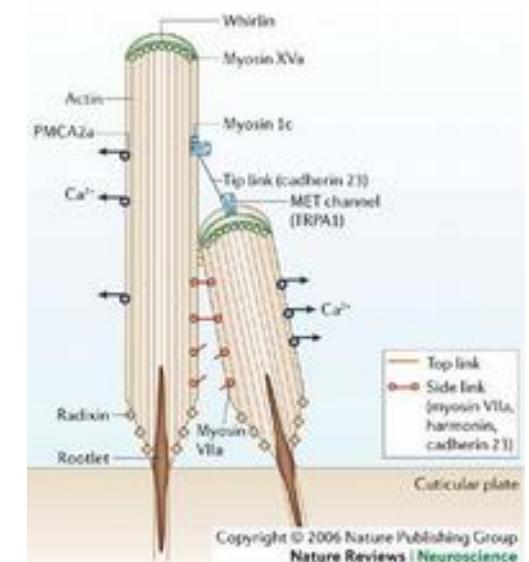
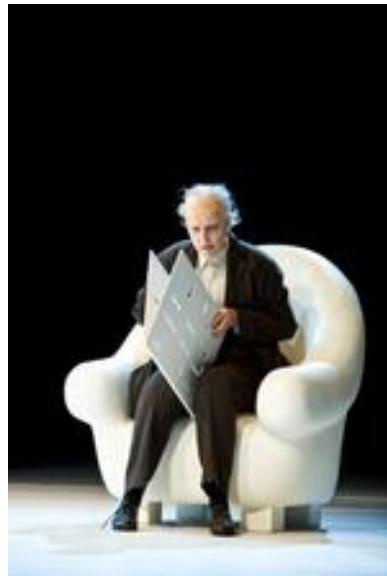


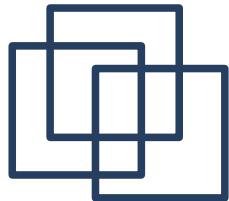
# Searching for the “language genes”



LSA2013  
Universality and Variability:  
New Insights from Genetics  
29<sup>th</sup> of June, 2013



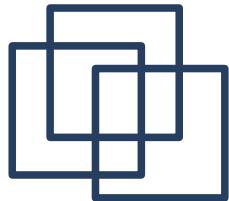
Dan Dediu  
Language and Genetics  
Max Planck Institute for Psycholinguistics  
Nijmegen  
The Netherlands



# Overview

---

- Heritability
- Linkage
- Association
- Sequencing
- Examples (hearing loss, dyslexia, SLI, stuttering)
- Conclusions
- Suggested readings



## Basic concepts

---

- **Phenotype** → observable/measurable properties
  - height





# Basic concepts

---

- **Phenotype** → observable/measurable properties
  - height
  - eye color

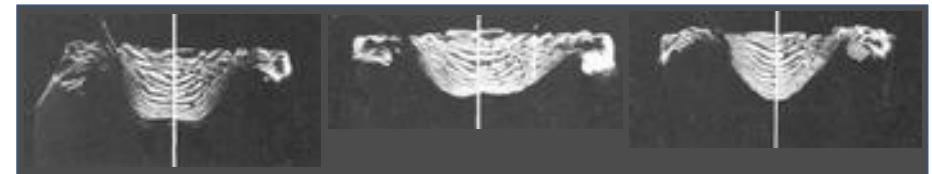




# Basic concepts

---

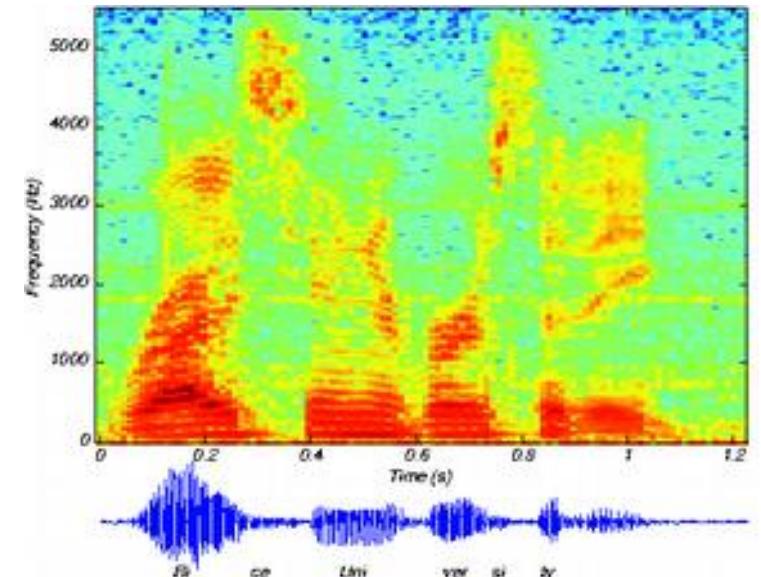
- **Phenotype** → observable/measurable properties
  - height
  - eye color
  - hard palate shape





# Basic concepts

- **Phenotype** → observable/measurable properties
  - height
  - eye color
  - hard palate shape
  - rate of speech

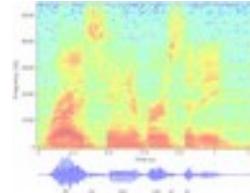
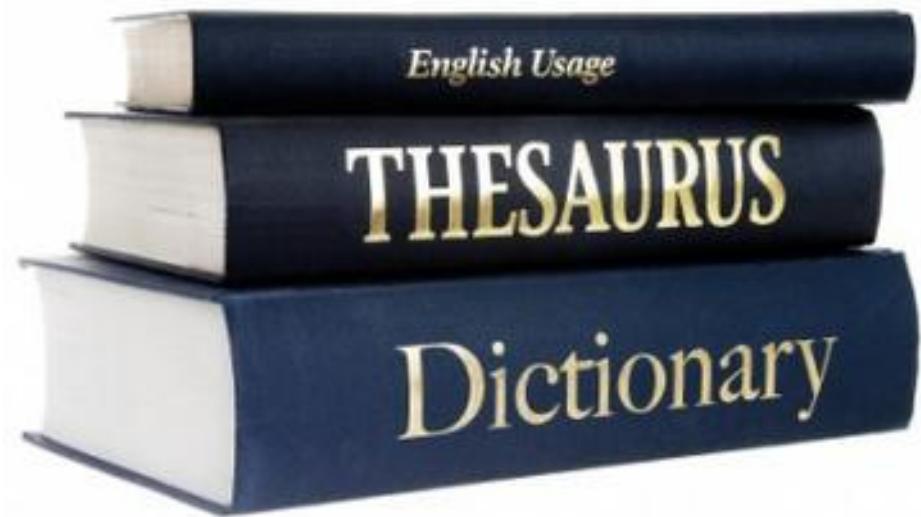




## Basic concepts

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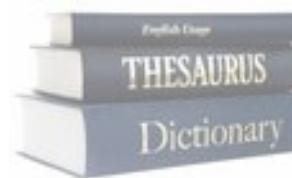
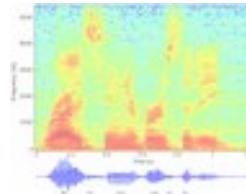
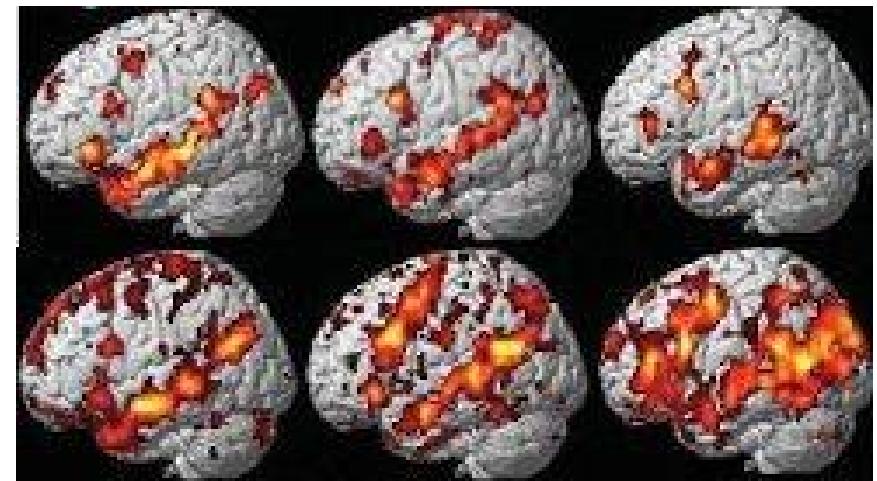
- **Phenotype** → observable/measurable properties
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  - hard palate shape
  - rate of speech
  - vocabulary size





# Basic concepts

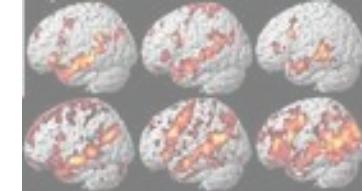
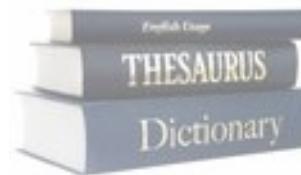
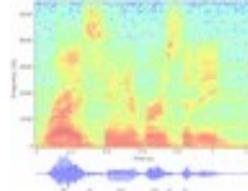
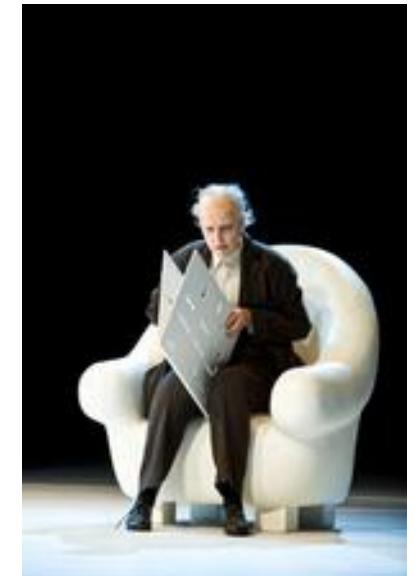
- **Phenotype** → observable/measurable properties
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  - hard palate shape
  - rate of speech
  - vocabulary size
  - brain activation





# Basic concepts

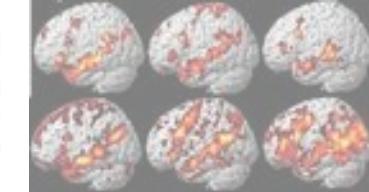
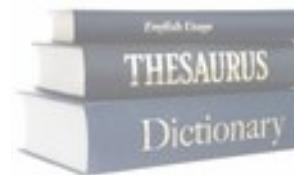
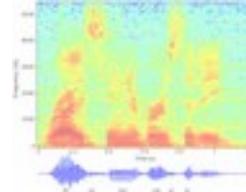
- **Phenotype** → observable/measurable properties
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  - rate of speech
  - vocabulary size
  - brain activation
  - grammaticality judgments

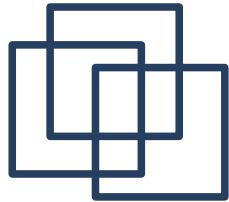




# Basic concepts

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  - eye color
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# Basic concepts

---

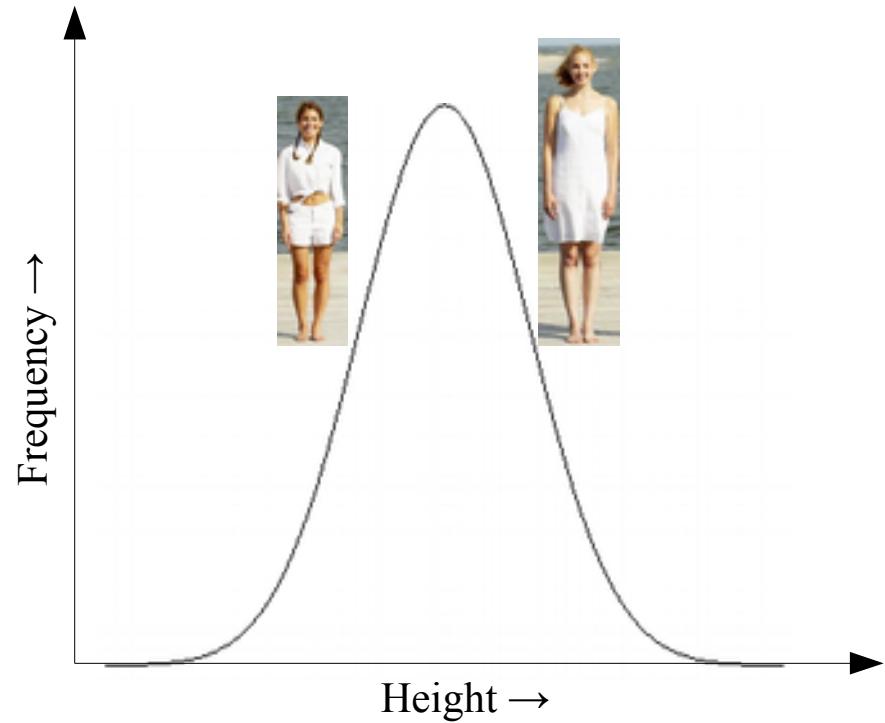
- Phenotype → variation



# Basic concepts

---

- Phenotype → variation
  - normal





# Basic concepts

- Phenotype → variation
  - normal
  - extreme/pathological





# Basic concepts

---

- **Phenotype** → variation
    - normal
    - extreme/pathological
- [measurement](#)





# Basic concepts

---

- Phenotype → variation
    - normal
    - extreme/pathological
- measurement

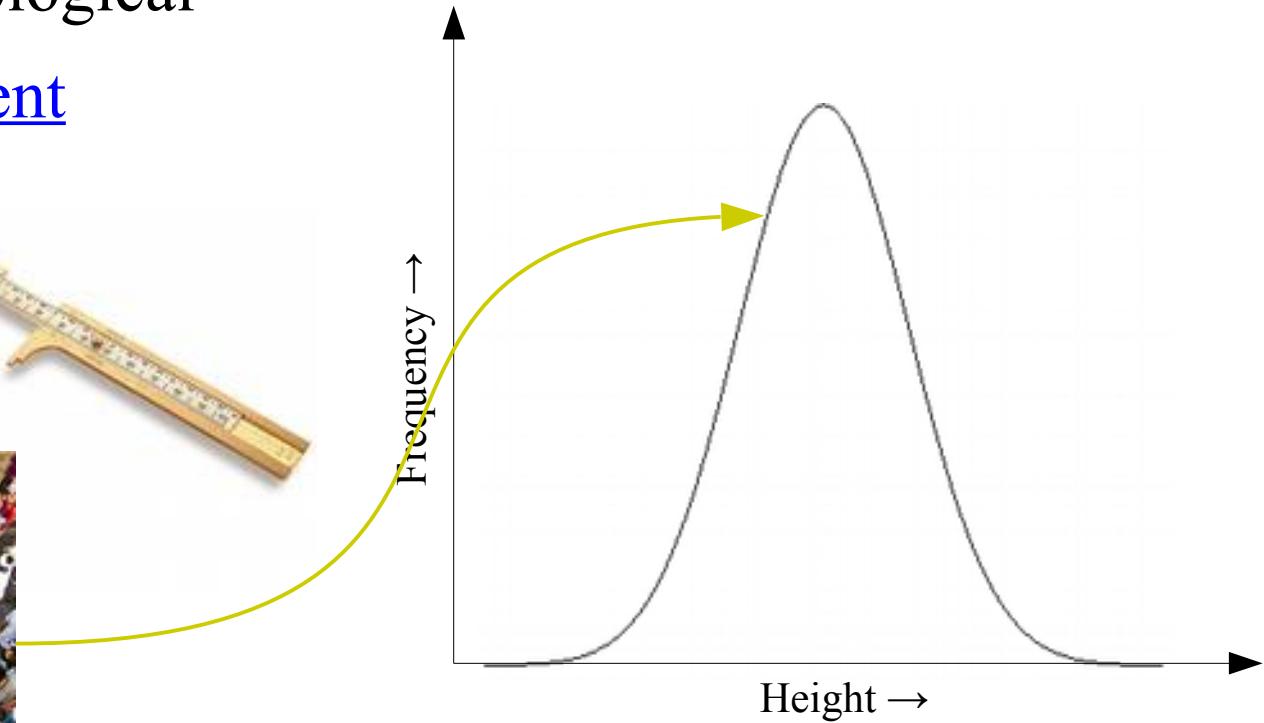


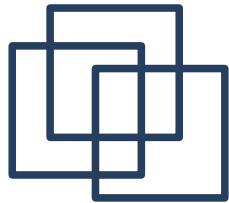


# Basic concepts

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    - normal
    - extreme/pathological
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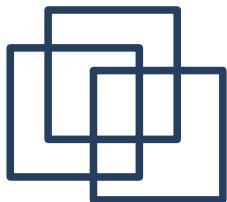




# Basic concepts

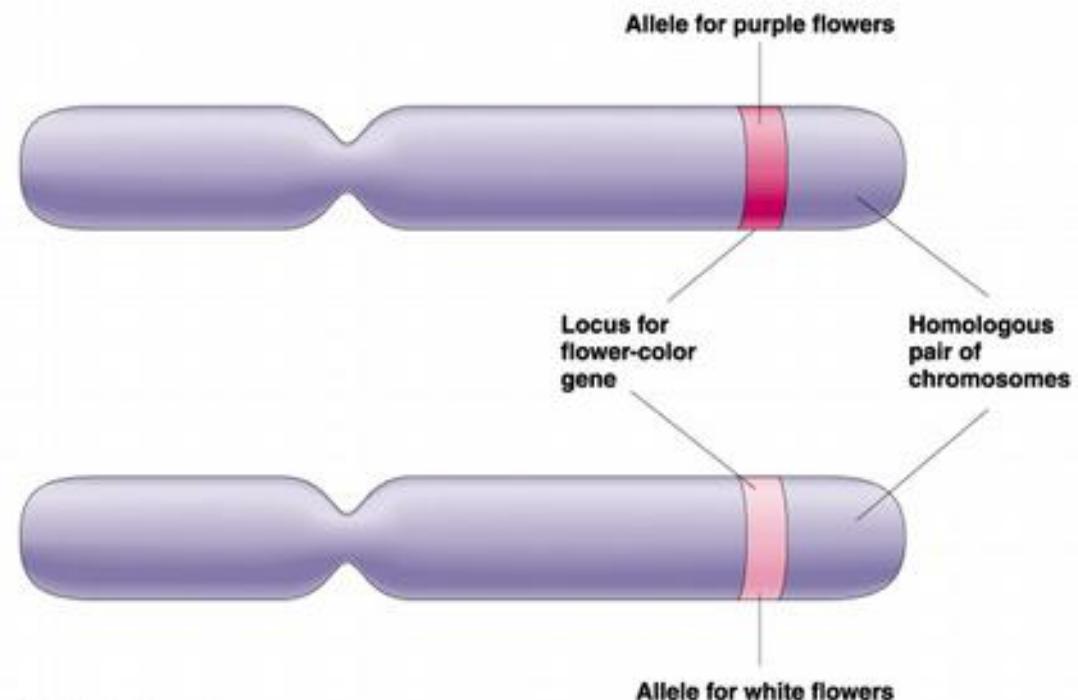
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- Genotype → abstract way



# Basic concepts

- Genotype → abstract way
  - gene → genetic locus
  - alleles/variants→ biallelic loci ( $A/a$ )

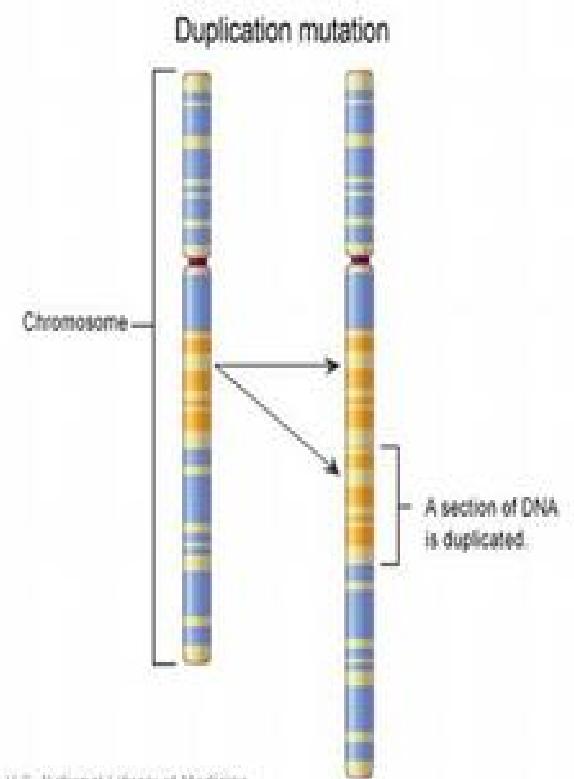


©1999 Addison Wesley Longman, Inc.

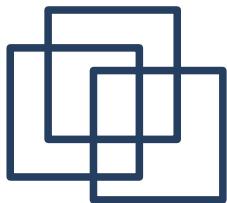


# Basic concepts

- Genotype → abstract way
  - gene → genetic locus
  - alleles/variants
  - biallelic loci ( $A/a$ )
  - CNVs

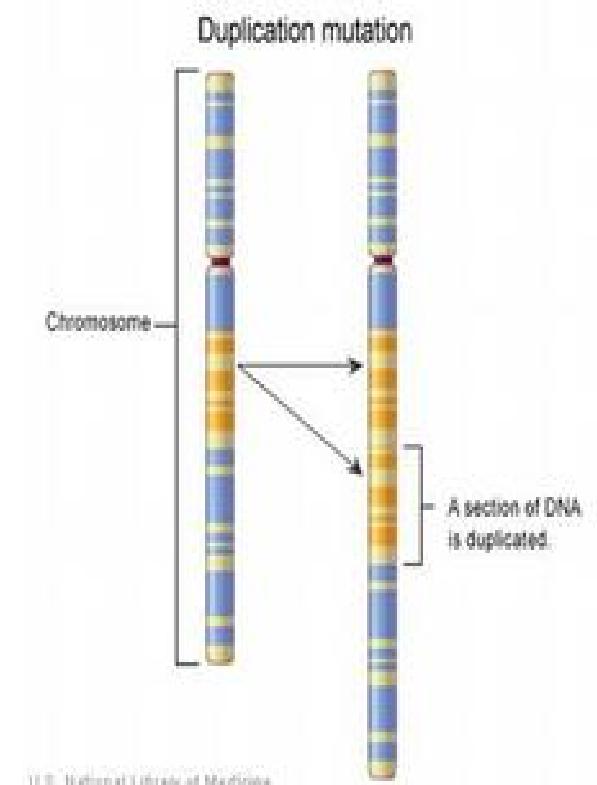
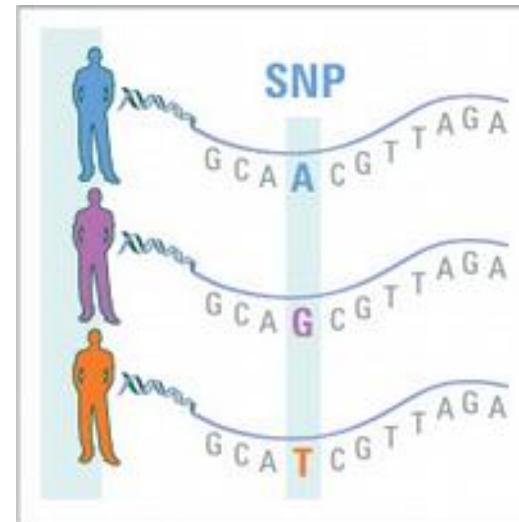


U.S. National Library of Medicine



# Basic concepts

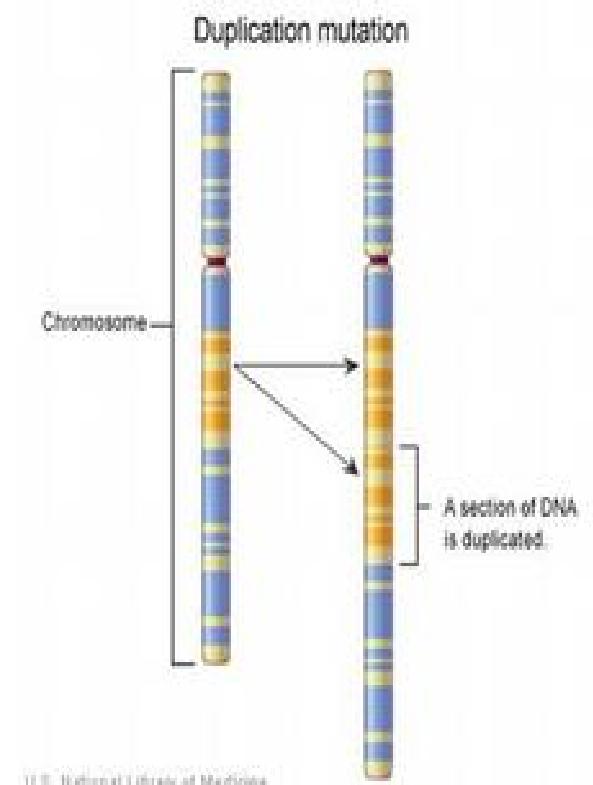
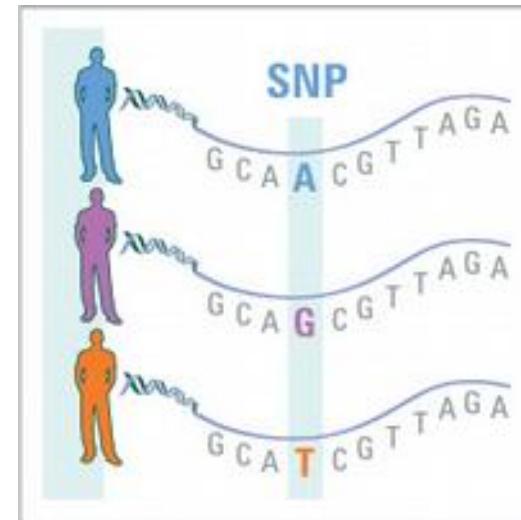
- Genotype → abstract way
  - gene → genetic locus
  - alleles/variants  
→ biallelic loci ( $A/a$ )
  - CNVs, SNPs





# Basic concepts

- Genotype → abstract way
  - gene → genetic locus
  - alleles/variants
    - biallelic loci ( $A/a$ )
  - CNVs, SNPs, etc...

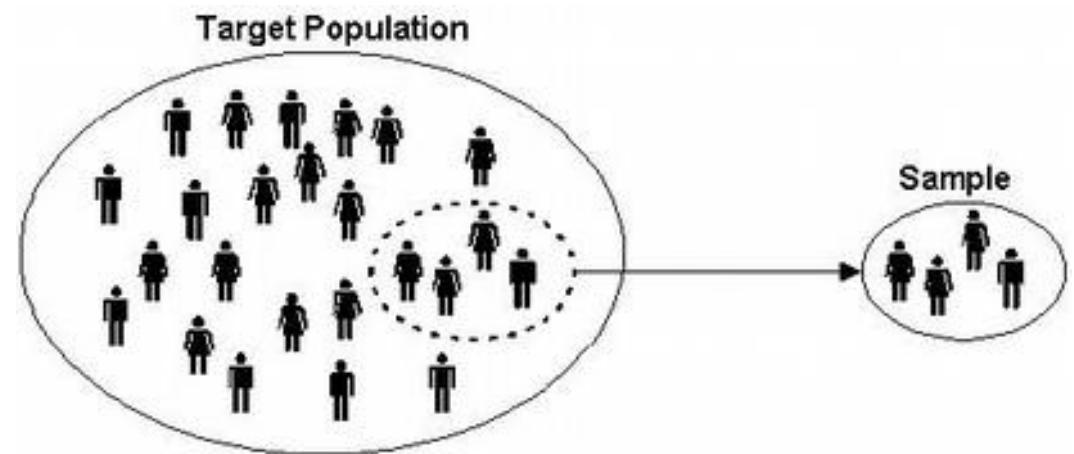


U.S. National Library of Medicine



# Basic concepts

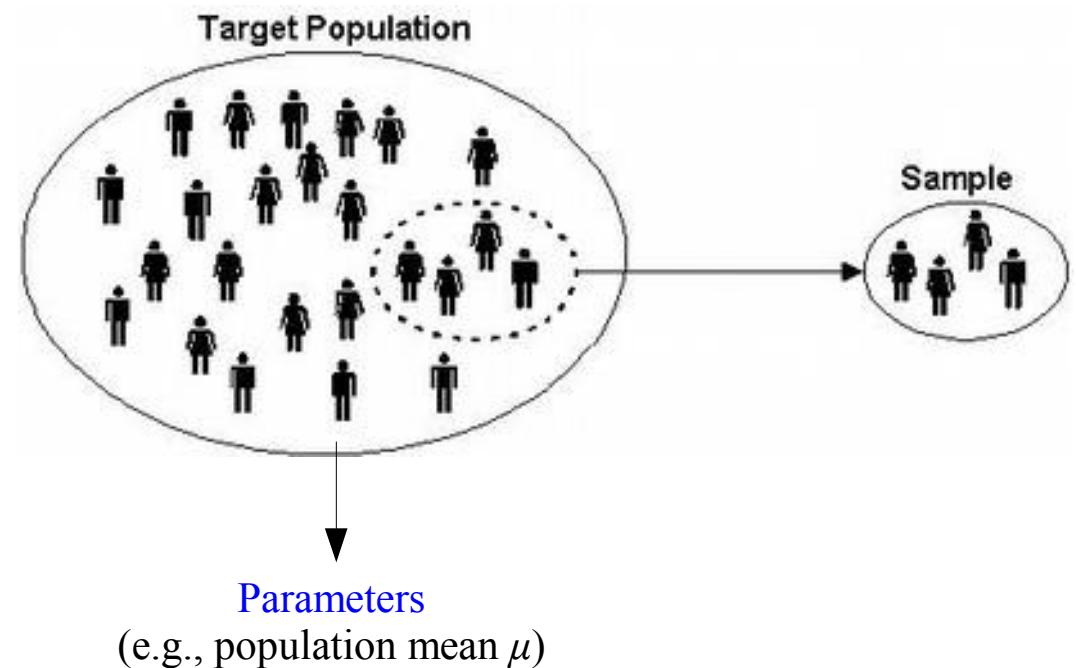
- Notions of statistics
  - (statistical) population  $\leftrightarrow$  sample & inference





# Basic concepts

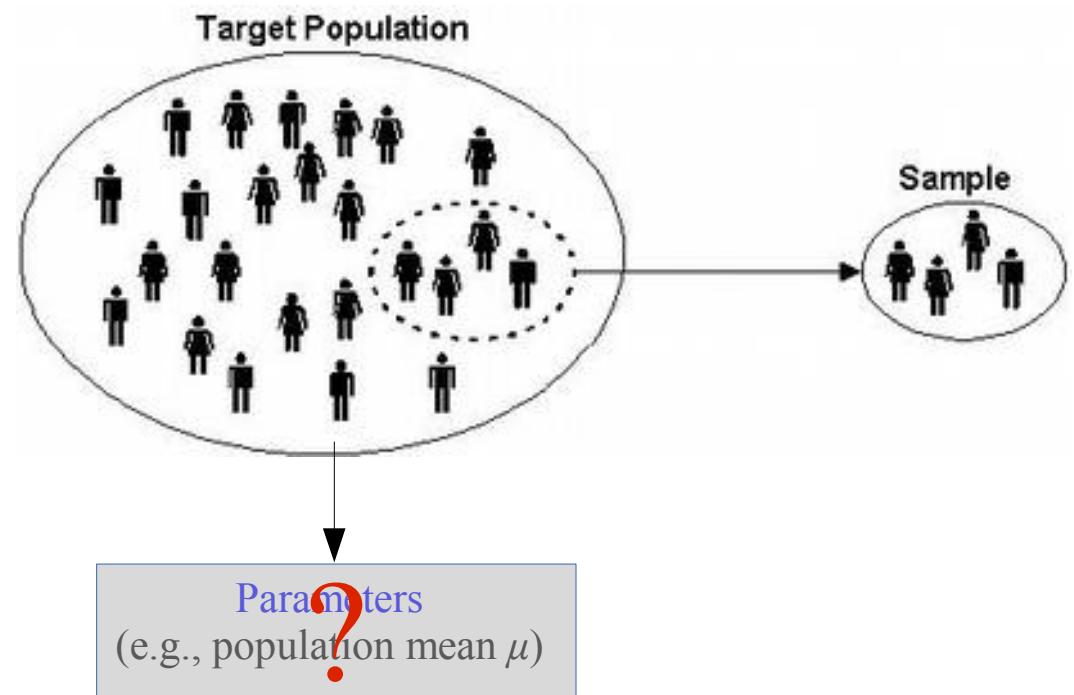
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# Basic concepts

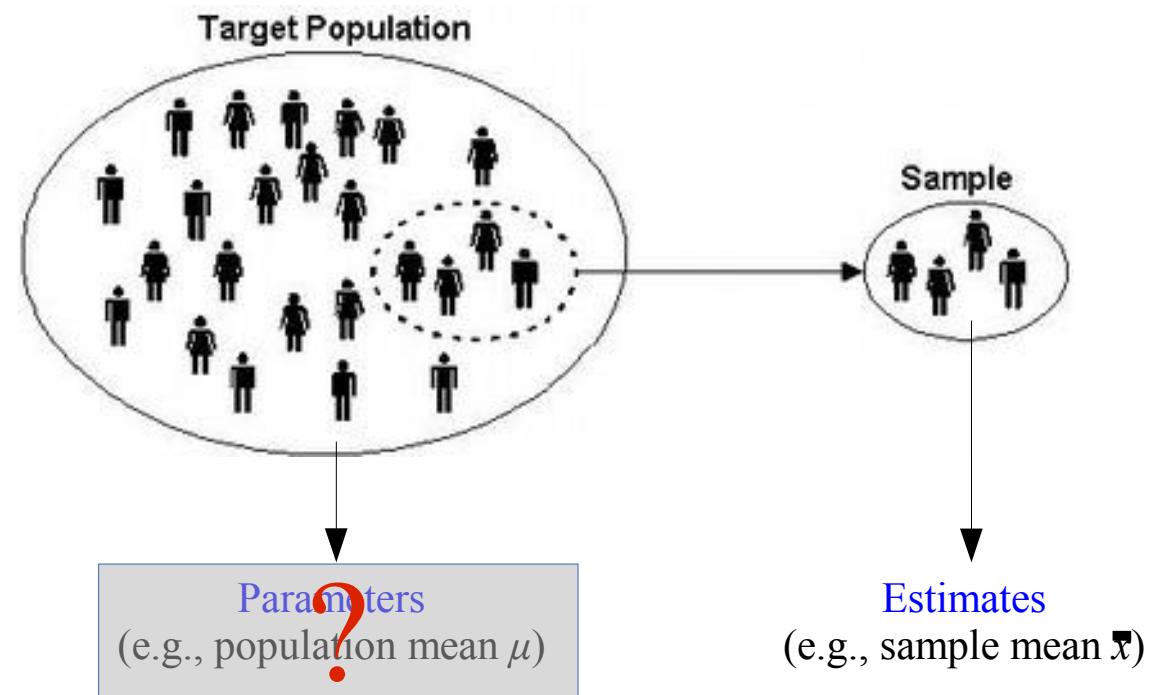
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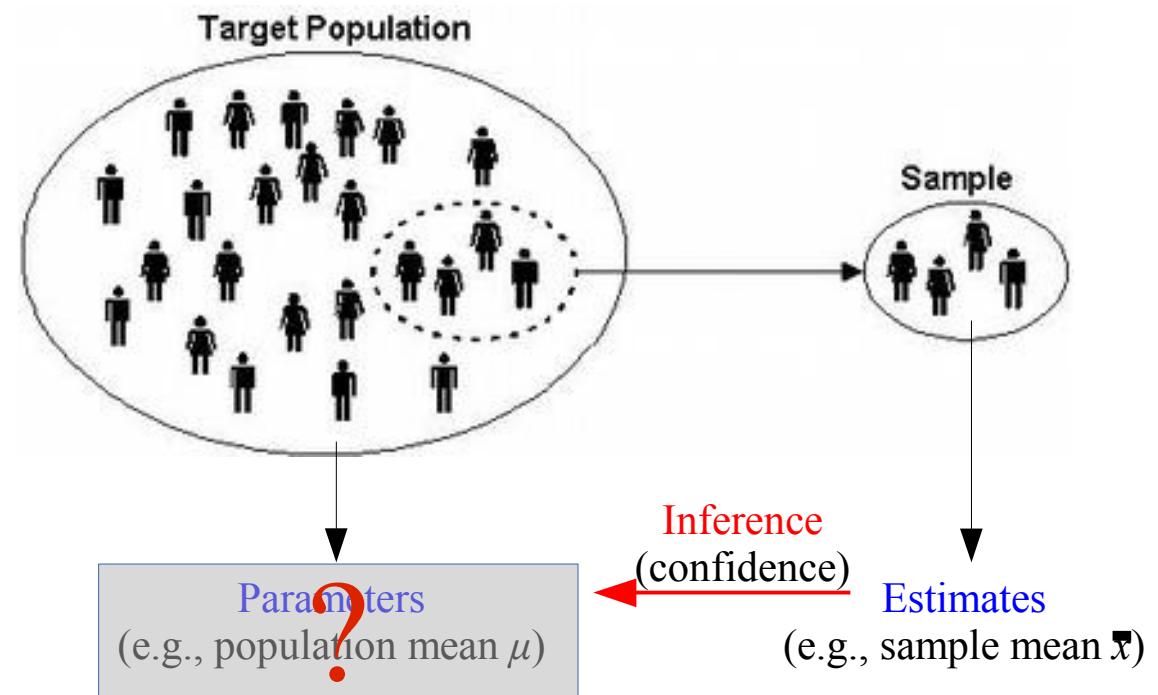
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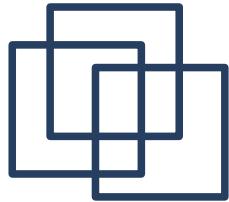




