



# Molecular Biology (3)

## The human genome

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# Resources



- This lecture
- Cooper, Ch. 5, pp.159-162, 166-171



SPECIES	BASE PAIRS (estimated)	GENES (estimated)	CHROMOSOMES
<b>Human</b> ( <i>Homo sapiens</i> )	3.2 billion	~ 25,000	46
<b>Mouse</b> ( <i>Mus musculus</i> )	2.6 billion	~ 25,000	40
<b>Fruit Fly</b> ( <i>Drosophila melanogaster</i> )	137 million	13,000	8
<b>Roundworm</b> ( <i>Caenorhabditis elegans</i> )	97 million	19,000	12
<b>Yeast</b> ( <i>Saccharomyces cerevisia</i> )	12.1 million	6,000	32
<b>Bacteria</b> ( <i>Escherichia coli</i> )	4.6 million	3,200	1
<b>Bacteria</b> ( <i>H. influenzae</i> )	1.8 million	1,700	1

# Nucleotides per genomes

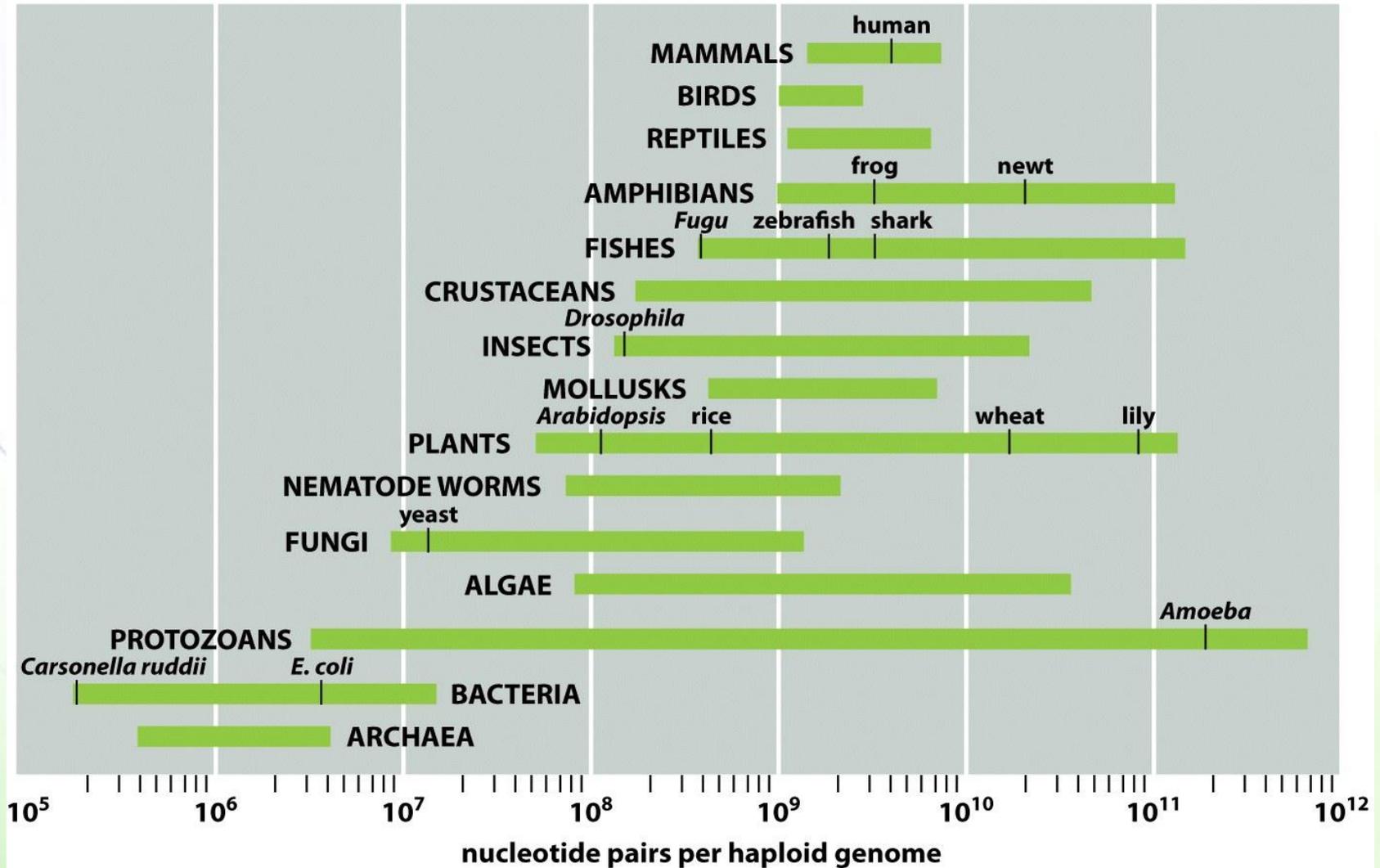
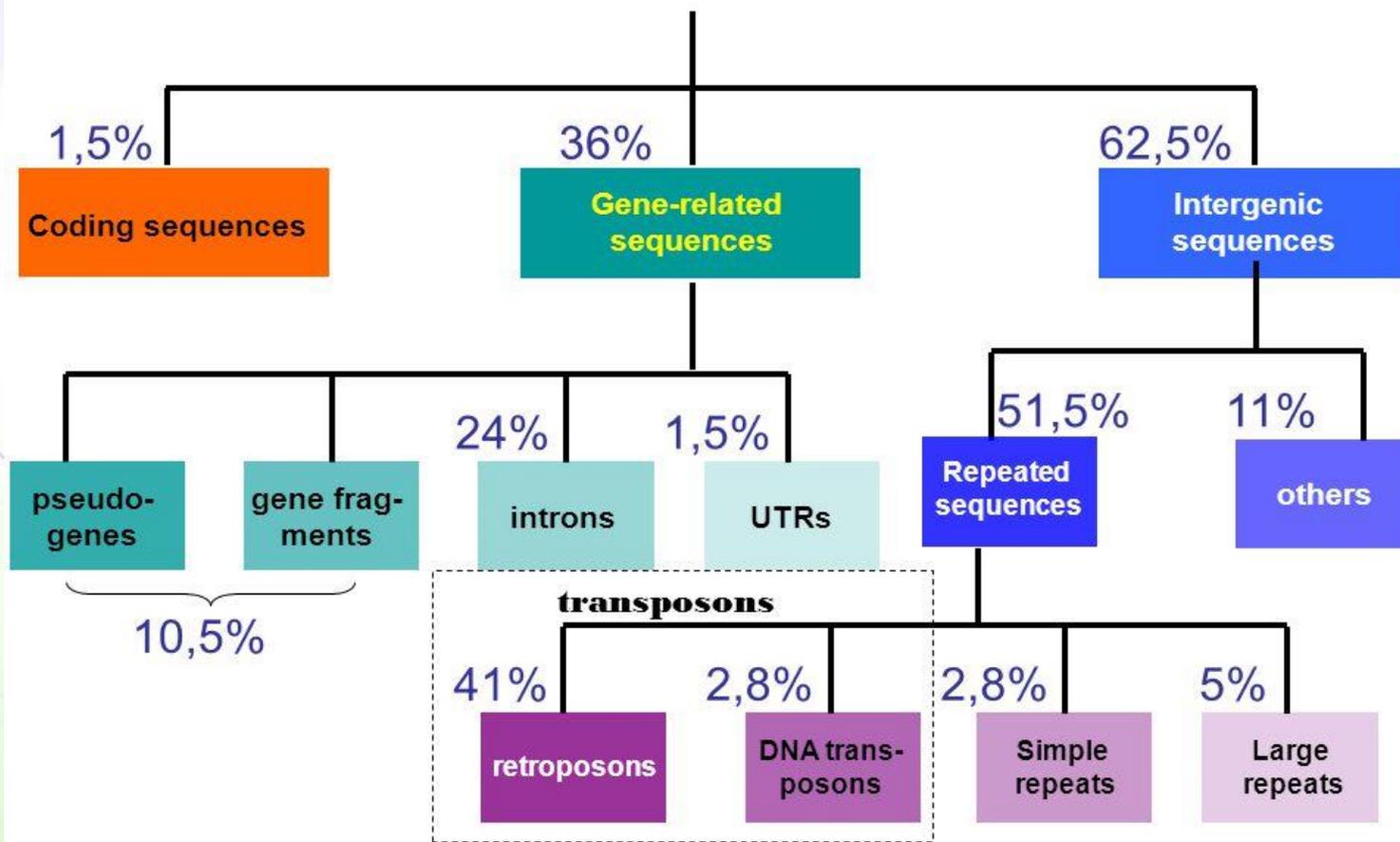


Figure 1-41 Essential Cell Biology 3/e (© Garland Science 2010)

