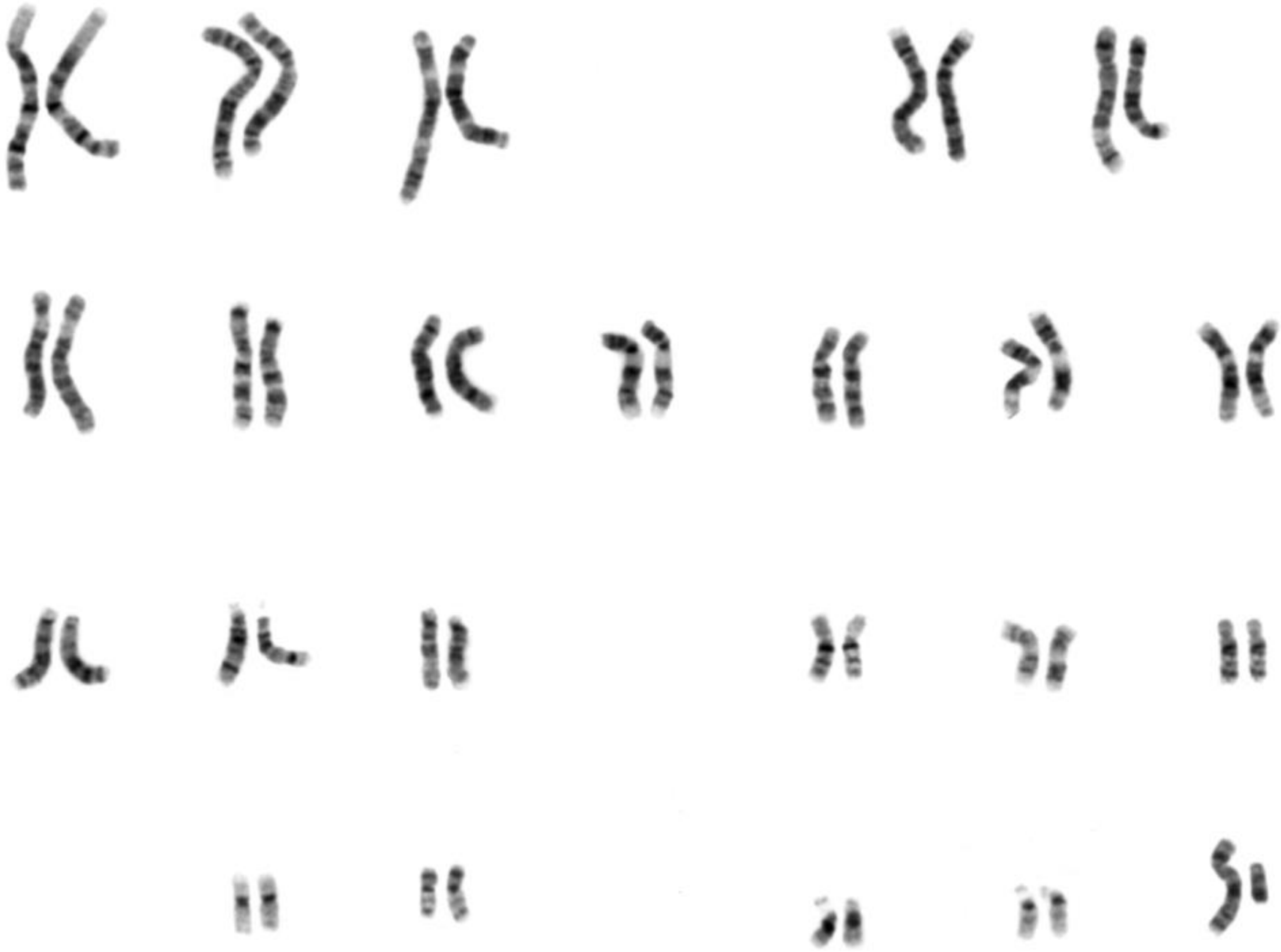
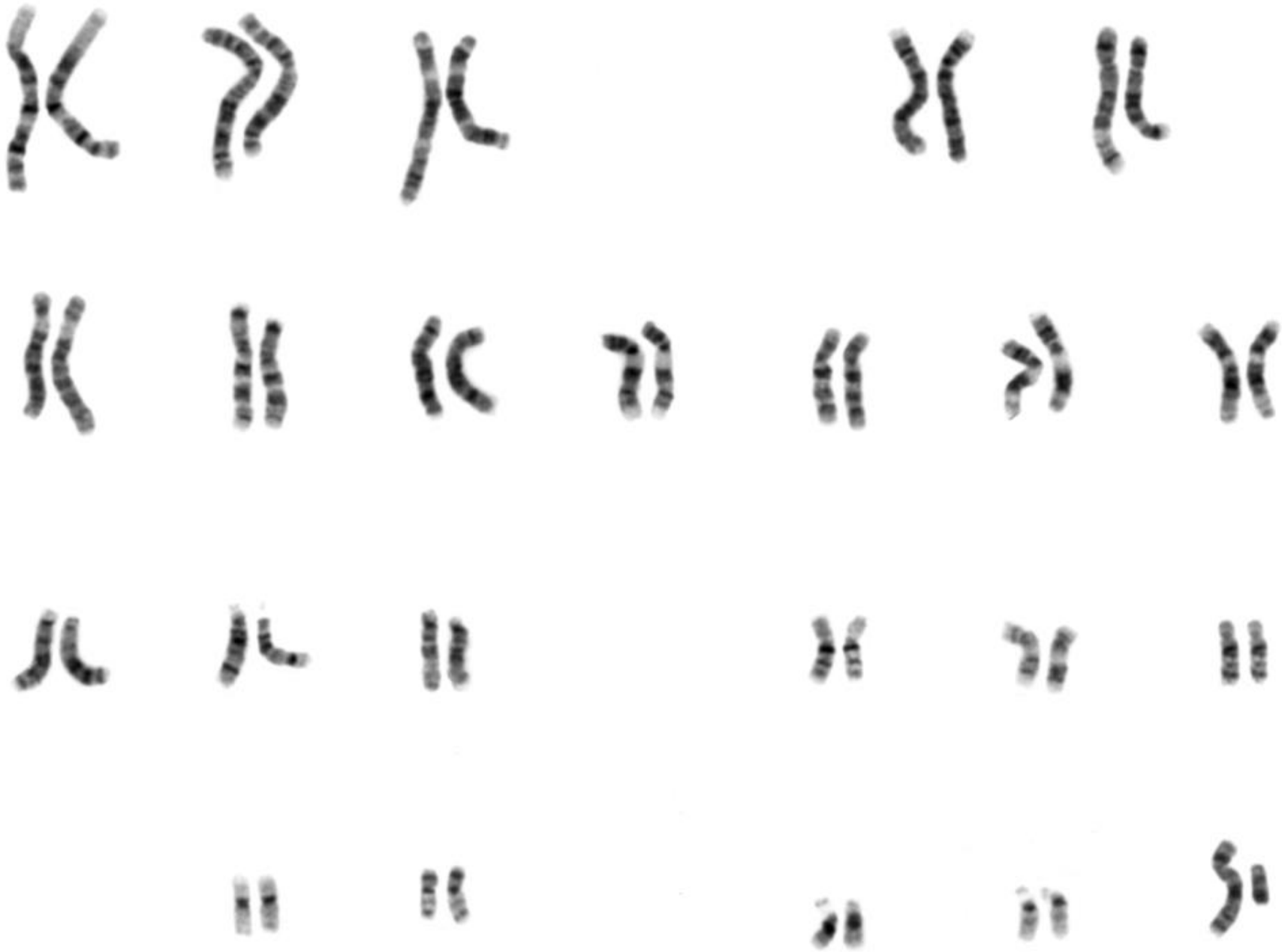
Human Genetic Variation

Section 3

Learning objectives

- Describe differences in types of genetic variation and how they affect phenotypes.
- Identify inheritance patterns of genotype-phenotype relationships.
- Describe the differences and the pros and cons of sequencing vs genotyping.