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# Basic concepts

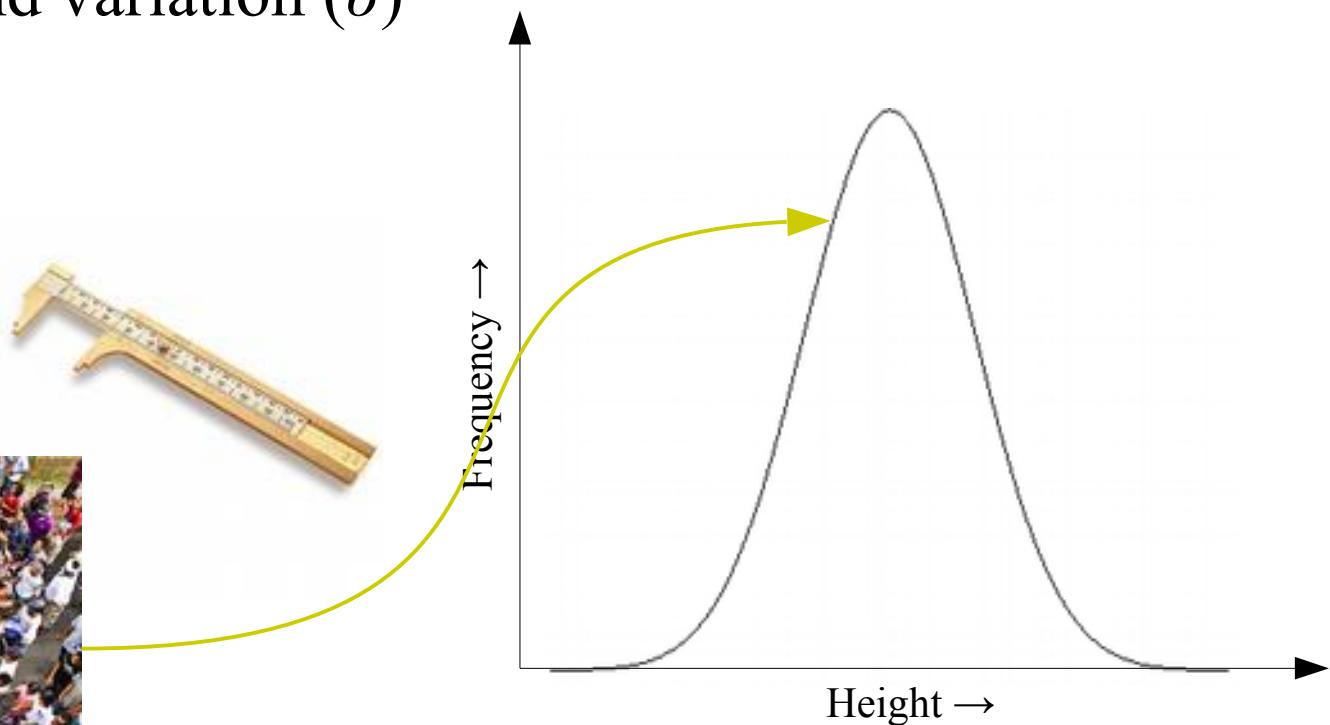
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- Notions of statistics
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  - mean ( $\mu$ ) and variation ( $\sigma$ )



# Basic concepts

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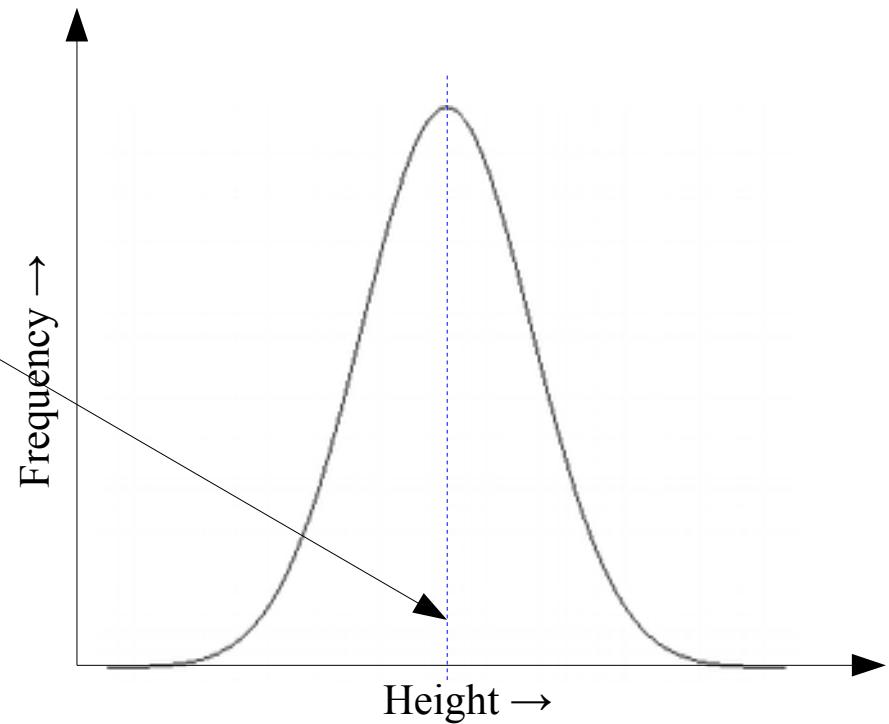




# Basic concepts

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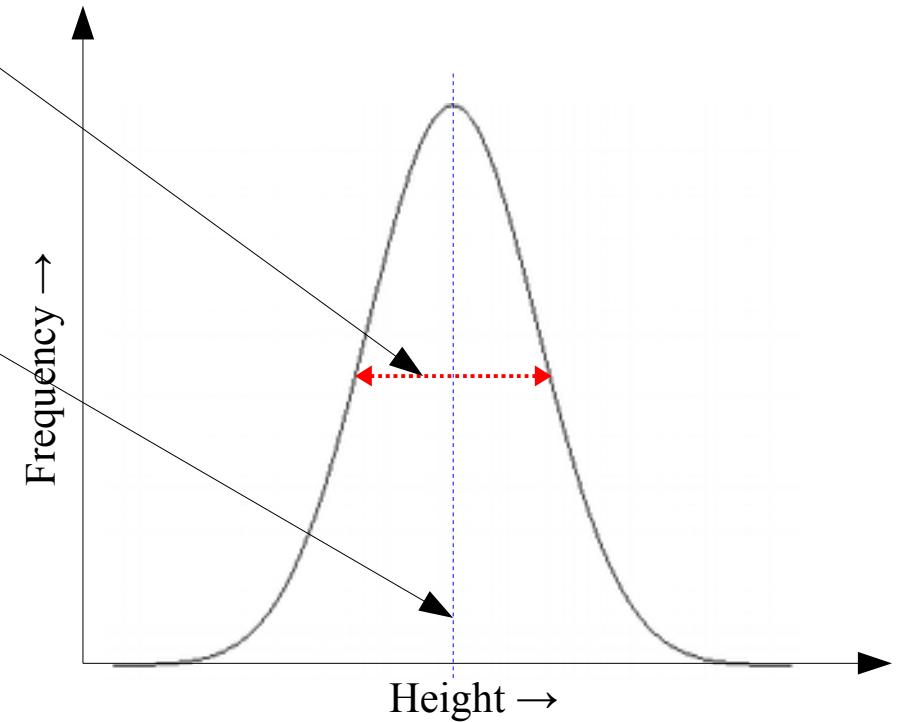
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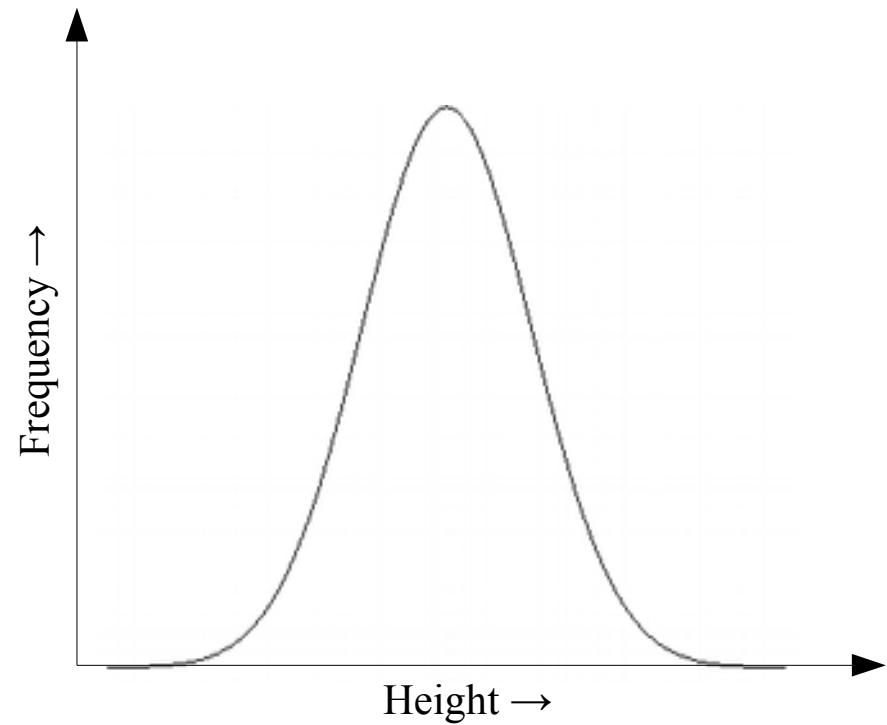




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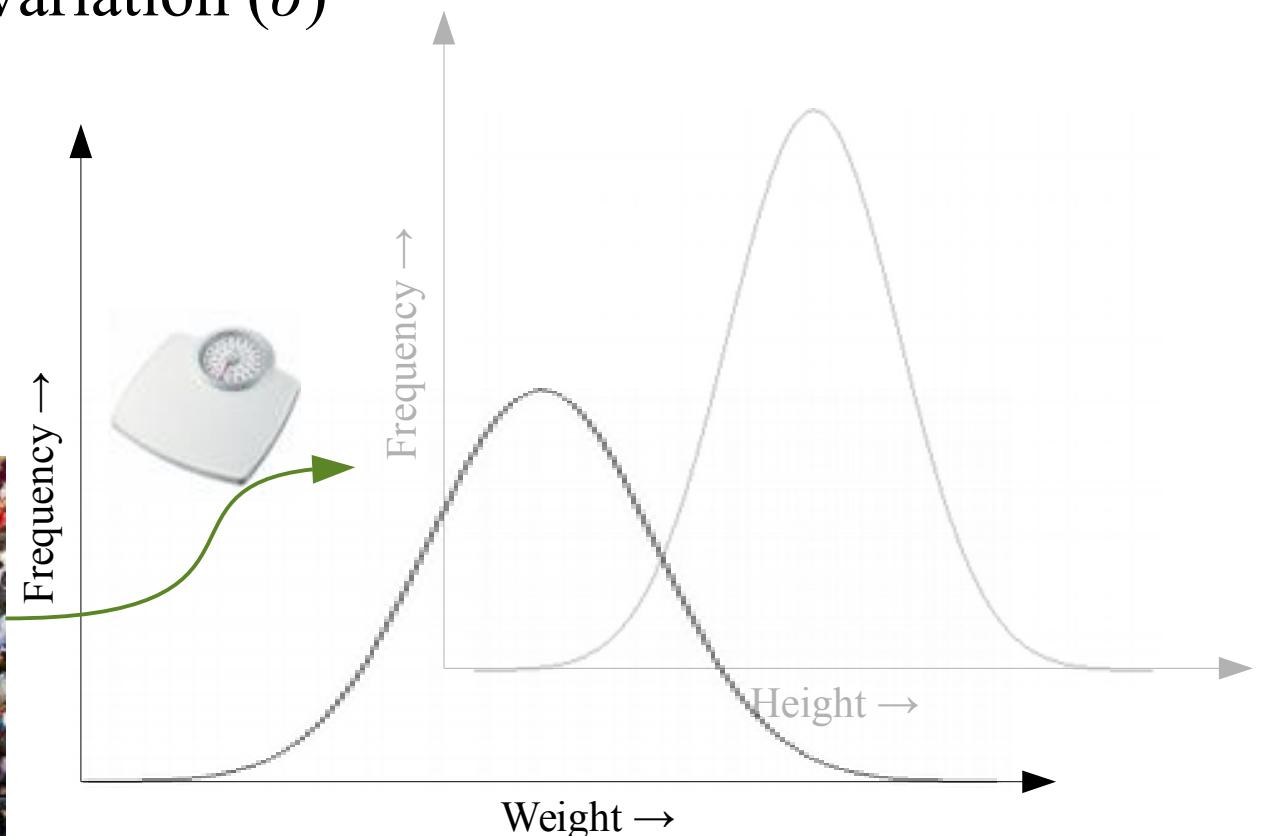
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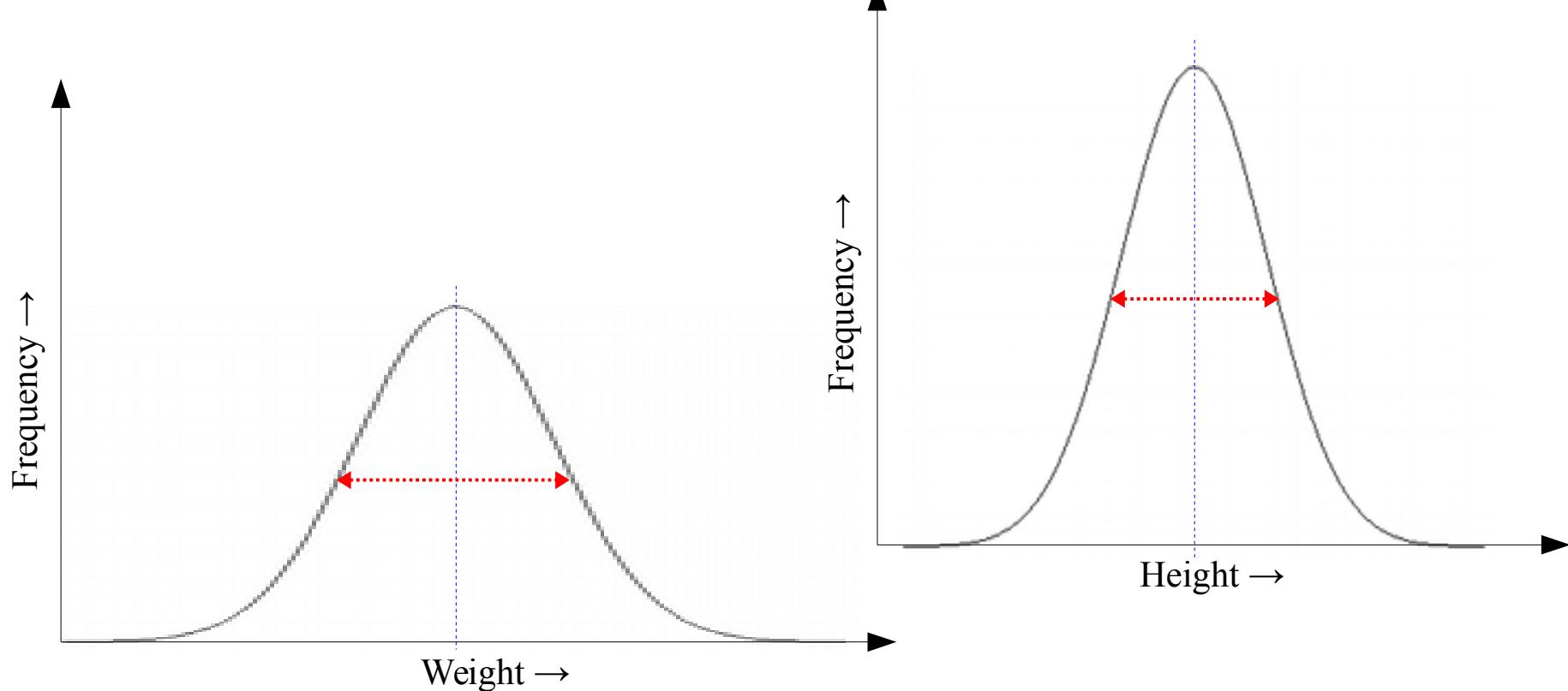
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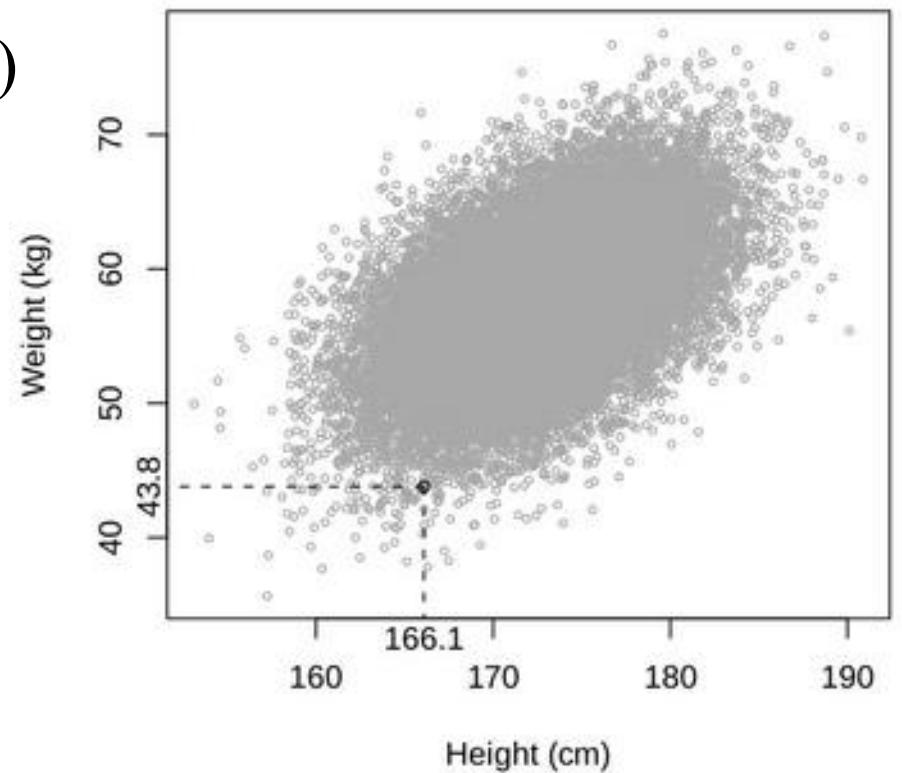


# Basic concepts

- Notions of statistics

- (statistical) population  $\leftrightarrow$  sample & inference
- mean ( $\mu$ ) and variation ( $\sigma$ )
- correlation  $r$  (covariation  $cov$ )

Scatterplot of height and weight



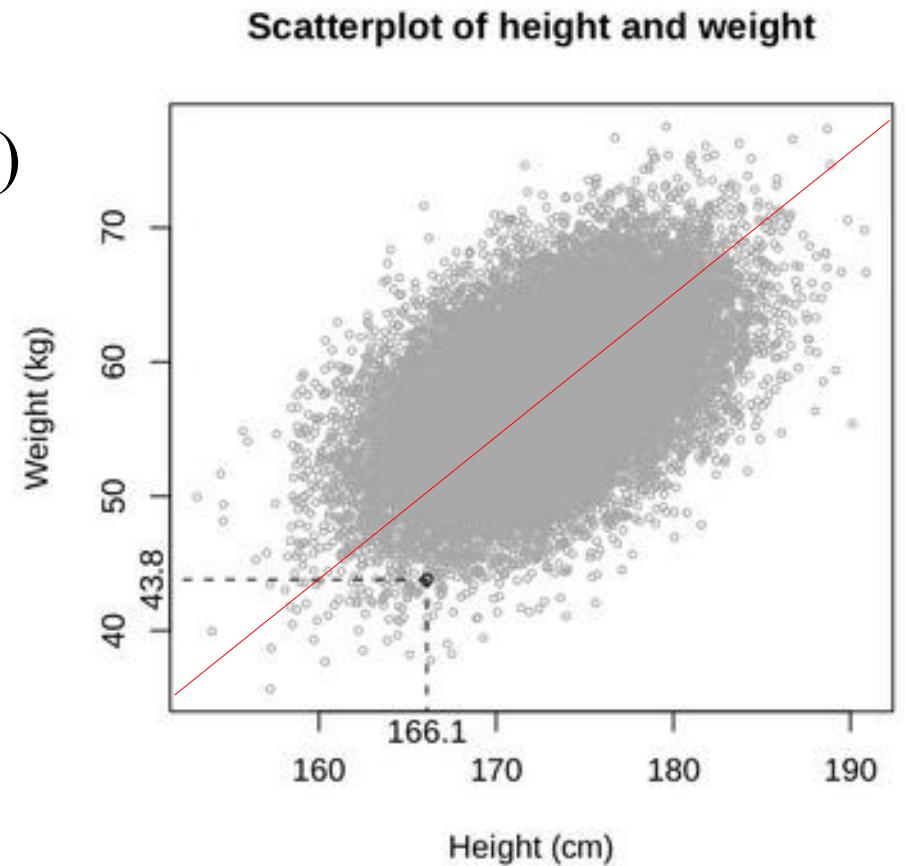


# Basic concepts

- Notions of statistics

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- correlation  $r$  (covariation  $cov$ )

$$r_{height, weight} = \frac{cov_{height, weight}}{\sigma_{height} \cdot \sigma_{weight}}$$



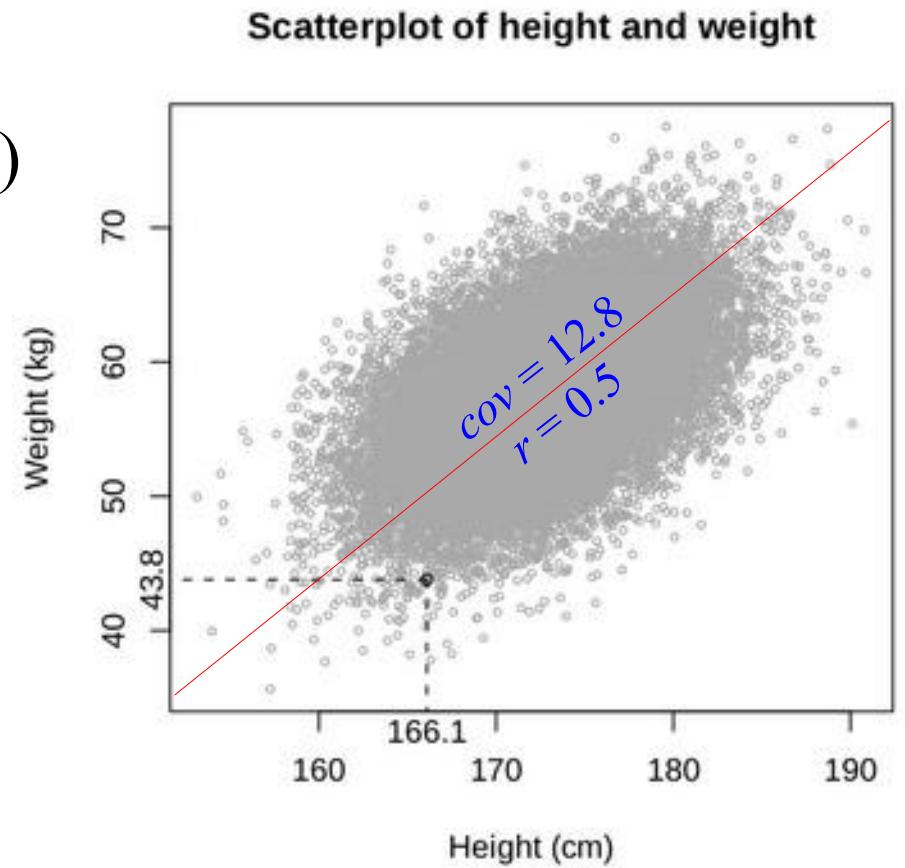


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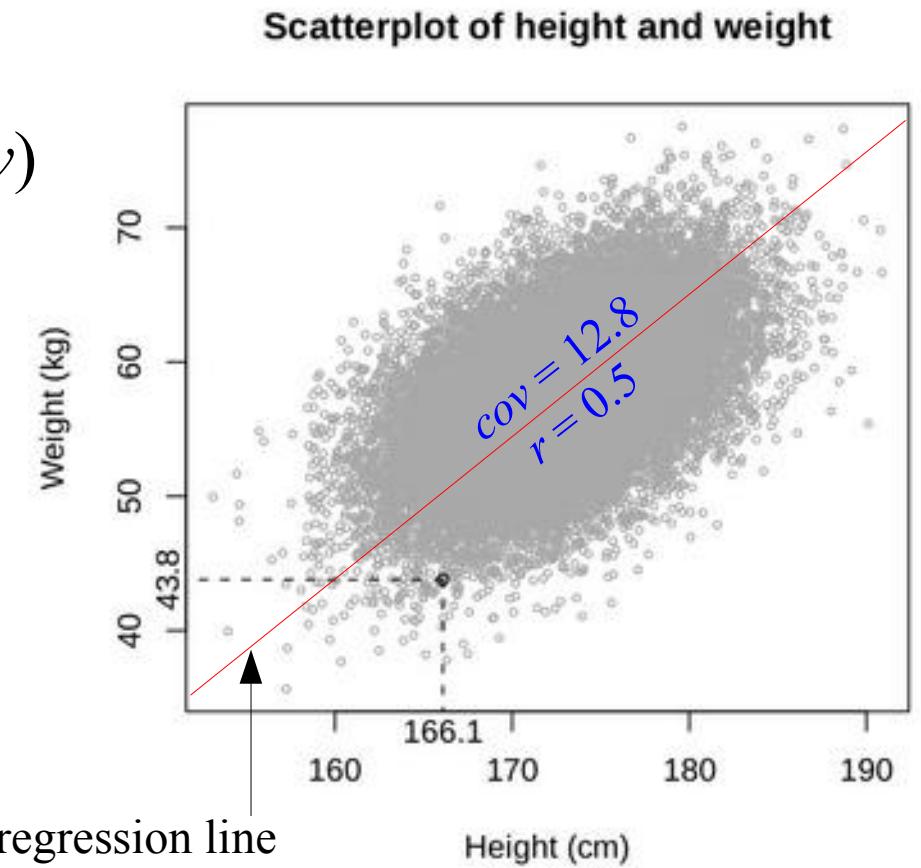


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$$r_{height, weight} = \frac{cov_{height, weight}}{\sigma_{height} \cdot \sigma_{weight}}$$





# Heritability

$$H^2 =$$



## Heritability

---

= proportion of phenotypic variation due to genotypic variation

$$H^2 = \text{_____}$$

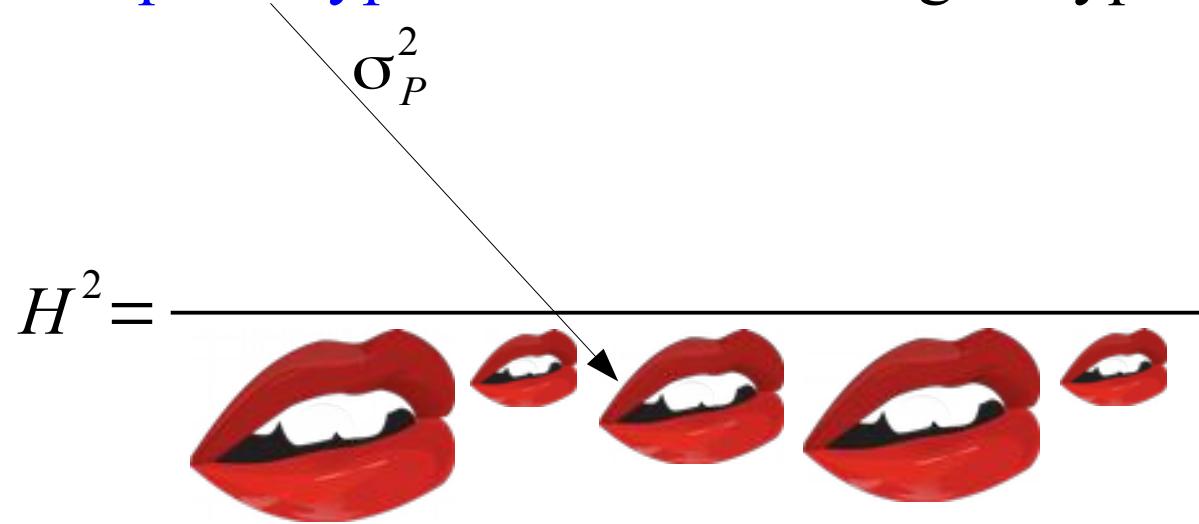
A mathematical equation where the symbol  $H^2$  is followed by a long horizontal line for an equals sign, with a small black arrowhead pointing towards the end of the line.



# Heritability

---

= proportion of **phenotypic variation** due to genotypic variation





# Heritability

---

= proportion of phenotypic variation due to genotypic variation

$$H^2 = \frac{\sigma_G^2}{\sigma_P^2}$$

The diagram illustrates the components of heritability. At the top, four DNA double helixes are shown, each with a unique color pattern. Below them, five pairs of human lips are depicted with red paint on the lips. An arrow points from the text 'genotypic variation' to the DNA helixes, indicating that genetic differences are represented by the different DNA structures. Another arrow points from the text 'phenotypic variation' to the lips, indicating that observable traits are represented by the different lip shapes.



# Heritability

---

= proportion of phenotypic variation due to genotypic variation

$$H^2 = \frac{\text{DNA Strands}}{\text{Lips}} = \frac{\sigma_G^2}{\sigma_P^2}$$



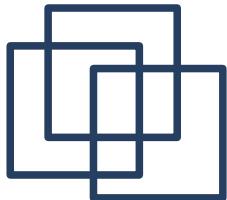

# Heritability

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$$H^2 = \frac{\text{DNA Strands}}{\text{Lips}} = \frac{\sigma_G^2}{\sigma_P^2}$$

$H^2$  (broad sense heritability)  $\neq h^2$  (narrow sense heritability)



# Heritability

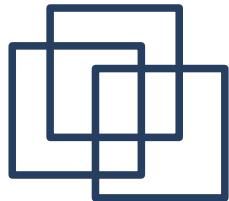
---

= proportion of phenotypic variation due to genotypic variation

$$H^2 = \frac{\text{genetic variation}}{\text{phenotypic variation}} = \frac{\sigma_G^2}{\sigma_P^2}$$


$H^2$  (broad sense heritability)  $\neq h^2$  (narrow sense heritability)

0 (genetic variation has no effect)  $\rightarrow$  1 (all phenotypic variation is genetic)

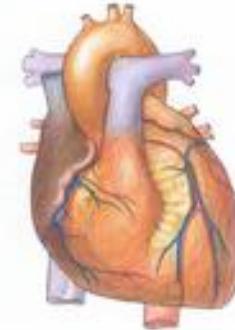


# Heritability

---

Caveats in interpretation:

- Uniform traits





# Heritability

---

Caveats in interpretation:

- Uniform traits
- Essential (fixed) genes





# Heritability

---

Caveats in interpretation:

- Uniform traits
- Essential (fixed) genes
- Constant vs variable environment





# Heritability

Caveats in interpretation:

- Uniform traits
- Essential (fixed) genes
- Constant vs variable environment
- Specific to **population & environment**

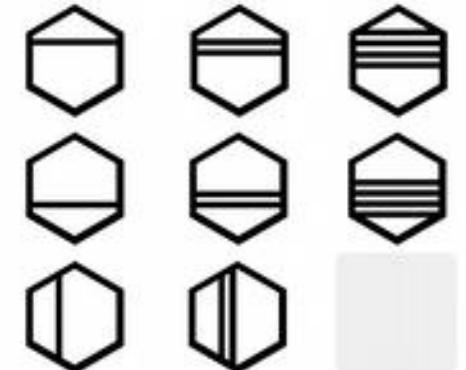




# Heritability

Caveats in interpretation:

- Uniform traits
- Essential (fixed) genes
- Constant vs variable environment
- Specific to population & environment
- **Changes** with age





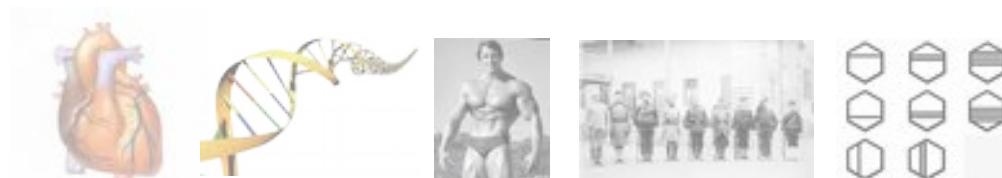
# Heritability

---

Caveats in interpretation:

- Uniform traits
- Essential (fixed) genes
- Constant vs variable environment
- Specific to population & environment
- Changes with age

→ **high heritability** ≠ innateness/“genetic determinism”





# Heritability

---

Estimation:

Twin studies



vs.



$$\rightarrow h^2 = 2(r_{MZ} - r_{DZ})$$



# Heritability

Estimation:

Twin studies



vs.



$$\rightarrow h^2 = 2(r_{MZ} - r_{DZ})$$

Adoption studies

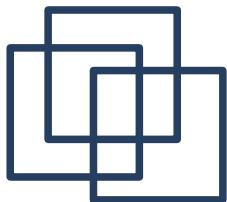


vs.



and





# Heritability

Estimation:

Twin studies



vs.



$$\rightarrow h^2 = 2(r_{MZ} - r_{DZ})$$

Adoption studies



vs.

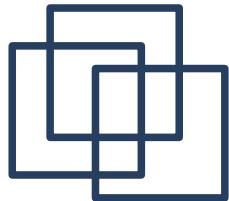


and



Non-related samples (genome-wide complex trait analysis; GCTA)





# Heritability

---

- Moderate → high heritabilities for:
  - almost all aspects of speech and language
  - normal and pathologic



# Heritability

---

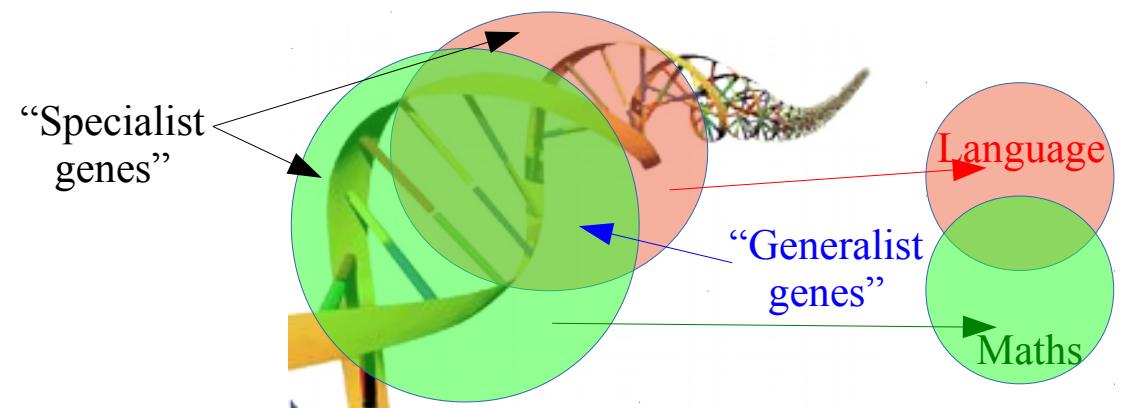
- Moderate → high heritabilities for:
  - almost all aspects of speech and language
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- Examples:
  - dyslexia (0.4 – 0.8), SLI (0.5), stuttering (0.7) ...
  - (I)SLA (0.7), conversational language (0.7), formal language (0.5), vocabulary size (0.7), “phonology & articulation” (0.7) ...

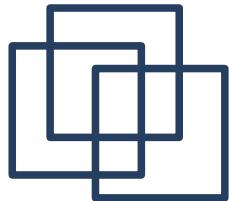


# Heritability

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  - (I)SLA (0.7), conversational language (0.7), formal language (0.5), vocabulary size (0.7), “phonology & articulation” (0.7) ...