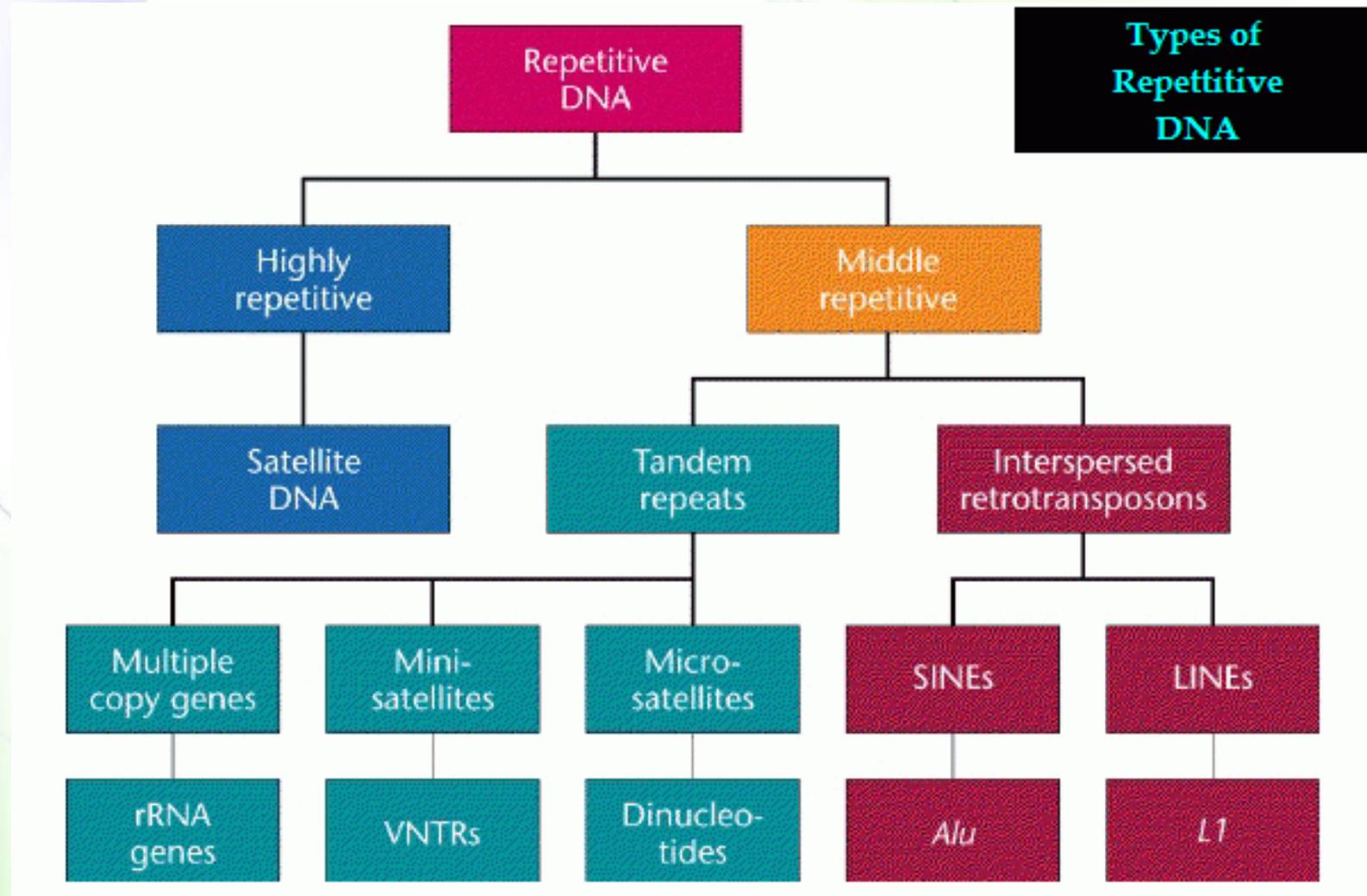
# Components of the human genome



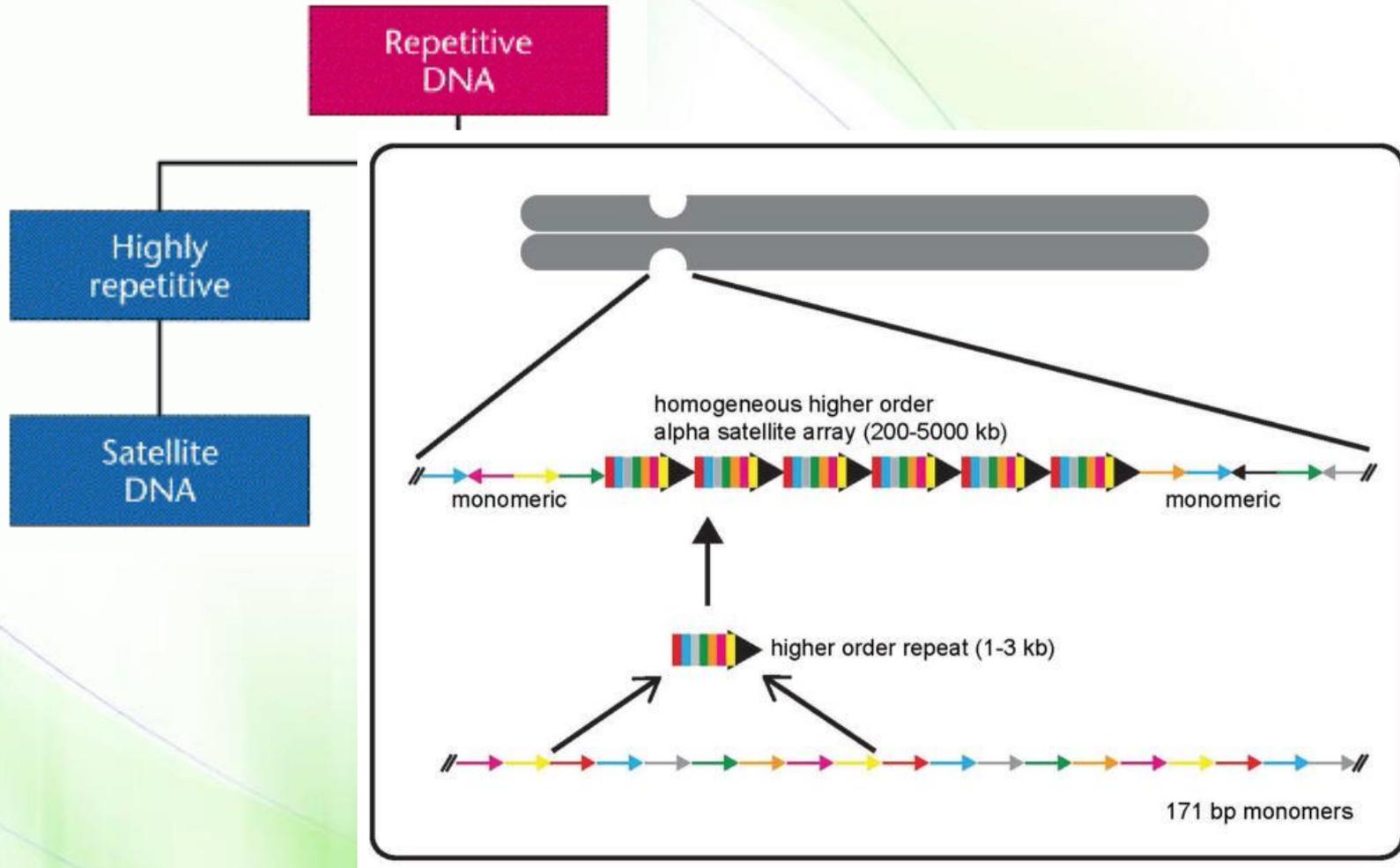
## Human genome



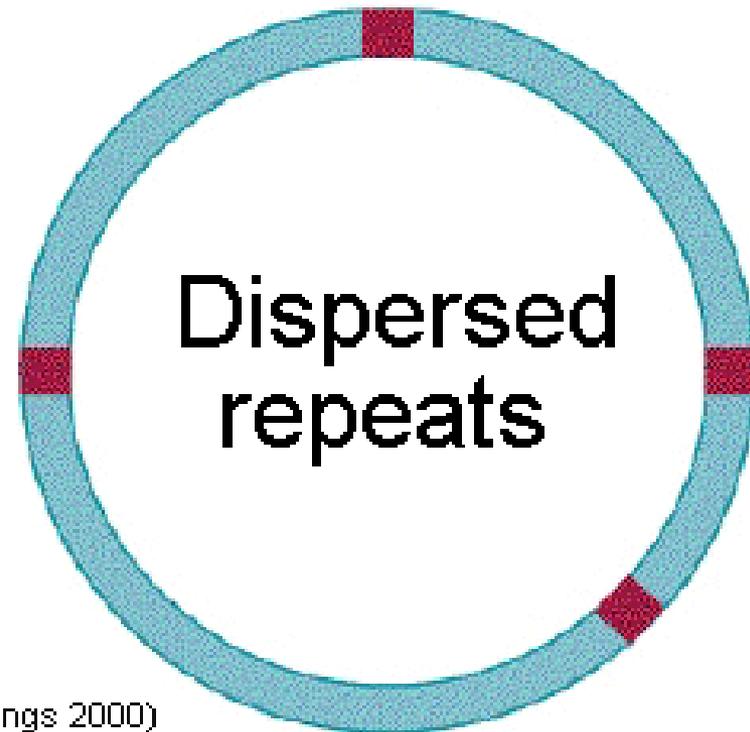
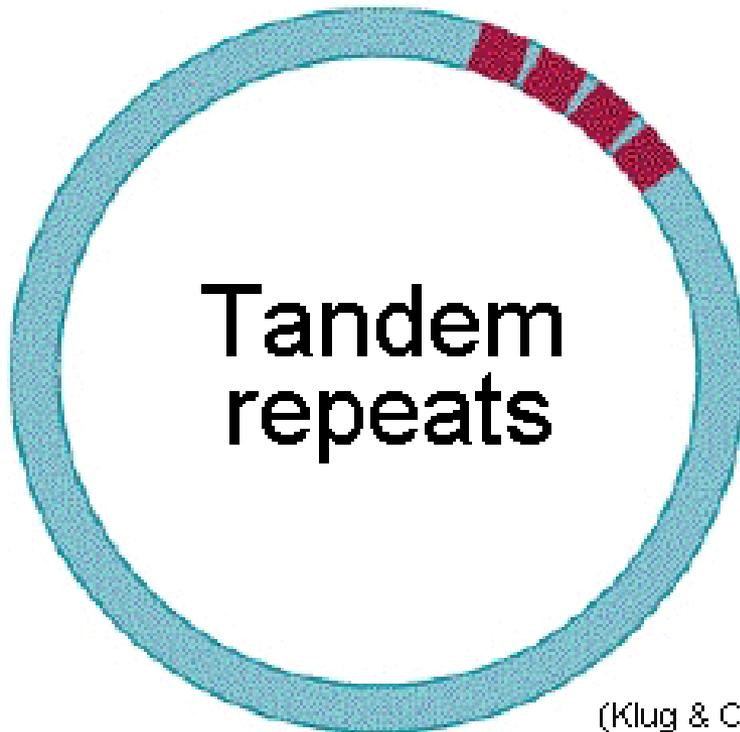
# Repetitive DNA sequences