Zoom Chat

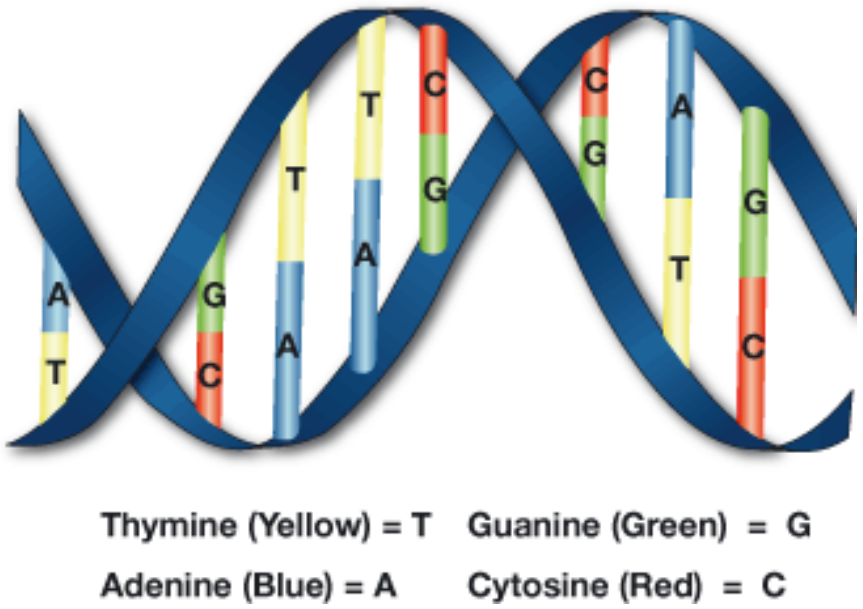
Our Genome in Numbers

23 chromosome pairs

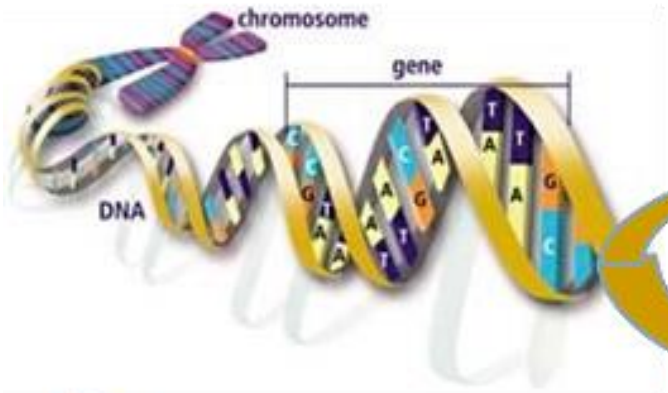
3.2 billion base-pairs (A,C,G,T)

~20,000 genes

~1.5% of the genome is coding DNA



Transcription and Translation



Coding Strand

ATGAAGCCGAGTCAT

UACUUCGGCUCAGUA ← mRNA

TACTTCGGCTCAGTA

Noncoding Strand

Nuclear Membrane

UACUUCGGCUCAGUA ← mRNA

Read as 3-letter "words" or triplets called "Codons"

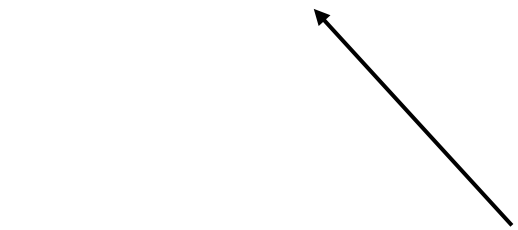
AUG | AAG | CCG | AGU | CAU

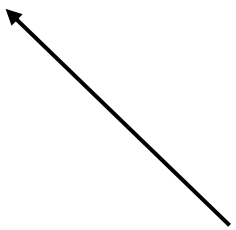
Met Lys Pro Ser Valine

"Anticodons" on tRNAs

Amino Acids

Genetic variation to phenotype variation



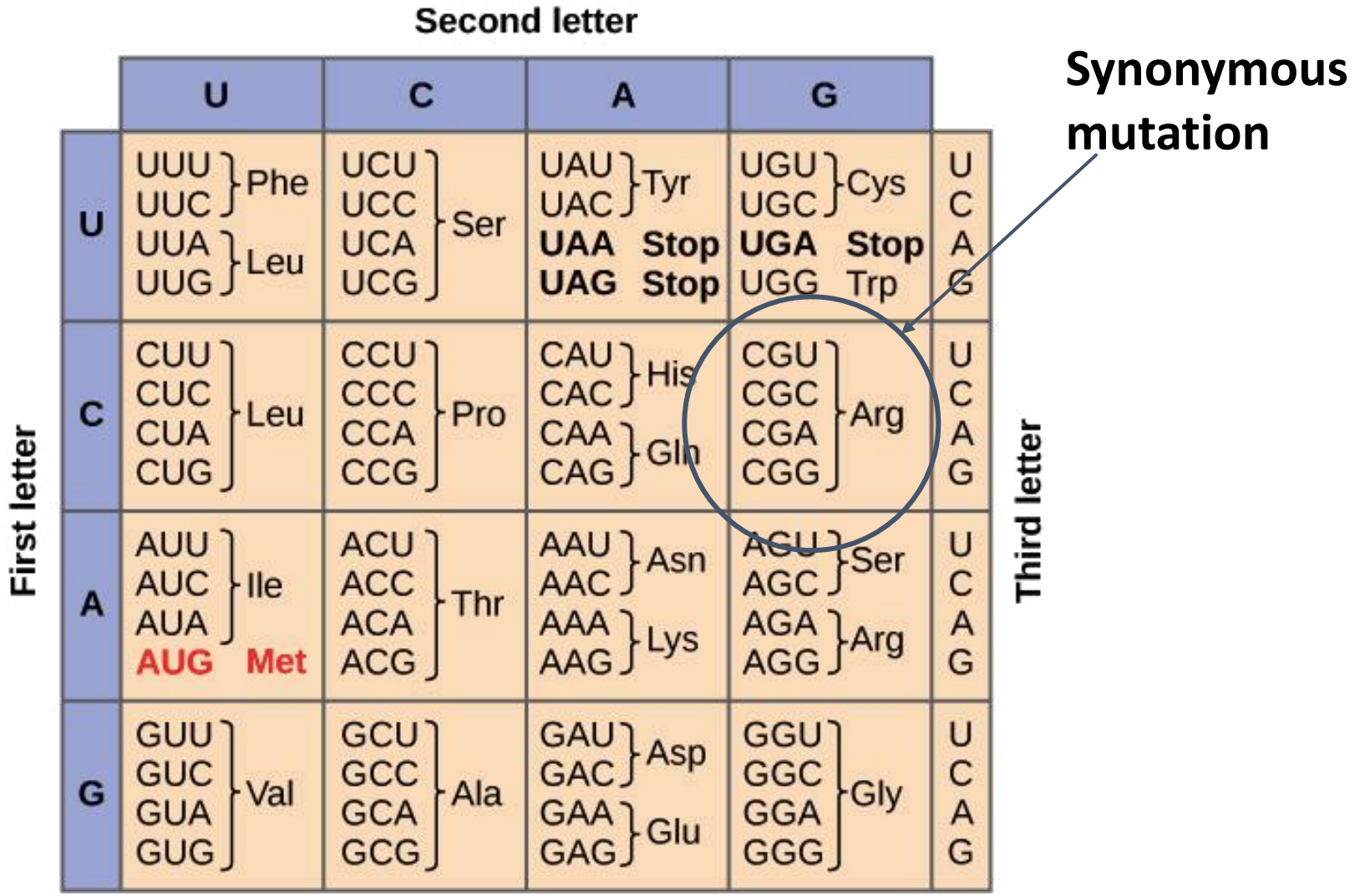


The changes in DNA

What we actually see (disease, trait)

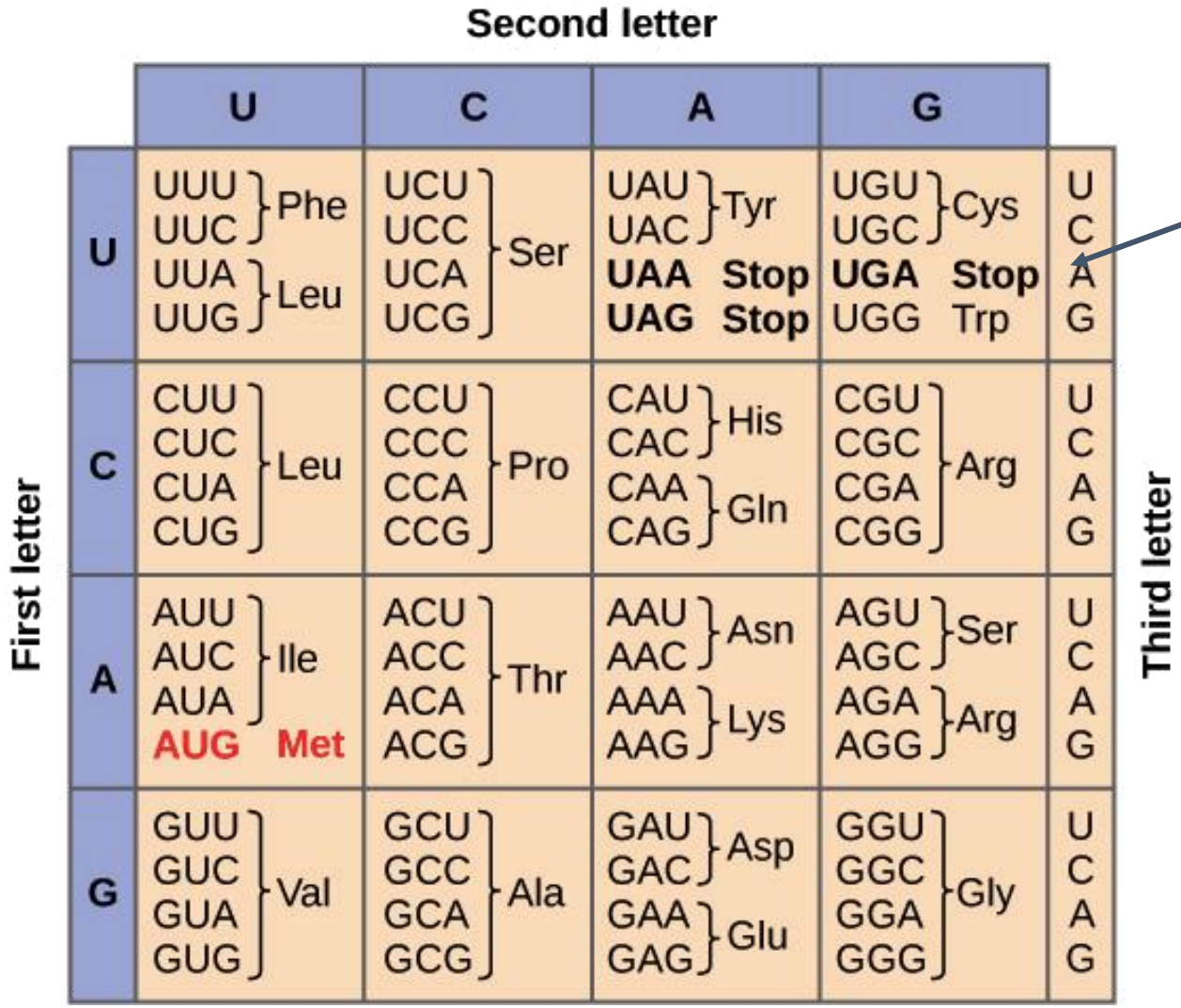
Single base change = Single Nucleotide Polymorphism/Variant (SNP/SNV)