Genetic correlations:

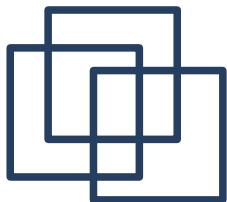




# Linkage

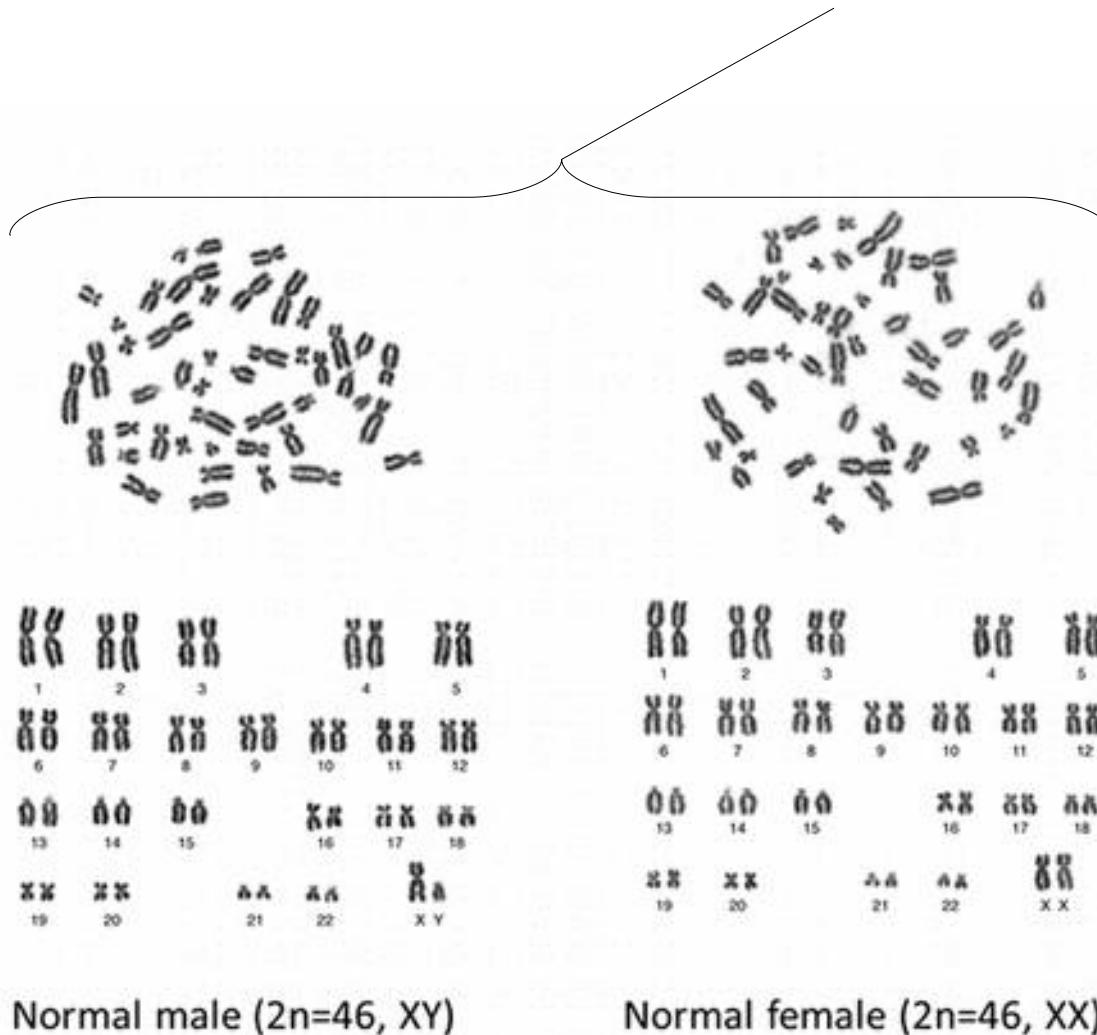
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- Genome: discrete linear molecules (chromosomes + mtDNA)



# Linkage

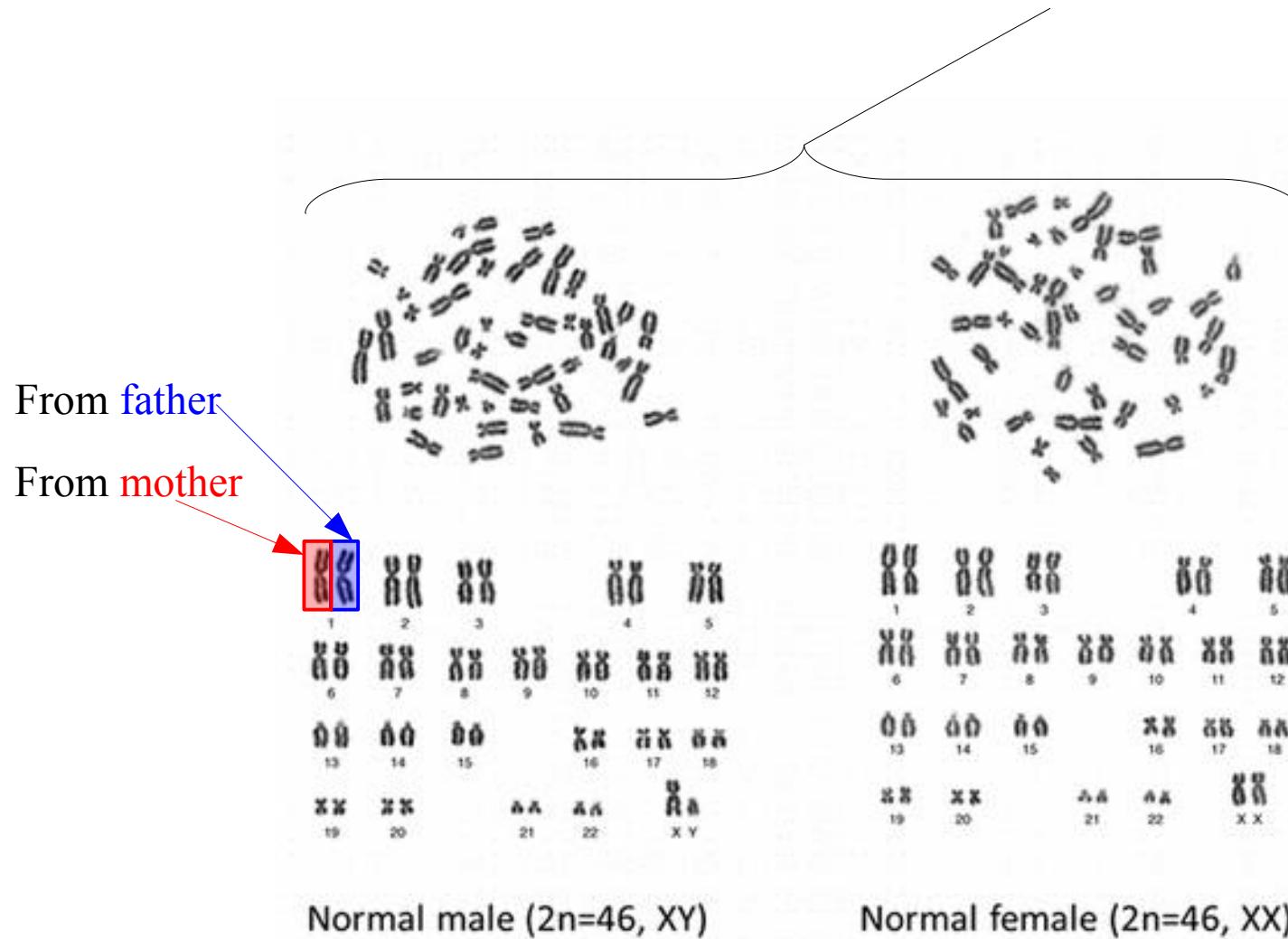
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# Linkage

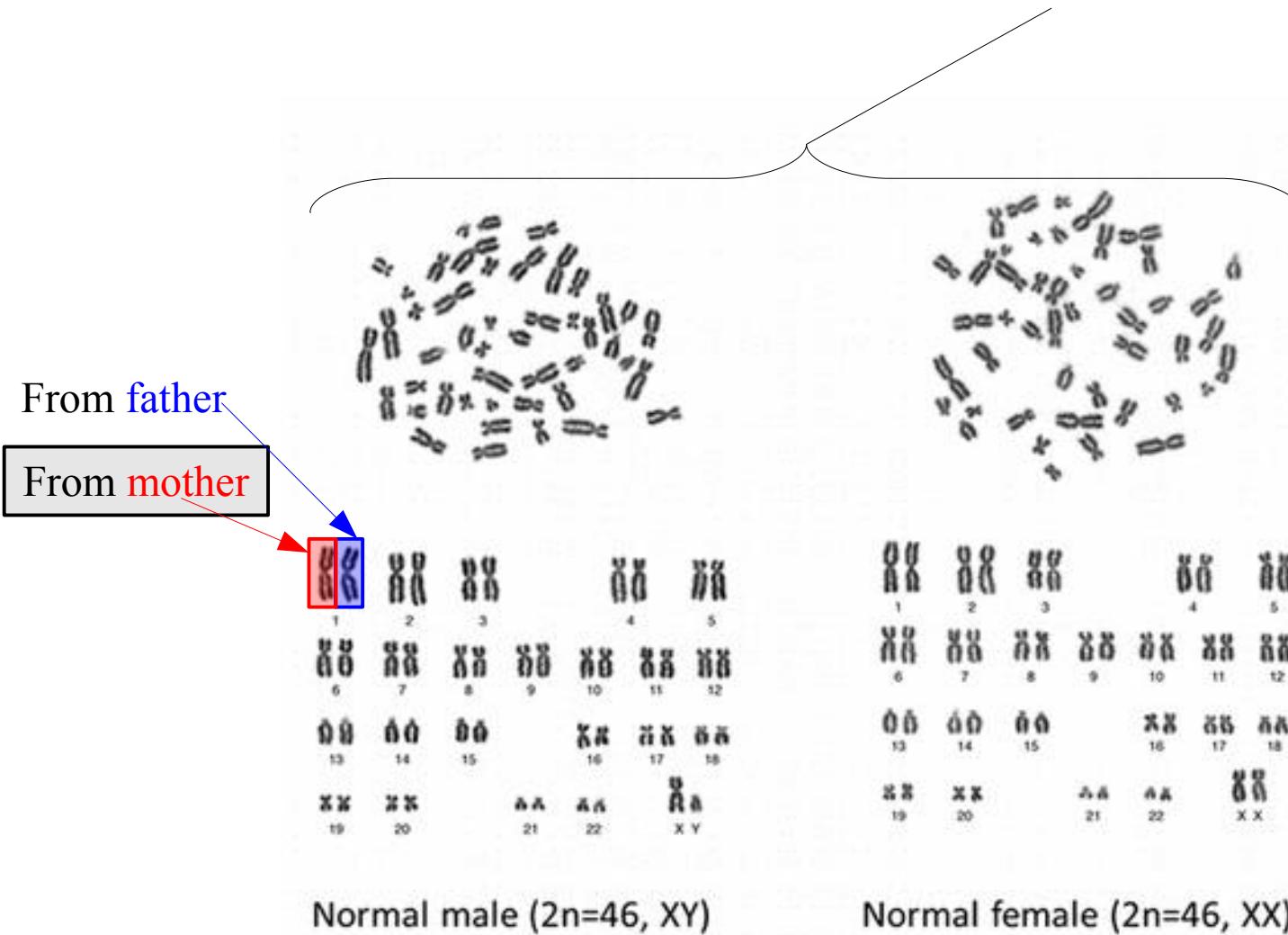
- Genome: discrete linear molecules (chromosomes + mtDNA)

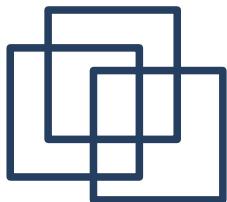




# Linkage

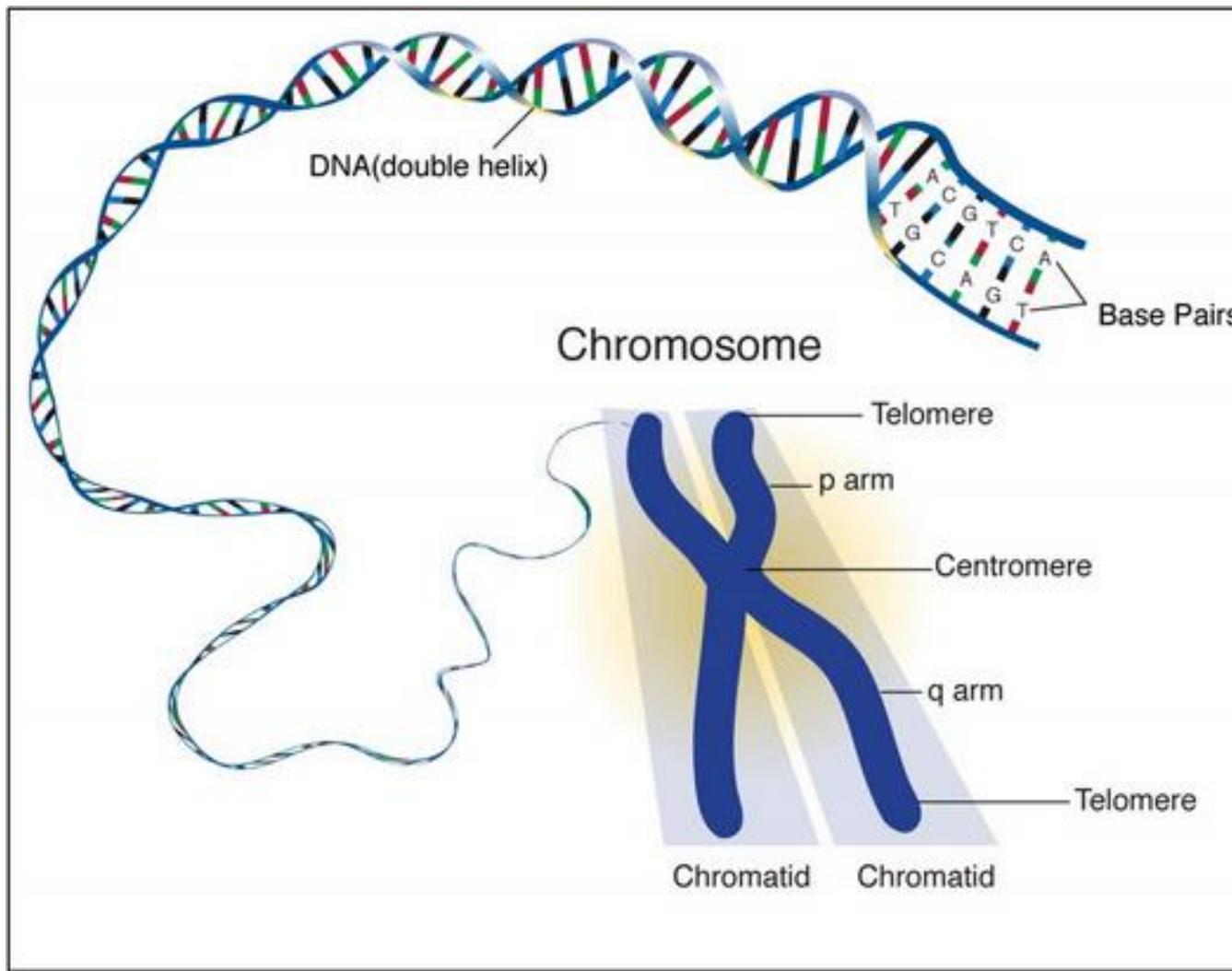
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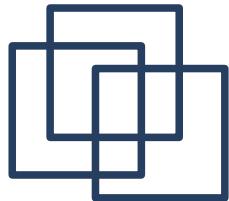




# Linkage

- Genome: discrete linear molecules (chromosomes + mtDNA)





# Linkage

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- Genome: discrete linear molecules  
→ independent loci (genes):

Peas plant

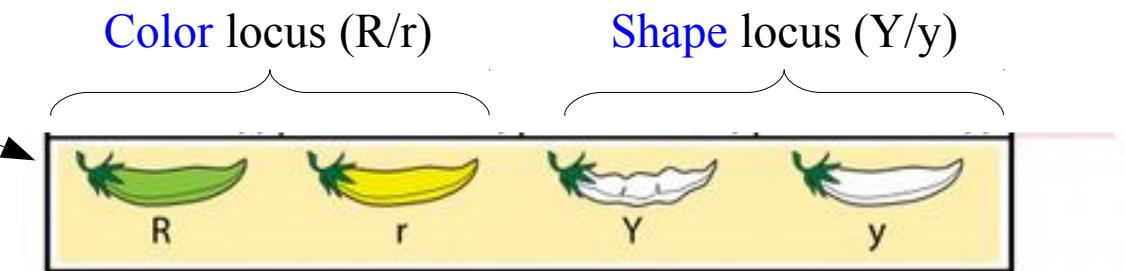




# Linkage

- Genome: discrete linear molecules  
→ independent loci (genes):

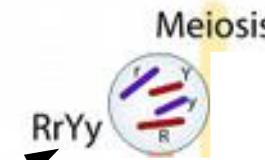
Peas plant



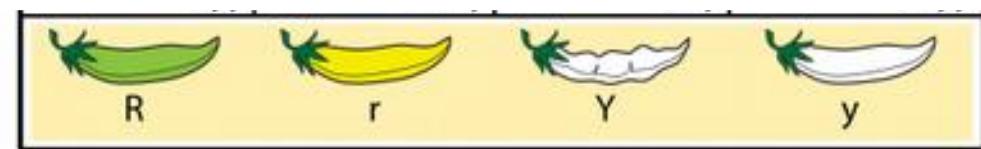


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- Genome: discrete linear molecules  
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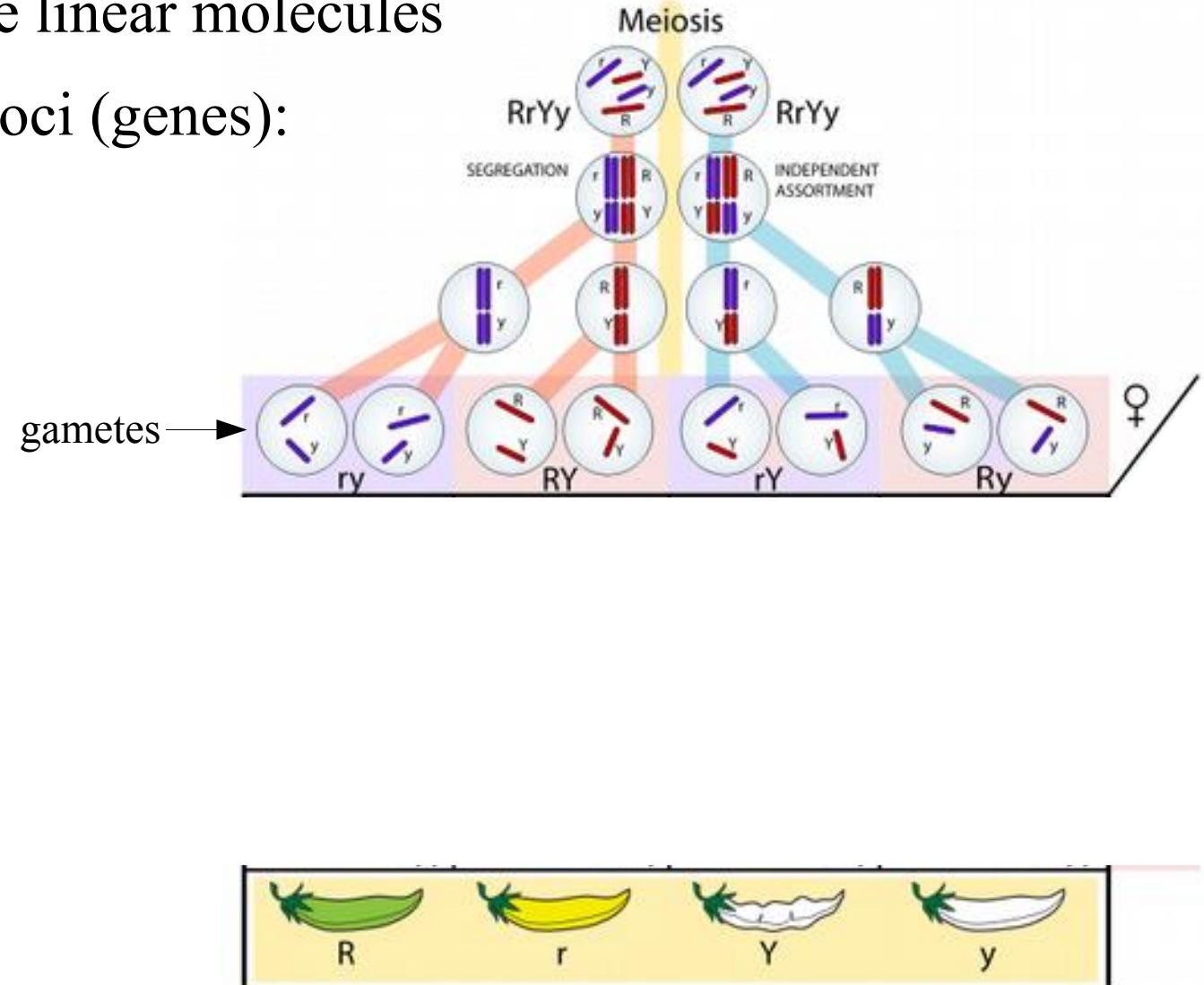




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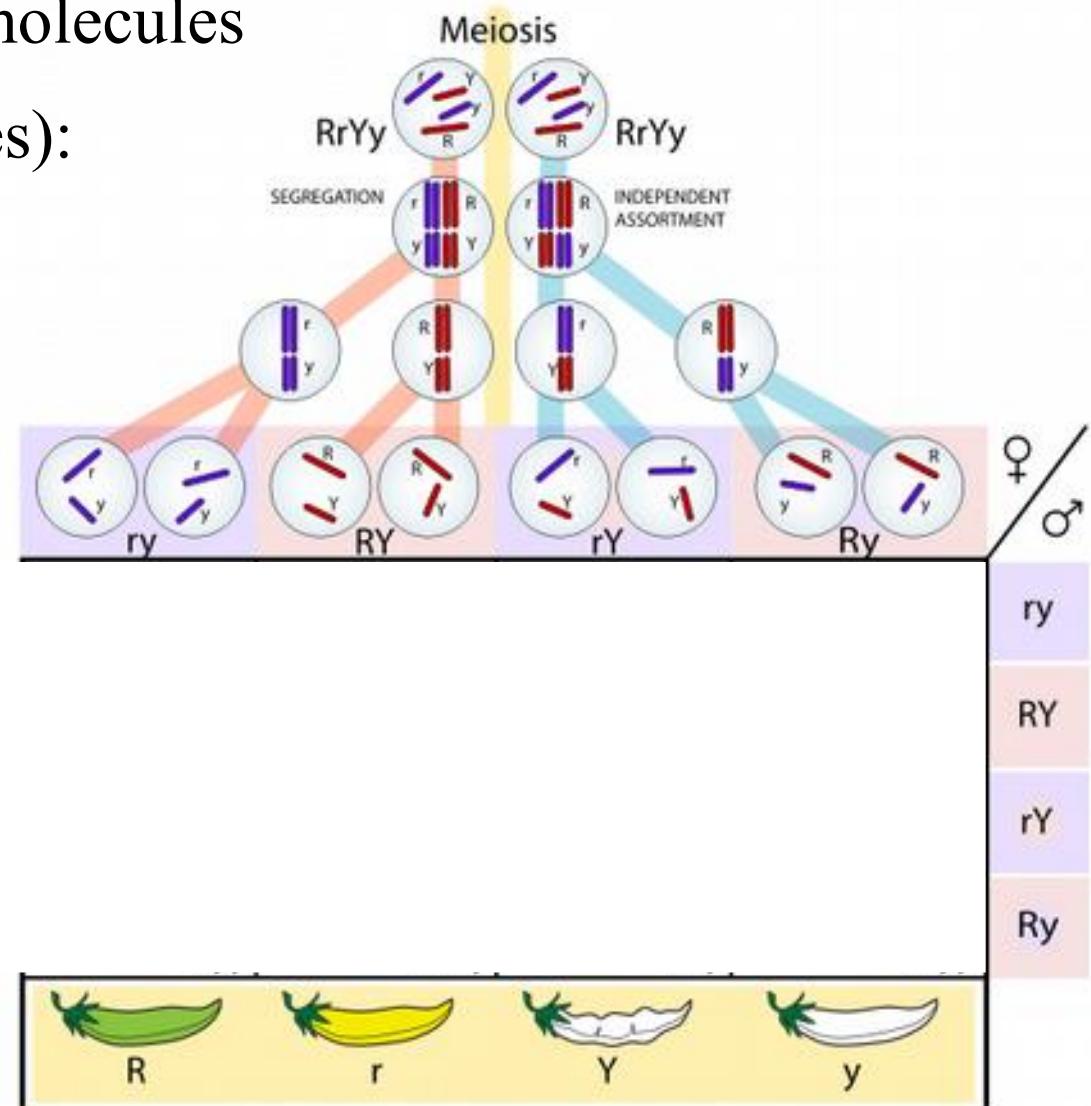




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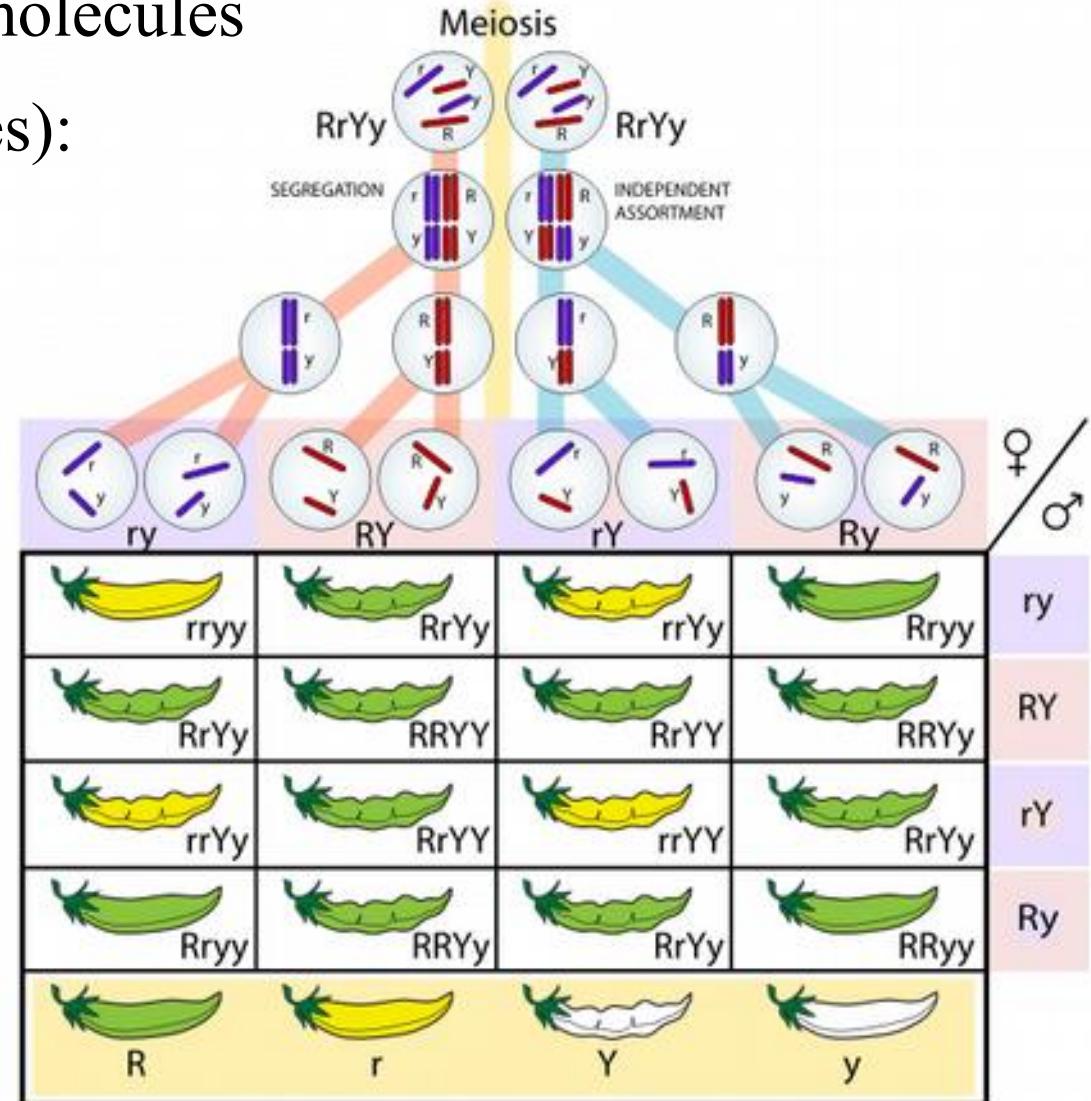
Peas plant

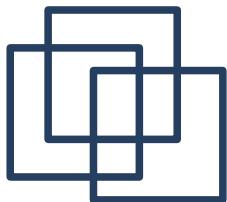




# Linkage

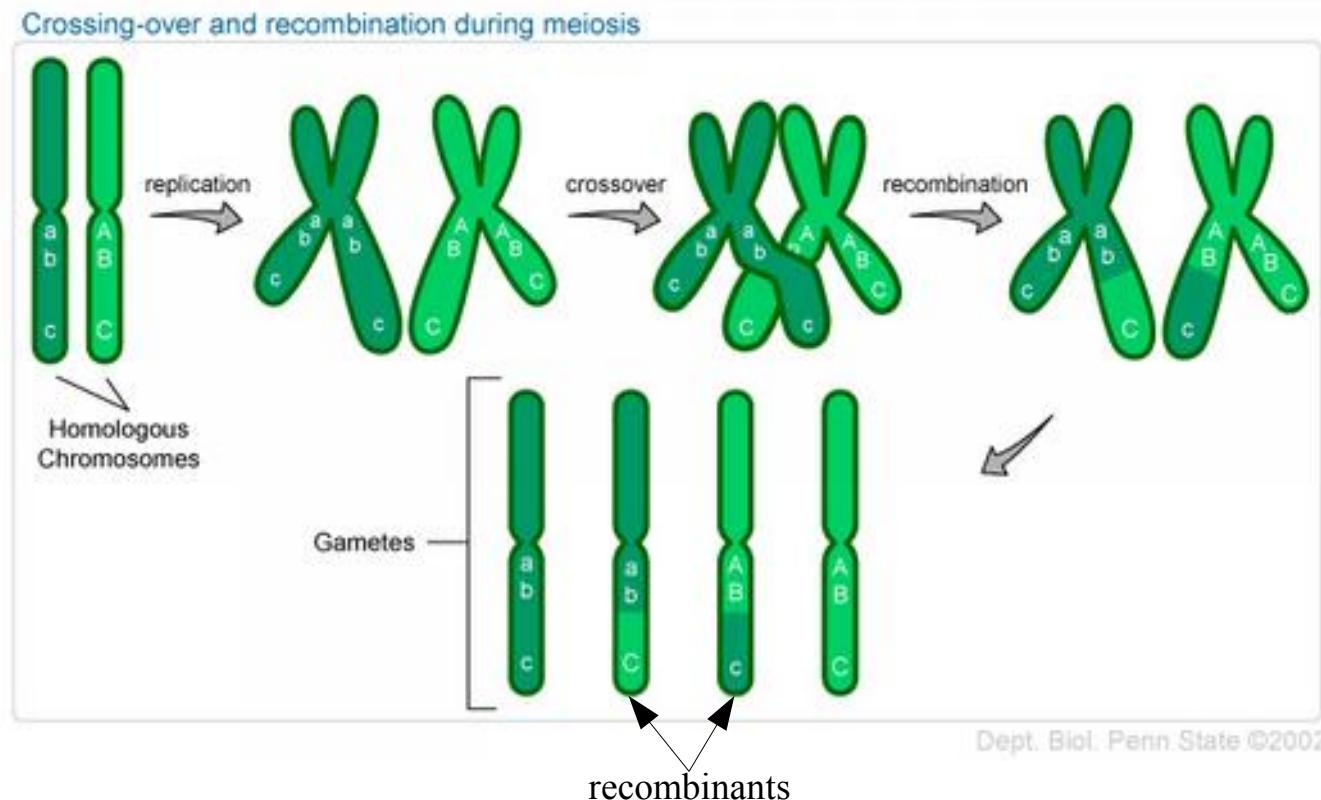
- Genome: discrete linear molecules  
→ independent loci (genes):





# Linkage

- Genome: discrete linear molecules
  - independent loci (genes)
  - **non-independent** loci → linkage + crossing over

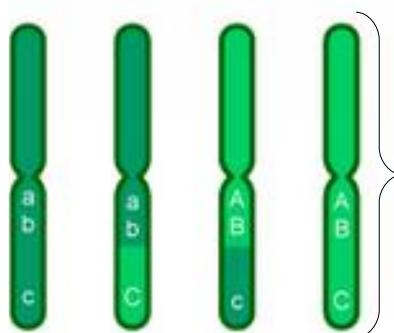




# Linkage

---

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  - independent loci (genes)
  - **non-independent** loci → linkage + crossing over

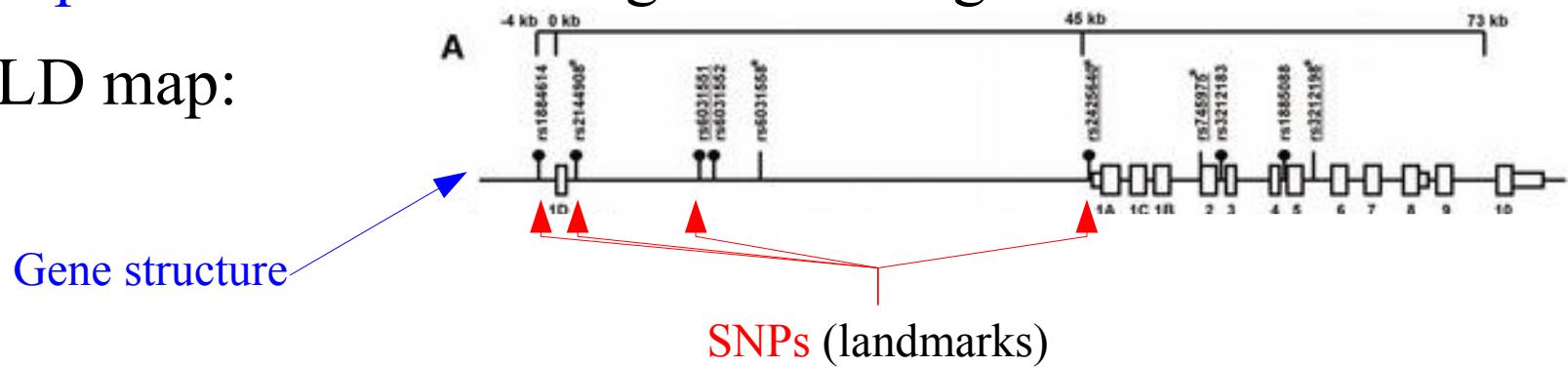


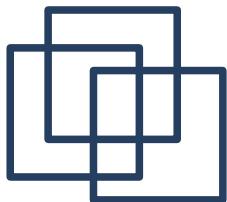
- recombination probability ~ physical distance
- 1 centiMorgan (cM) = 1% recombinants/generation



# Linkage

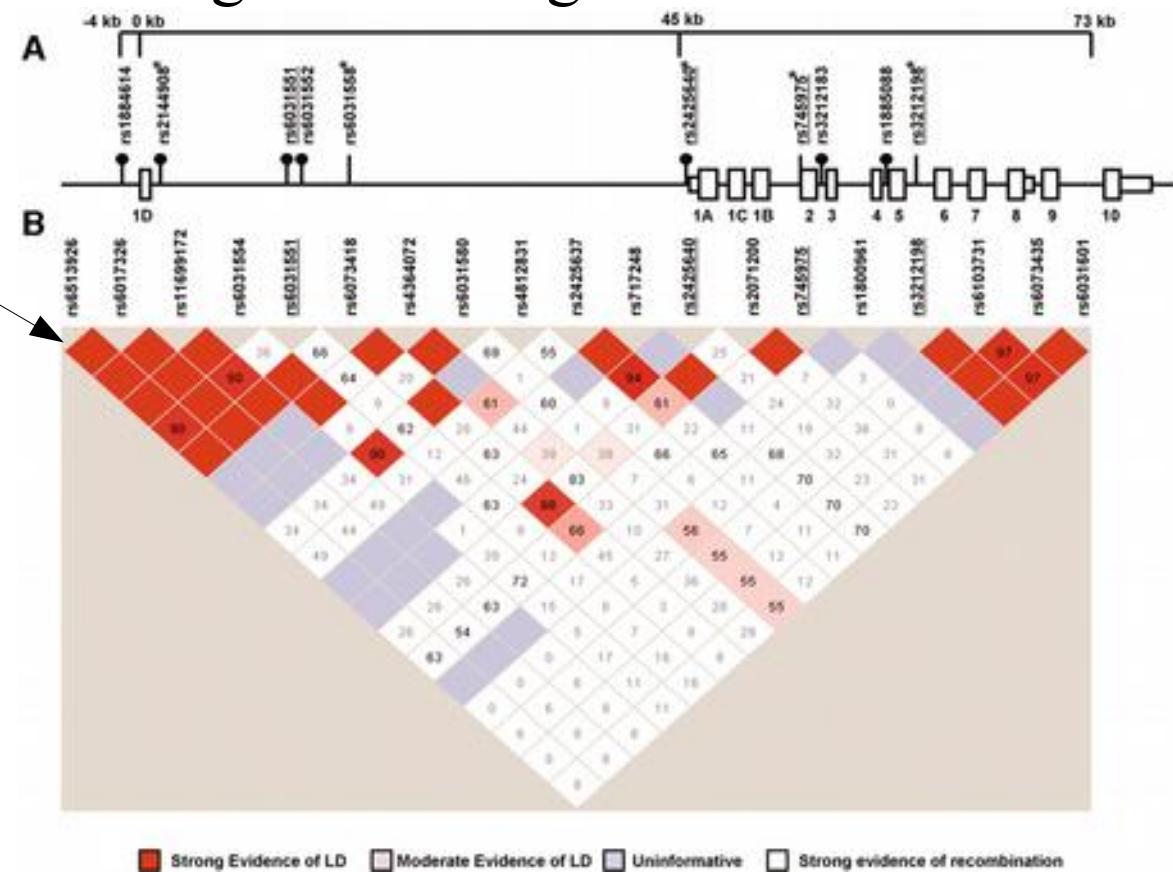
- Genome: discrete linear molecules
  - independent loci (genes)
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    - LD map:

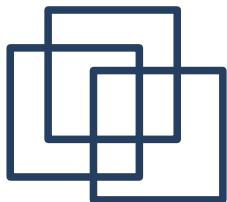




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  - independent loci (genes)
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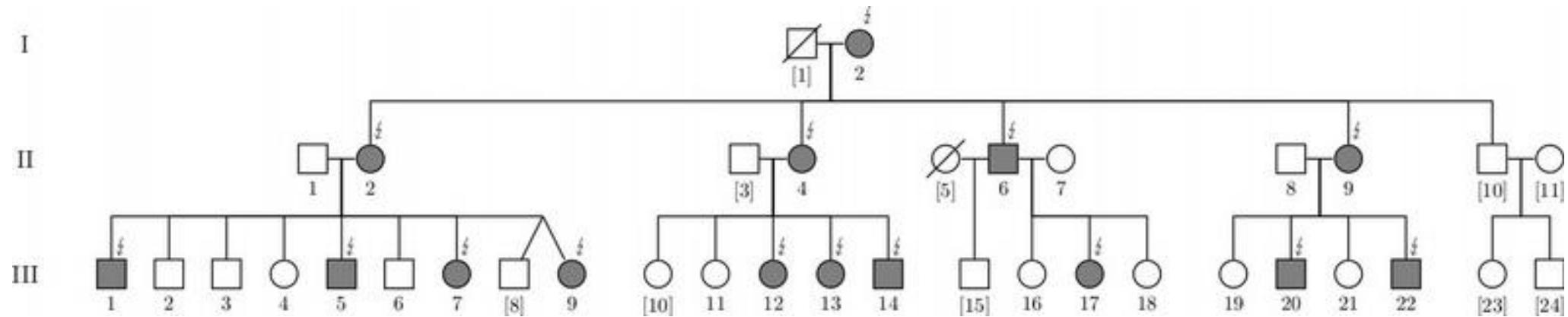