# Repetitive DNA sequences



# Tandem vs. dispersed

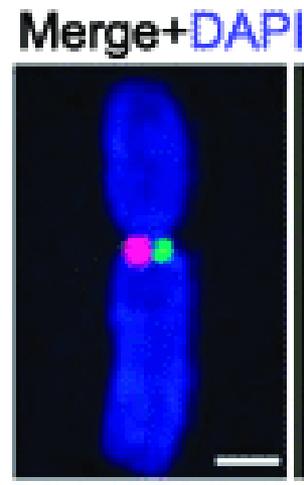
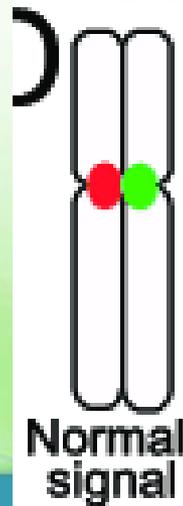
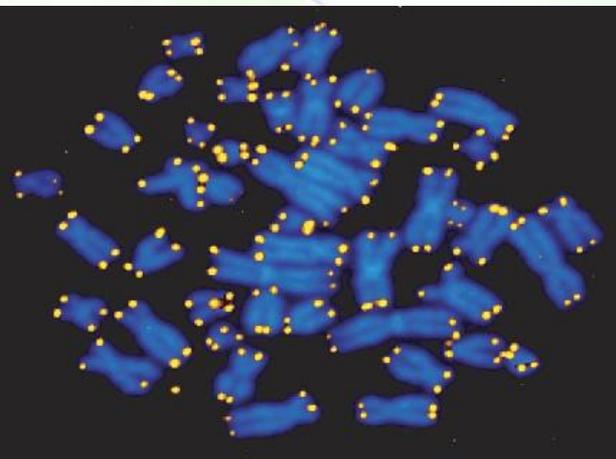
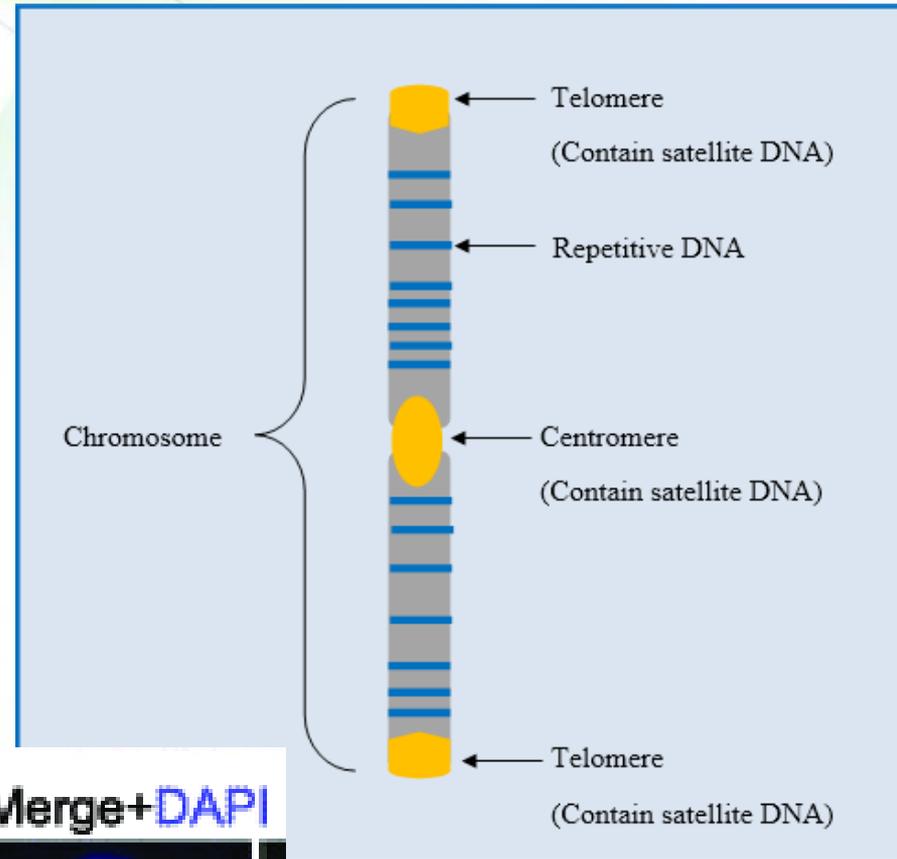


(Klug & Cummings 2000)