Genetic variant – changes in amino acid codons

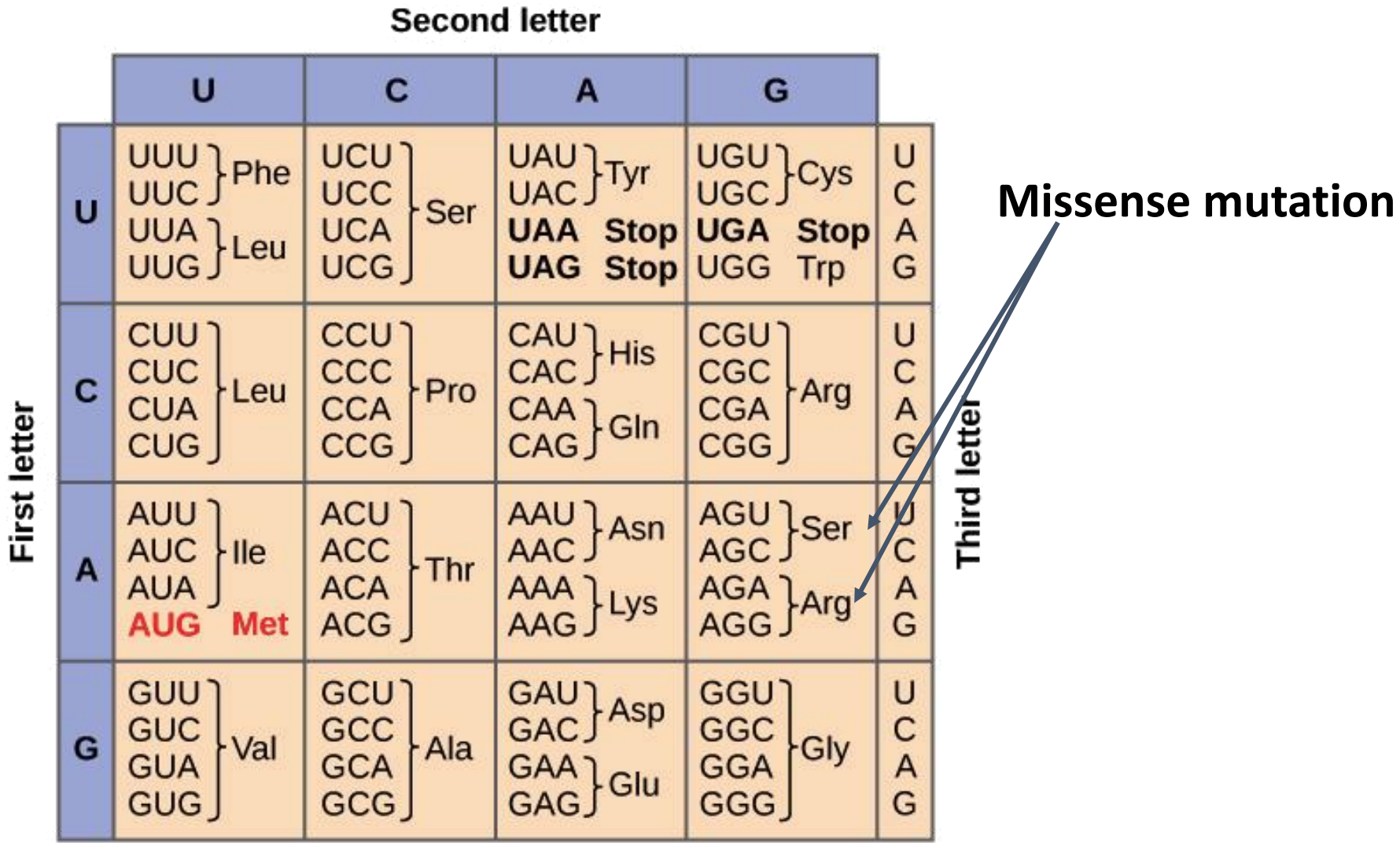


Nonsynonymous is usually worse than synonymous

Nonsense mutation

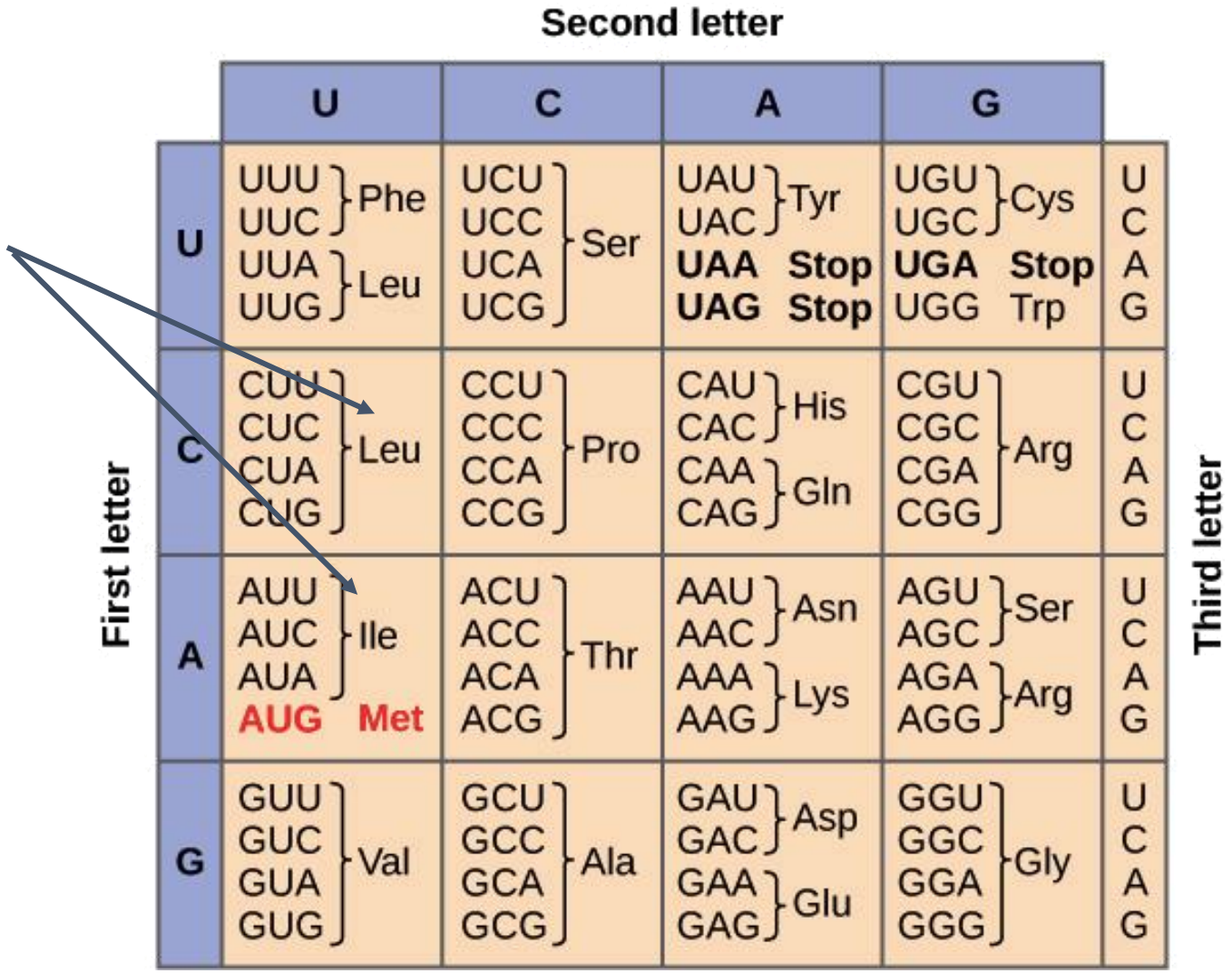


Nonsynonymous mutations



Some missense mutations can be less bad

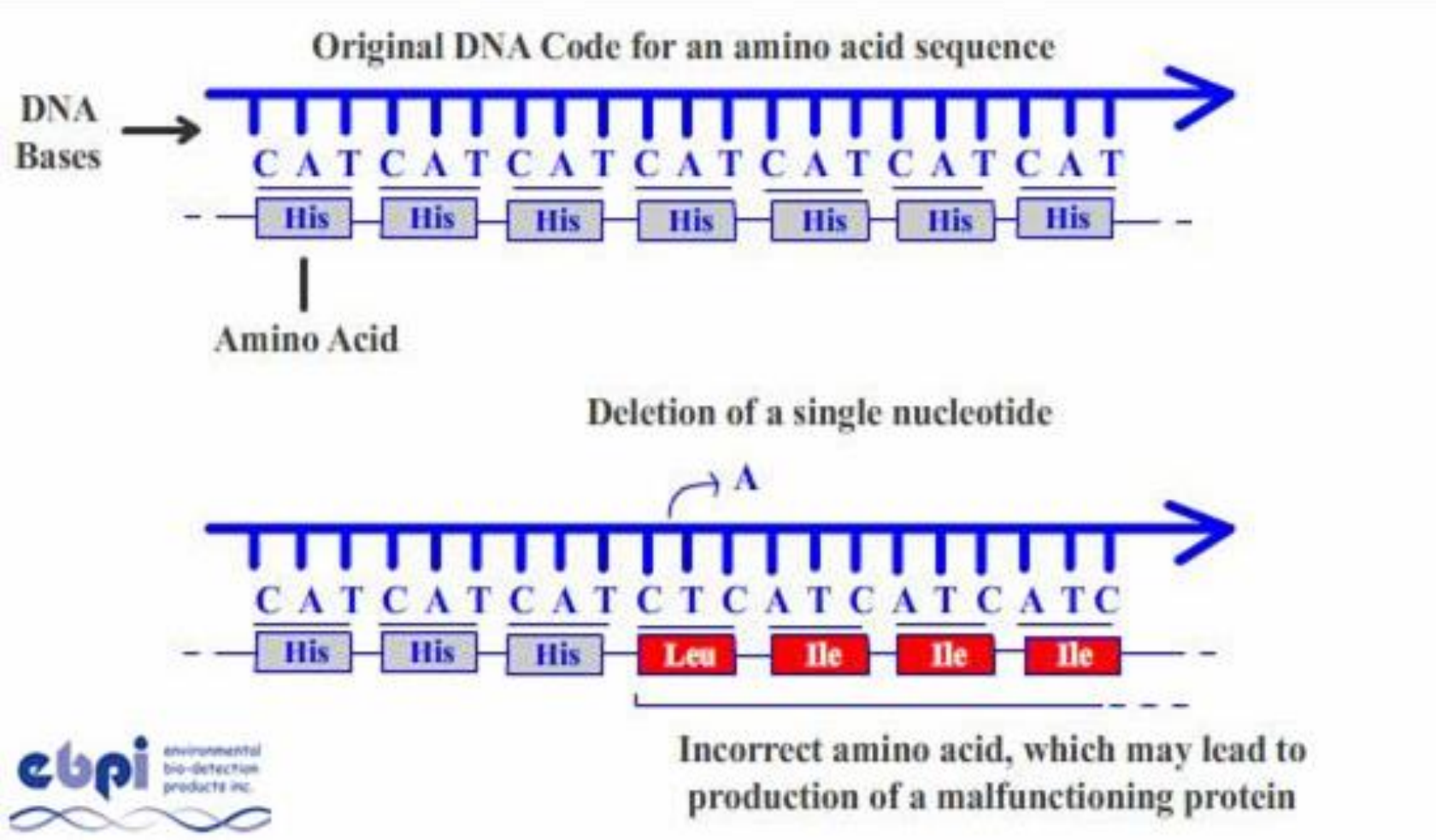
Both polar



First letter \ Second letter	U	C	A	G	Third letter
U	UUU, UUC: Phe UUA, UUG: Leu	UCU, UCC, UCA, UCG: Ser	UAU, UAC: Tyr **UAA Stop** **UAG Stop**	UGU, UGC: Cys **UGA Stop** UGG Trp	U C A G
C	CUU, CUC, CUA, CUG: Leu	CCU, CCC, CCA, CCG: Pro	CAU, CAC: His CAA, CAG: Gln	CGU, CGC, CGA, CGG: Arg	U C A G
A	AUU, AUC, AUA: Ile **AUG Met**	ACU, ACC, ACA, ACG: Thr	AAU, AAC: Asn AAA, AAG: Lys	AGU, AGC: Ser AGA, AGG: Arg	U C A G