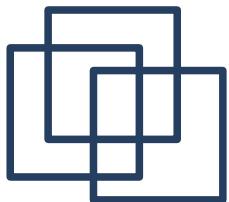


# Linkage

- Large pedigrees segregating the phenotype

The “KE” family



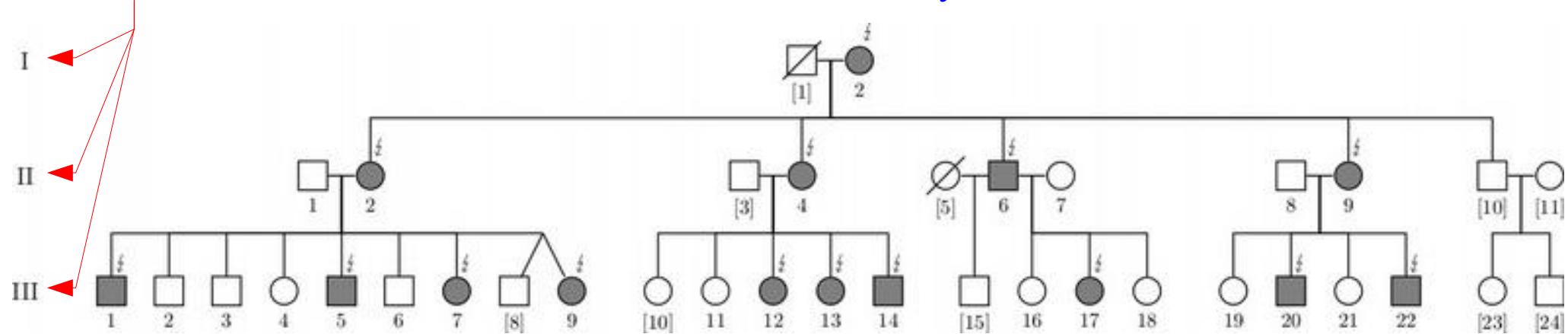


# Linkage

- Large pedigrees segregating the phenotype

generations

The “KE” family

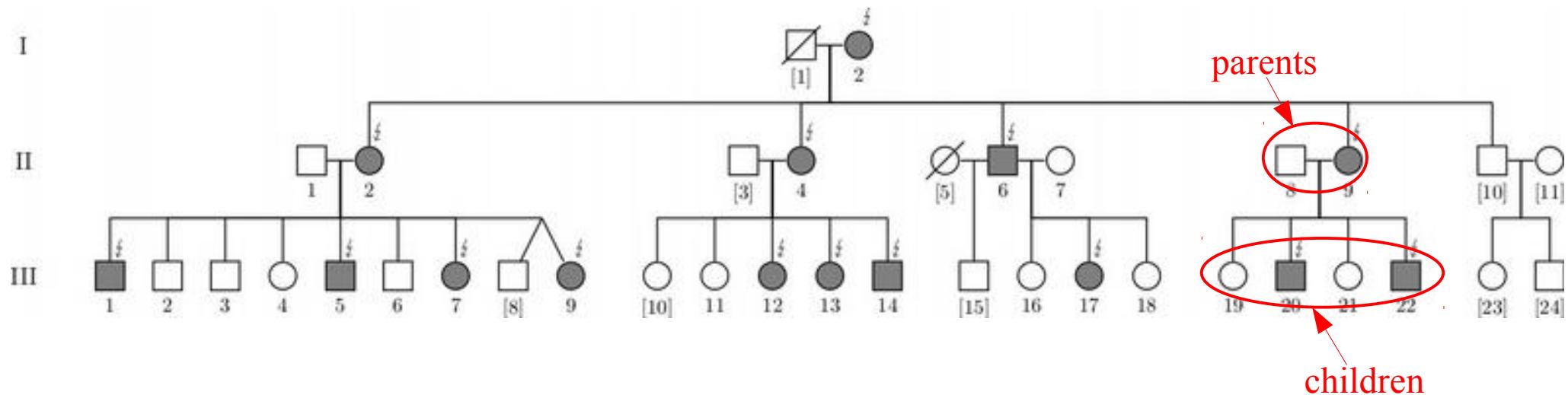




# Linkage

- Large pedigrees segregating the phenotype

The “KE” family

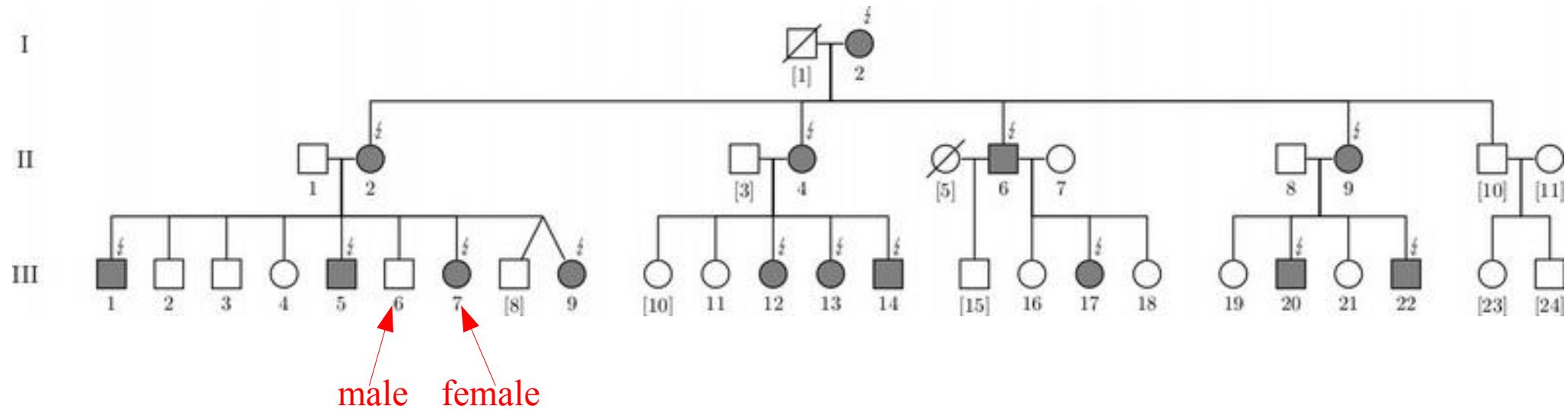


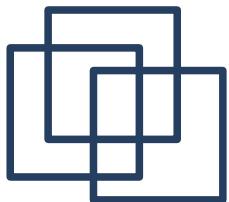


# Linkage

- Large pedigrees segregating the phenotype

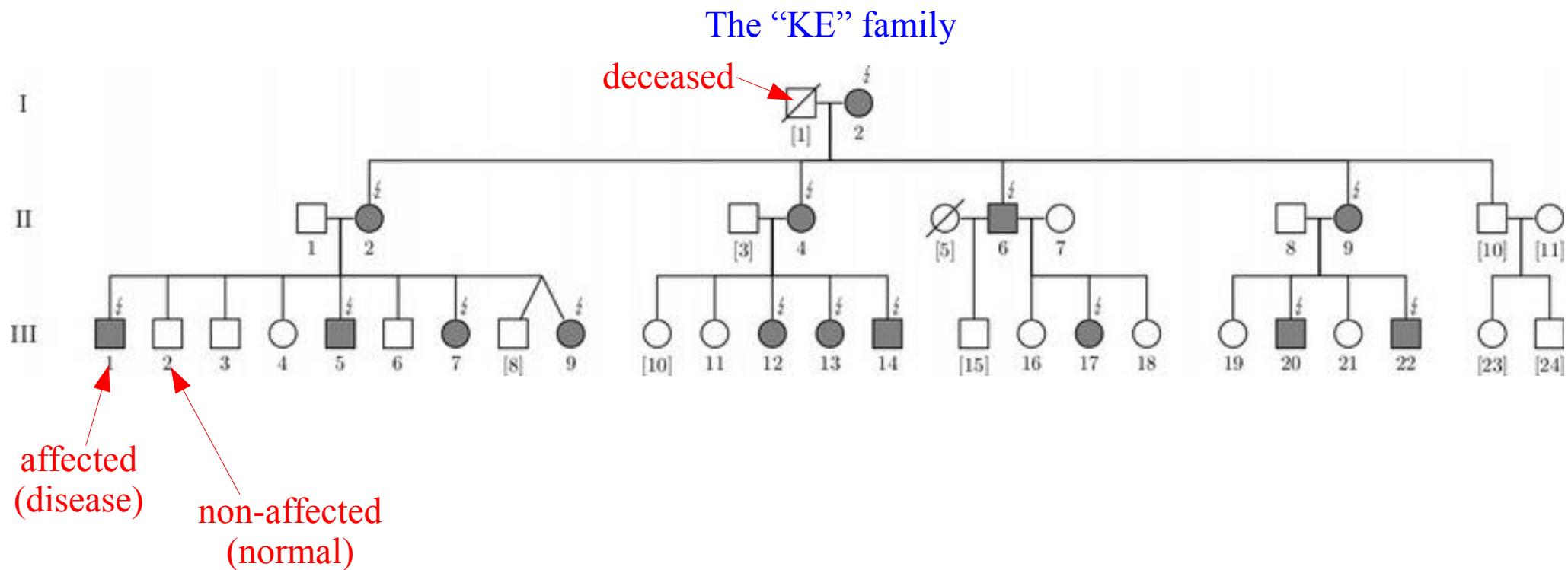
The “KE” family





# Linkage

- Large pedigrees segregating the phenotype

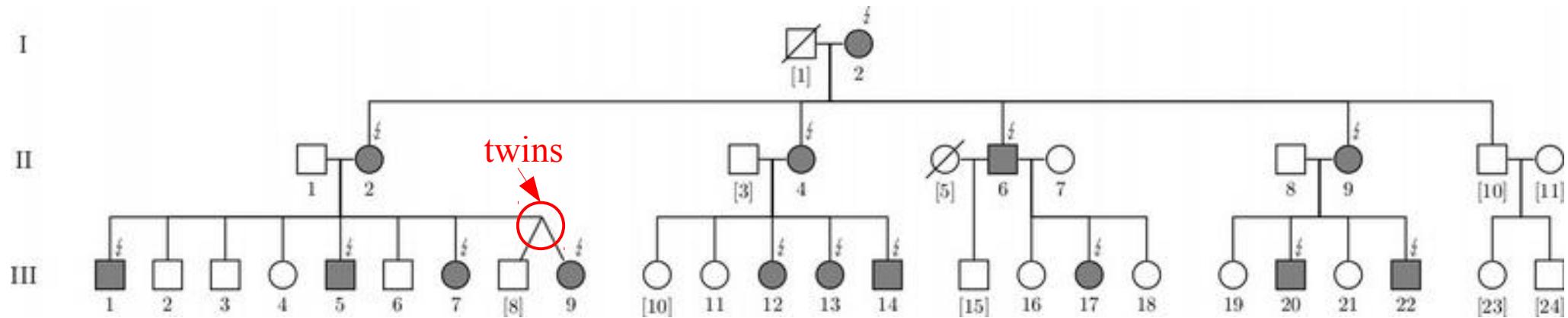




# Linkage

- Large pedigrees segregating the phenotype

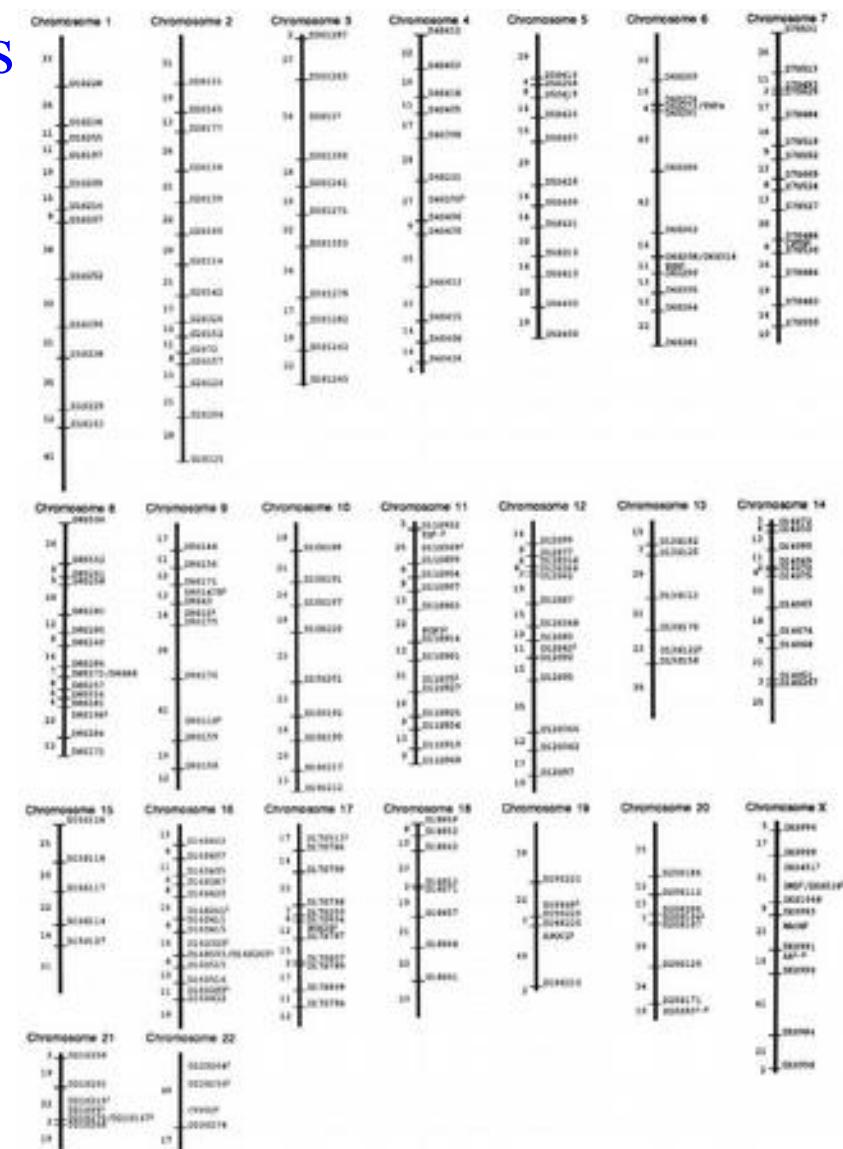
The “KE” family





# Linkage

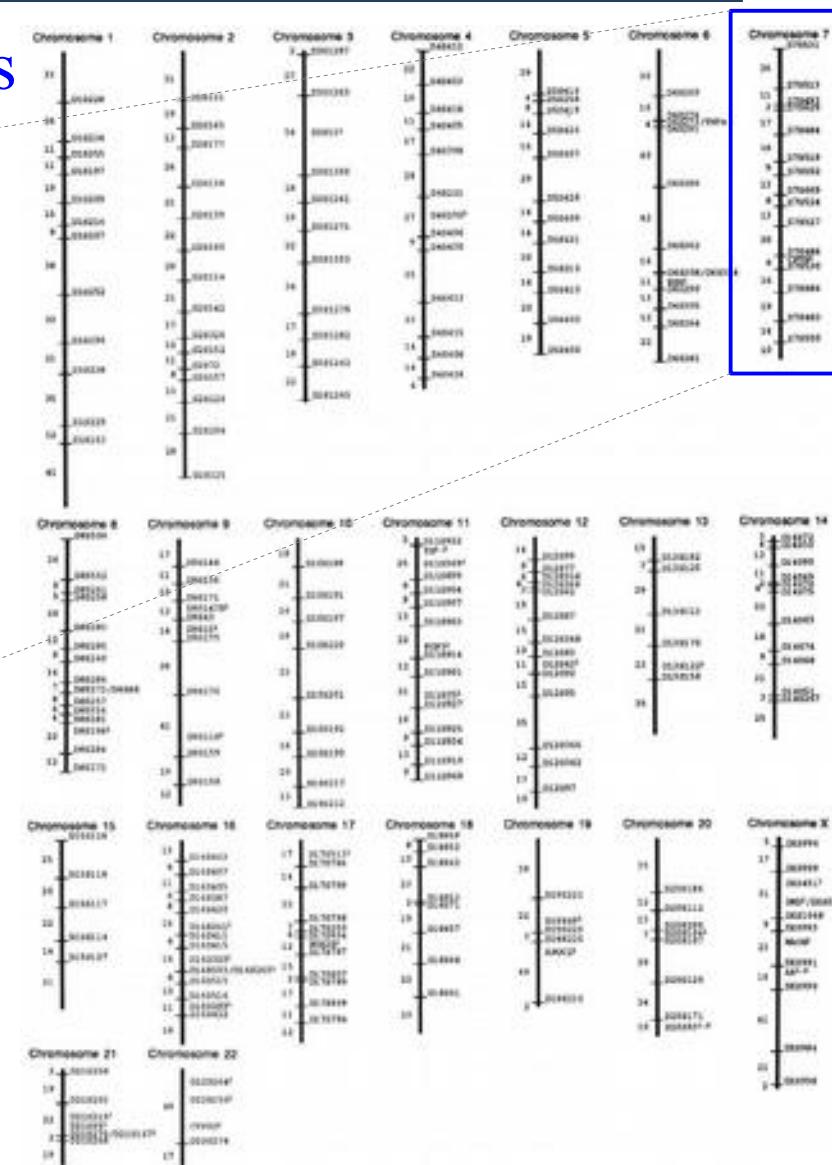
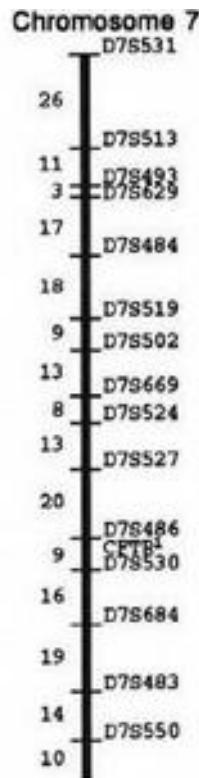
- Large set (genome-wide) of landmarks





# Linkage

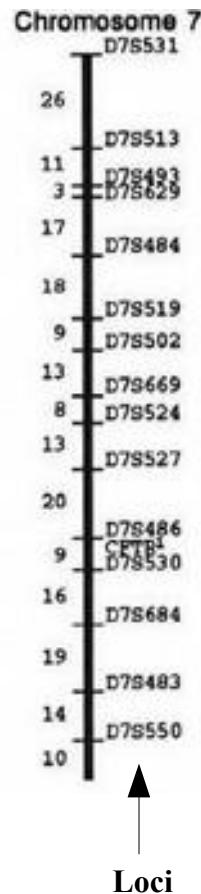
- Large set (genome-wide) of landmarks





# Linkage

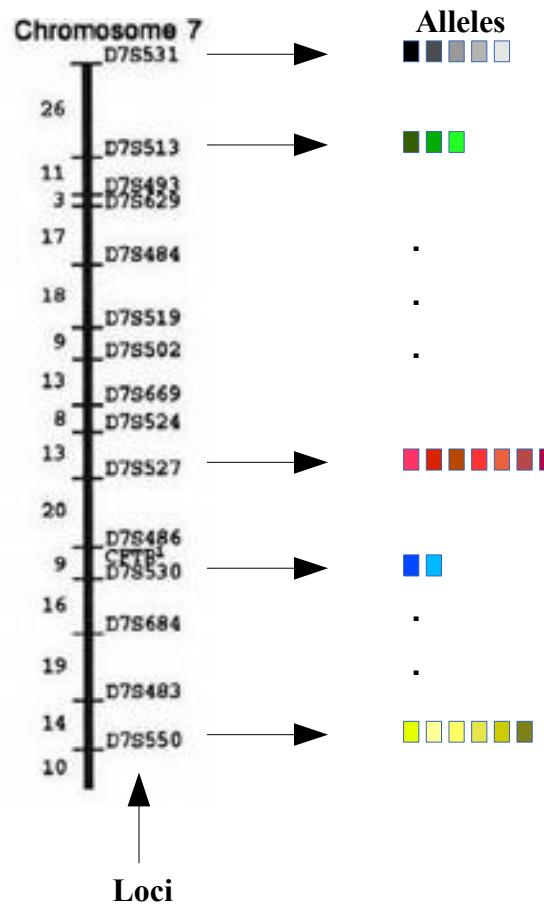
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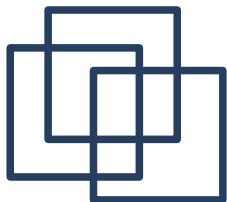




# Linkage

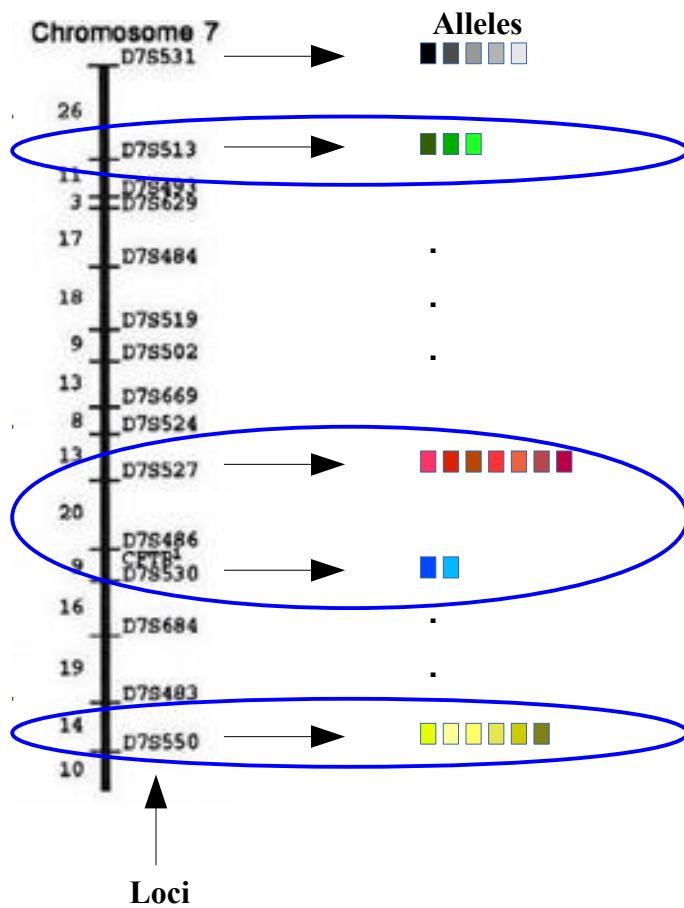
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# Linkage

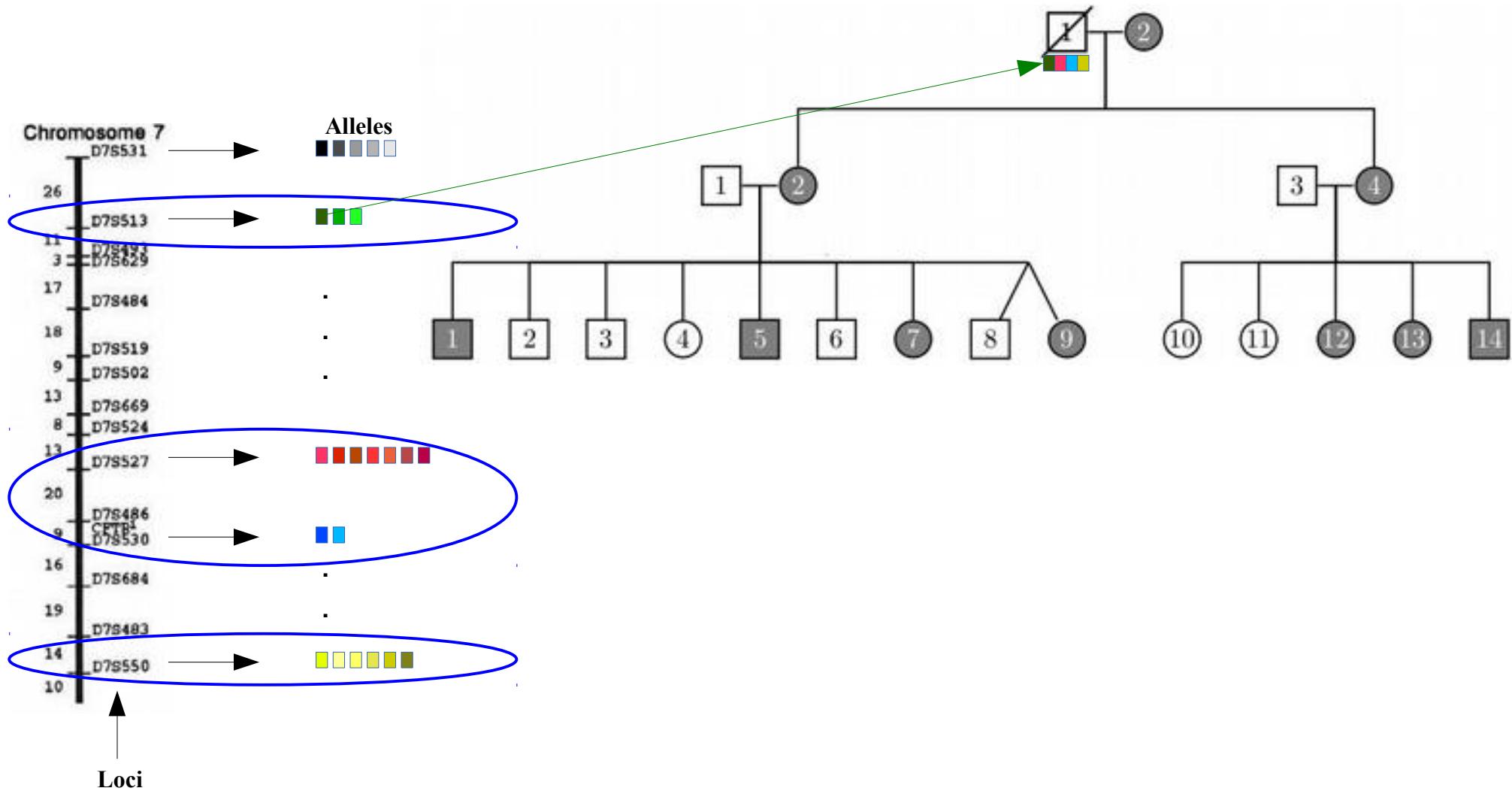
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# Linkage

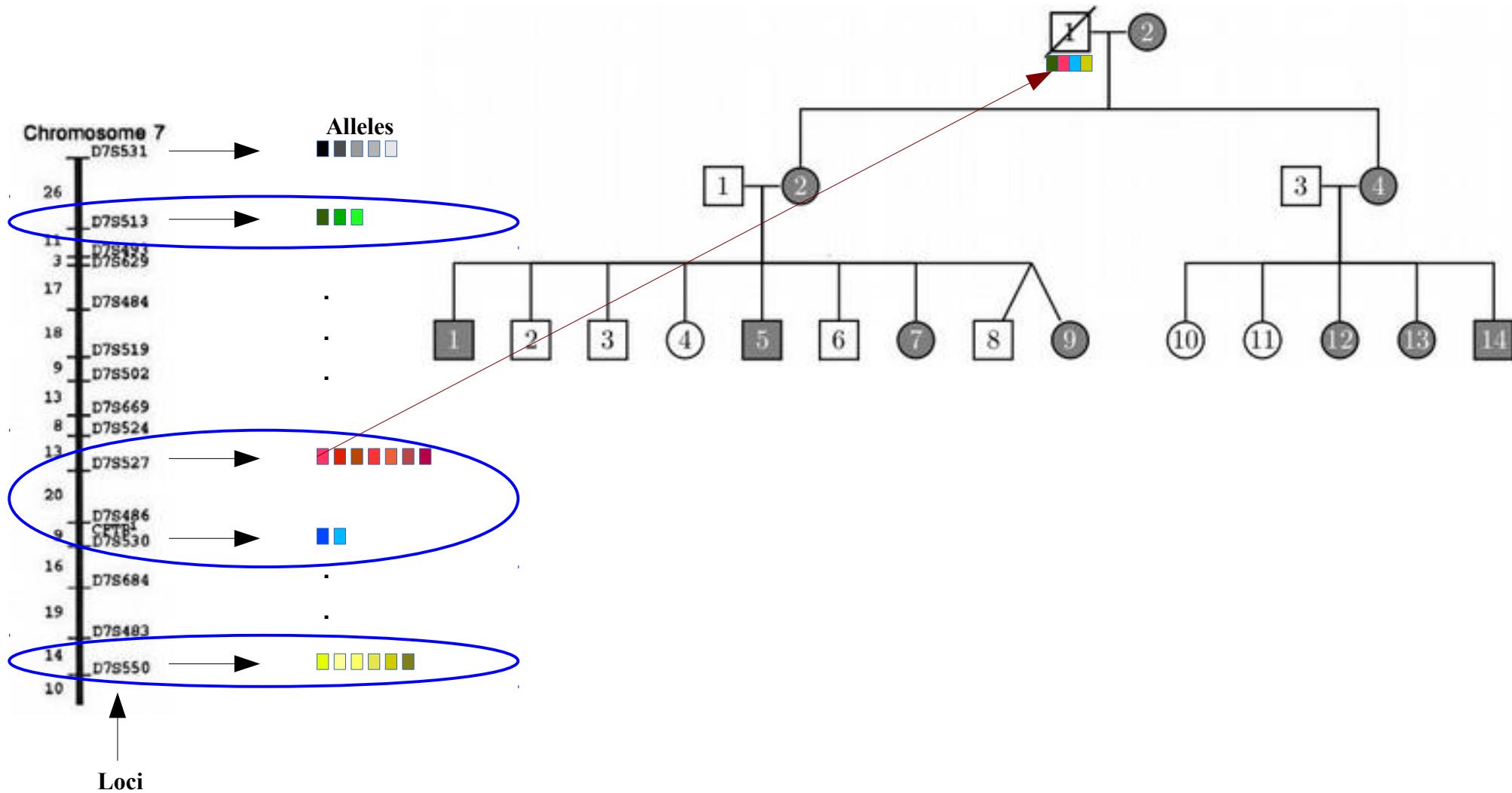
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# Linkage

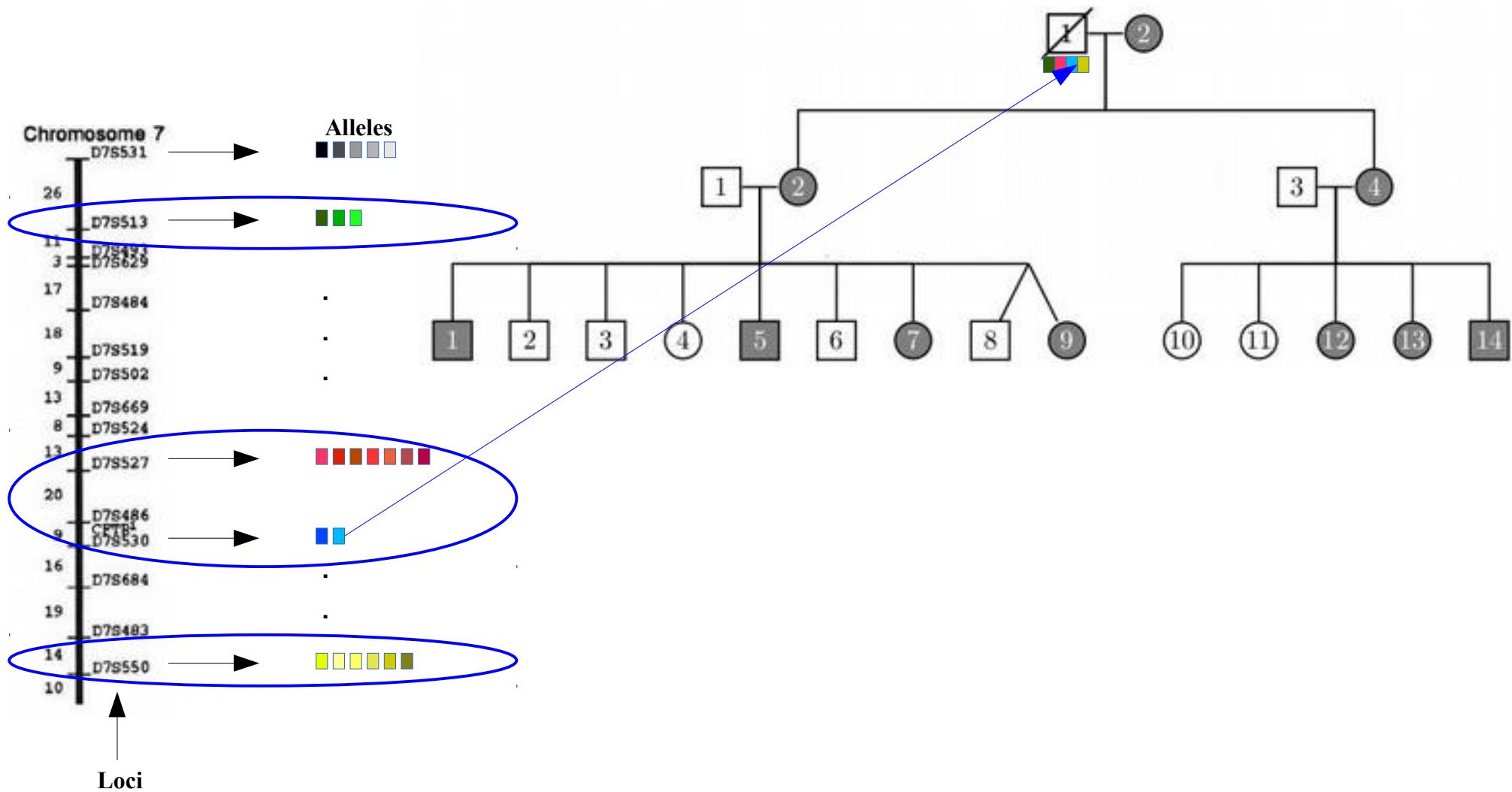
- Large set (genome-wide) of landmarks





# Linkage

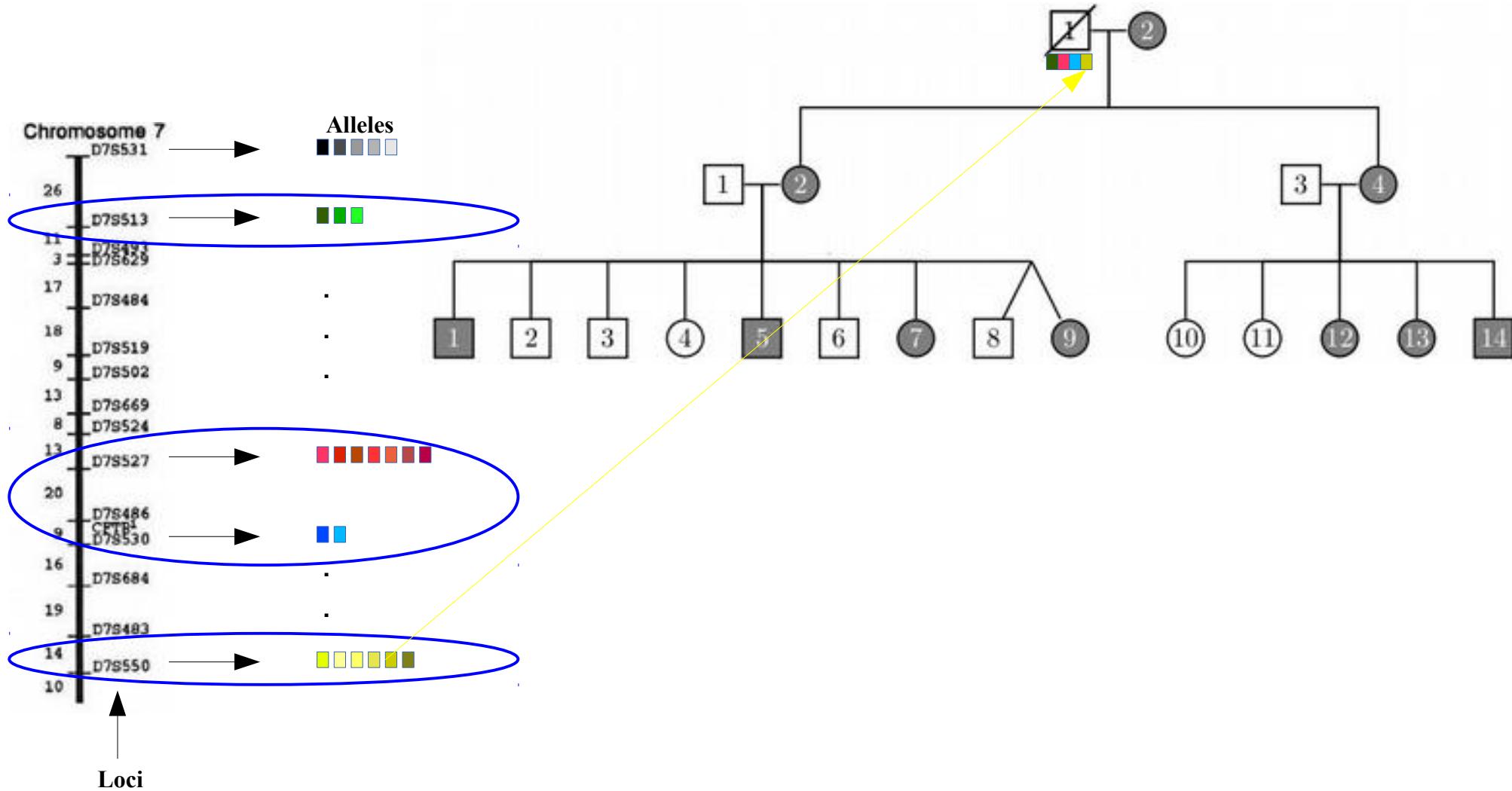
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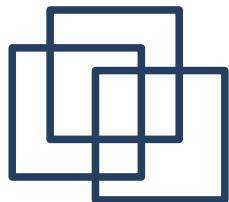




# Linkage

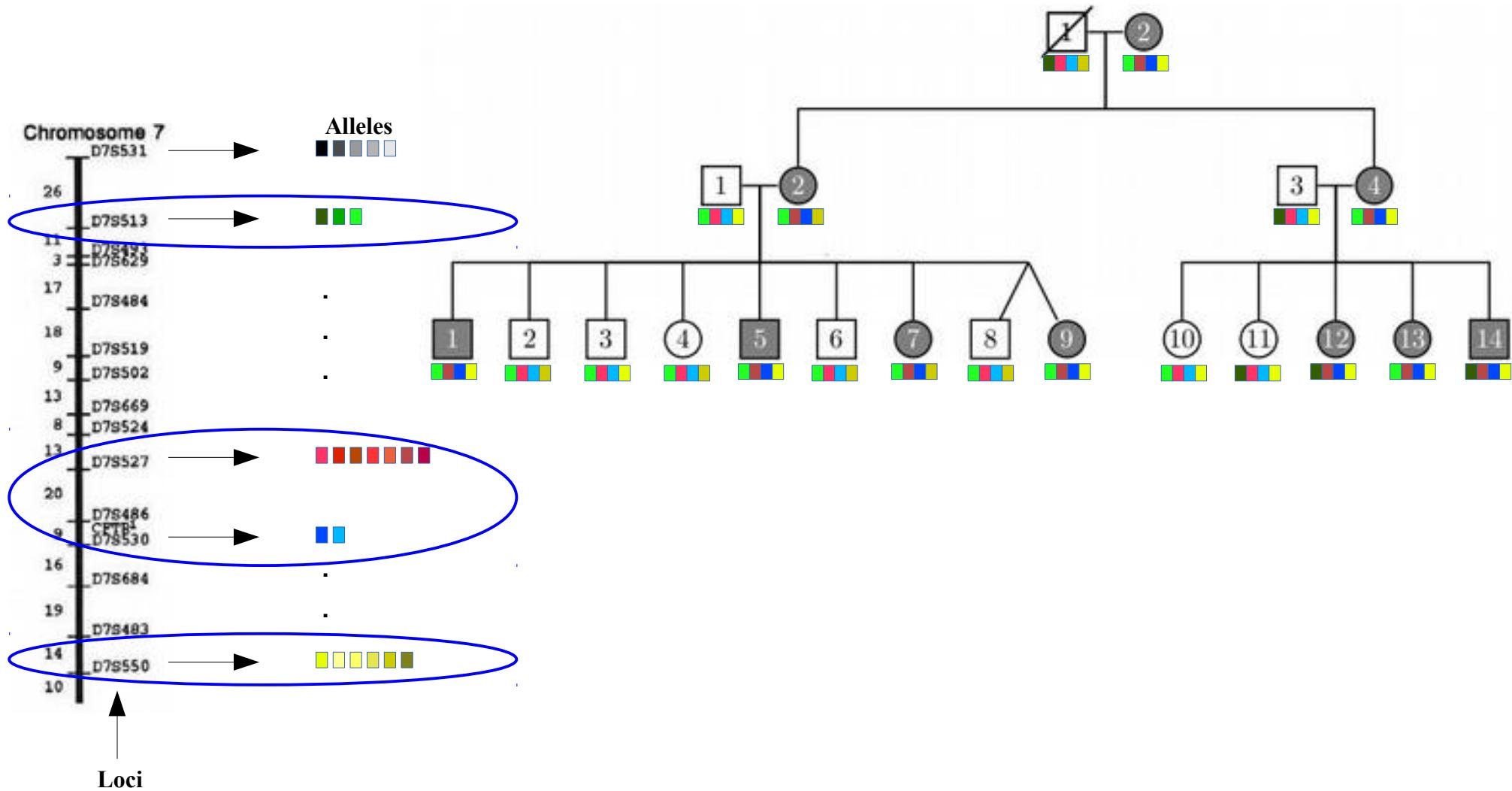
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# Linkage

