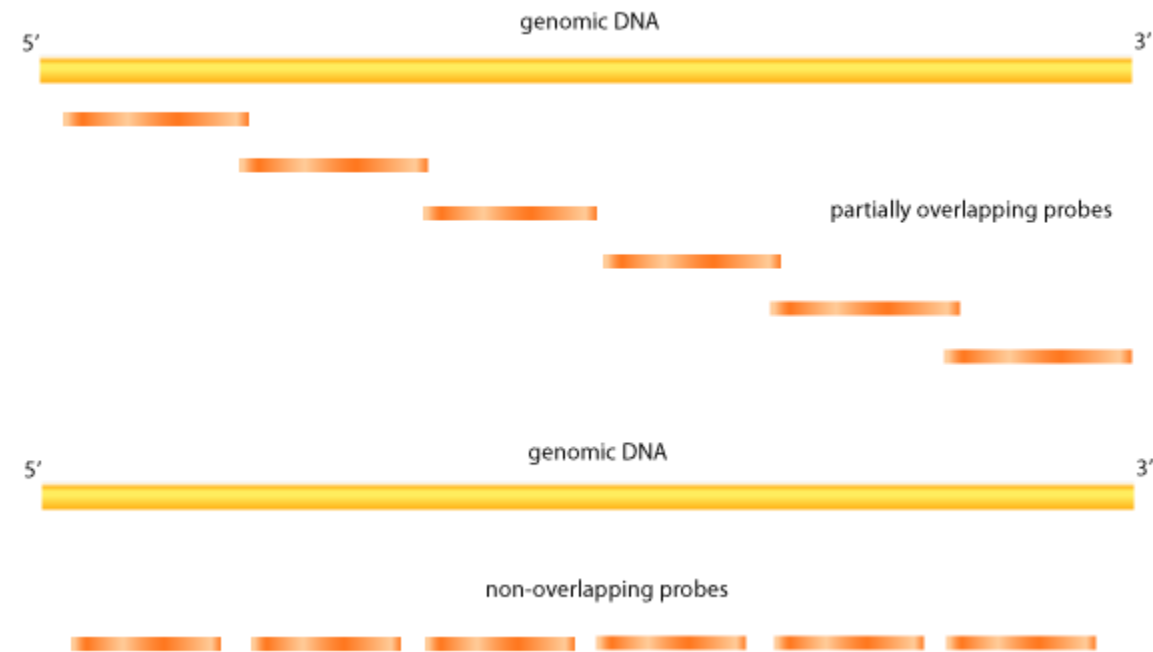
SNP genotyping



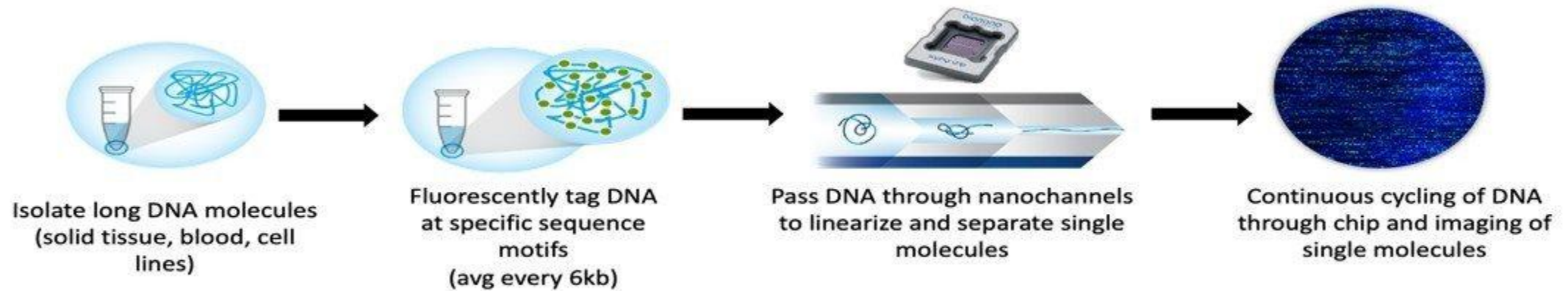
NGS (Roche 454, Illumina Solexa, ABI SOLiD)



Tiling arrays



Optical mapping



- Thank you for your attention!



Questions?