G	GUU, GUC, GUA, GUG: Val	GCU, GCC, GCA, GCG: Ala	GAU, GAC: Asp GAA, GAG: Glu	GGU, GGC, GGA, GGG: Gly	U C A G

Deletions/insertions

“Frameshifts”



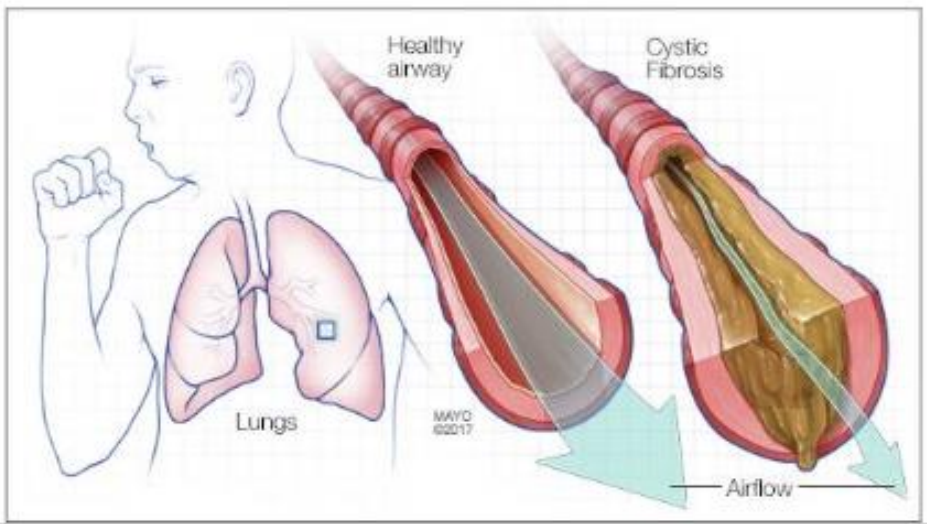
Deletion – cystic fibrosis F508del

Functioning CFTR sequence:

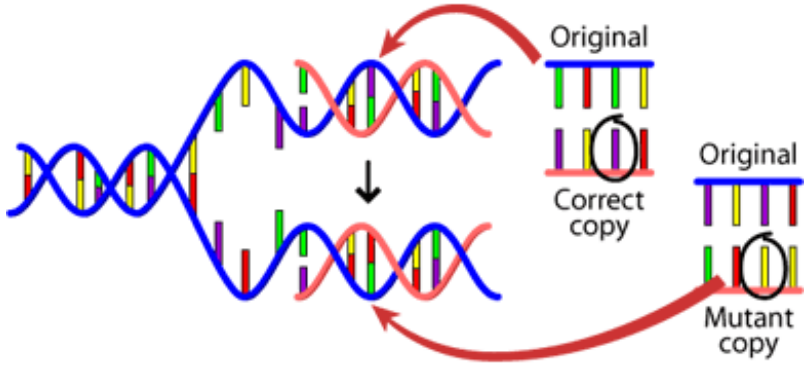
Nucleotide	ATC	ATC	TTT	GGT	GTT
Amino acid	Ile	Ile	Phe	Gly	Val

F508Del variant inactivating chloride channel:

Nucleotide	ATC	ATT	GGT	GTT
Amino acid	Ile	Ile	Gly	Val



Mutations happen all the time, with every replication



Human genome mutation rate is ~1.1×10^{-8} per site per generation.

Human genome is over 3 billion base pairs.