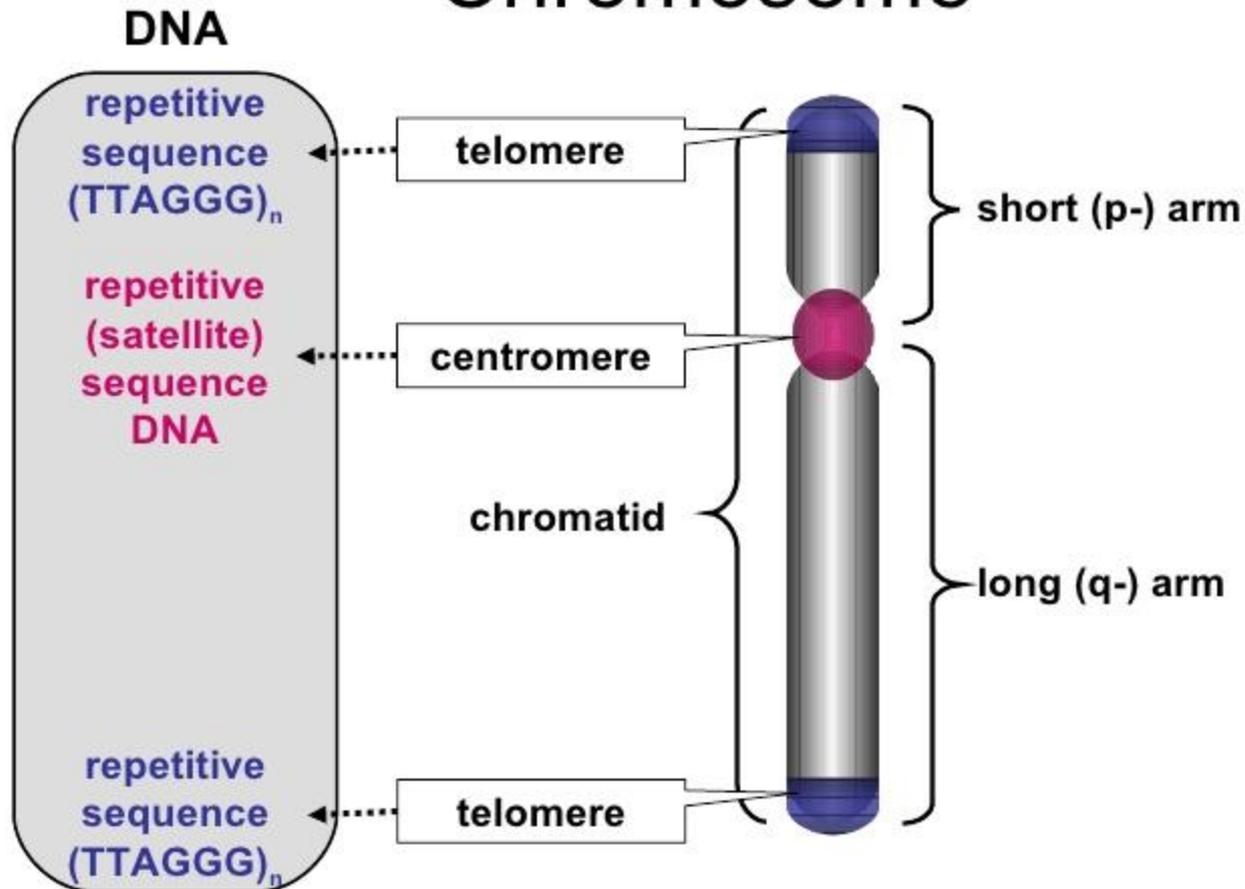
# Satellite (macro-satellite) DNA



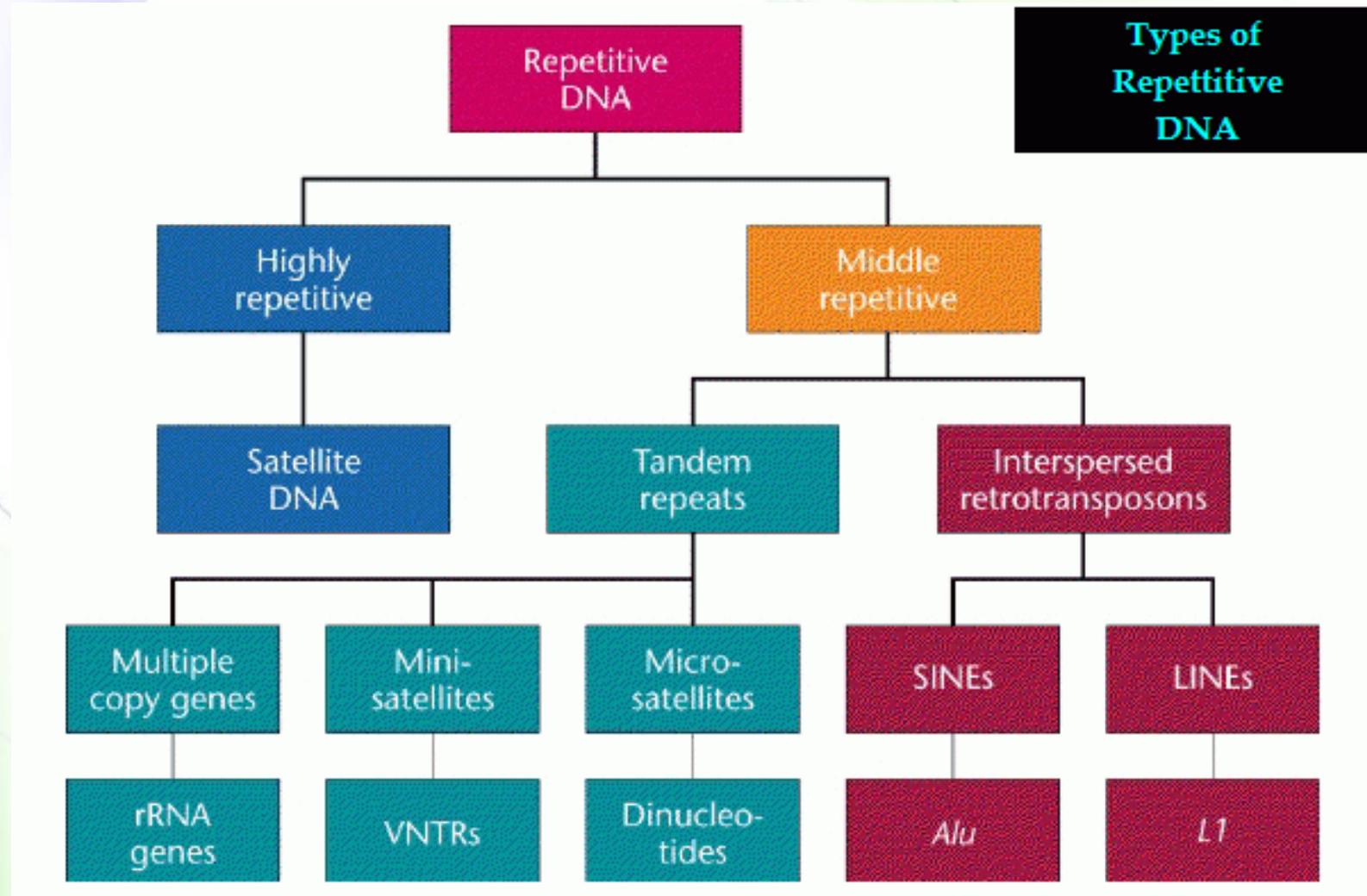
- Regions of 5-300 bp repeated  $10^6$ - $10^7$  times (10% of genome)
- Centromeric repeats (171 bp) unique to each chromosome (you make chromosome-specific probes) by **fluorescent in situ hybridization**.
- Telomeric repeats



# Chromosome



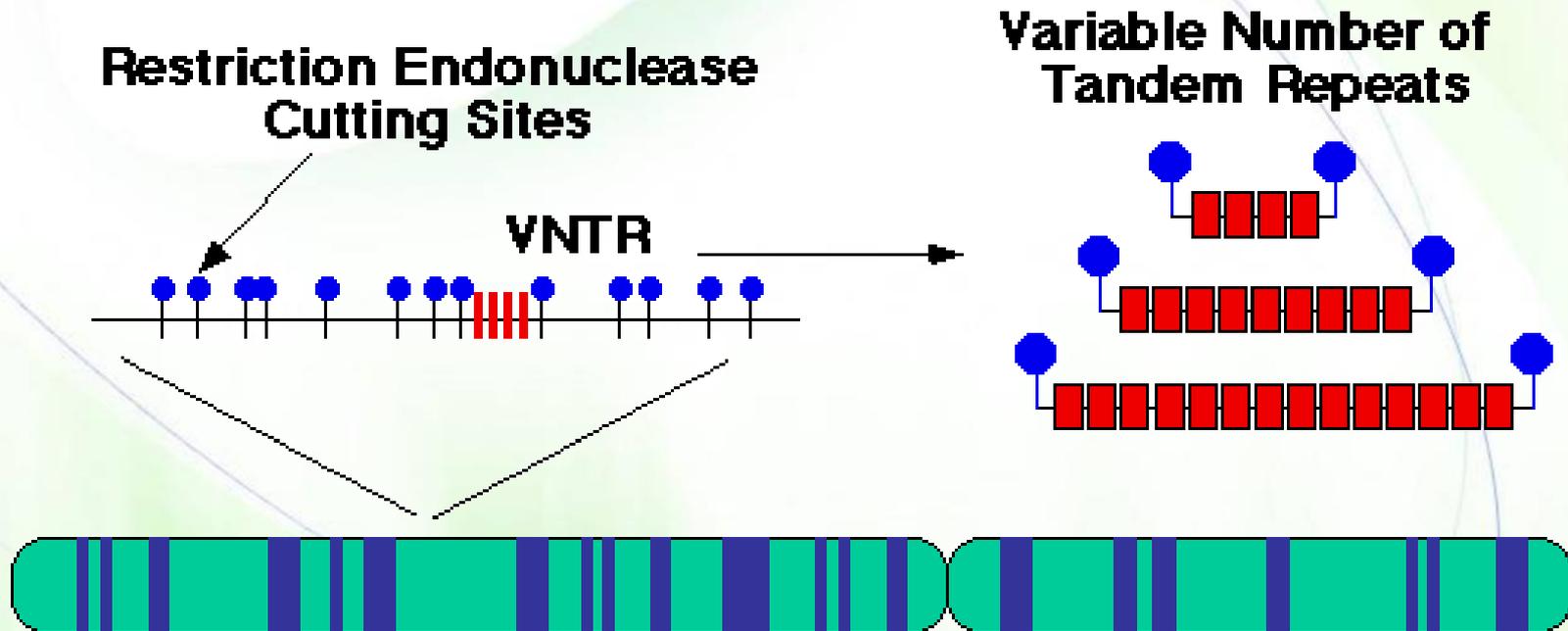
# Repetitive DNA sequences



# Mini-satellite DNA



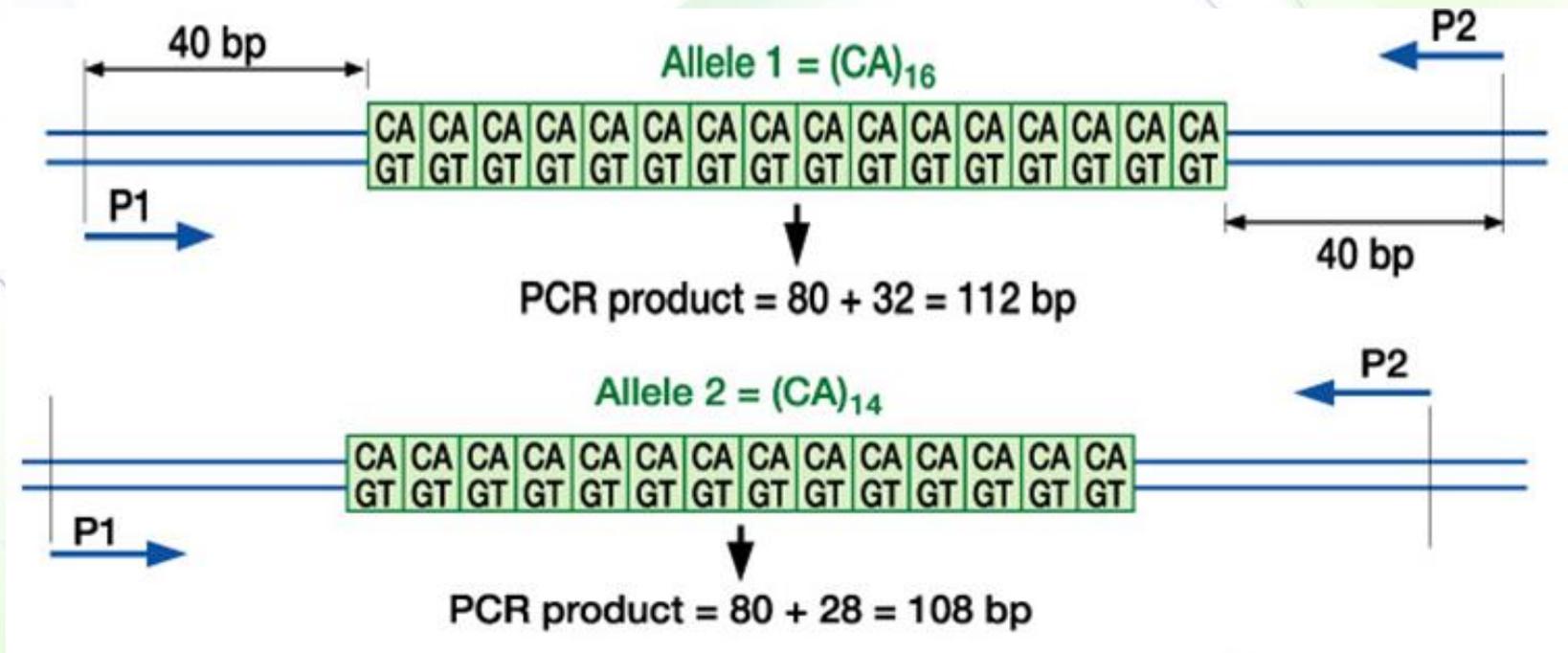
- Mini satellite sequences or VNTRs (variable number of tandem repeats) of 20 to 100 bp repeated 20-50 times