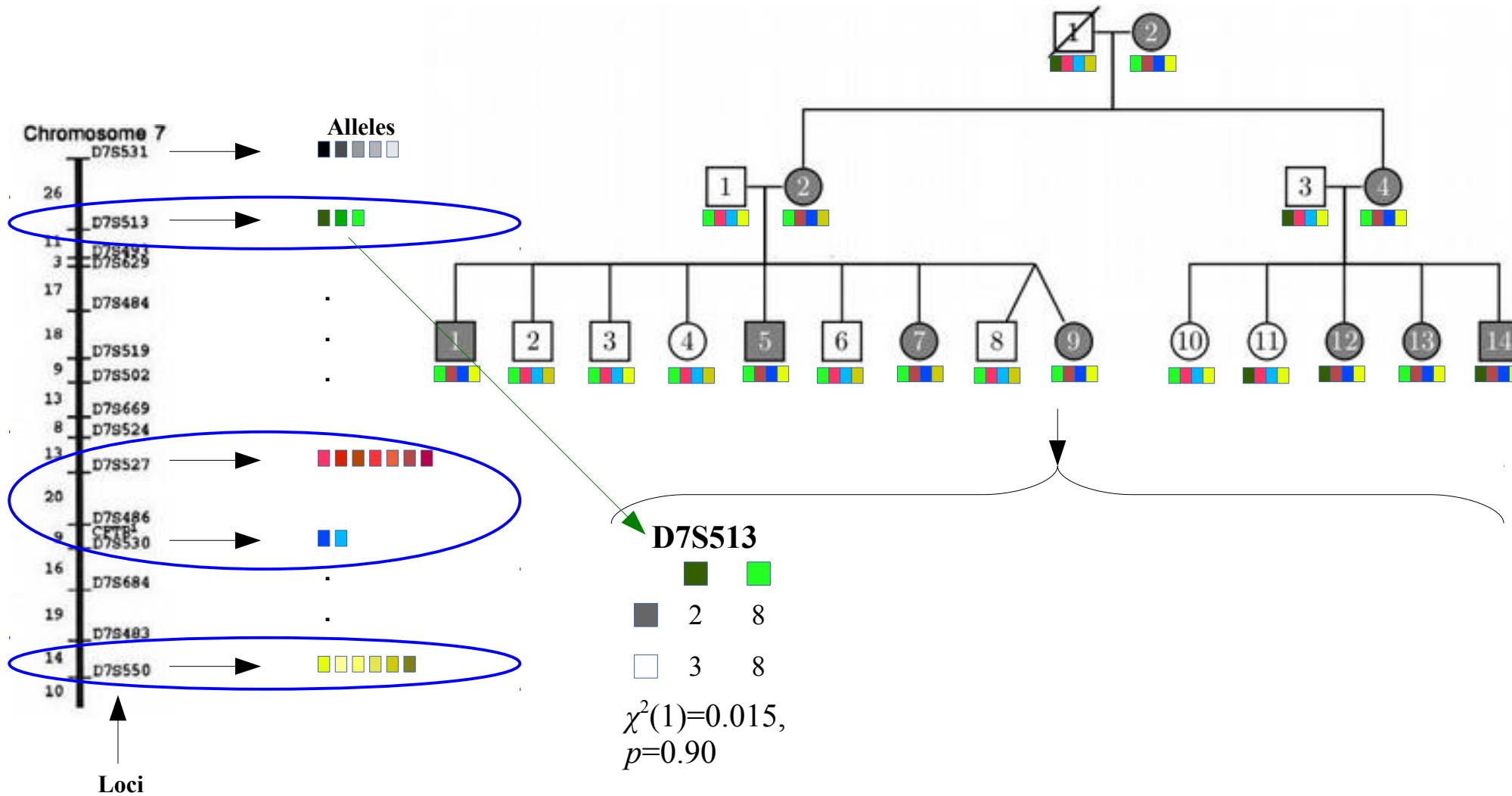
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# Linkage

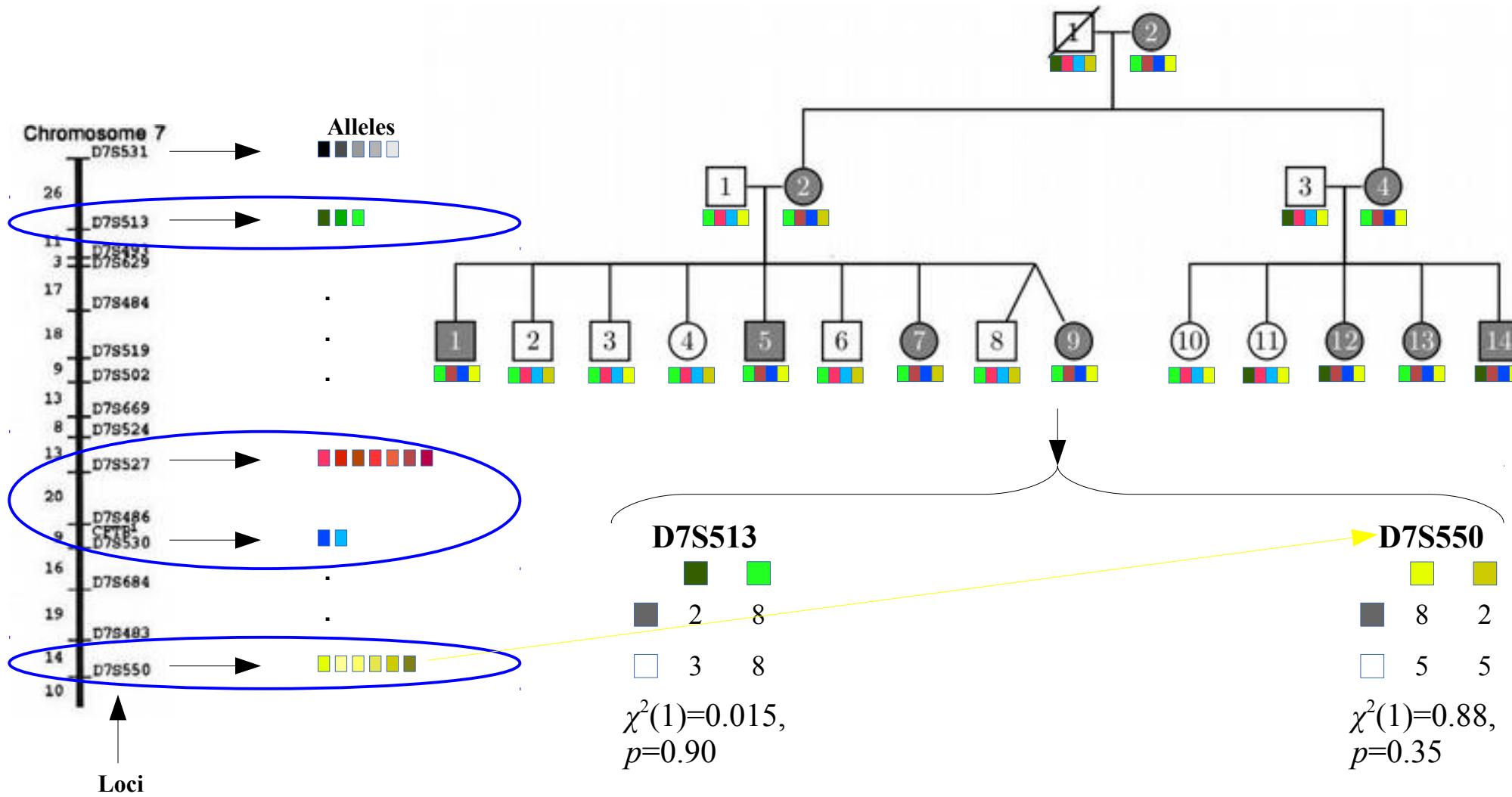
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# Linkage

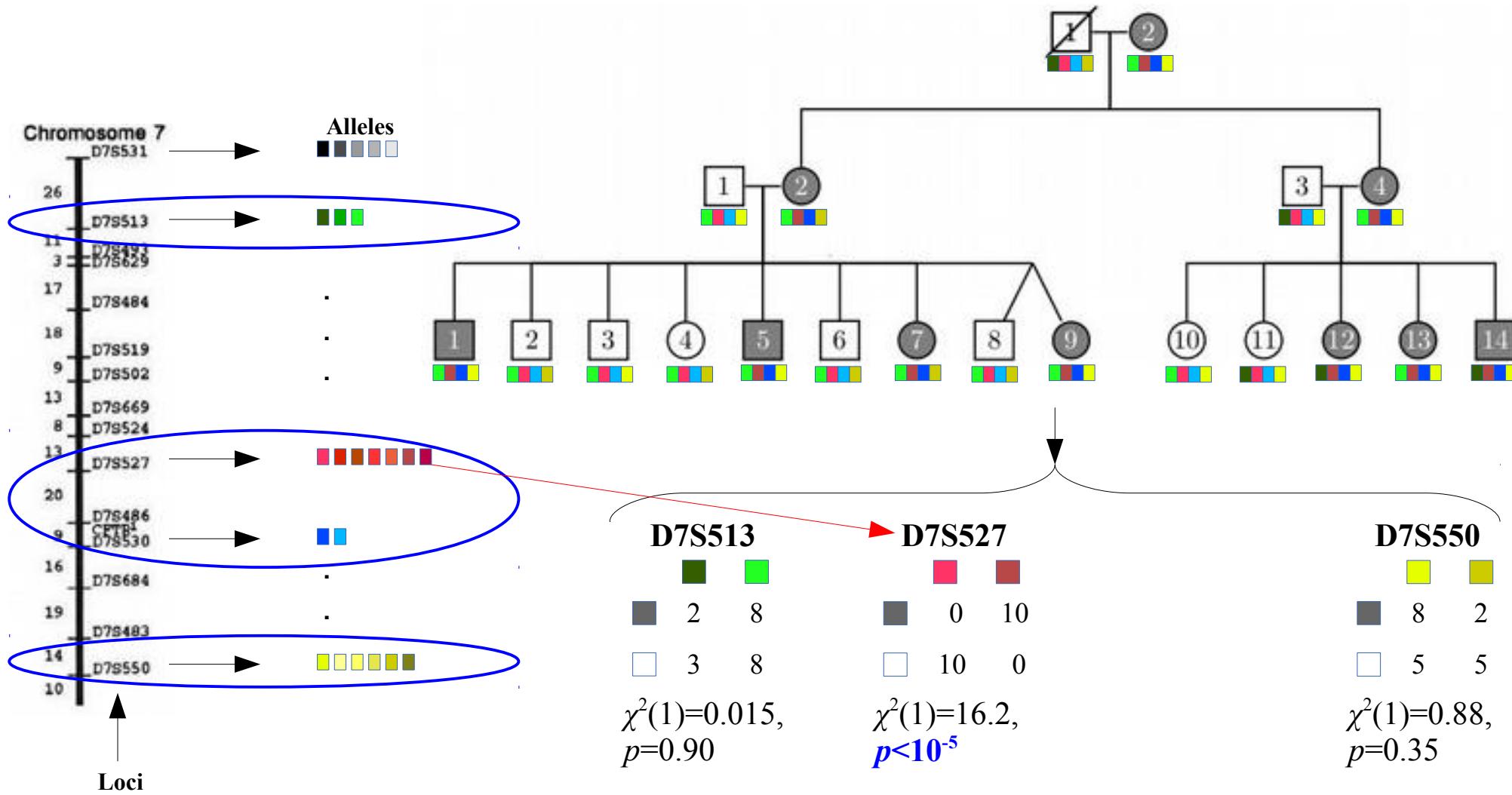
- Large set (genome-wide) of landmarks





# Linkage

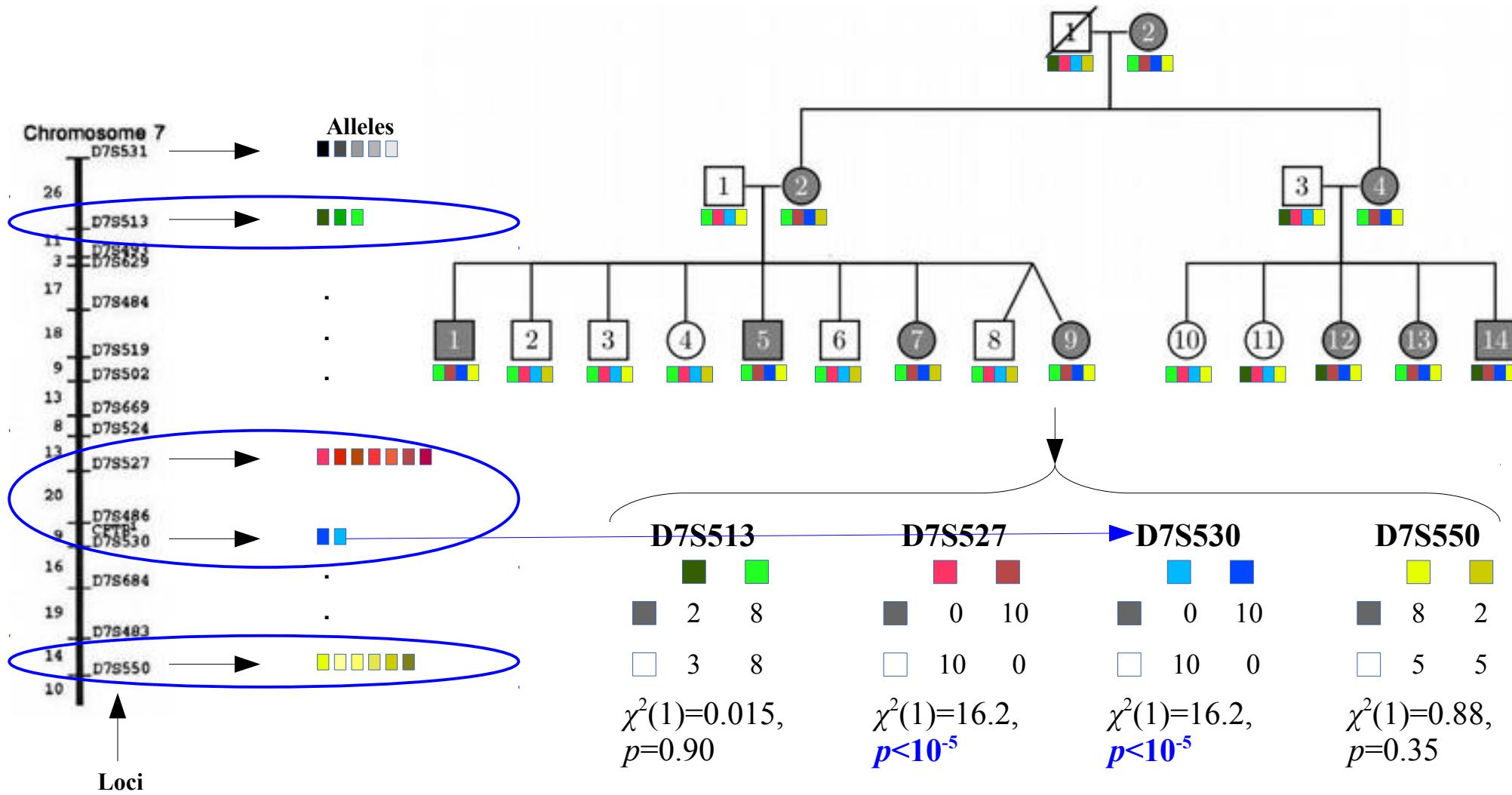
- Large set (genome-wide) of landmarks





# Linkage

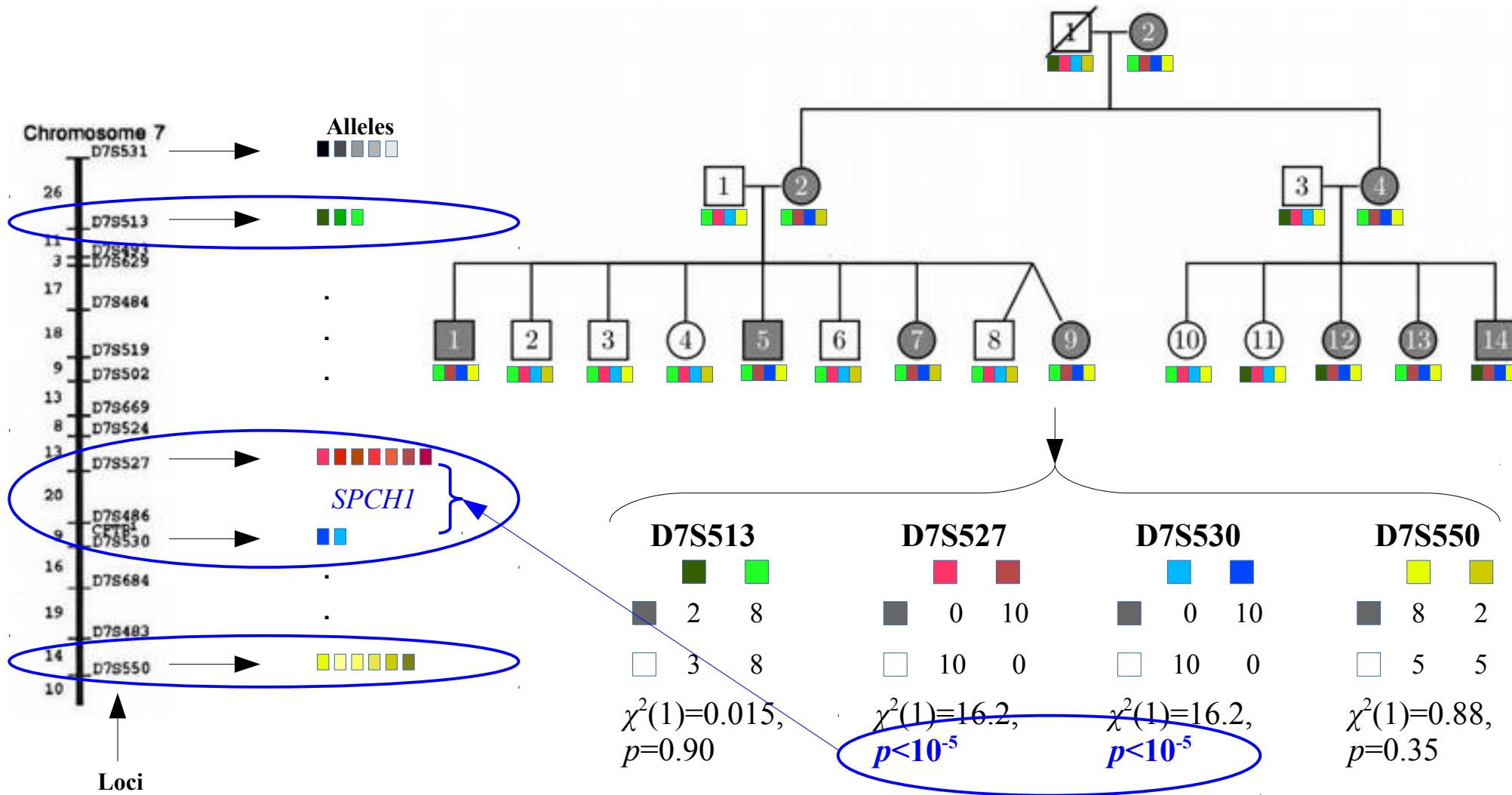
- Large set (genome-wide) of landmarks





# Linkage

- Large set (genome-wide) of landmarks





## Linkage

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- Large set (genome-wide) of landmarks
- In practice:
  - LOD score (Logarithm of Odds)  $> 3$



## Linkage

---

- Large set (genome-wide) of landmarks
- In practice:
  - LOD score (Logarithm of Odds)  $> 3$
  - Specialized **software** (MERLIN, GENEHUNTER)



## Linkage

---

- Large set (genome-wide) of landmarks
- In practice:
  - LOD score (Logarithm of Odds)  $> 3$
  - Specialized software (MERLIN, GENEHUNTER)
  - Relatively **low resolution**  
→ complementary techniques



## Linkage

---

- Large set (genome-wide) of landmarks
  - In practice:
    - LOD score (Logarithm of Odds)  $> 3$
    - Specialized software (MERLIN, GENEHUNTER)
    - Relatively low resolution
- complementary techniques



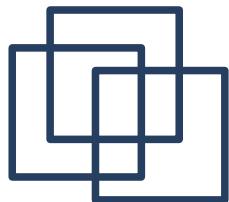
# Linkage

---

- Large set (genome-wide) of landmarks
- In practice:
  - LOD score (Logarithm of Odds)  $> 3$
  - Specialized software (MERLIN, GENEHUNTER)
  - Relatively low resolution  
→ complementary techniques

here, a case (CS) unrelated to KE

- with same phenotype
- chromosomal abnormality affecting the *SPCH1* interval on chromosome 7 → more precisely *FOXP2*

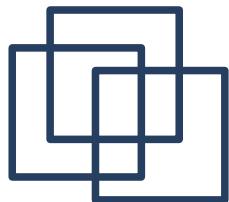


## Association studies

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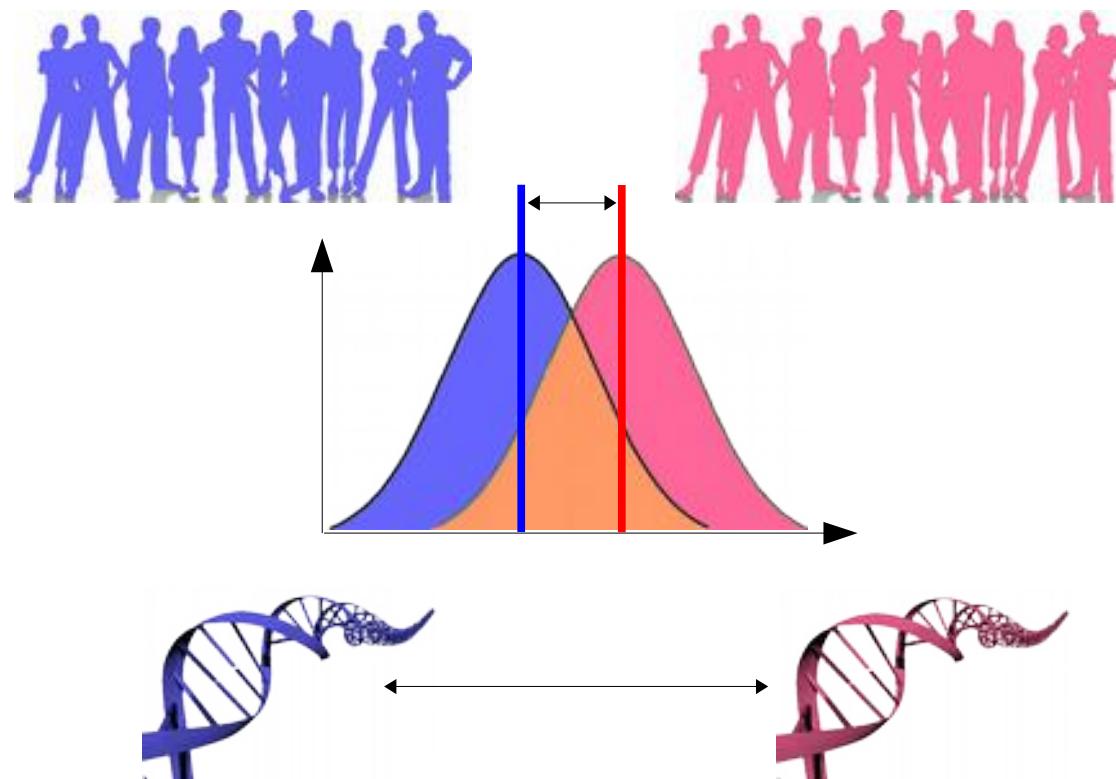
- Large **unrelated** samples → variation in the phenotype of interest

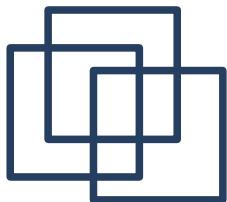




# Association studies

- Large **unrelated** samples → variation in the phenotype of interest
- **Correlation** between each marker and differences in phenotype

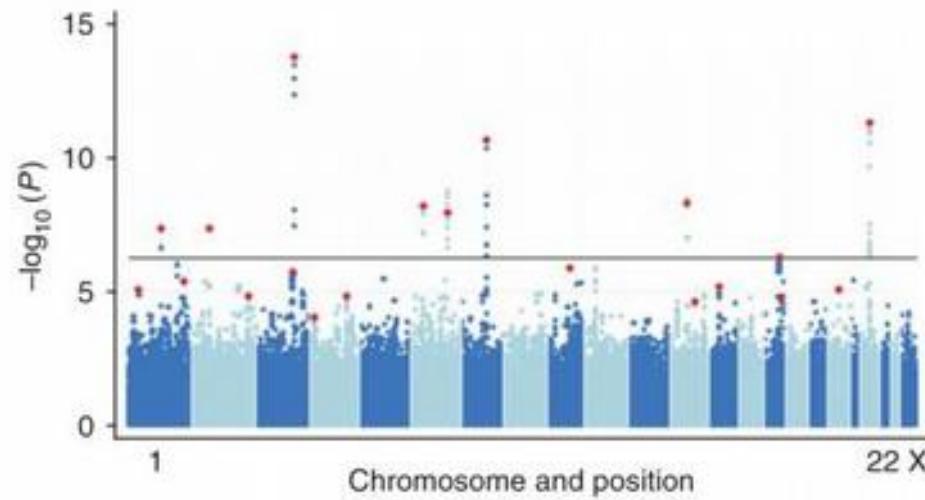


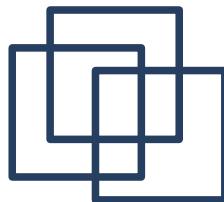


## Association studies

- Large **unrelated** samples → variation in the phenotype of interest
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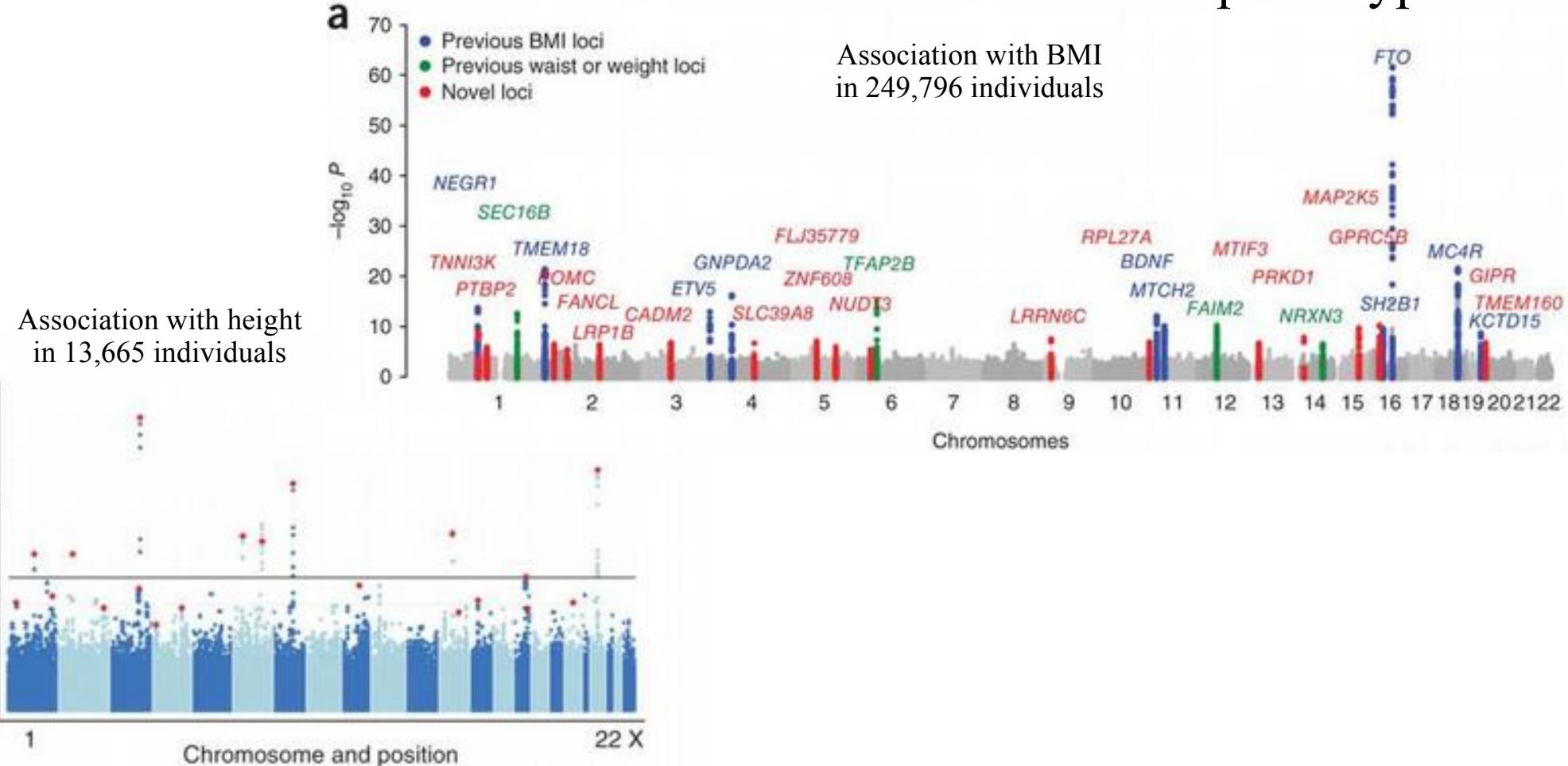
Association with height  
in 13,665 individuals





# Association studies

- Large **unrelated** samples → variation in the phenotype of interest
- **Correlation** between each marker and differences in phenotype





# Association studies

---

- Large **unrelated** samples → variation in the phenotype of interest
- **Correlation** between each marker and differences in phenotype
- Issues:
  - multiple testing correction ( $p < 5 \cdot 10^{-8}$ )



## Association studies

---

- Large **unrelated** samples → variation in the phenotype of interest
- **Correlation** between each marker and differences in phenotype
- Issues:
  - multiple testing correction ( $p < 5 \cdot 10^{-8}$ )
  - **replication**



## Association studies

---

- Large **unrelated** samples → variation in the phenotype of interest
- **Correlation** between each marker and differences in phenotype
- Issues:
  - multiple testing correction ( $p < 5 \cdot 10^{-8}$ )
  - replication
  - **huge sample sizes** (1,000+ → 100,000+) → **tiny effect sizes**

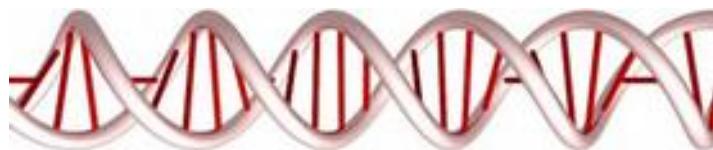




## Exome & genome sequencing

---

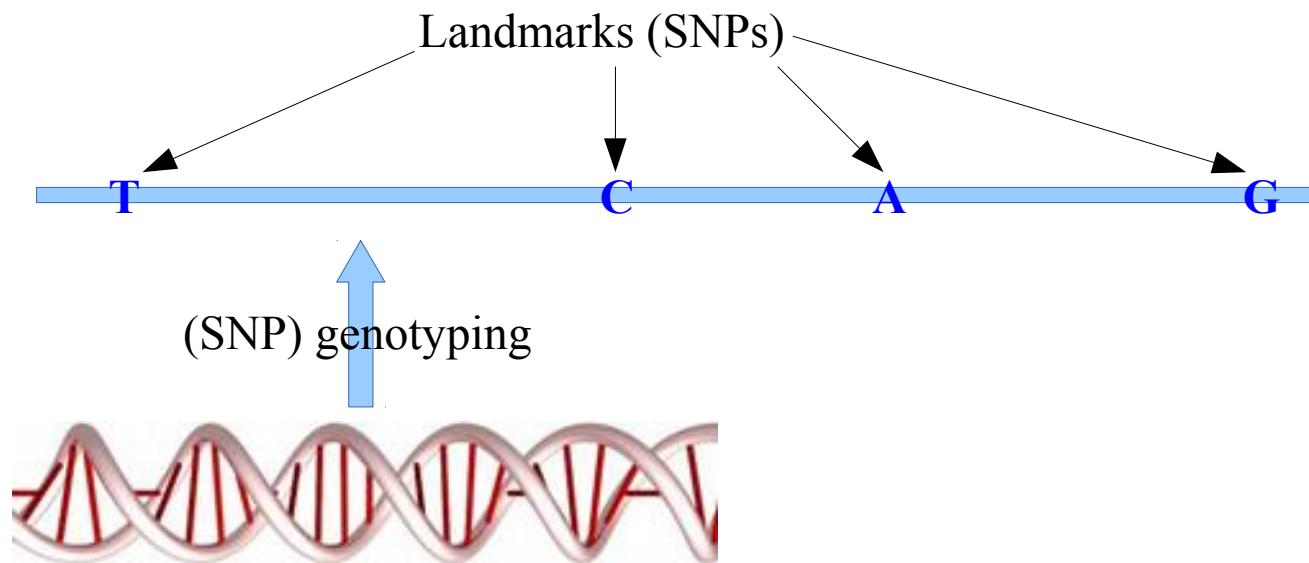
- Sequencing → full message instead of (dense) landmarks

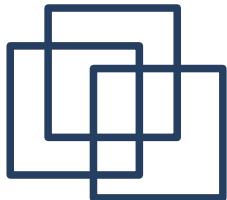




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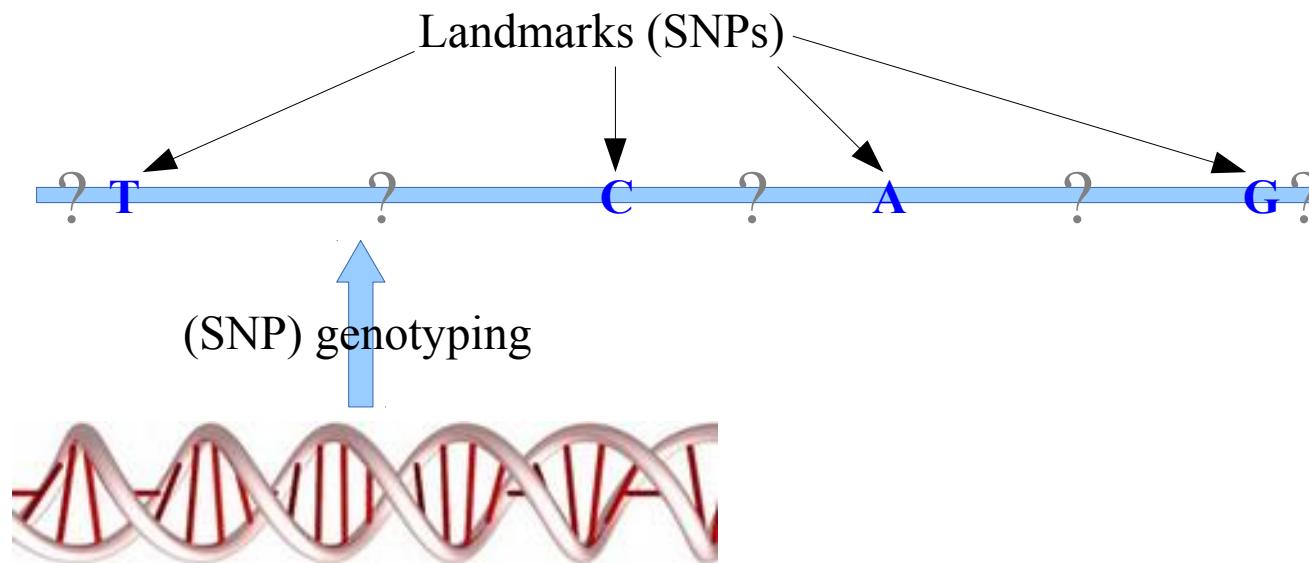
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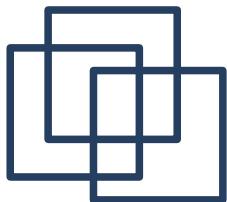




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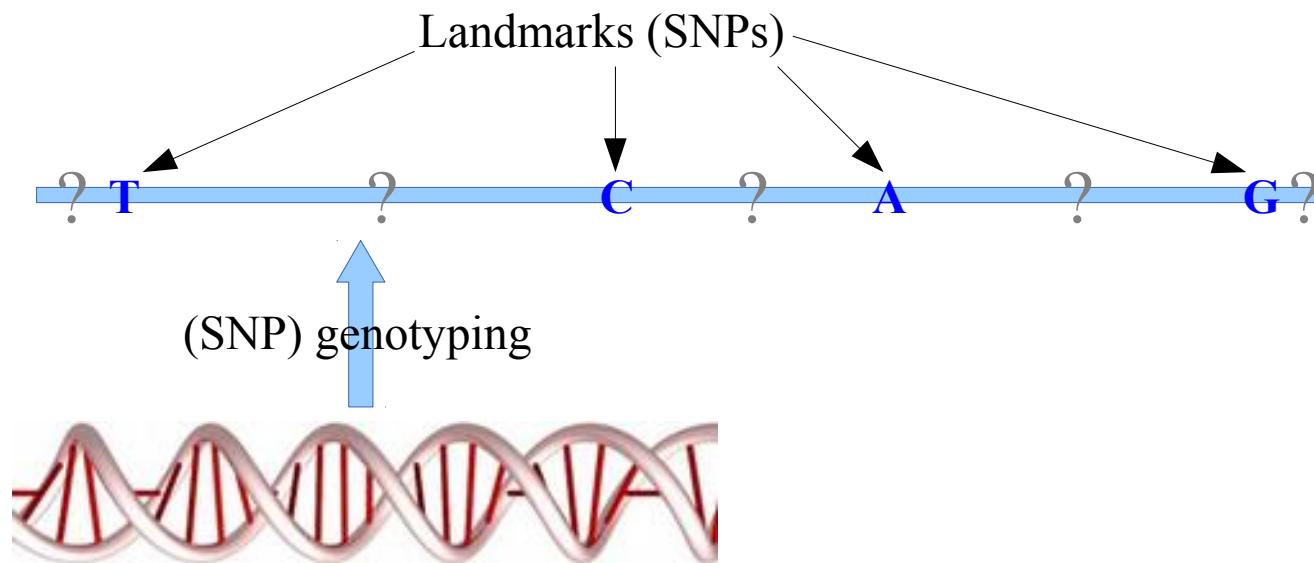
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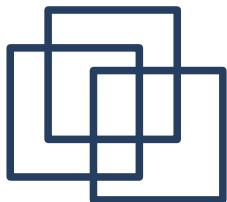