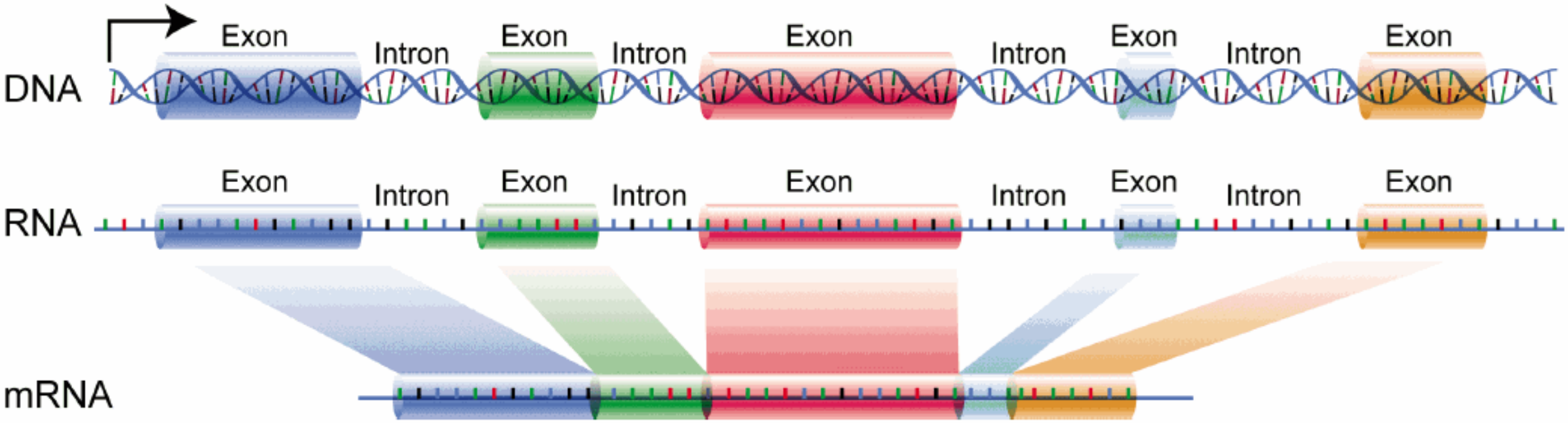
Each genome: 3,000,000,000 sites
Mutation rate: 0.000000011 errors/site

How many new mutations do you expect in each cell replication?

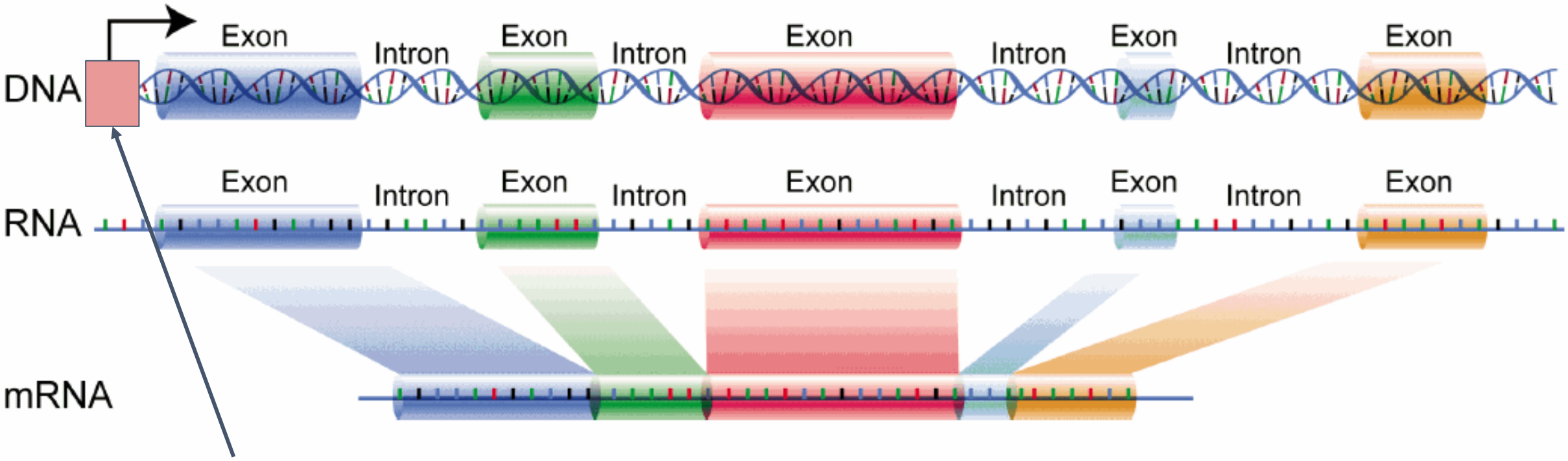
Zoom Poll

Sometimes we don’t change the protein itself…

A gene includes a lot of DNA that doesn't become protein

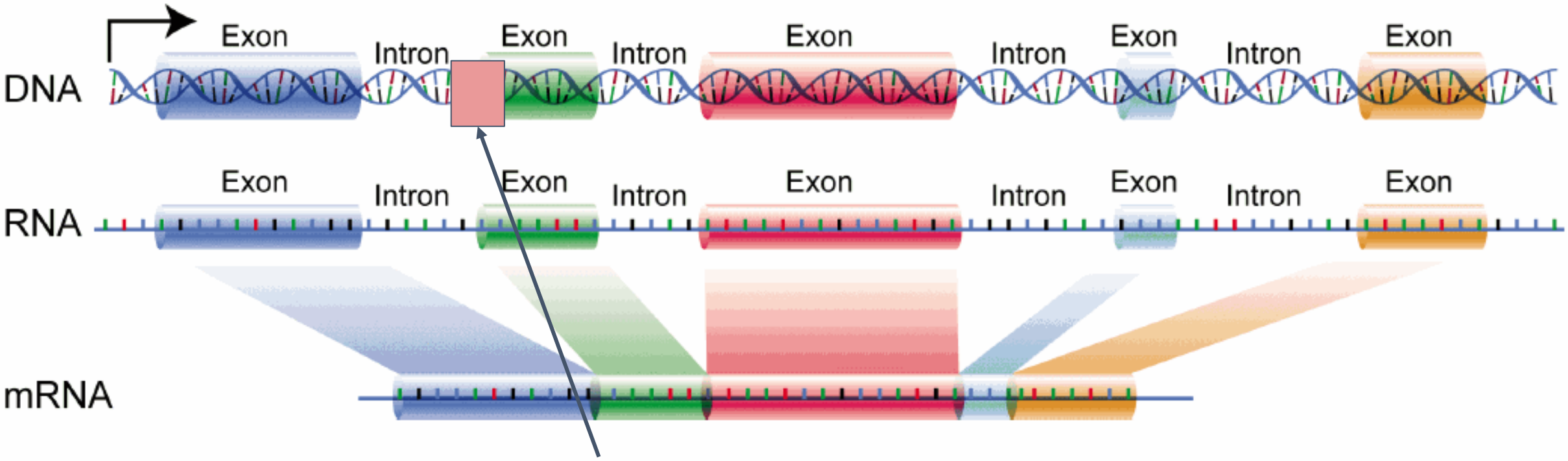


A gene includes a lot of DNA that doesn't become protein



A variant here can change gene "expression"

A gene includes a lot of DNA that doesn't become protein



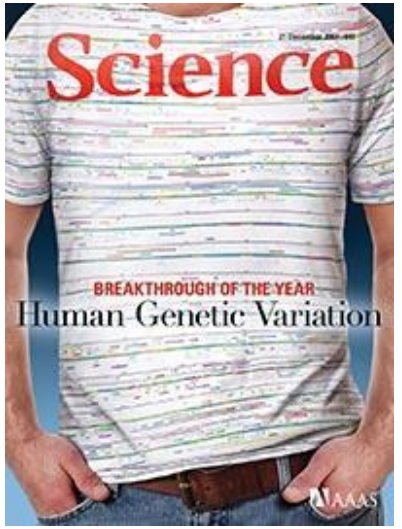
Or here can change the "splice site" to make a different protein