# Micro-satellite DNA



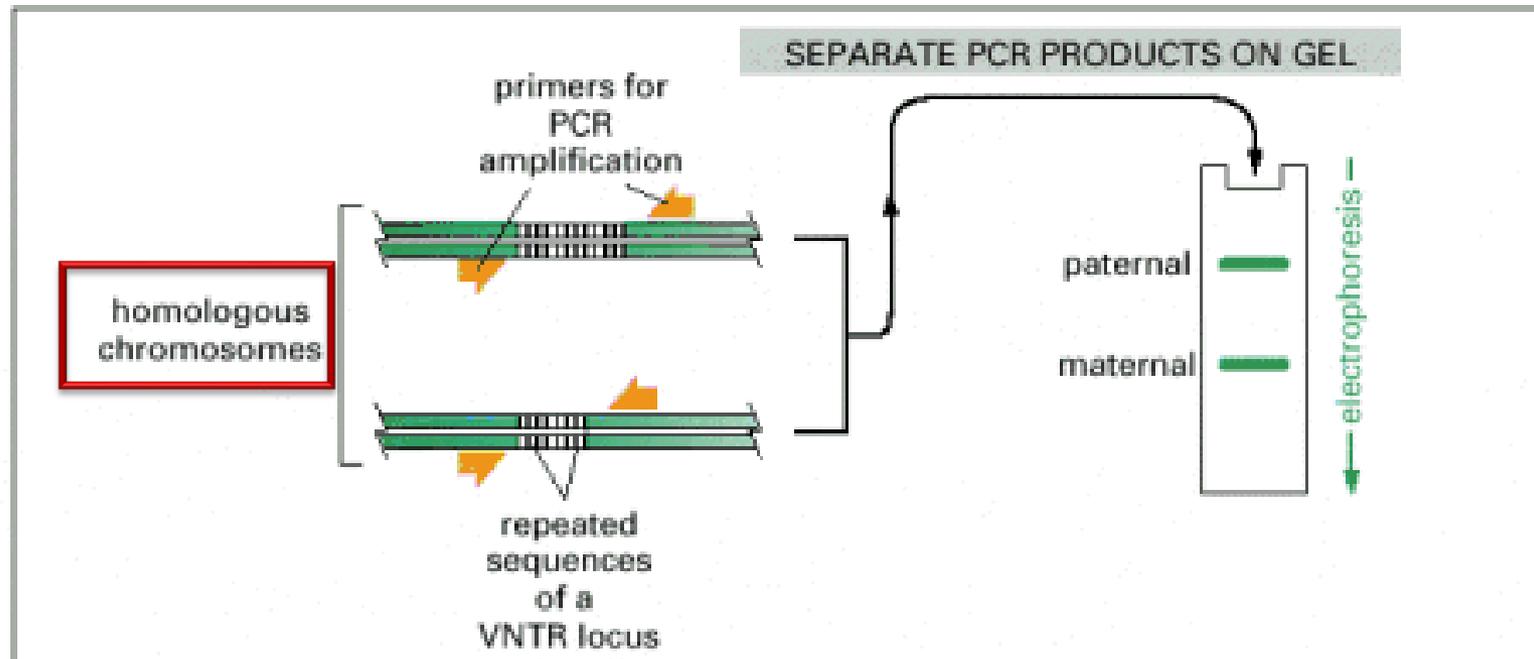
- STRs (short tandem repeats) of 2 to 10 bp repeated 10-100 times



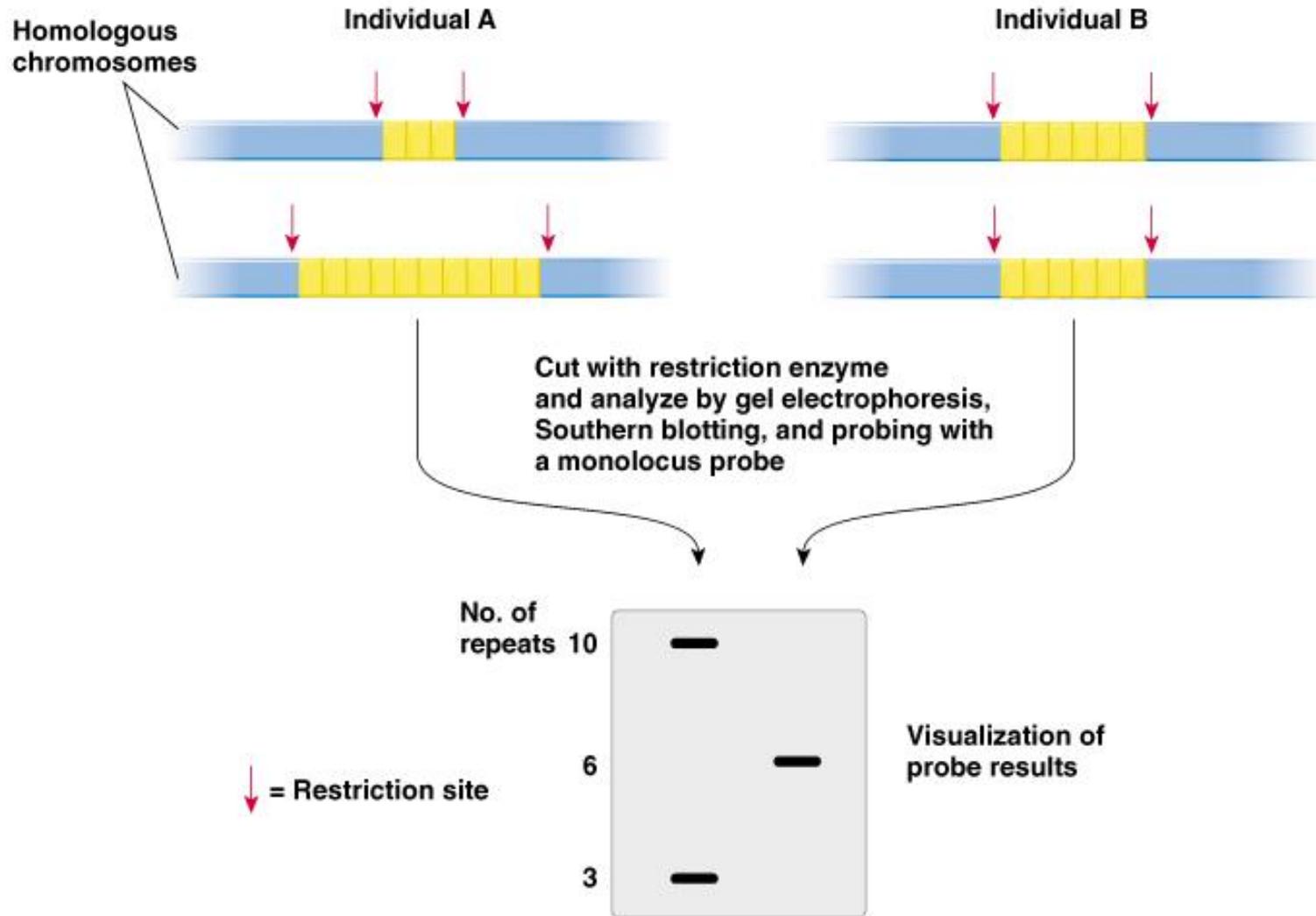
# Polymorphisms of VNTR and STR



- STRs and VNTRs are highly variable among individuals (polymorphic)
  - Thus, they are useful in DNA profiling for forensic testing