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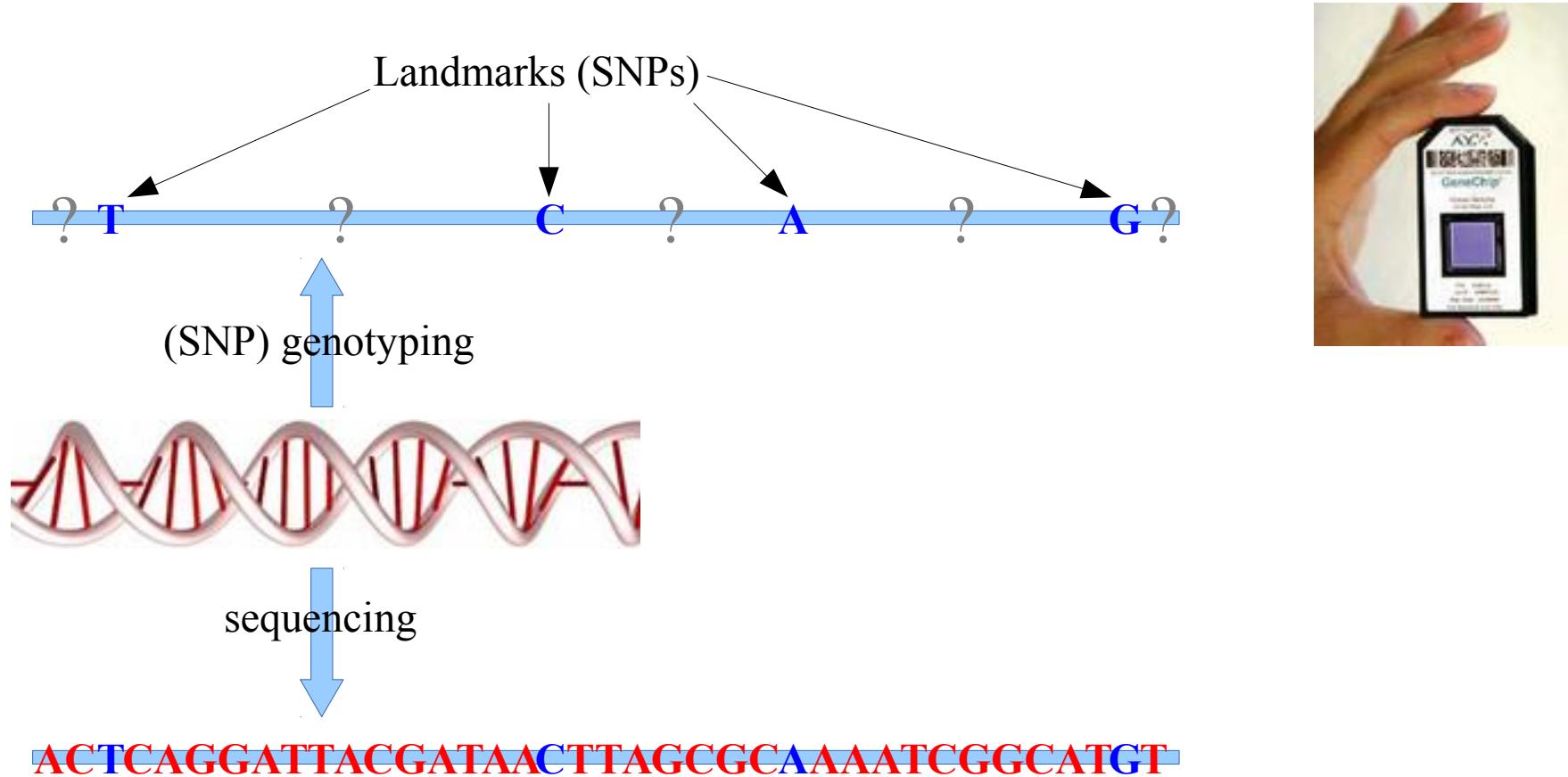
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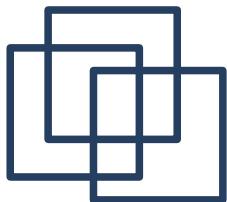




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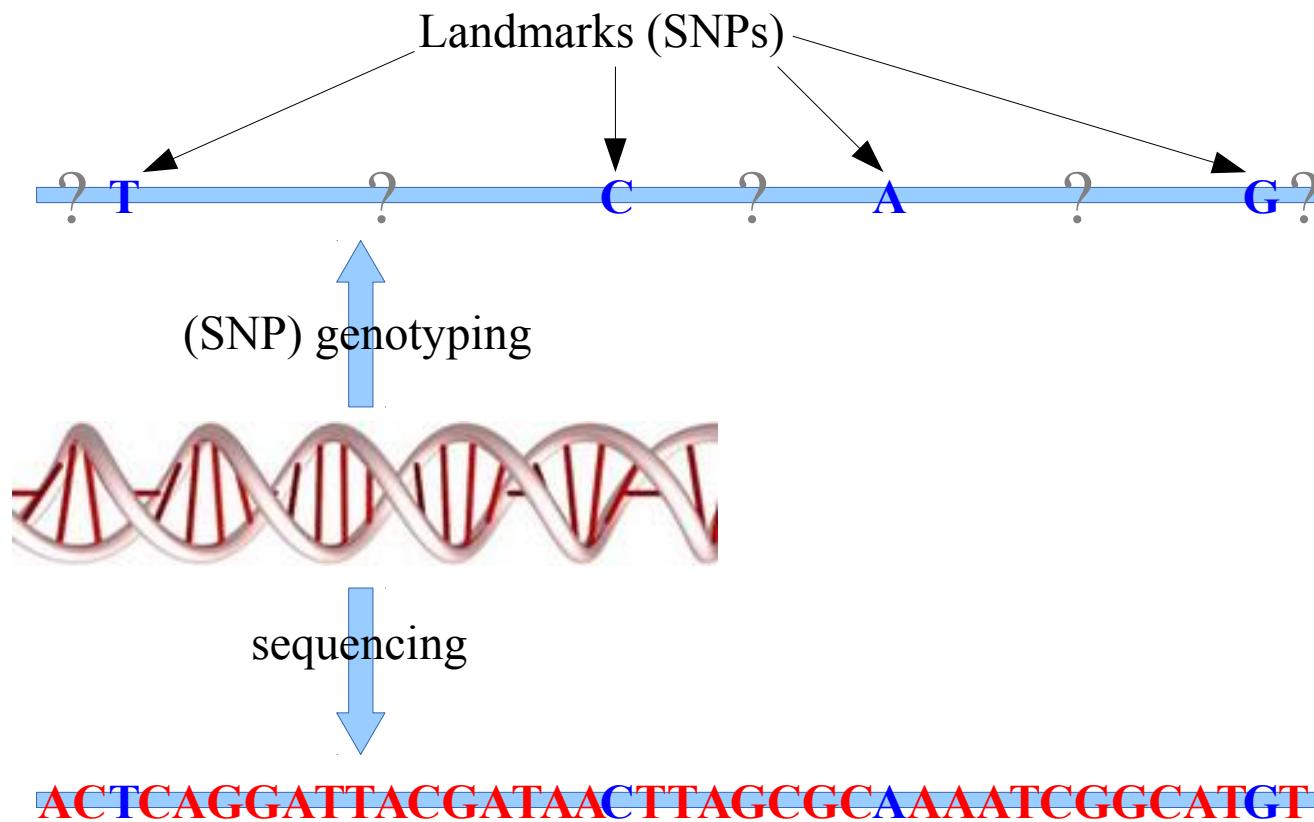
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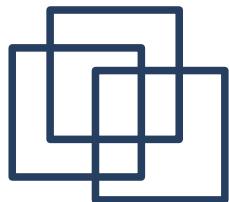




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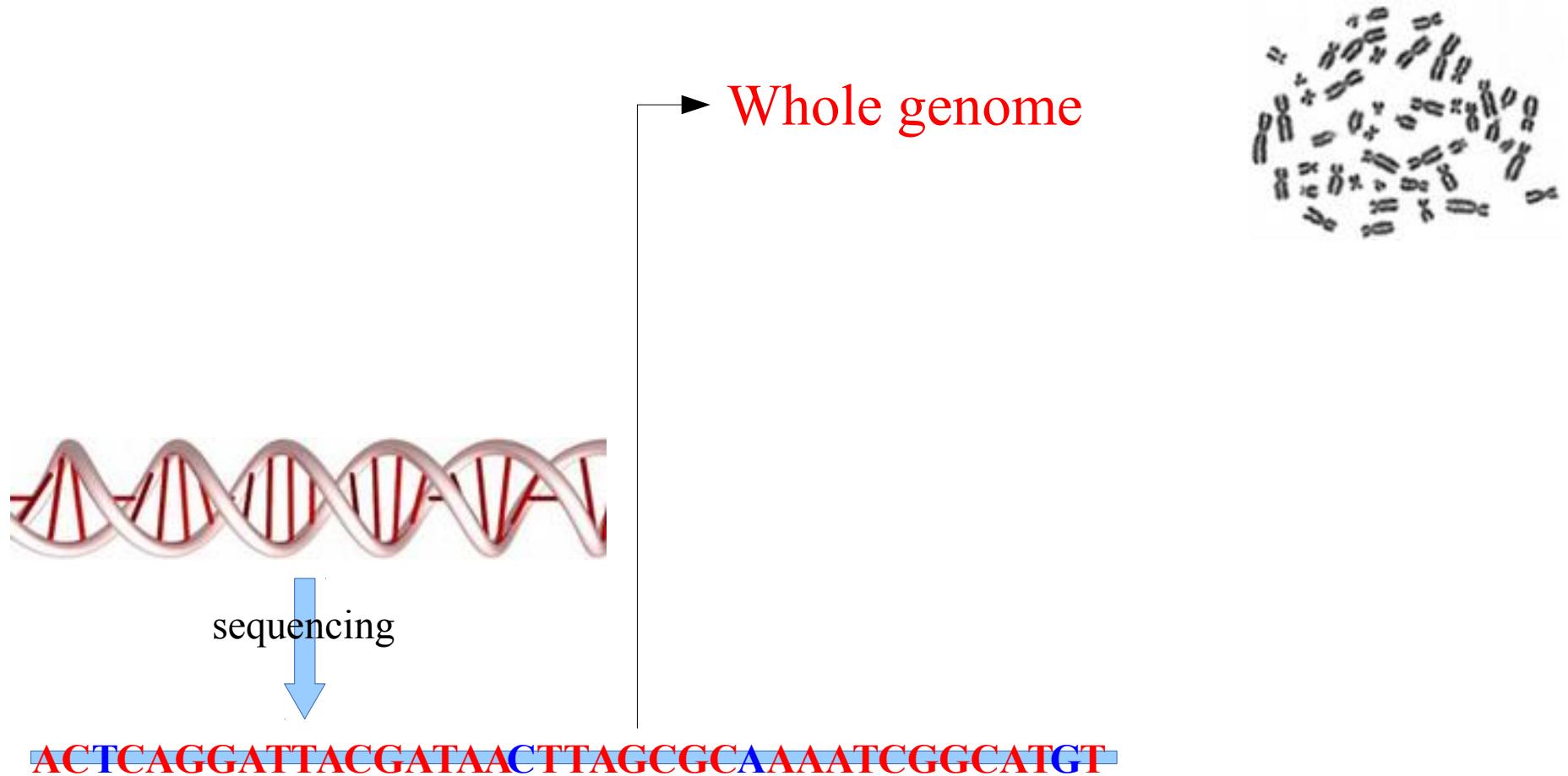
- Sequencing → full message instead of (dense) landmarks





## Exome & genome sequencing

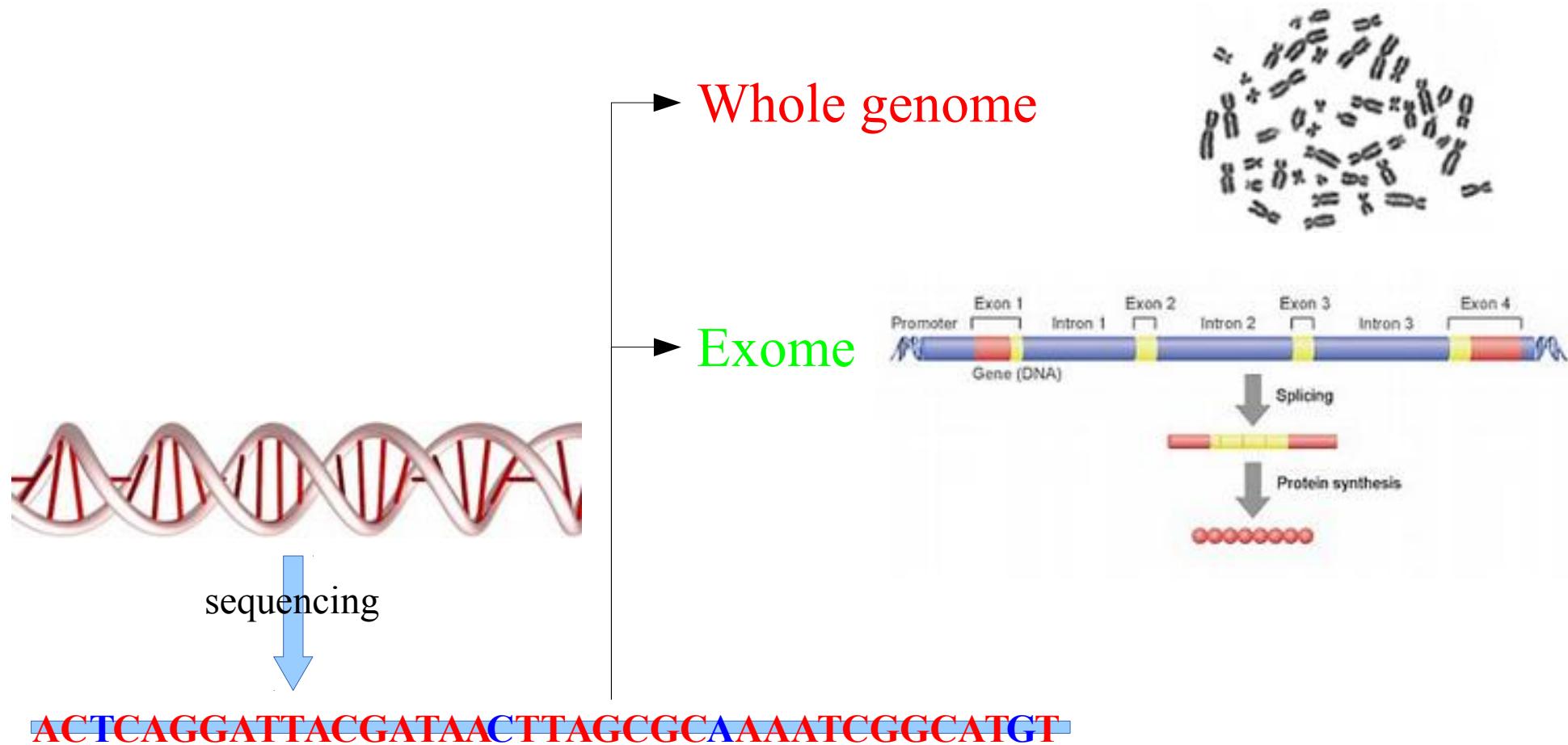
- Sequencing → full message instead of (dense) landmarks





# Exome & genome sequencing

- Sequencing → full message instead of (dense) landmarks





# Exome & genome sequencing

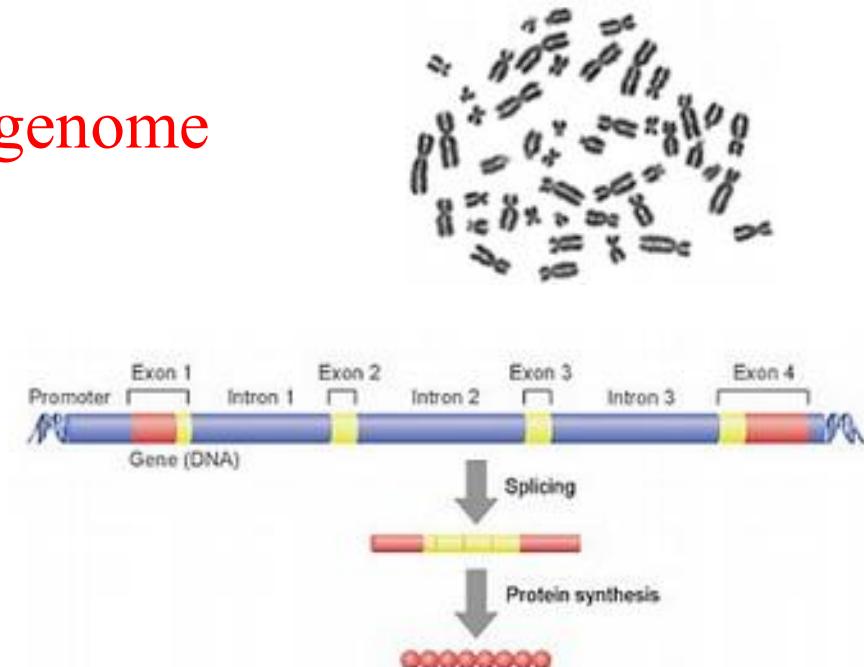
- Sequencing → full message instead of (dense) landmarks

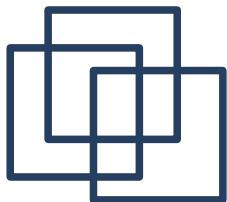


lots of data

Whole genome

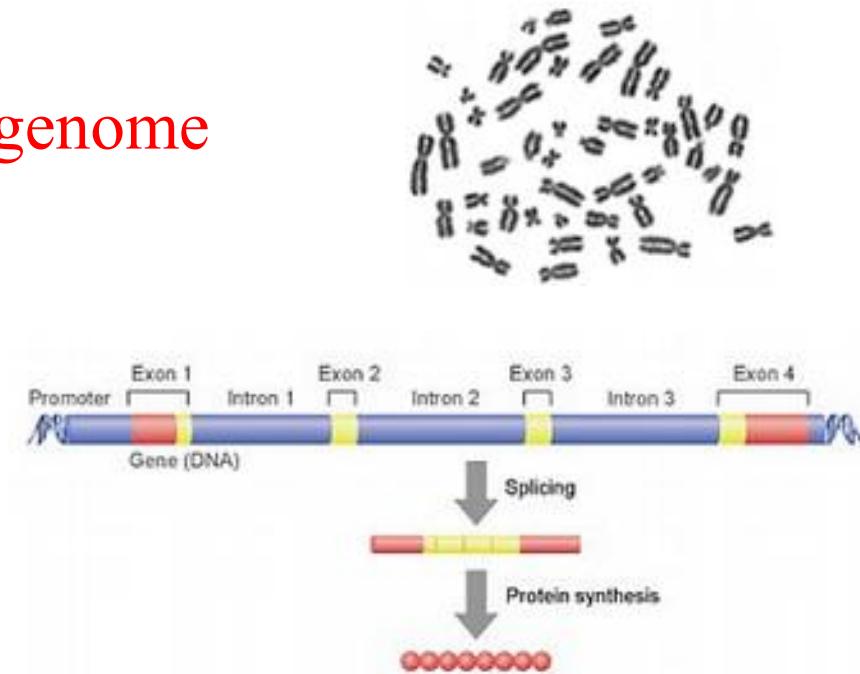
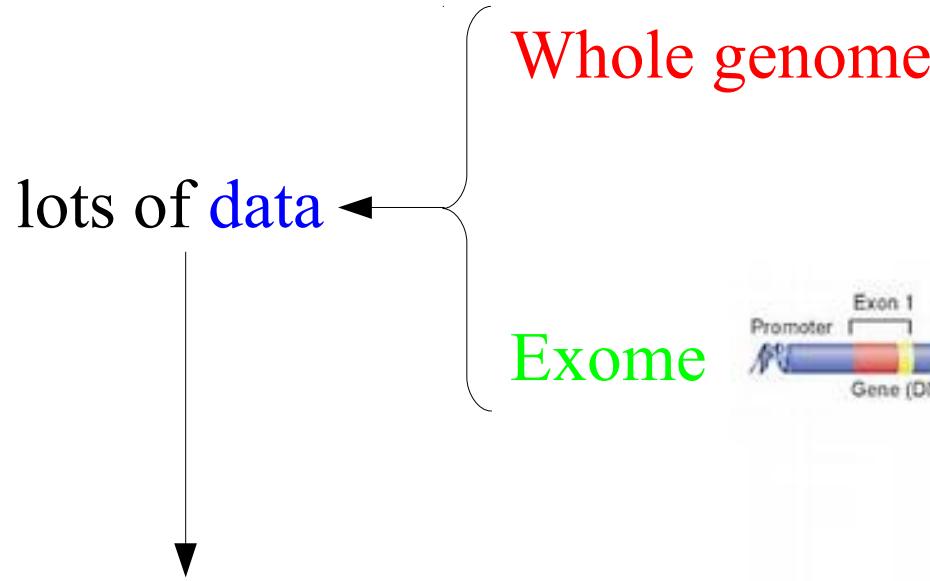
Exome





# Exome & genome sequencing

- Sequencing → full message instead of (dense) landmarks



Difficult to analyze:  
- heaps of genetic variation → what is relevant?



## Examples of genes

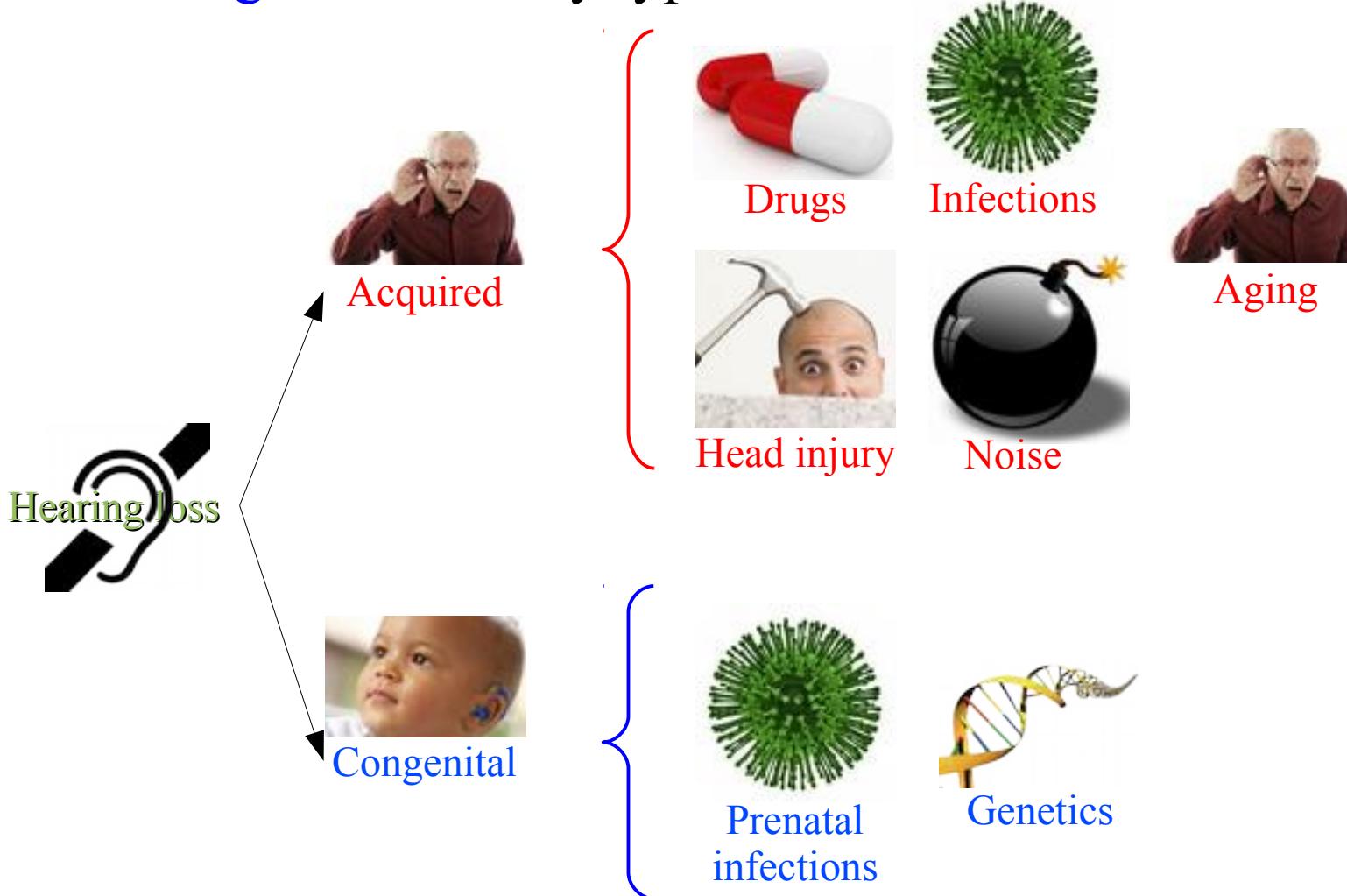
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- Hearing loss



## Examples of genes

- Hearing loss → many types

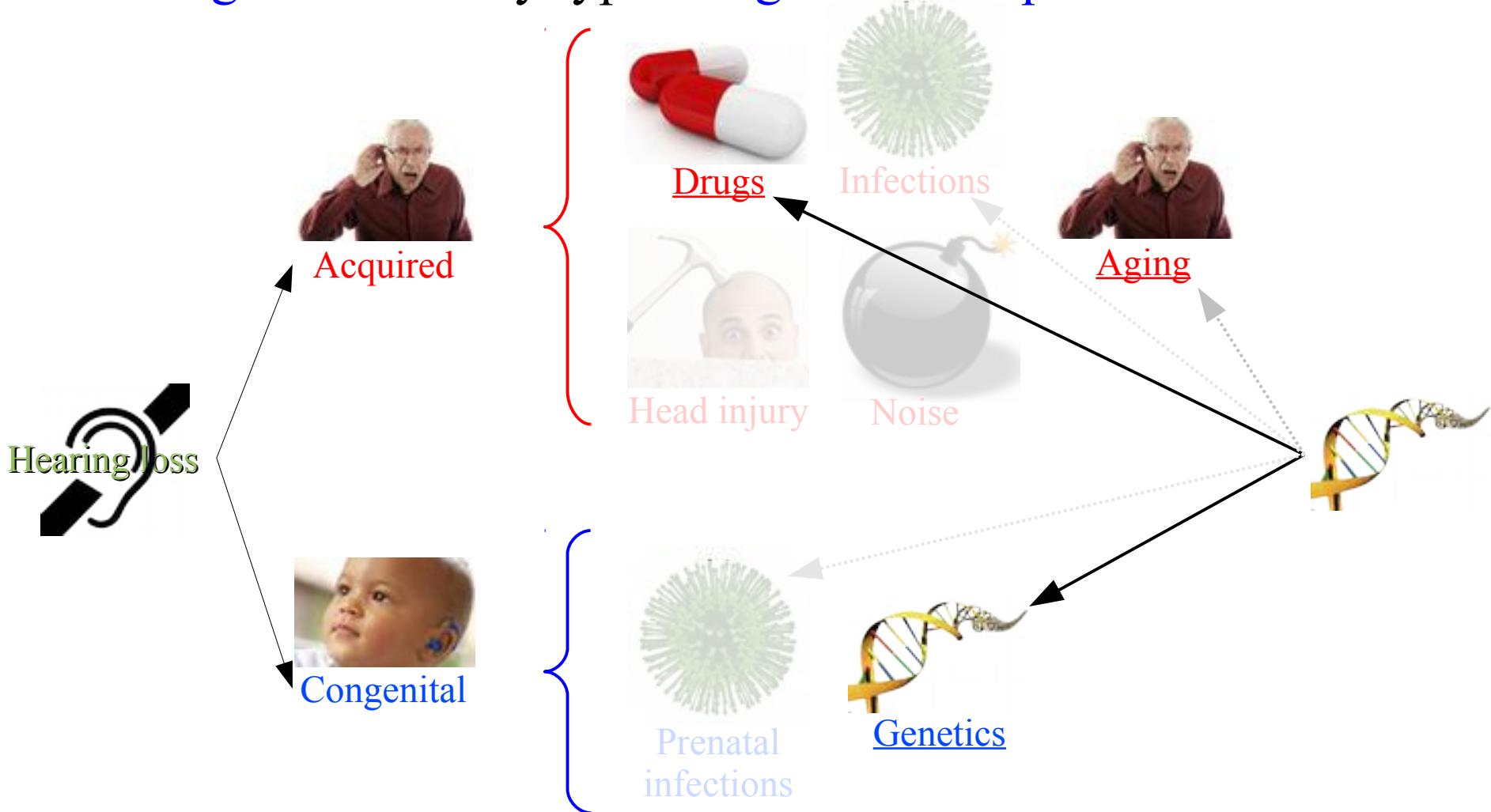


Examples: hearing loss



# Examples of genes

- Hearing loss → many types → genetic component

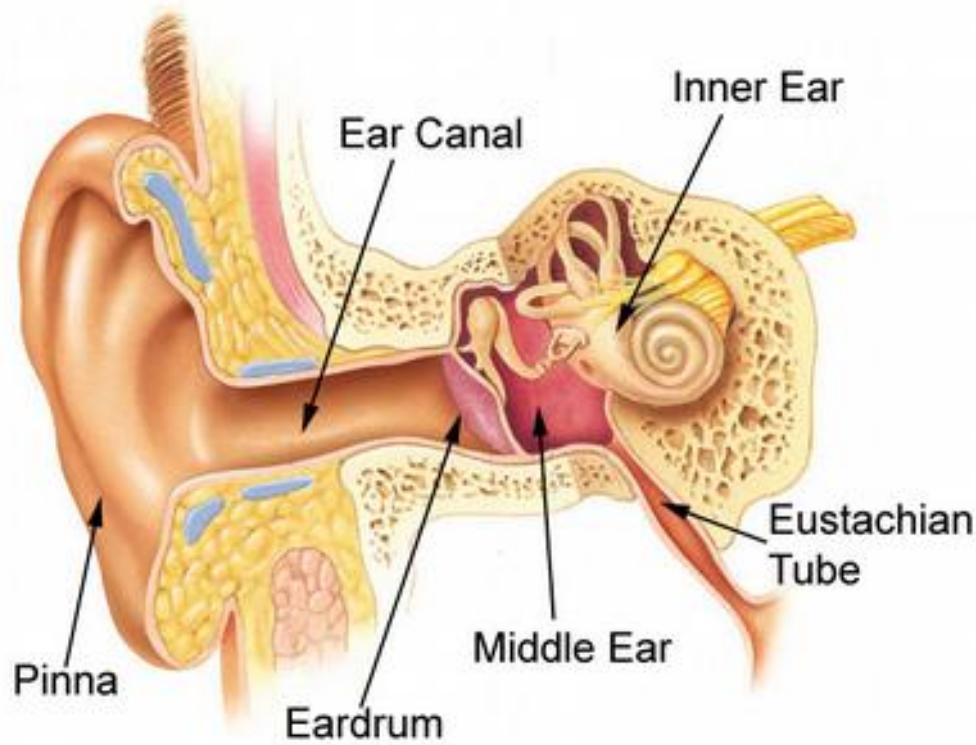


Examples: hearing loss



## Some examples: TECTA

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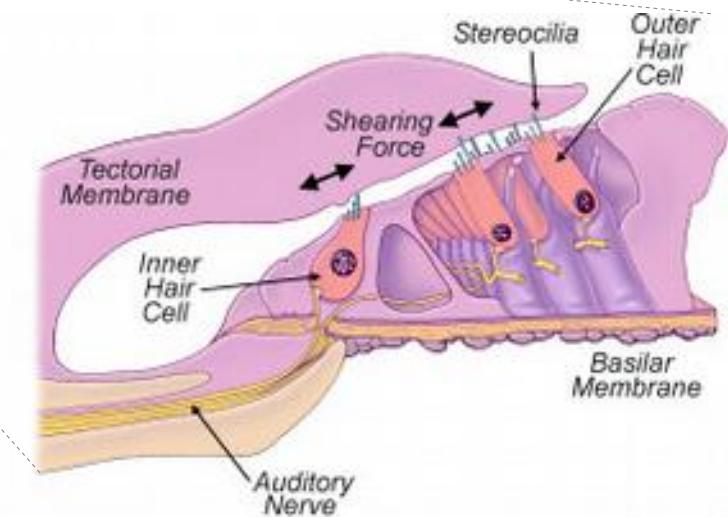
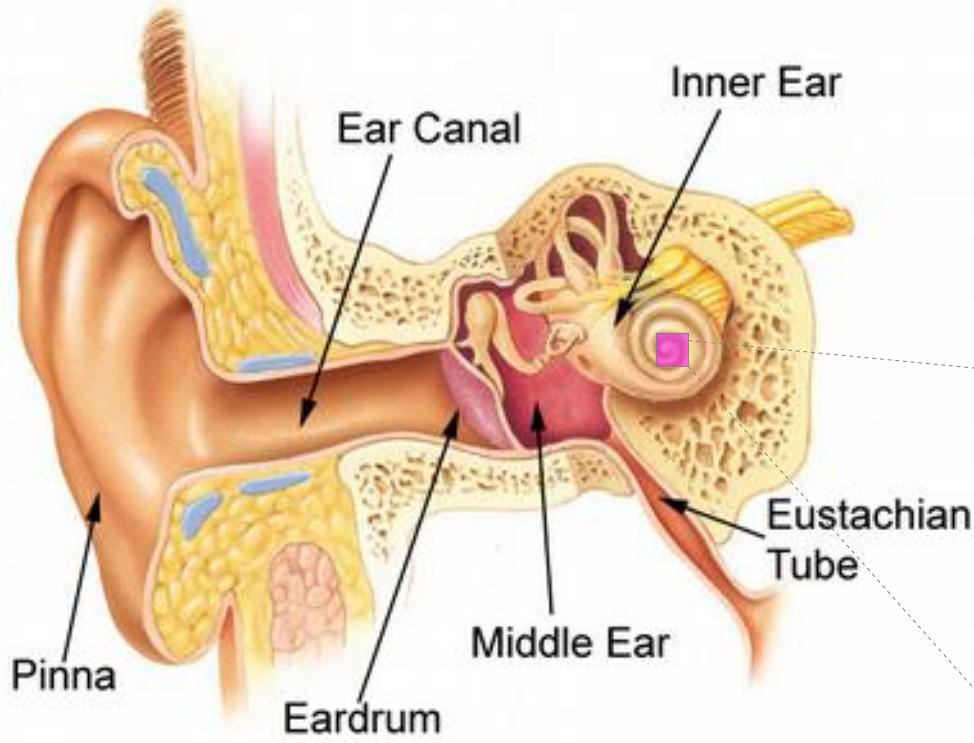


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Examples: hearing loss



## Some examples: TECTA



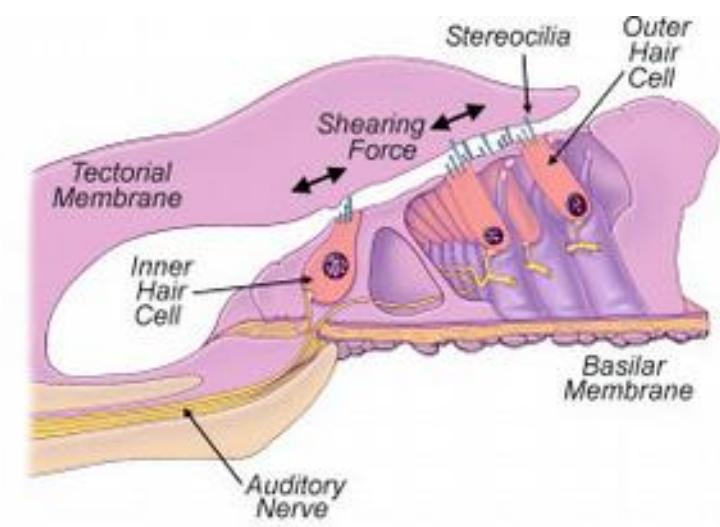
The Organ of Corti

Examples: hearing loss

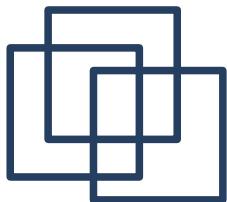


## Some examples: TECTA

- Tectorial membrane:

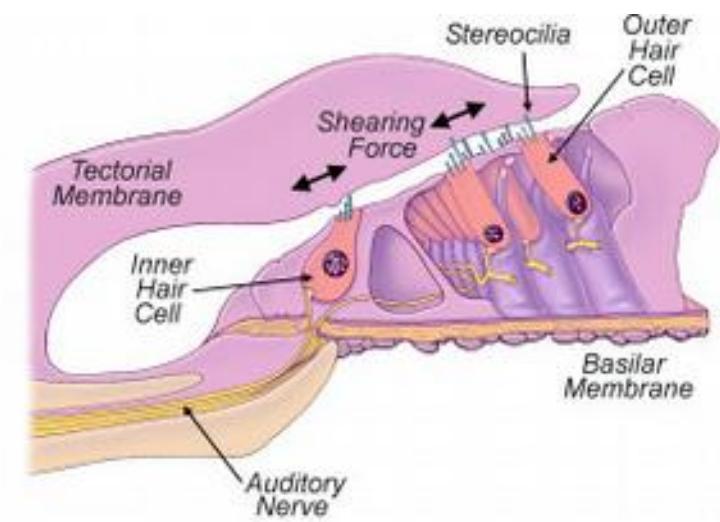
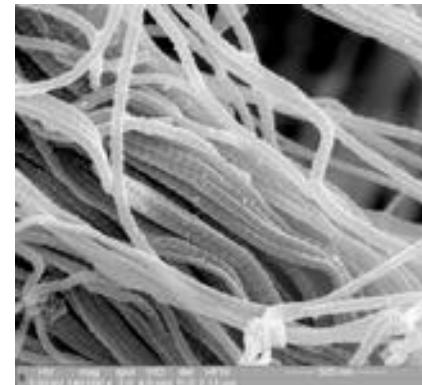