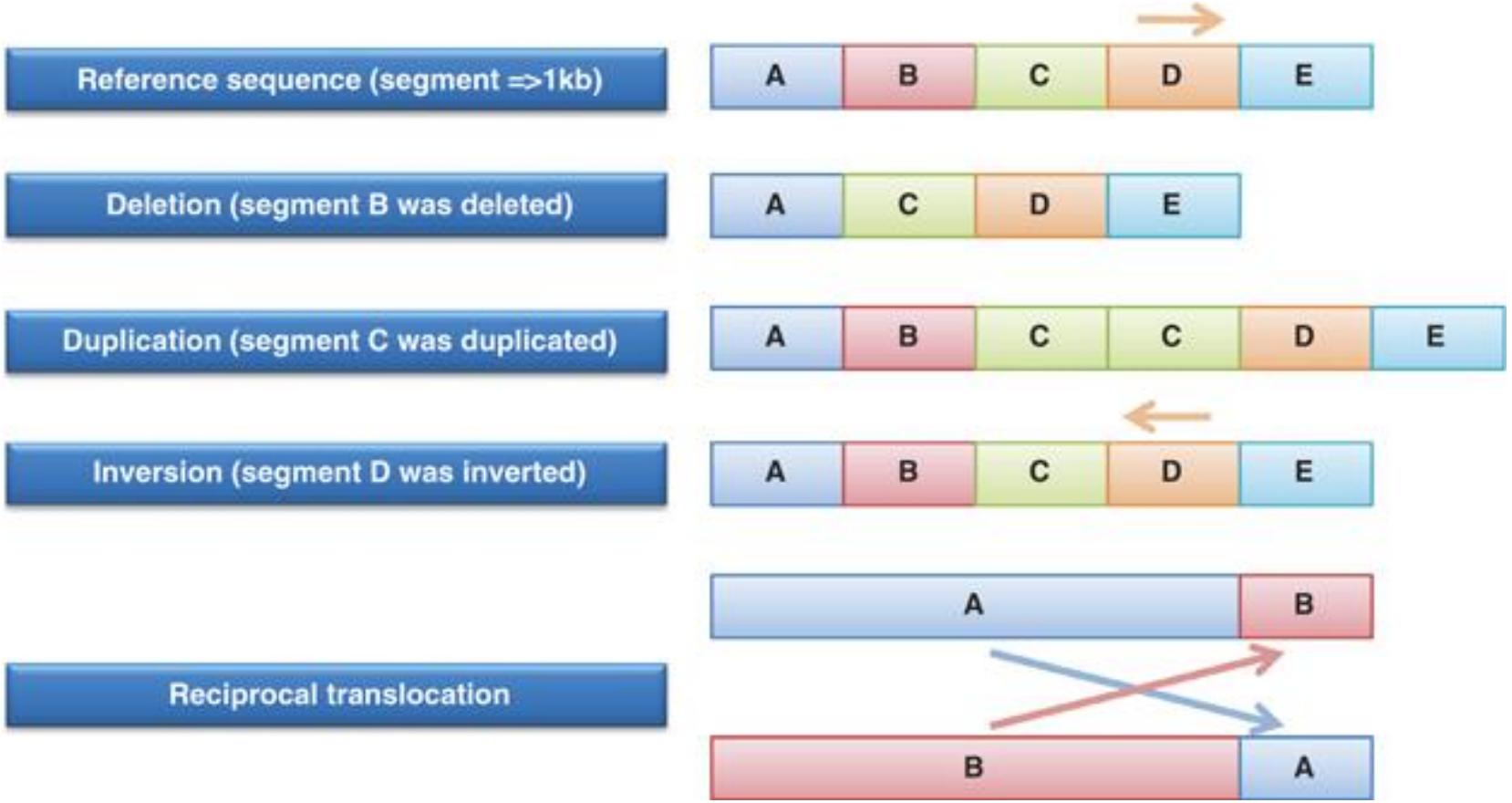
Zoom breakout – discuss Q1

A recent study sequenced the genome of 2,504 individuals and identified 84.7 million SNPs (single nucleotide polymorphisms) between the participants. On average, each individual carried 3.5-4.3 million SNPs each. About 0.5% of those SNPs were in coding regions of genes. Remember, 1.5% of the genome is in a coding region. Why might only 0.5% of variants be in coding regions compared to what would be expected if SNPs were randomly allocated throughout the genome?

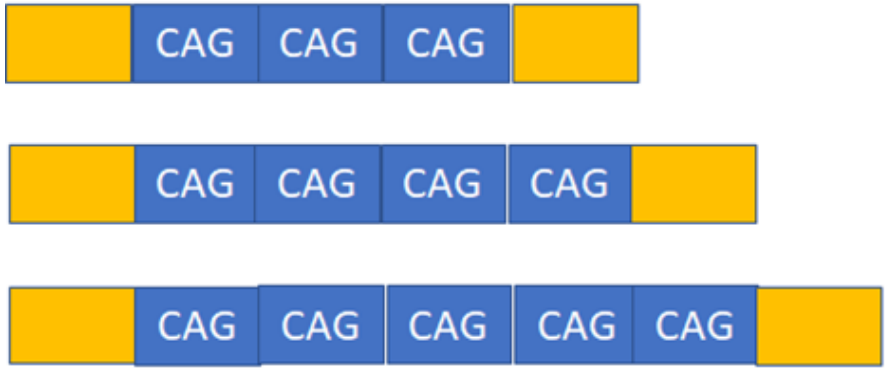
Besides single base changes, what types of changes can we have?

Genetic Variation – structural variation





tandem repeats (Huntington's disease)



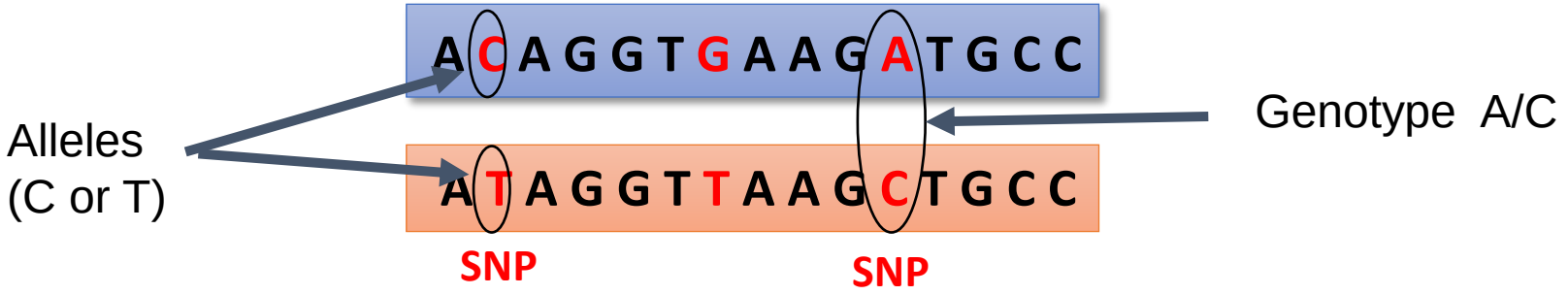
The normal function of huntingtin is unknown. The CAG repeats (polyglutamine) is in some way neurotoxic.

Repeat count	Classification	Disease status
<28	Normal	Unaffected
28–35	Intermediate	Unaffected
36–40	Reduced-penetrance	May be affected
>40	Full-penetrance	Affected

Alleles to genotypes and phenotypes

Allele vs. Genotype

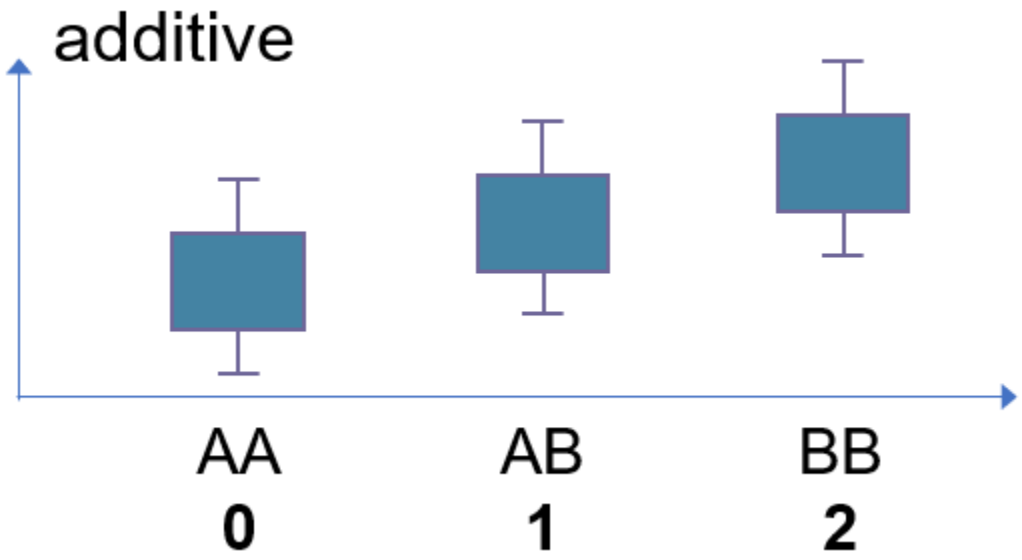
We inherit two copies of each chromosome