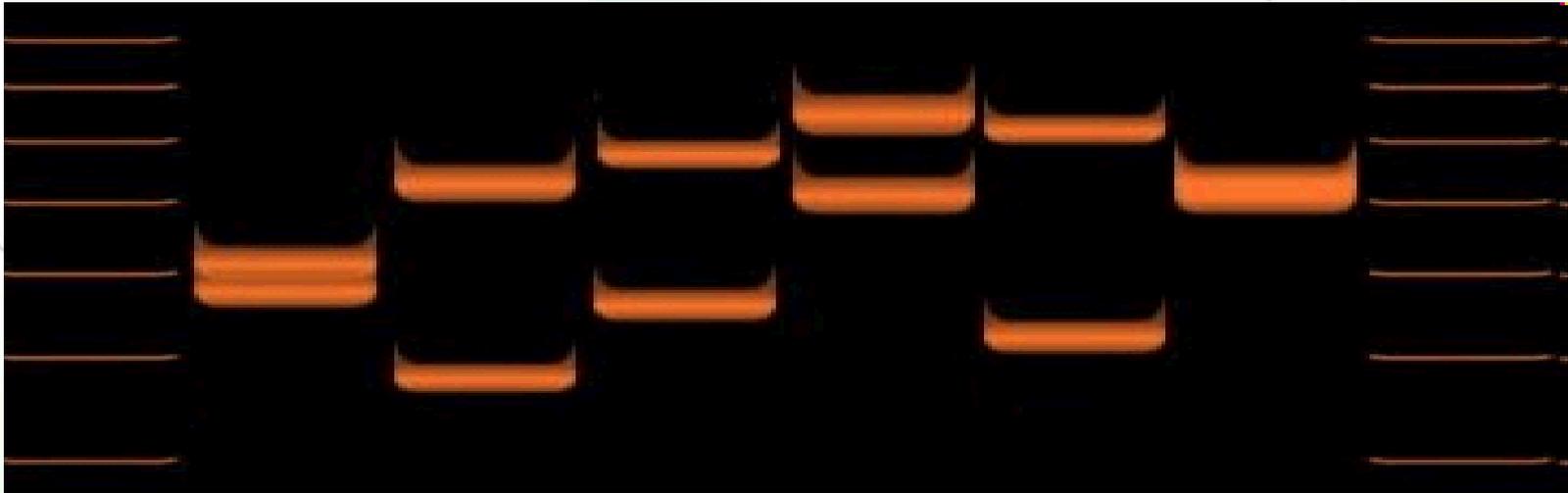
# Microsatellites and VNTRs as DNA Markers



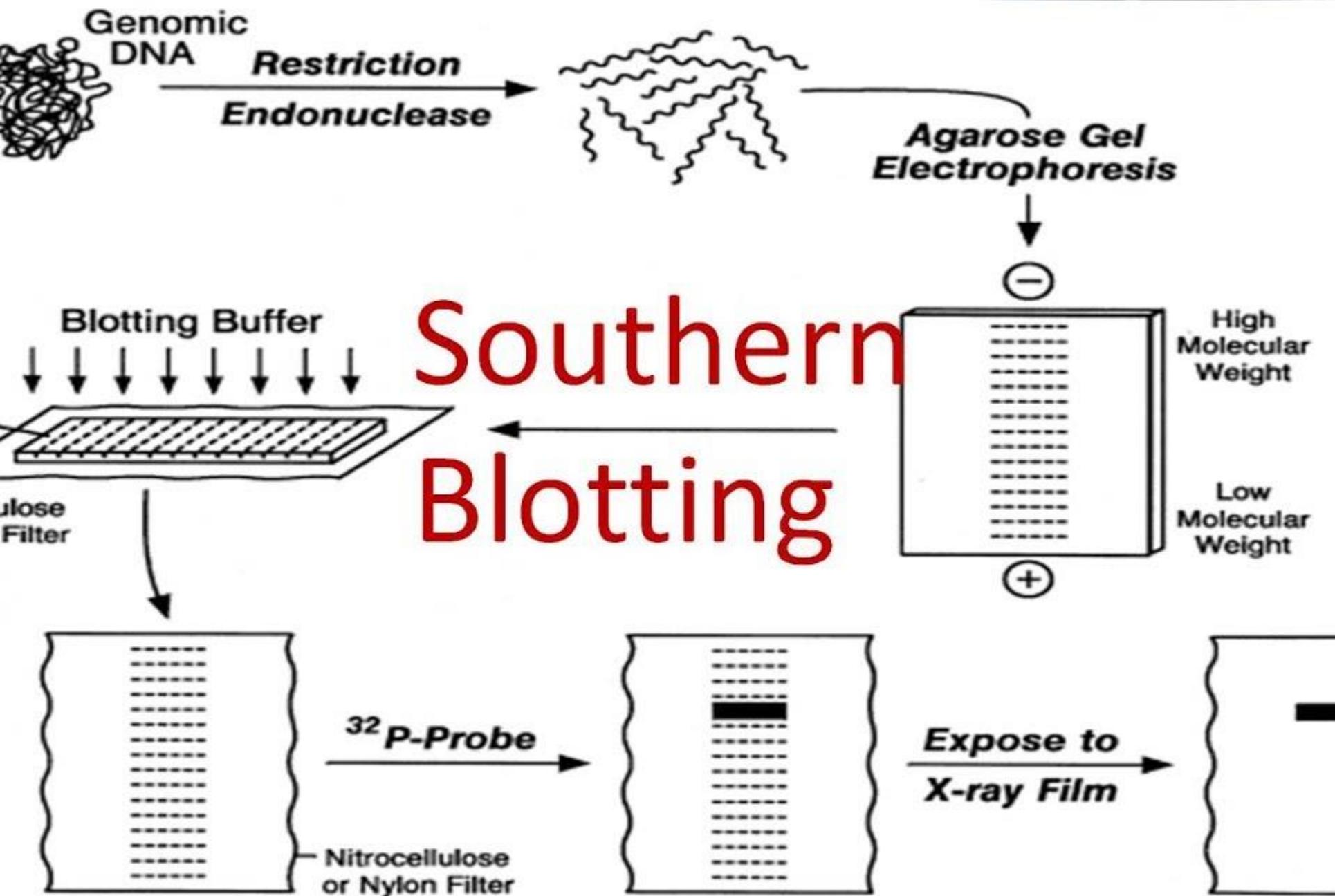
# VNTR in medicine and more



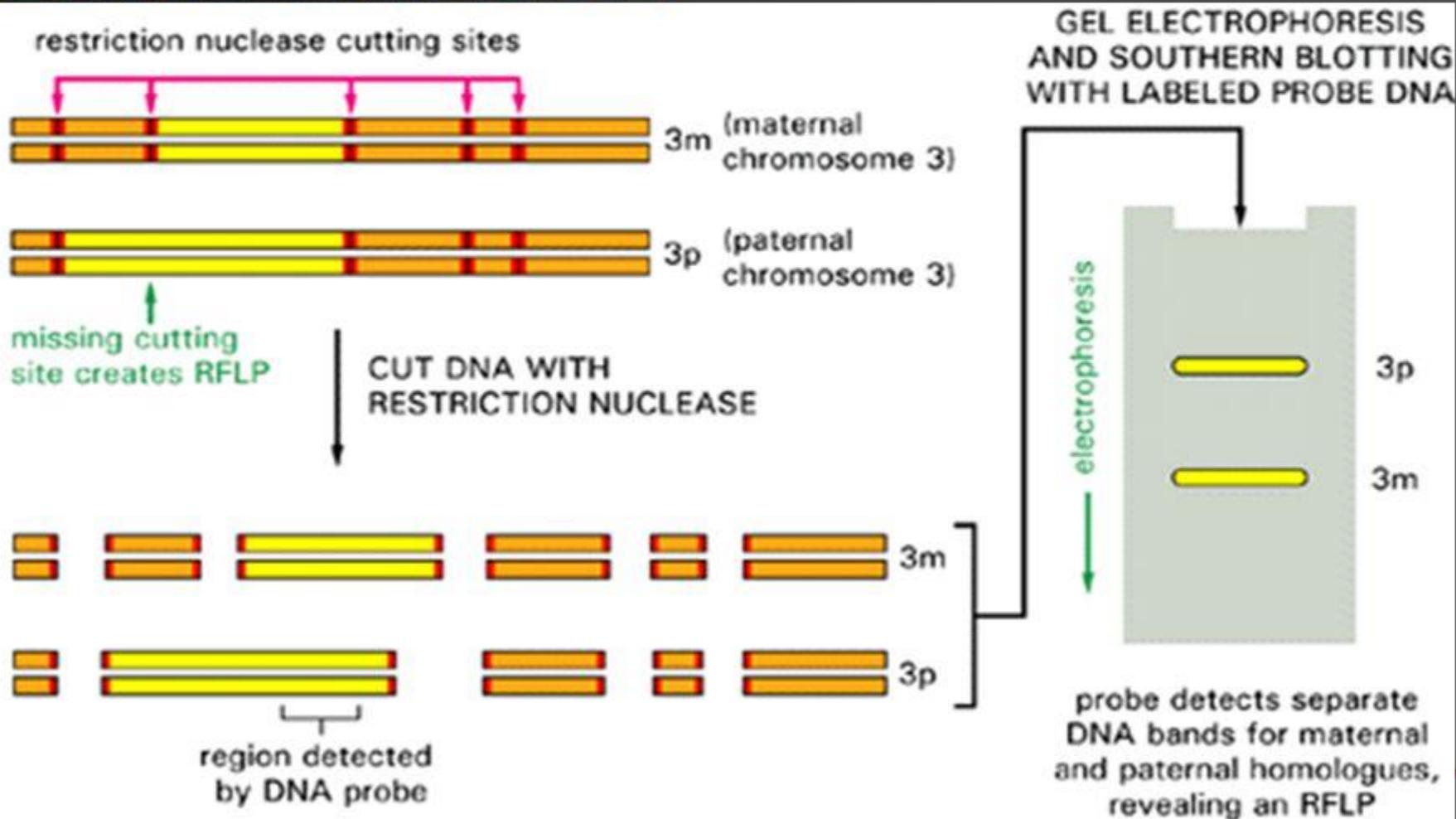
- The picture below illustrates VNTR allelic length variation among 6 individuals.