Examples: hearing loss



## Some examples: TECTA

- Tectorial membrane:  
→ collagen



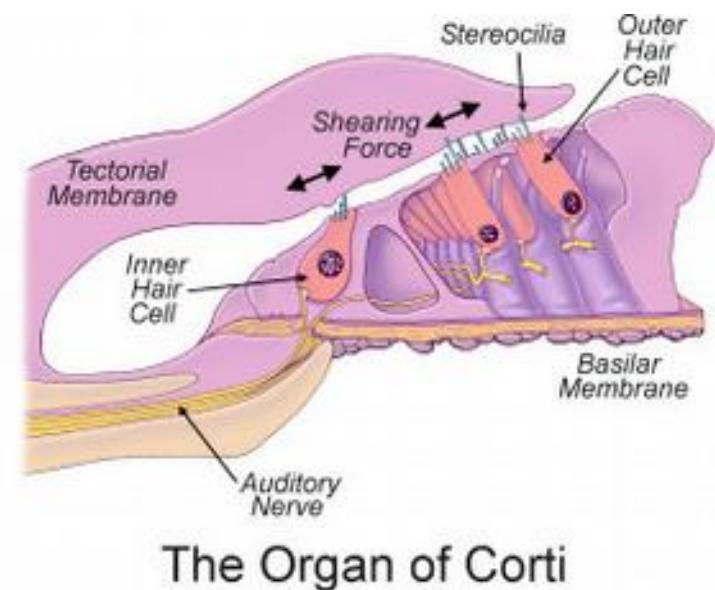
The Organ of Corti

Examples: hearing loss



## Some examples: TECTA

- Tectorial membrane:
  - collagen
  - non-collagenous proteins



Examples: hearing loss



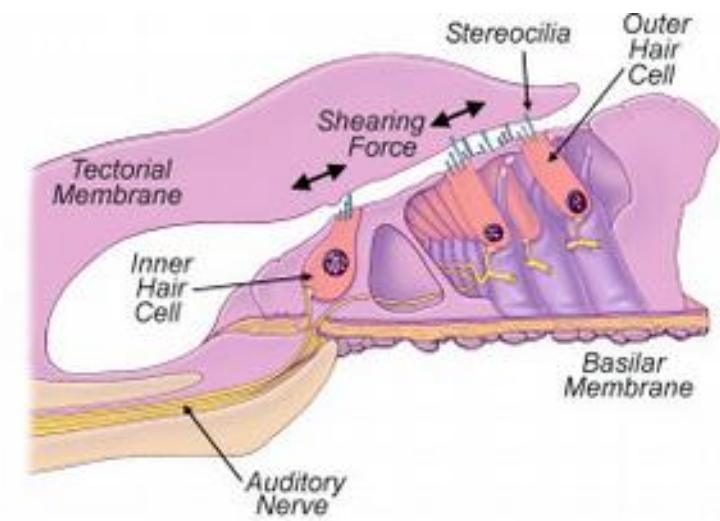
## Some examples: TECTA

- Tectorial membrane:

→ collagen

→ non-collagenous proteins

→  $\alpha$ -tectorin



The Organ of Corti



## Some examples: *TECTA*

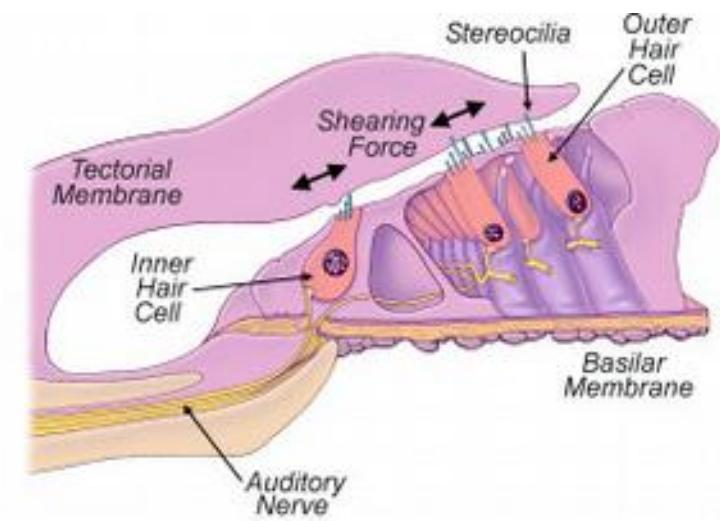
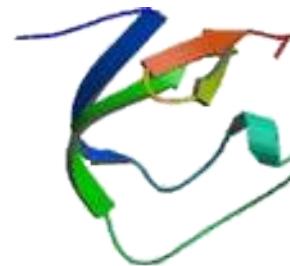
- Tectorial membrane:

→ collagen

→ non-collagenous proteins

→  $\alpha$ -tectorin

↓  
*TECTA* gene



The Organ of Corti



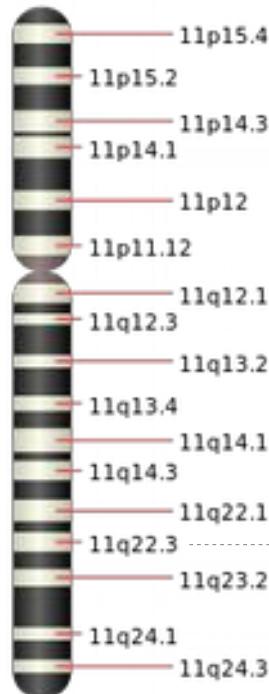
## Some examples: *TECTA*

- Tectorial membrane:

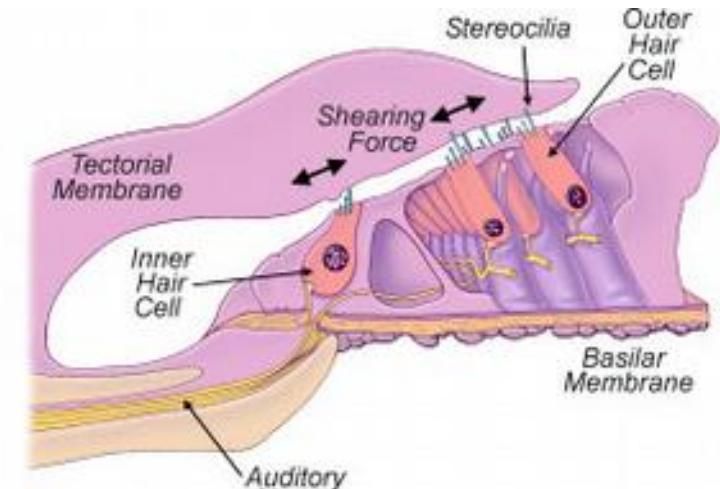
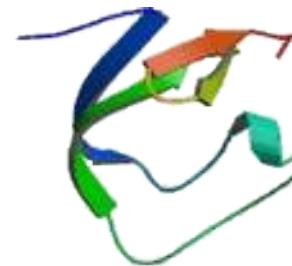
→ collagen

→ non-collagenous proteins

→  $\alpha$ -tectorin

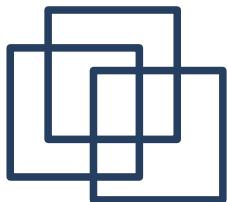


*TECTA* gene (11q23.3)



The Organ of Corti

Examples: hearing loss



## Some examples: *TECTA*

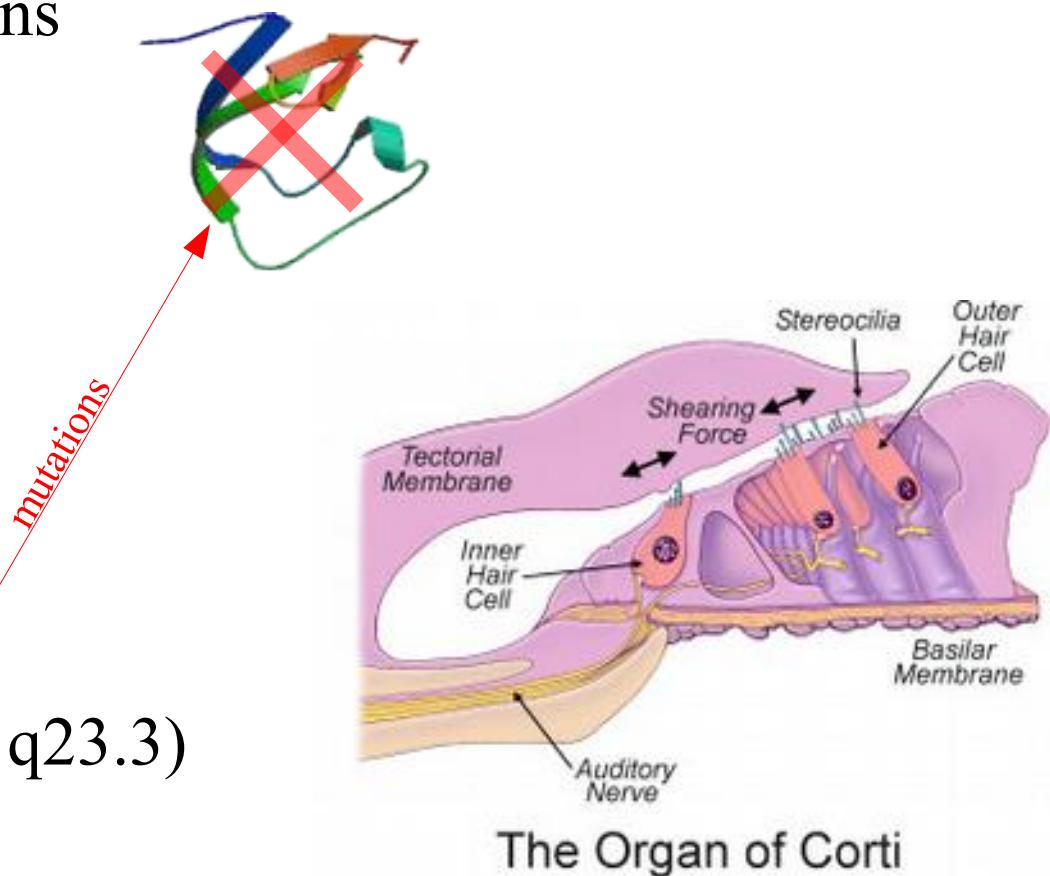
- Tectorial membrane:

→ collagen

→ non-collagenous proteins

→  $\alpha$ -tectorin

*TECTA* gene (11q23.3)





## Some examples: *TECTA*

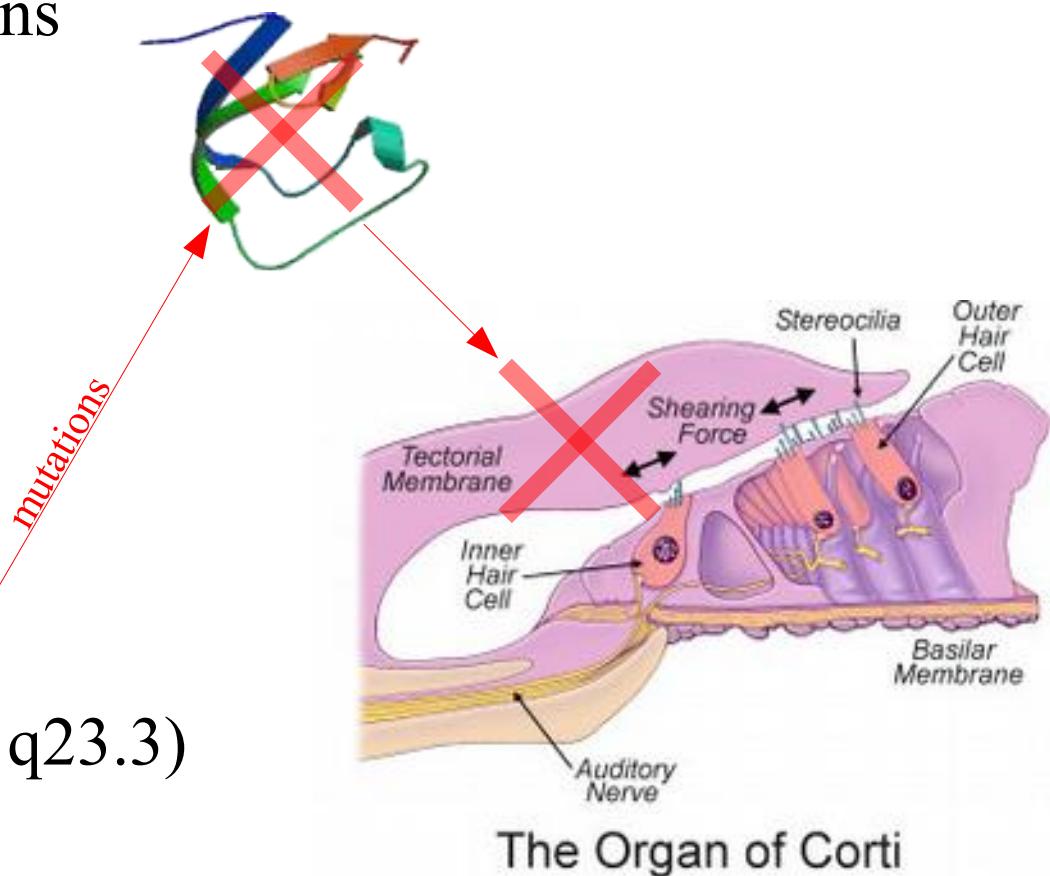
- Tectorial membrane:

→ collagen

→ non-collagenous proteins

→  $\alpha$ -tectorin

*TECTA* gene (11q23.3)





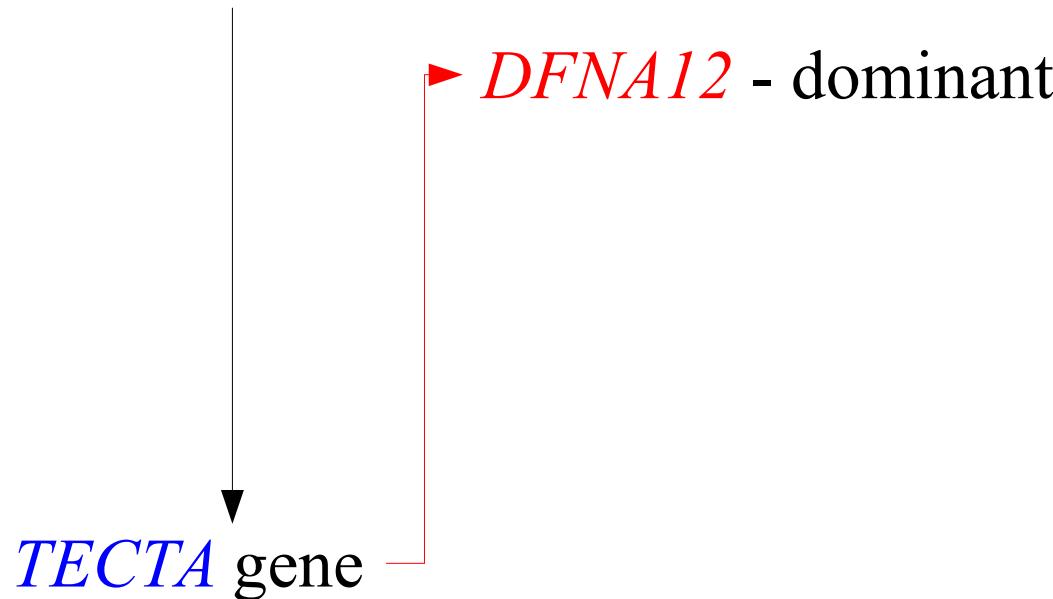
## Some examples: *TECTA*

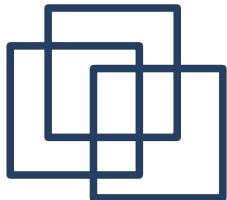
- Tectorial membrane:

→ collagen

→ non-collagenous proteins

→  $\alpha$ -tectorin





## Some examples: *TECTA*

- Tectorial membrane:

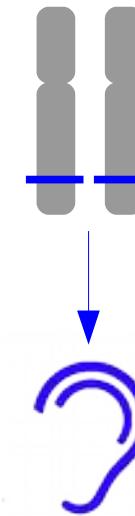
→ collagen

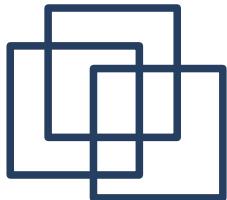
→ non-collagenous proteins

→  $\alpha$ -tectorin

*TECTA* gene

► *DFNA12* - dominant





## Some examples: *TECTA*

- Tectorial membrane:

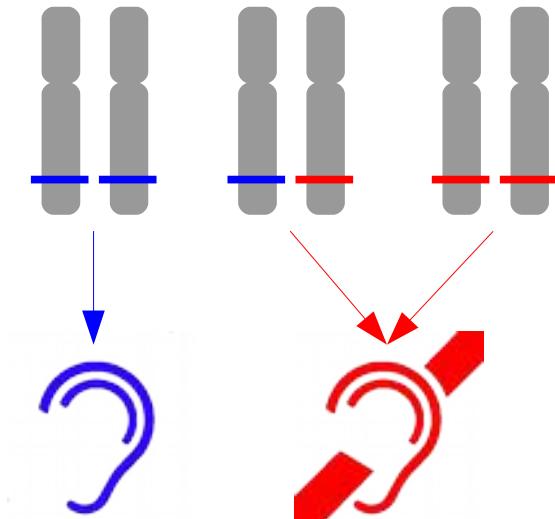
→ collagen

→ non-collagenous proteins

→  $\alpha$ -tectorin

*TECTA* gene

► *DFNA12* - dominant





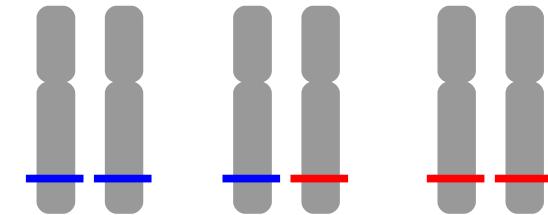
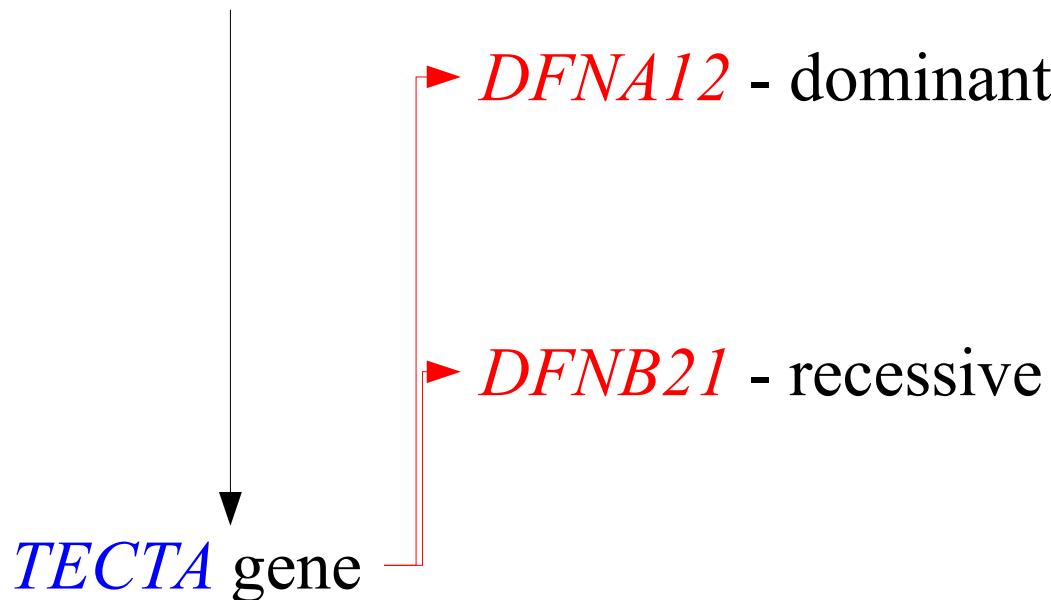
## Some examples: *TECTA*

- Tectorial membrane:

→ collagen

→ non-collagenous proteins

→  $\alpha$ -tectorin





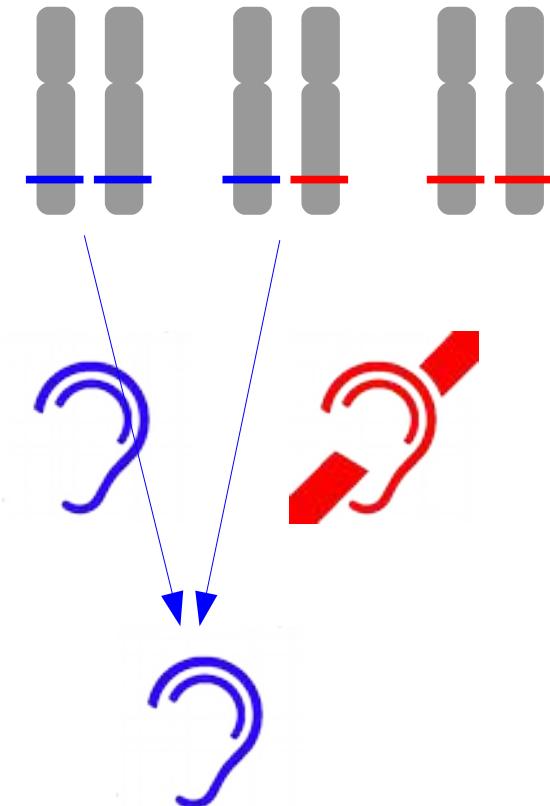
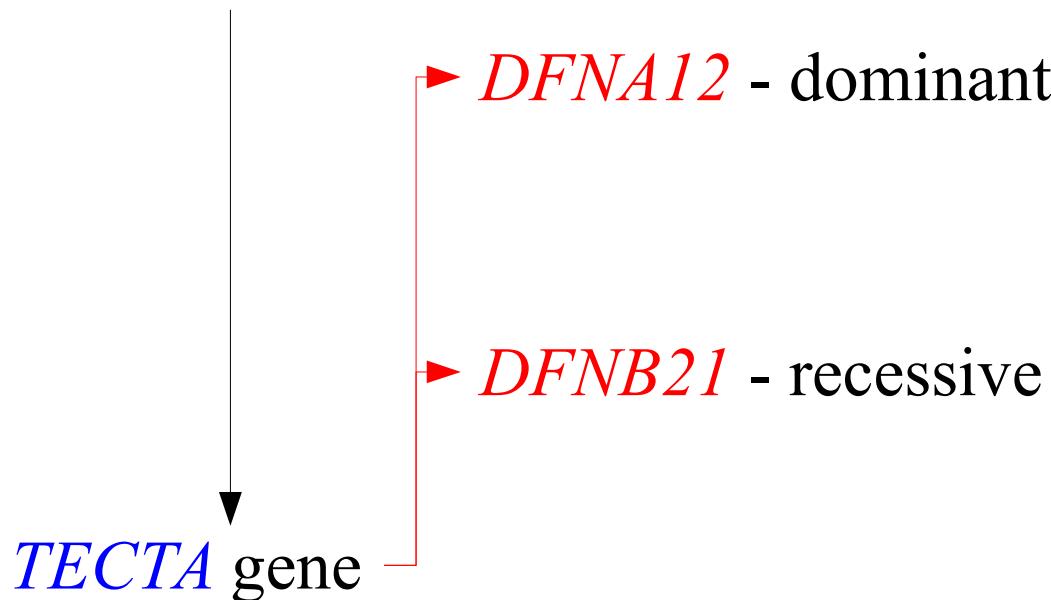
## Some examples: *TECTA*

- Tectorial membrane:

→ collagen

→ non-collagenous proteins

→  $\alpha$ -tectorin





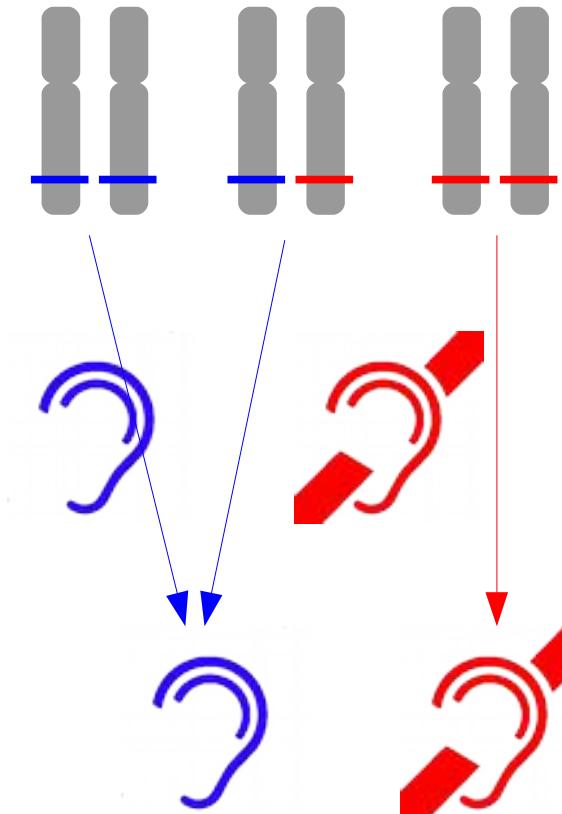
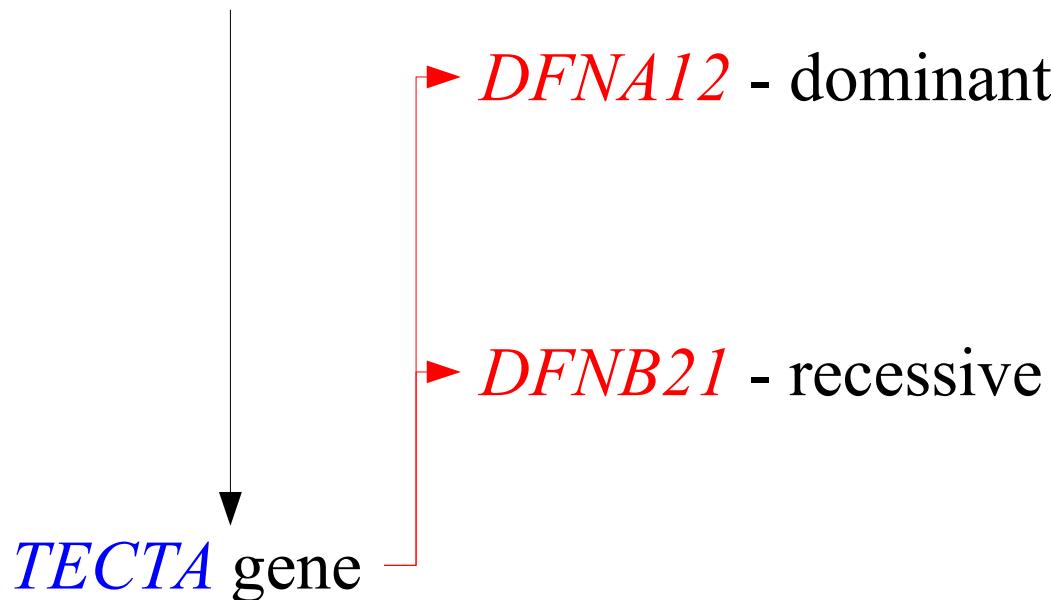
## Some examples: *TECTA*

- Tectorial membrane:

→ collagen

→ non-collagenous proteins

→  $\alpha$ -tectorin





## Some examples: *TECTA*

- Tectorial membrane:

→ collagen

→ non-collagenous proteins

→  $\alpha$ -tectorin

*TECTA* gene

► *DFNA12* - dominant

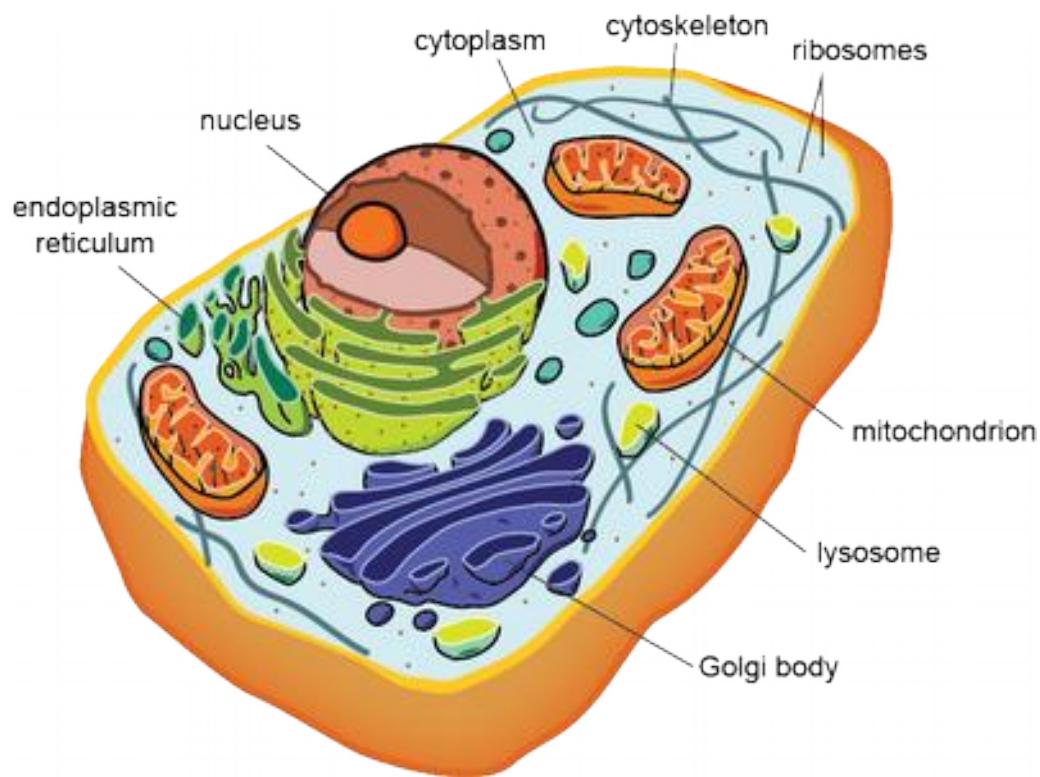


► *DFNB21* - recessive





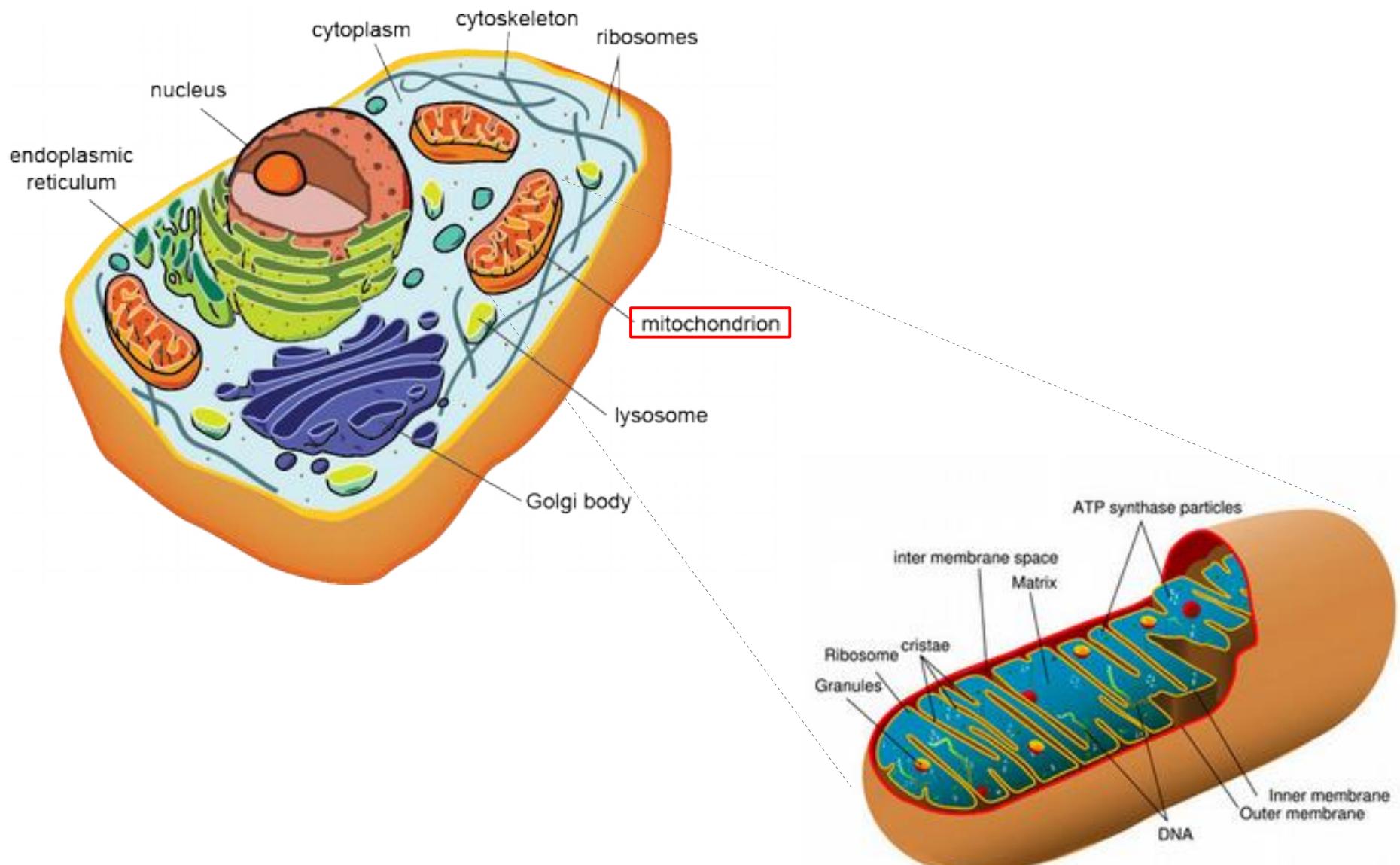
## Some examples: mitochondrial 12S rRNA



Examples: hearing loss



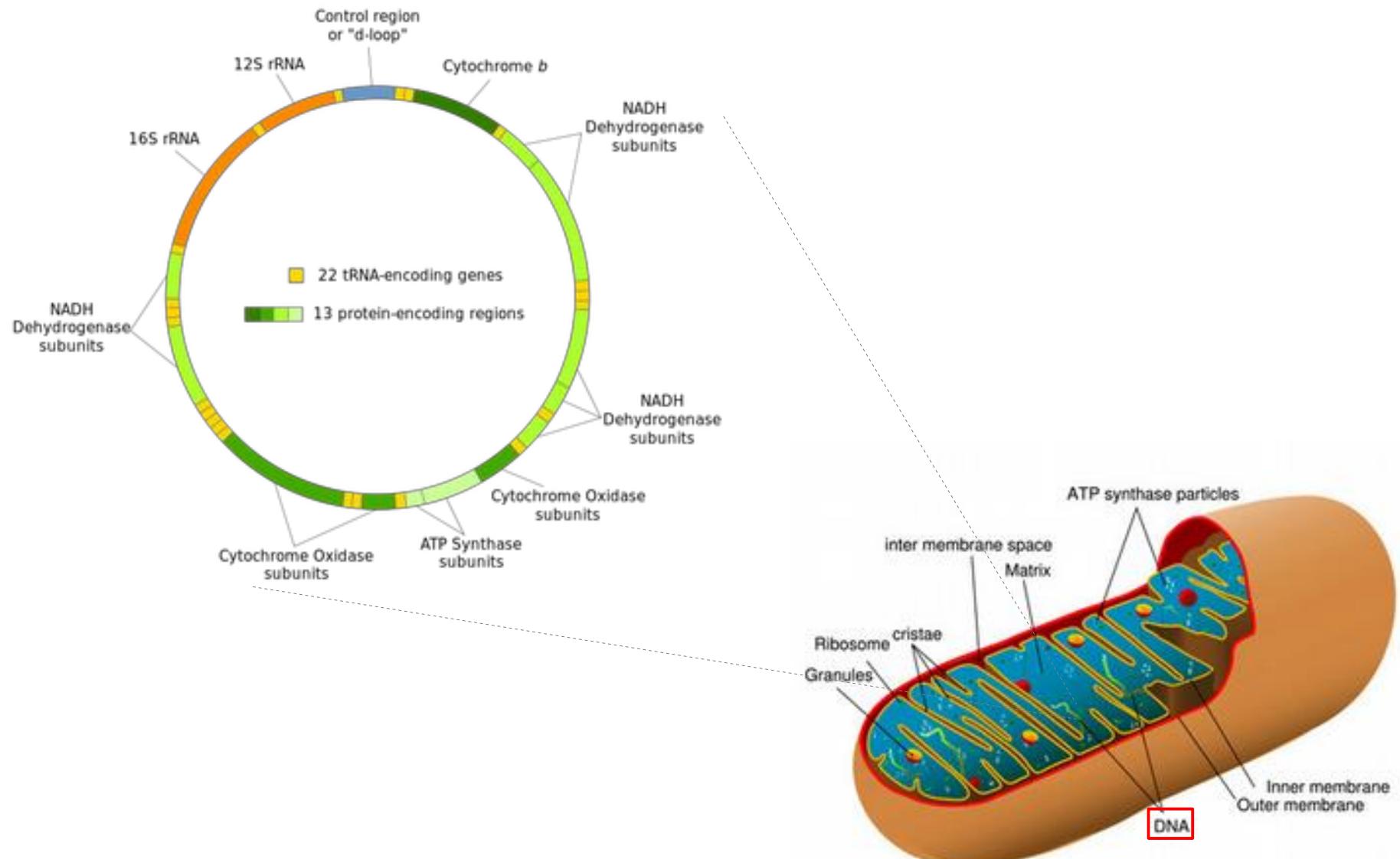
## Some examples: mitochondrial 12S rRNA



Examples: hearing loss



## Some examples: mitochondrial 12S rRNA

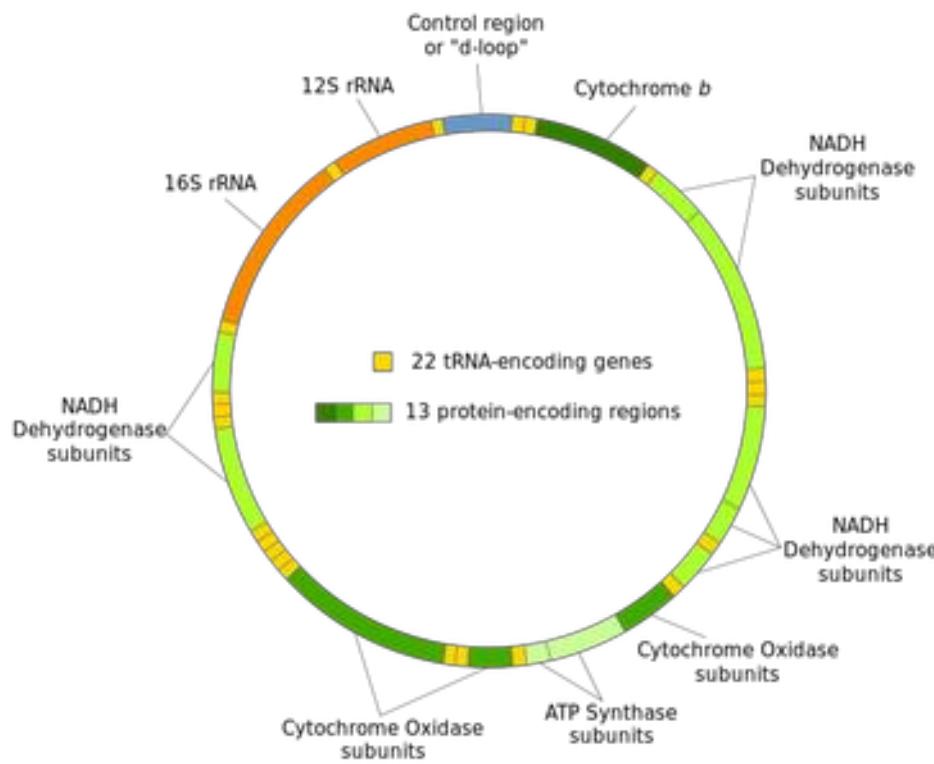


Examples: hearing loss



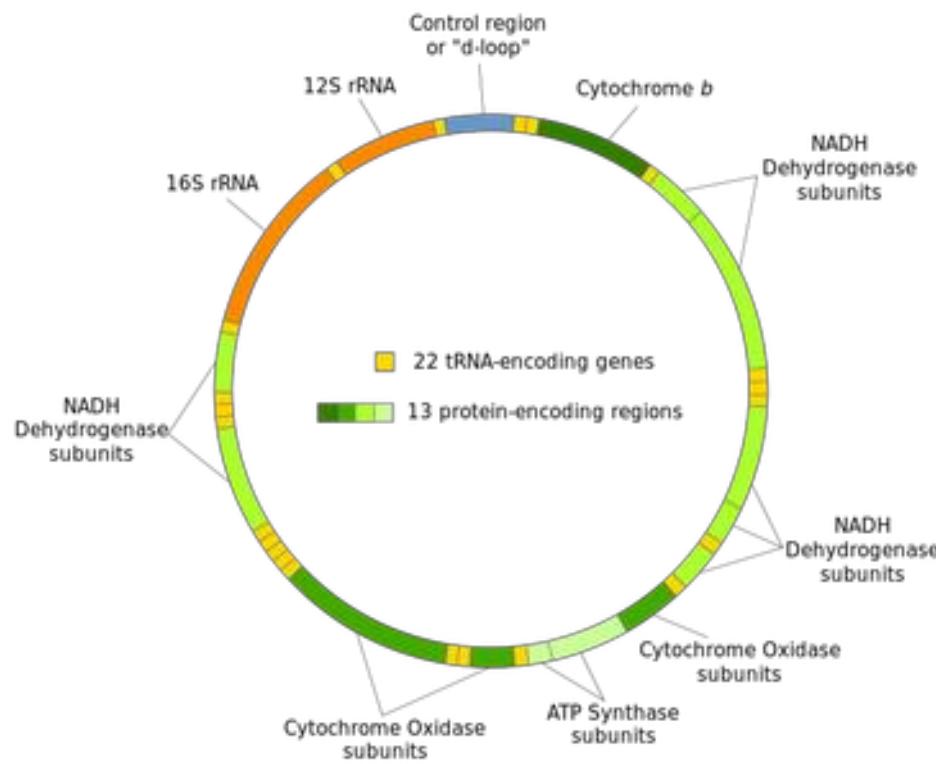
## Some examples: mitochondrial 12S rRNA