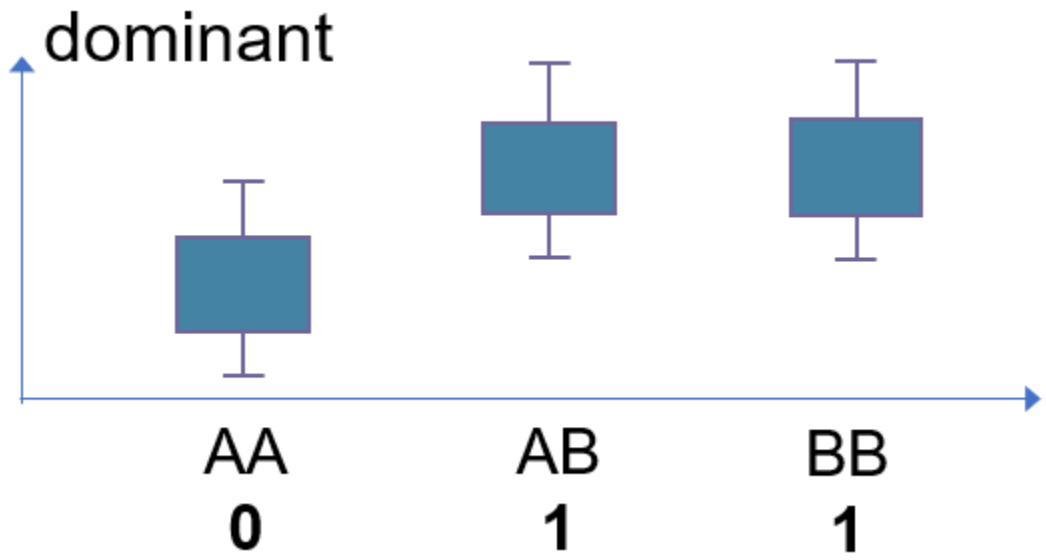


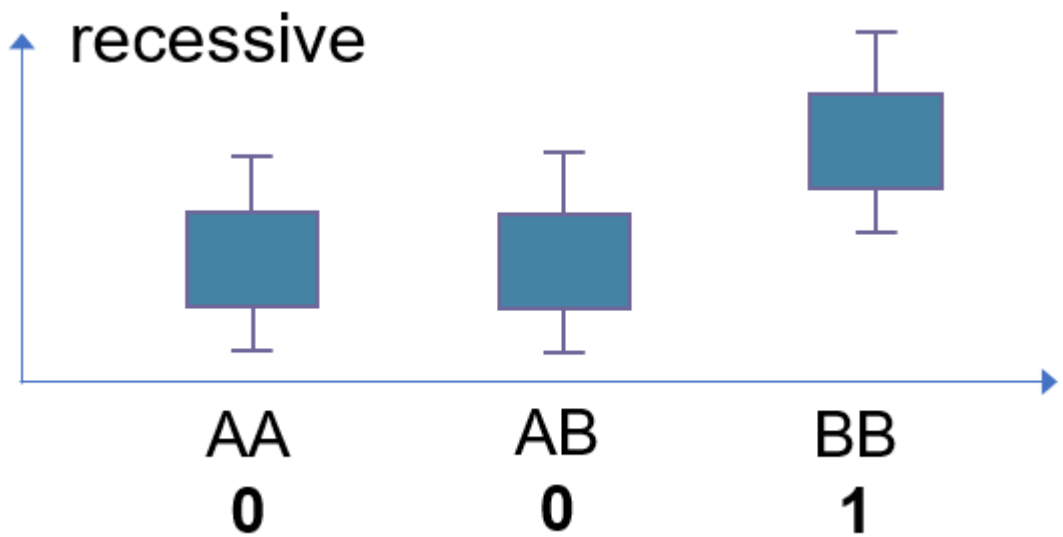
Genotypes
(A/A) – homozygous
(A/C) – heterozygous
(C/C) - homozygous

Inheritance patterns: genotype->phenotype

- 2 copies of every gene/chromosome (most common)
- Dominant (only need one copy of a variant to see the effect)
- Recessive (need two copies of the variant to see the effect)
- Additive (the effect of one variant is ½ that of two variants)

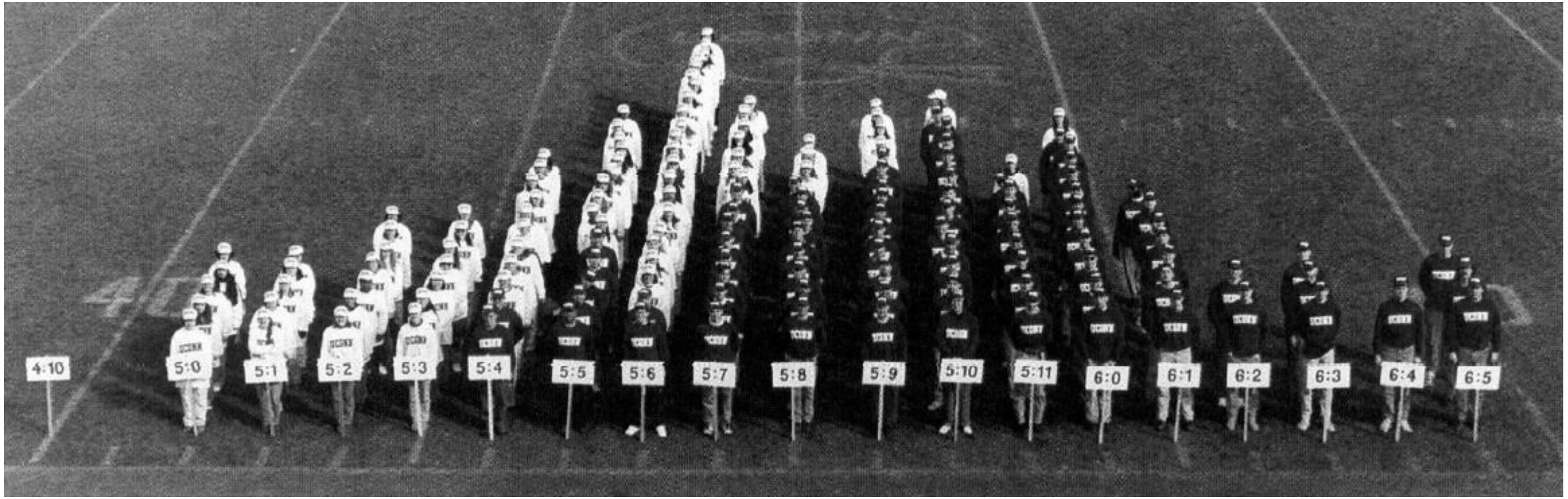

additive
AA
0
AB
1
BB
2


dominant
AA
0
AB
1
BB
1


recessive
AA
0
AB
0
BB
1

Genotypes and Phenotypes

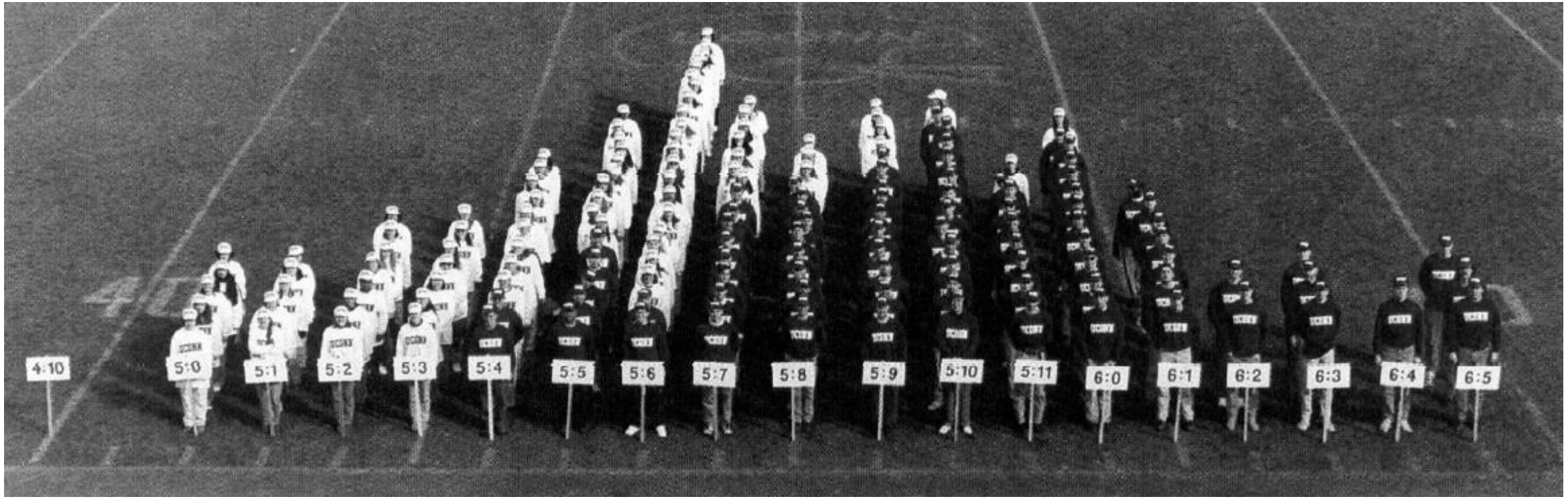
- **Binary outcomes** (yes/no, i.e. disease status)
- **Quantitative outcomes** (continuous, i.e. height)



Zoom chat: How might you turn “height” into a binary variable?
What would be your approach?