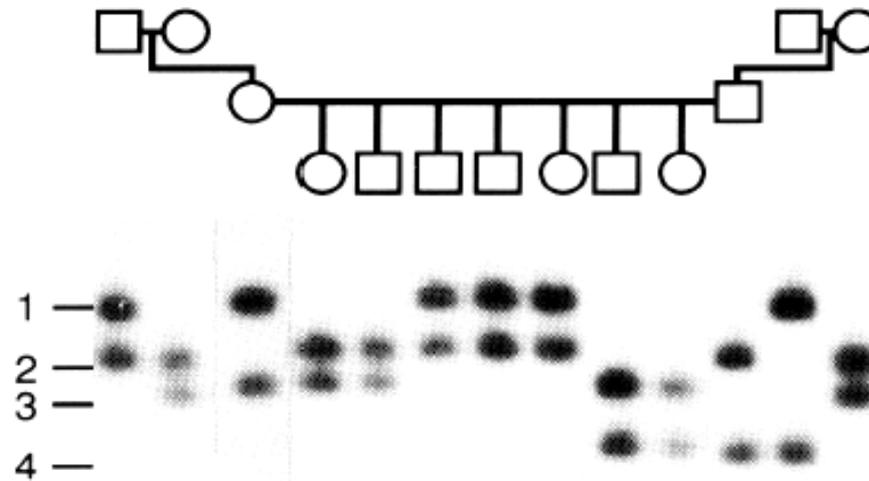
**The likelihood of 2 unrelated individuals having same allelic pattern extremely improbable**



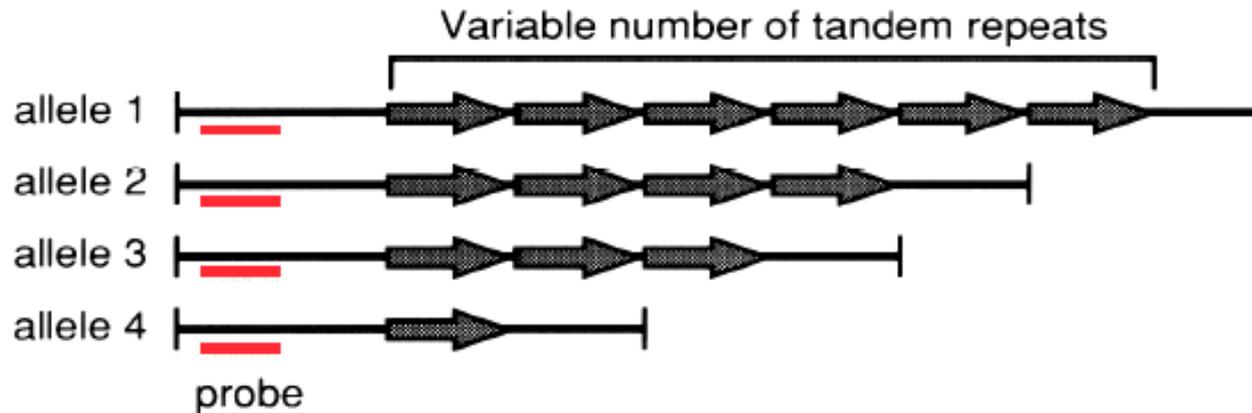
# Detection of an RFLP by Southern blotting

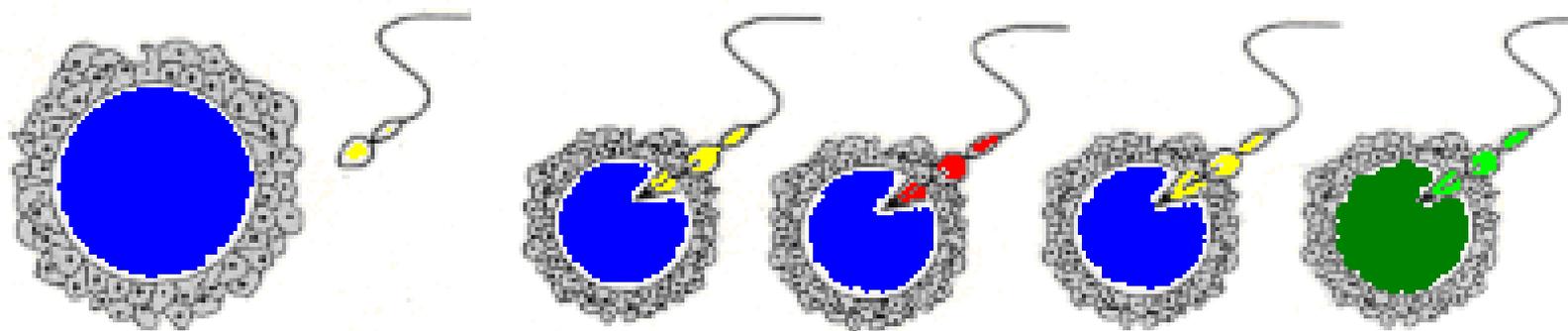
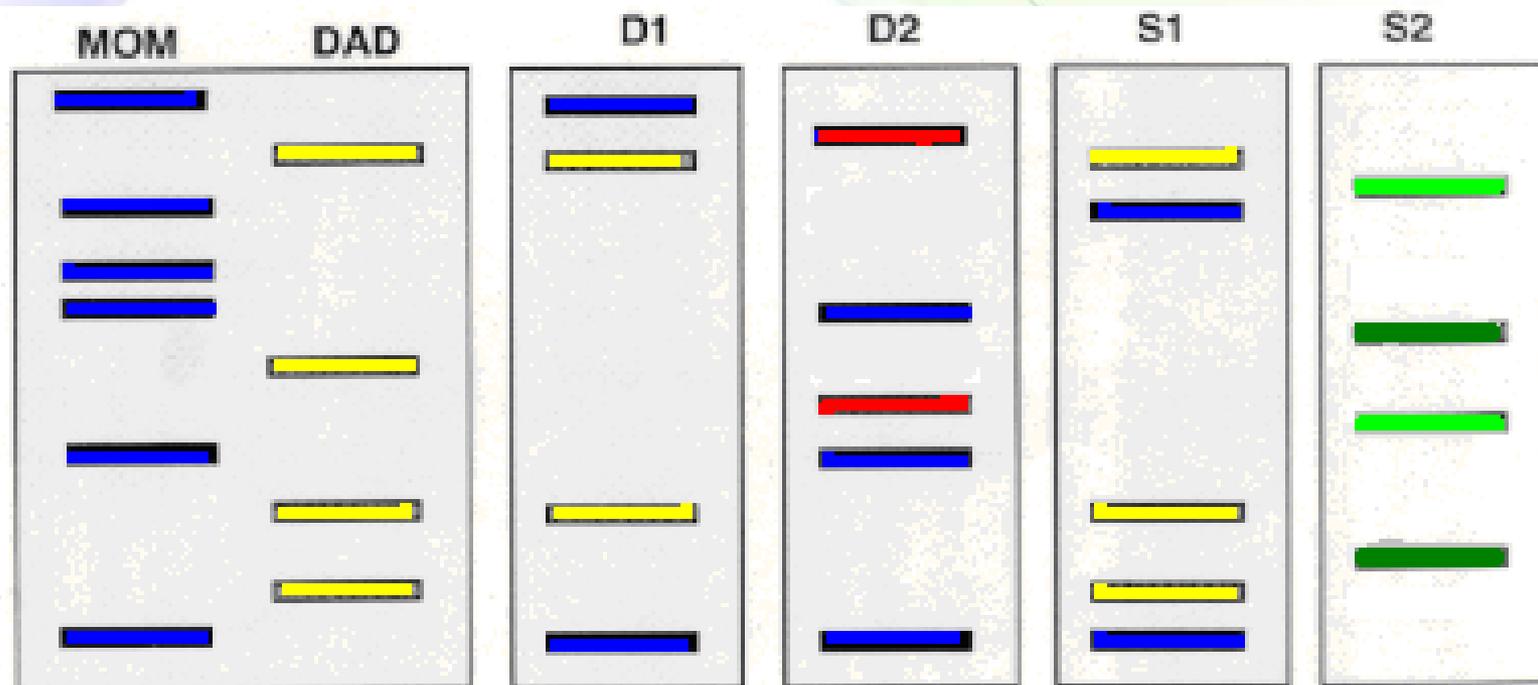


# Real example



single-locus probe but multiple alleles





# Single nucleotide polymorphism (SNPs)



- Another source of genetic variation
- Single-nucleotide substitutions of one base for another
- Two or more versions of a sequence must each be present in at least one percent of the general population
- SNPs occur throughout the human genome - about one in every 300 nucleotide base pairs.
  - ~10 million SNPs within the 3-billion-nucleotide human genome
  - Only 500,000 SNPs are thought to be relevant