Genotypes and Phenotypes

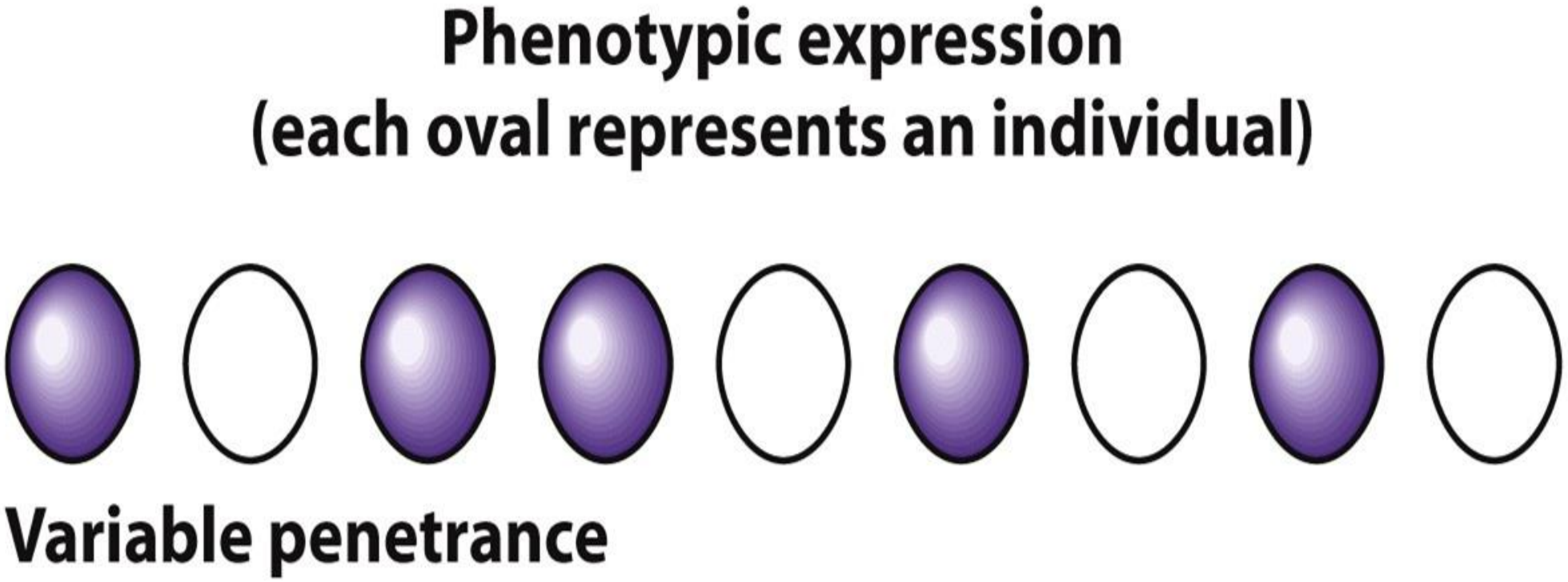
- **Binary outcomes** (yes/no, i.e. disease status)
- **Quantitative outcomes** (continuous, i.e. height)



Genotypes and Phenotypes

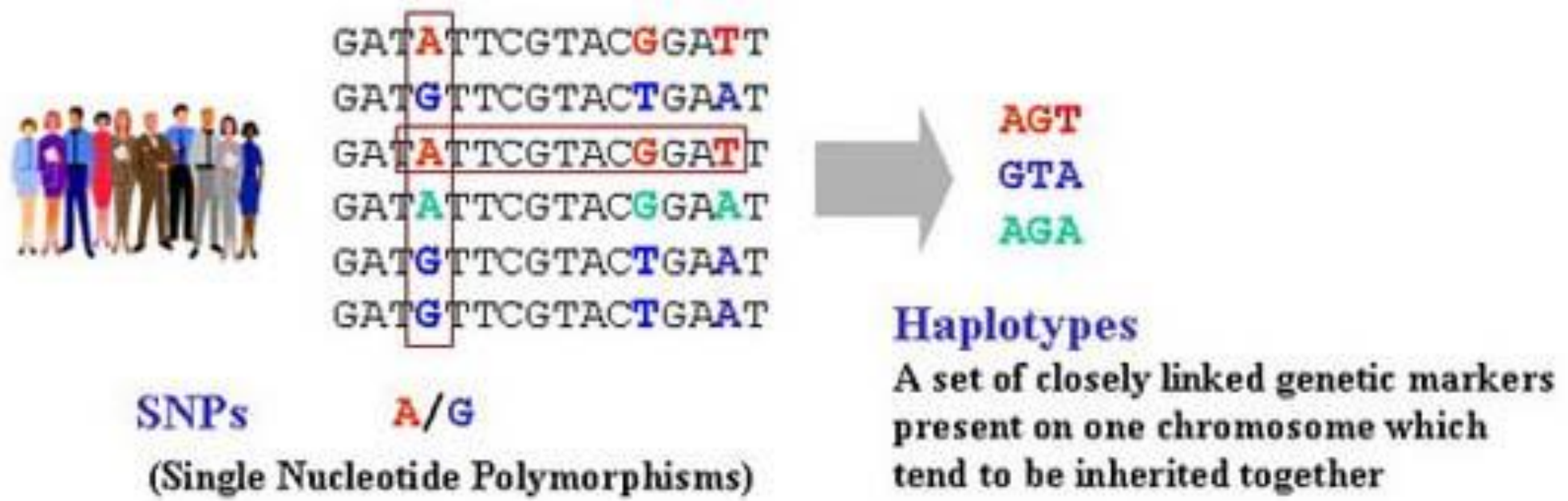
- **Mendelian phenotype** is one driven by variation at a single genetic locus.
- **Complex phenotype** does not show such simple patterns of inheritance.
  - oligogenic (a few genetic loci)
  - polygenic (many genetic loci)

Same genetic pattern, different phenotype



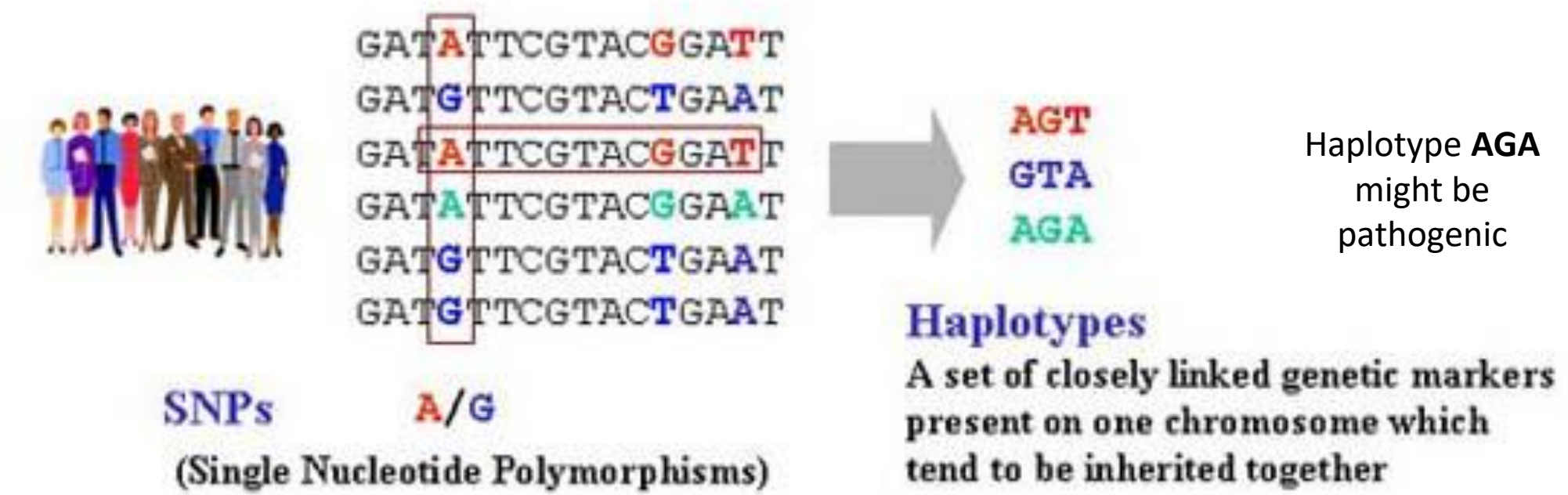
Haplotypes

Specific combination of SNPs occurring on the same segment of chromosome. This depends on Linkage Disequilibrium, which we will discuss later



Haplotypes

Specific combination of SNPs occurring on the same segment of chromosome. This depends on Linkage Disequilibrium, which we will discuss later



Haplotype **AGA** might be pathogenic

Reference SNP (rs) Report

Download

Switch to classic site

rs776746

Current Build 152
Released October 2, 2018

Organism	*Homo sapiens*
Position	chr7:99672916 (GRCh38.p12)
Alleles	T>C
Variation Type	SNV Single Nucleotide Variation
Frequency	T=0.28922 (36317/125568, TOPMED) T=0.2653 (8204/30920, GnomAD) T=0.379 (1896/5008, 1000G) (+ 3 more)
Clinical Significance	Reported in ClinVar
Gene : Consequence	CYP3A5 : Splice Acceptor Variant ZSCAN25 : Intron Variant
Publications	386 citations
Genomic View	See rs on genome

FEEDBACK

Variant Details

Clinical Significance

Frequency

Genomic Placements

Sequence name	Change
GRCh37.p13 chr 7	NC_000007.13:g.99270539C>T
GRCh38.p12 chr 7	NC_000007.14:g.99672916T>C

Navigate to dbSNP: https://www.ncbi.nlm.nih.gov/snp

- Search: rs4646438

Zoom breakout exercises #2 and #3

- Terminology matching and dbSNP navigation

Zoom breakout

- #2: matching – can view this in answer key
- #3: Missense mutation in APOE

Summary

- Genetic variation can affect single nucleotides or longer segments through structural changes.
- Changes in DNA affect what we see (phenotypes) depending on where they are in the genome and their role in protein production.