# Categories of SNPs



TTGGCCAGCTGGACGAGGGGCGATGAC  
TTGGCCAGCTGGATGAGGGGCGATGAC

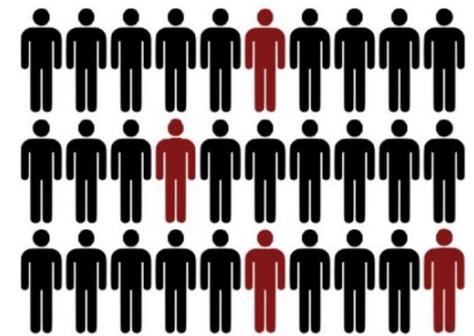
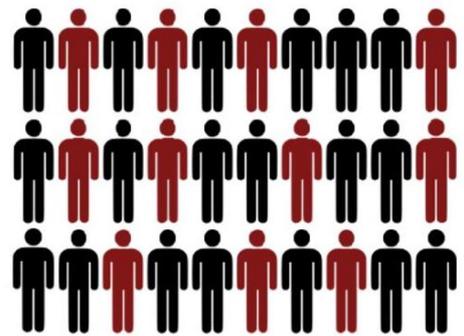
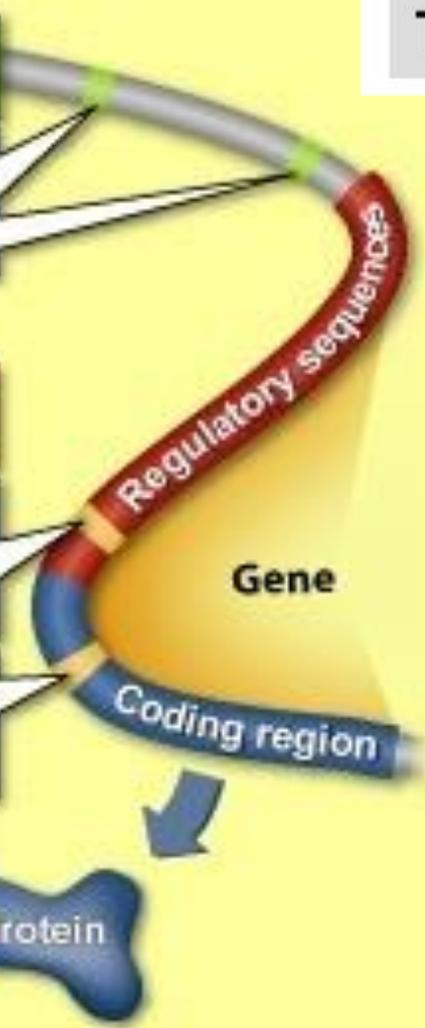
**Linked SNPs**  
outside of gene

no effect on protein production or function

**Causative SNPs**  
in gene

**Non-coding SNP:**  
● changes amount of protein produced

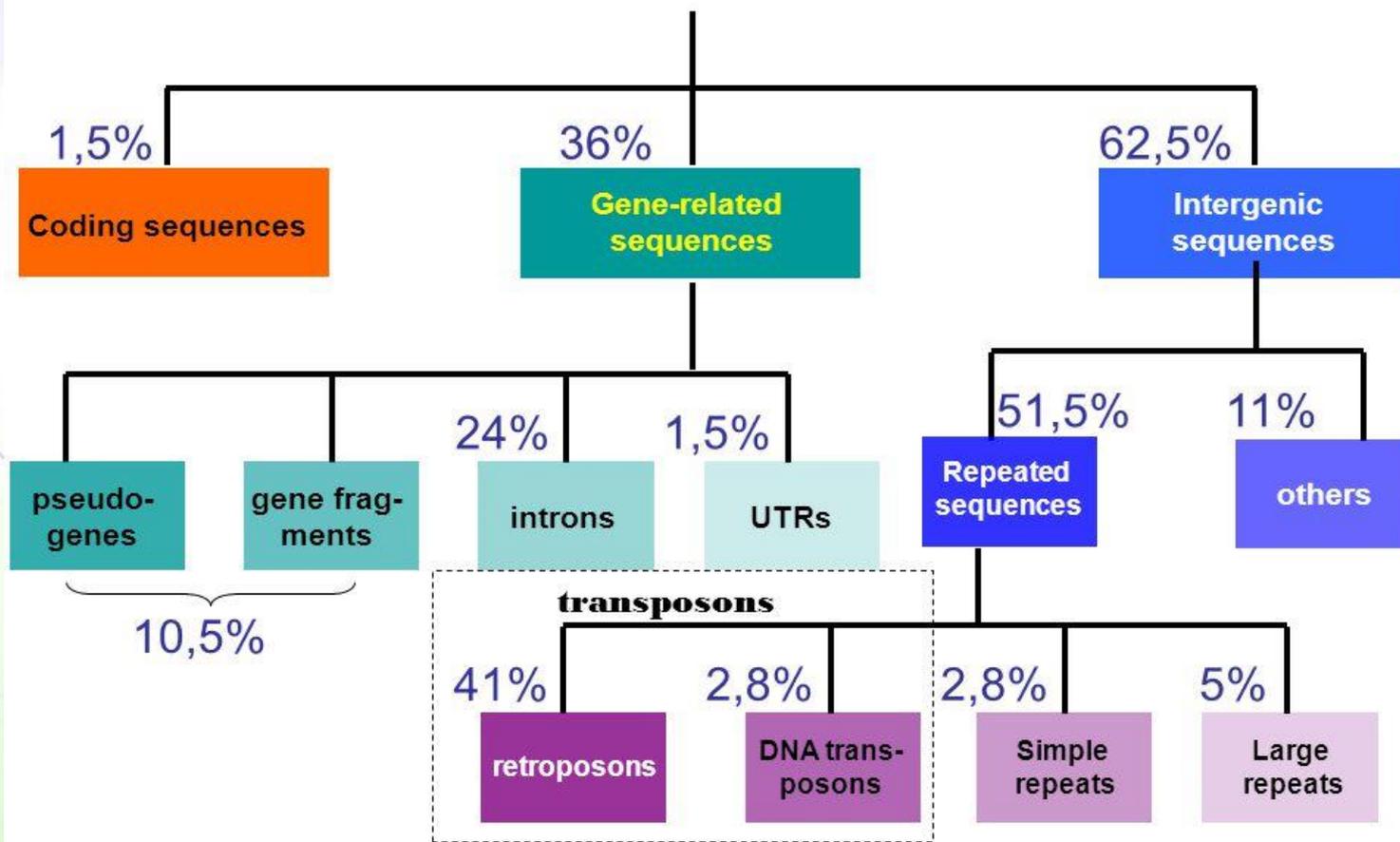
**Coding SNP:**  
● changes amino acid sequence



# Components of the human genome



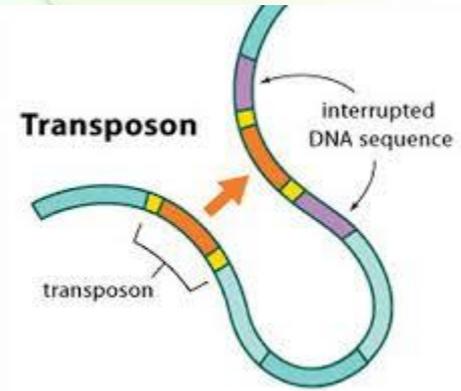
## Human genome



# Transposons (jumping genes)

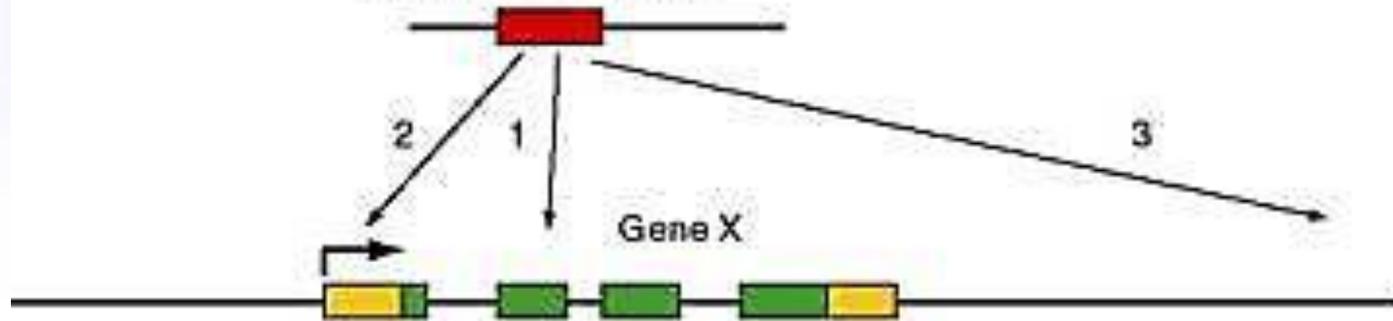


- They are segments of DNA that can move from their original position in the genome to a new location.



- Two classes:
  - DNA transposons (2-3% of human genome)
  - RNA transposons or retrotransposons (40% of human genome).
    - Long interspersed elements (LINEs)
    - Short interspersed elements (SINEs) – An example is Alu (300 bp)
- Diseases often caused by transposons include hemophilia A and B, severe combined immunodeficiency, porphyria, predisposition to cancer, and Duchenne muscular dystrophy.

Transposable element



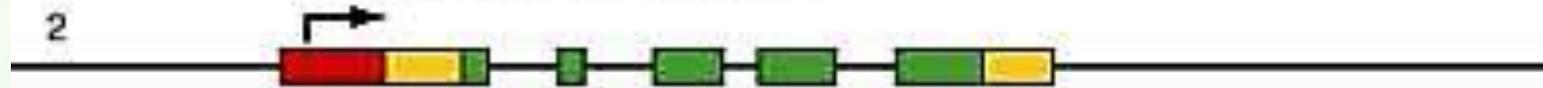
Transcribed in certain cell types, protein product is active

1



Protein product not functional

2



Transcription activated in other cell types

3



No effect