Own genetic code





## Some examples: mitochondrial 12S rRNA

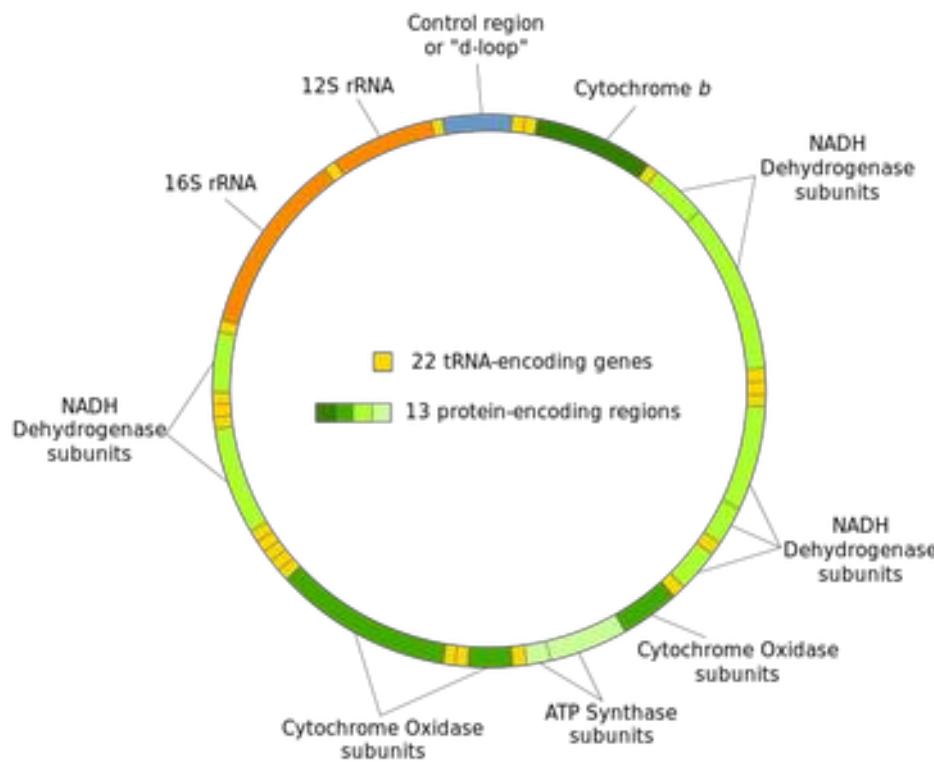


Own genetic code

→ own translation machinery



## Some examples: mitochondrial 12S rRNA



Own genetic code

- own translation machinery
- own **ribosomes**

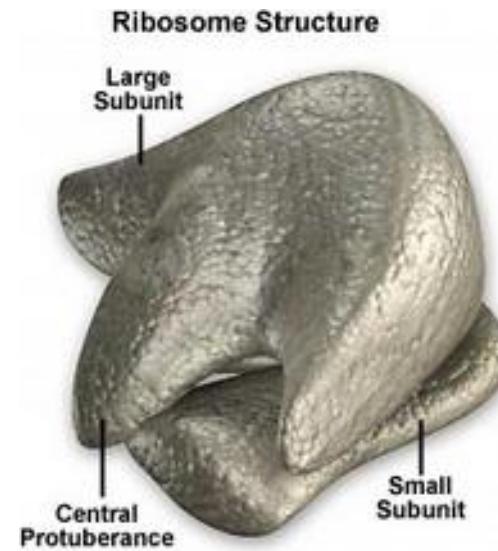
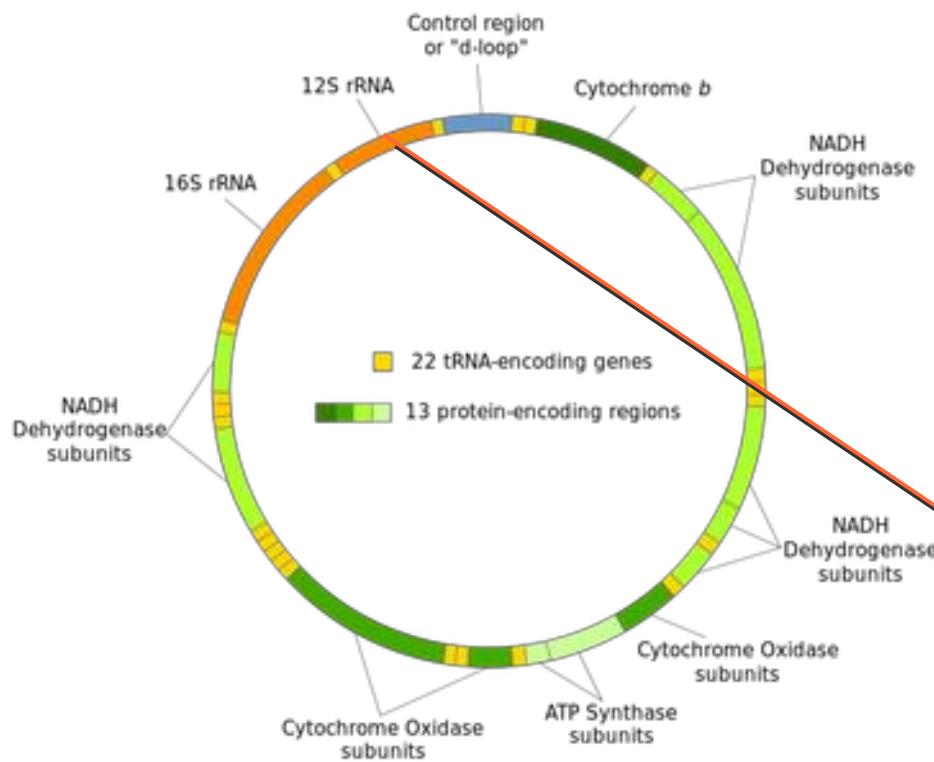


Figure 1



## Some examples: mitochondrial 12S rRNA



Own genetic code

- own translation machinery
- own ribosomes

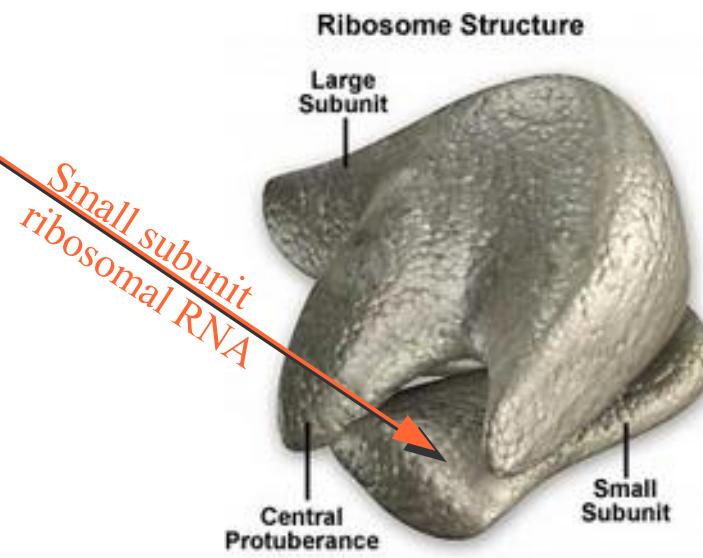


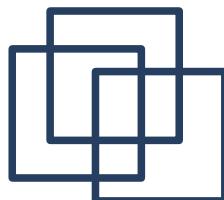
Figure 1



## Some examples: mitochondrial 12S rRNA

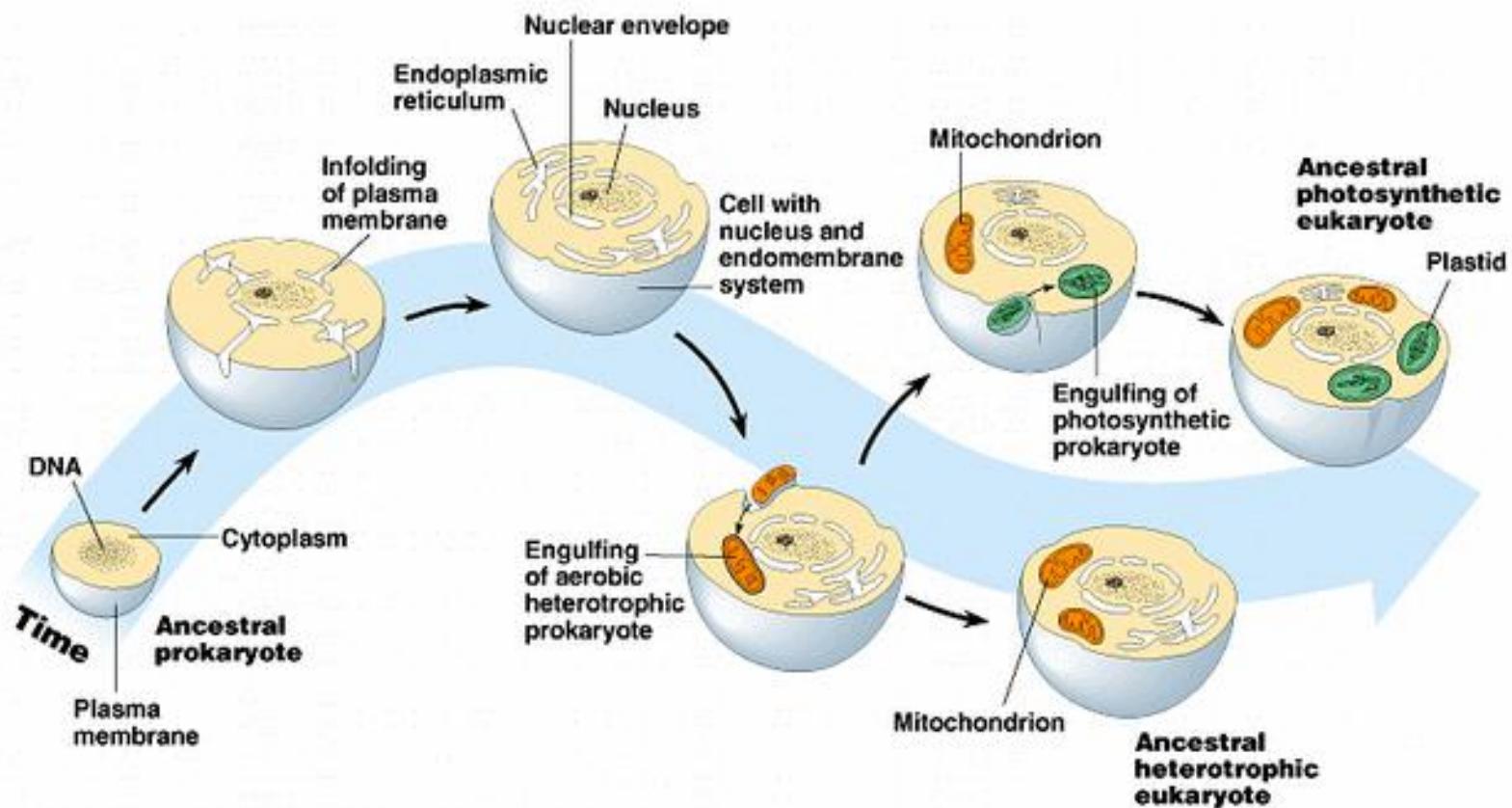
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Mitochondria → ancient bacteria



## Some examples: mitochondrial 12S rRNA

Mitochondria → ancient bacteria (endosymbiotic theory)



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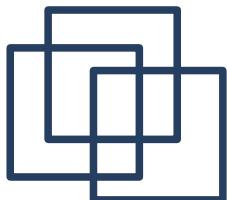
Examples: hearing loss



## Some examples: mitochondrial 12S rRNA

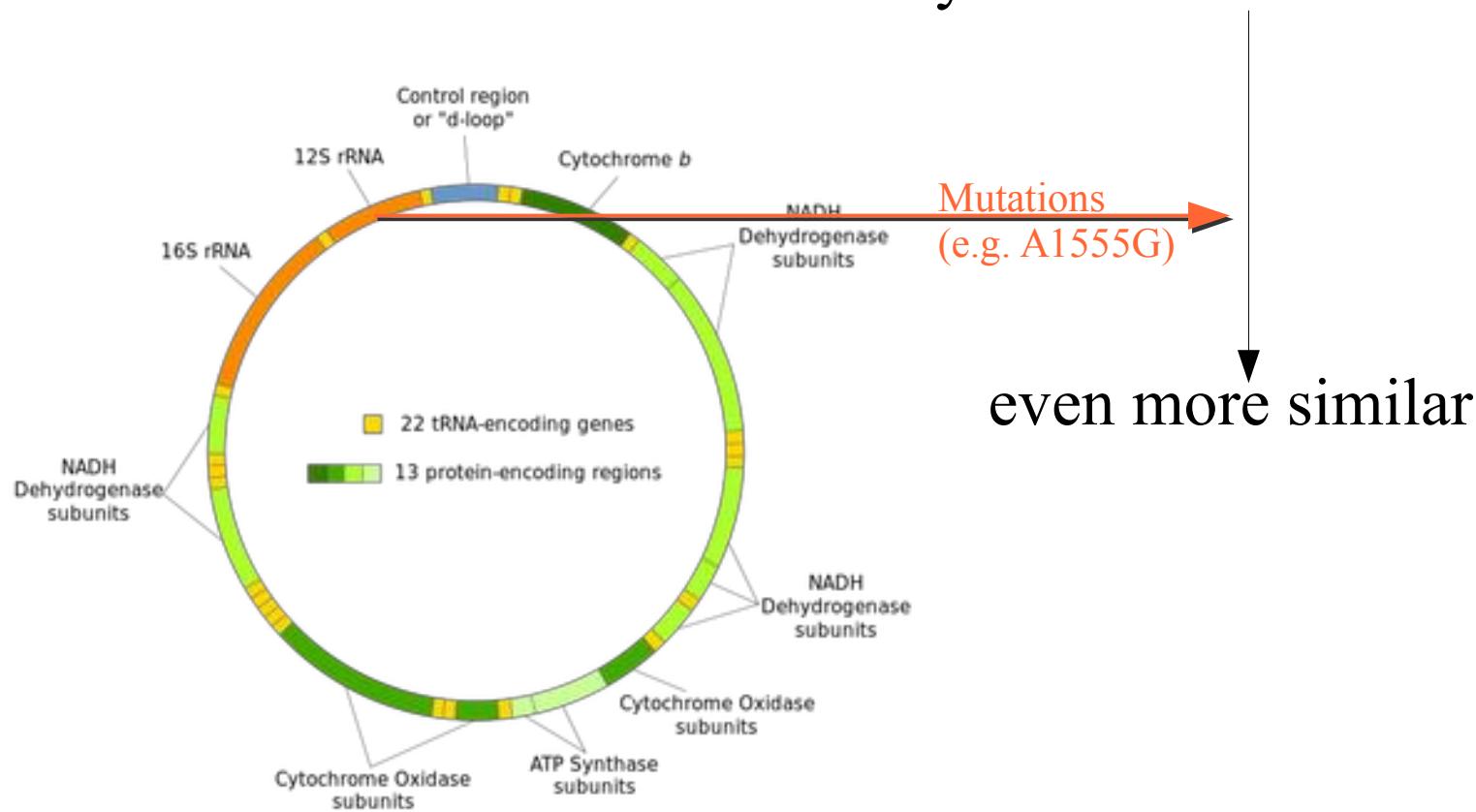
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Mitochondria → ancient bacteria ([endosymbiotic theory](#))  
→ mitochondrial ribosomes are very similar to bacterial ribosomes



## Some examples: mitochondrial 12S rRNA

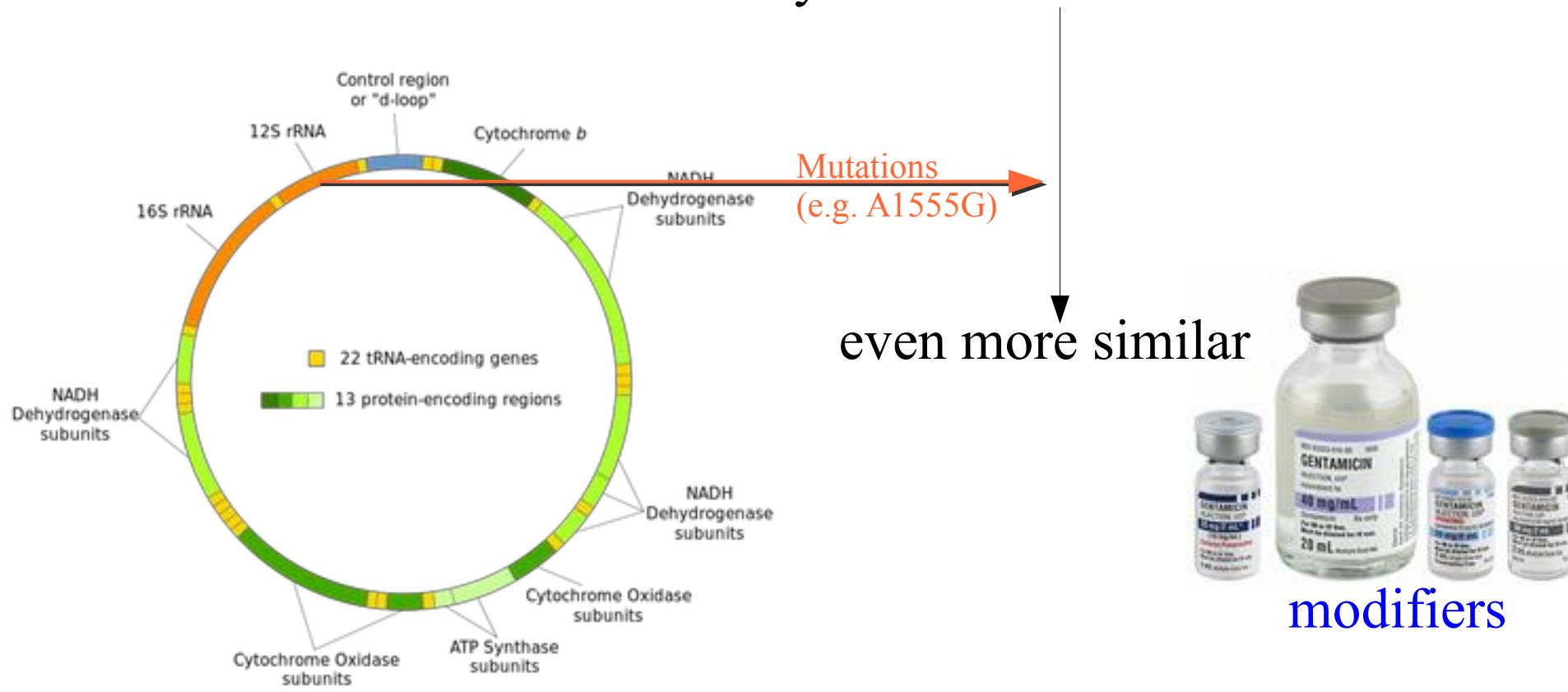
Mitochondria → ancient bacteria (endosymbiotic theory)  
→ mitochondrial ribosomes are very similar to bacterial ribosomes





## Some examples: mitochondrial 12S rRNA

Mitochondria → ancient bacteria (endosymbiotic theory)  
→ mitochondrial ribosomes are very similar to bacterial ribosomes



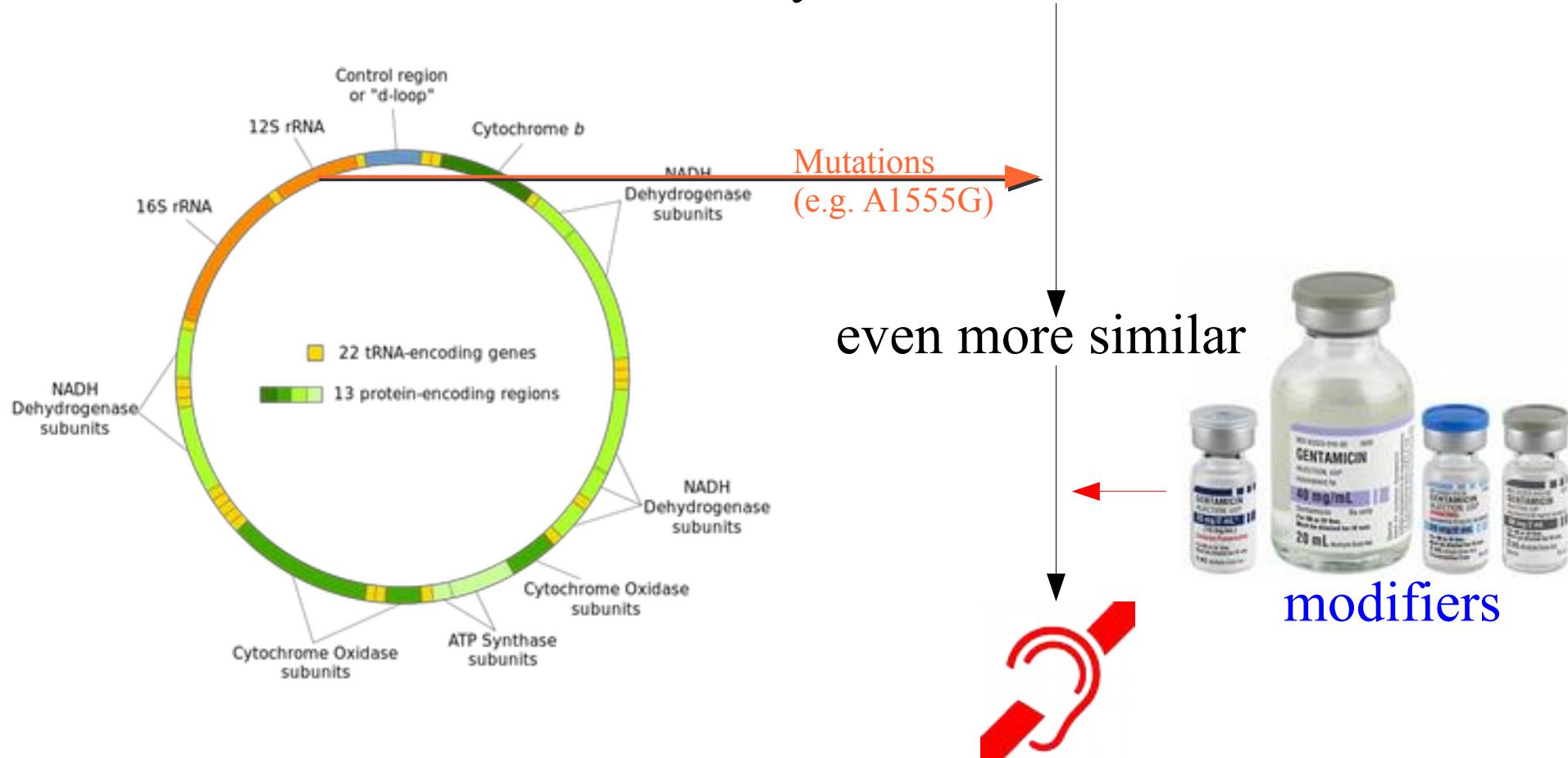
Examples: hearing loss



## Some examples: mitochondrial 12S rRNA

Mitochondria → ancient bacteria (endosymbiotic theory)

→ mitochondrial ribosomes are very similar to bacterial ribosomes

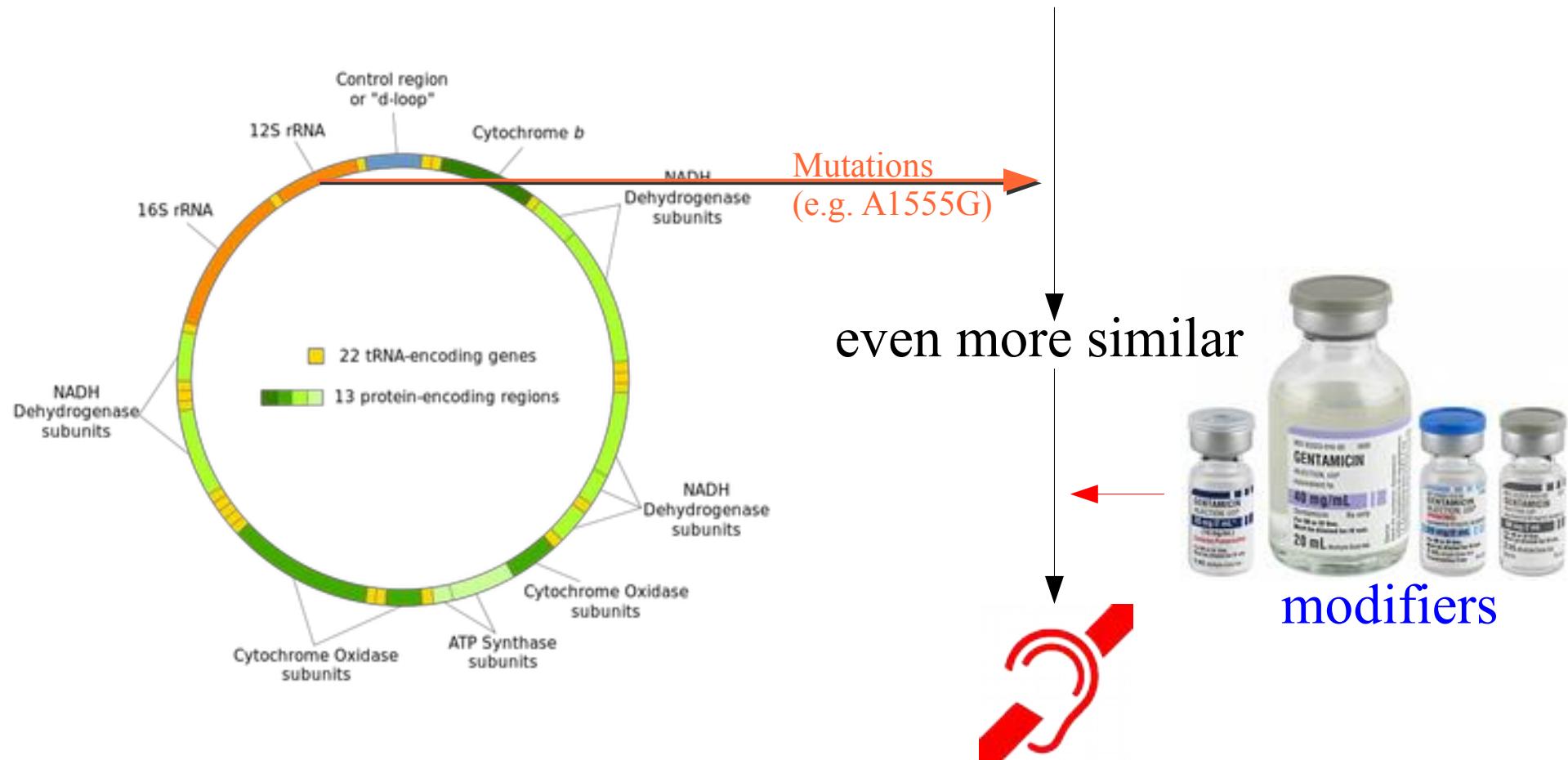


Examples: hearing loss



## Some examples: mitochondrial 12S rRNA

Hair cells are more affected by mitochondrial ribosomal impaired function more than other cells?

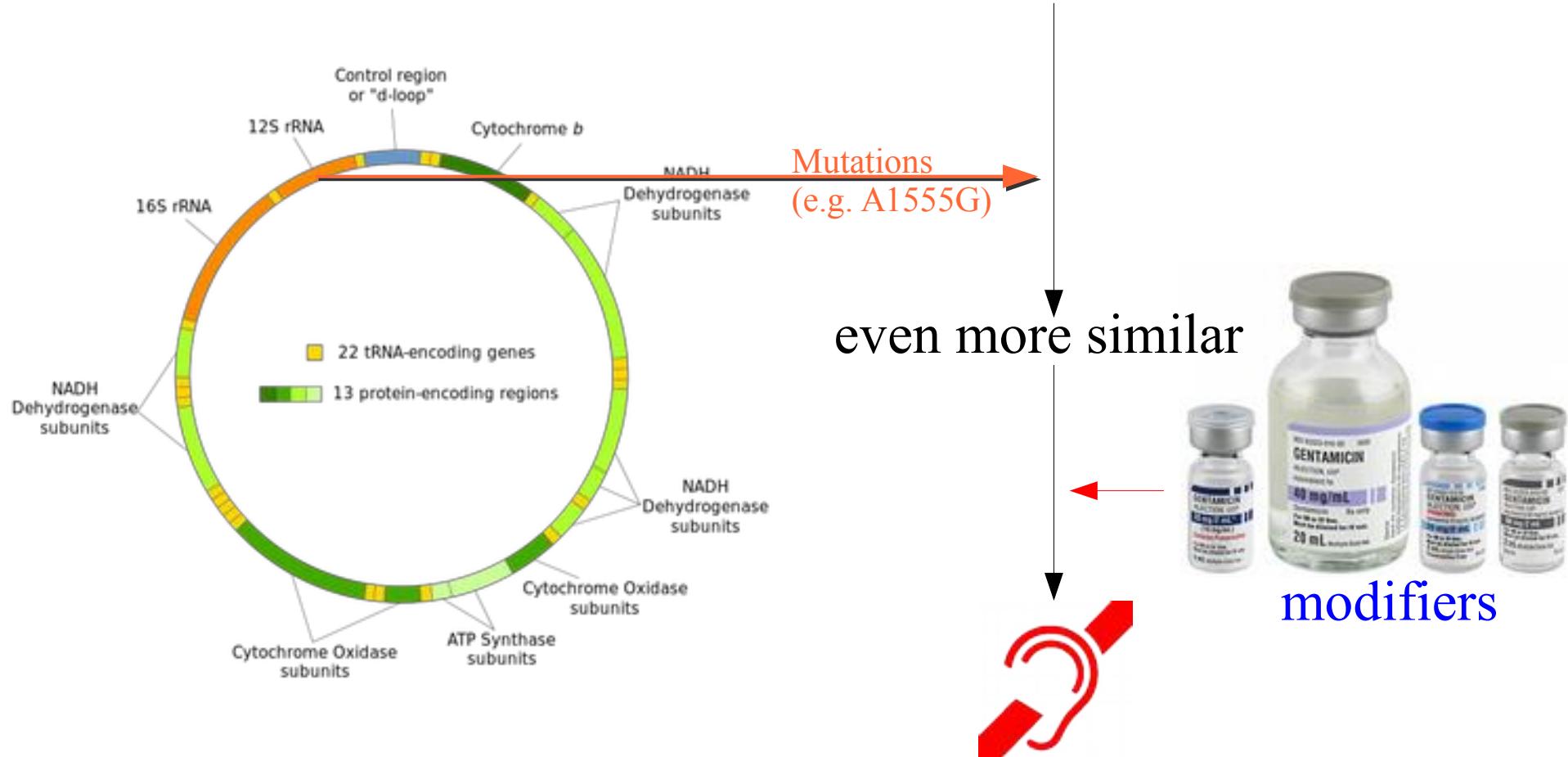


Examples: hearing loss



## Some examples: mitochondrial 12S rRNA

Hair cells are more affected by mitochondrial ribosomal impaired function more than other cells? → specific phenotype



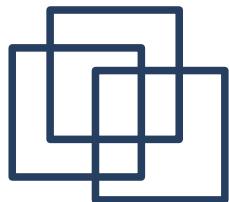
Examples: hearing loss



## Congenital non-syndromic deafness

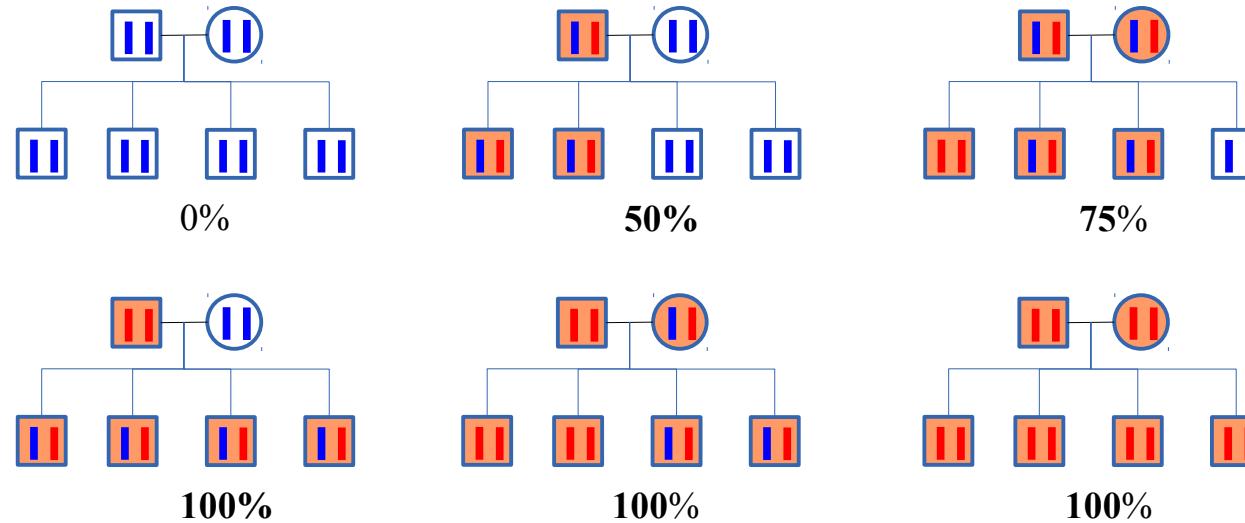
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- Many loci (e.g., <http://hereditaryhearingloss.org/main.aspx?c=.HHH&n=86163>)



# Congenital non-syndromic deafness

- Many loci (e.g., <http://hereditaryhearingloss.org/main.aspx?c=.HHH&n=86163>)
- Autosomal dominant: *DFNAnn* ( $\sim 25$ )

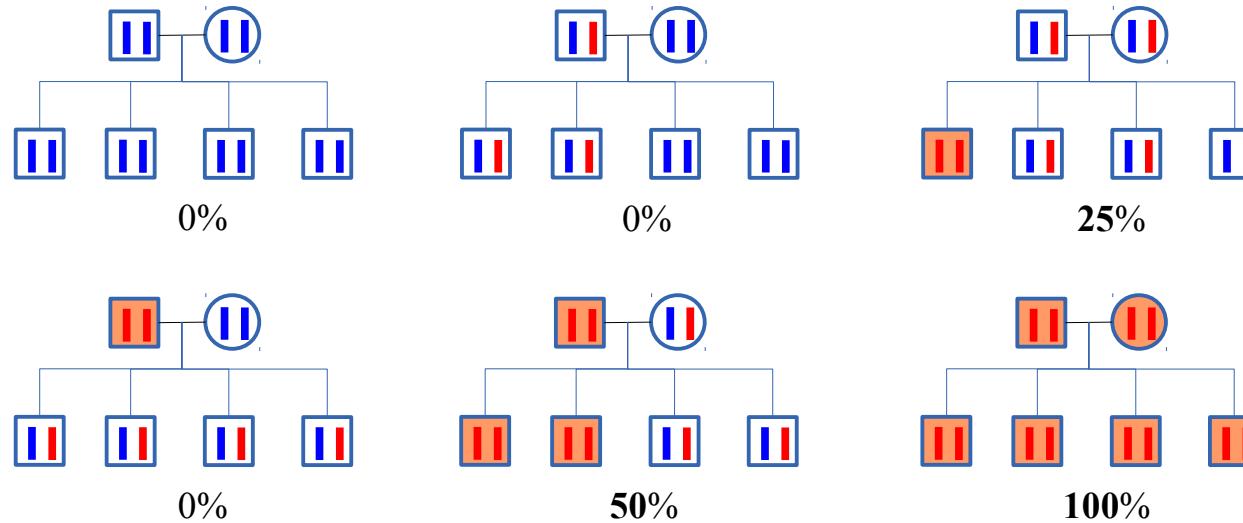


Examples: hearing loss



# Congenital non-syndromic deafness

- Many loci (e.g., <http://hereditaryhearingloss.org/main.aspx?c=.HHH&n=86163>)
- Autosomal dominant: *DFNAnn*, recessive: *DFN~~B~~nn* (~40)



Examples: hearing loss



## Congenital non-syndromic deafness

- Many loci (e.g., <http://hereditaryhearingloss.org/main.aspx?c=.HHH&n=86163>)
- Autosomal recessive: *DFNB1* and *DFNB3*



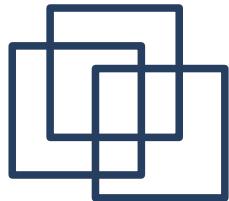
## ***DFNB1A/B (GJB2 and GJB6)***

---

- Autosomal recessive
- 13q12.11

---

*Examples: hearing loss*



## ***DFNB1A/B (GJB2 and GJB6)***

---

- Autosomal recessive
- 13q12.11
- *GJB2* (Gap junction beta-2; Connexin 26) and *GJB6* (Gap junction beta-6; Connexin 30)

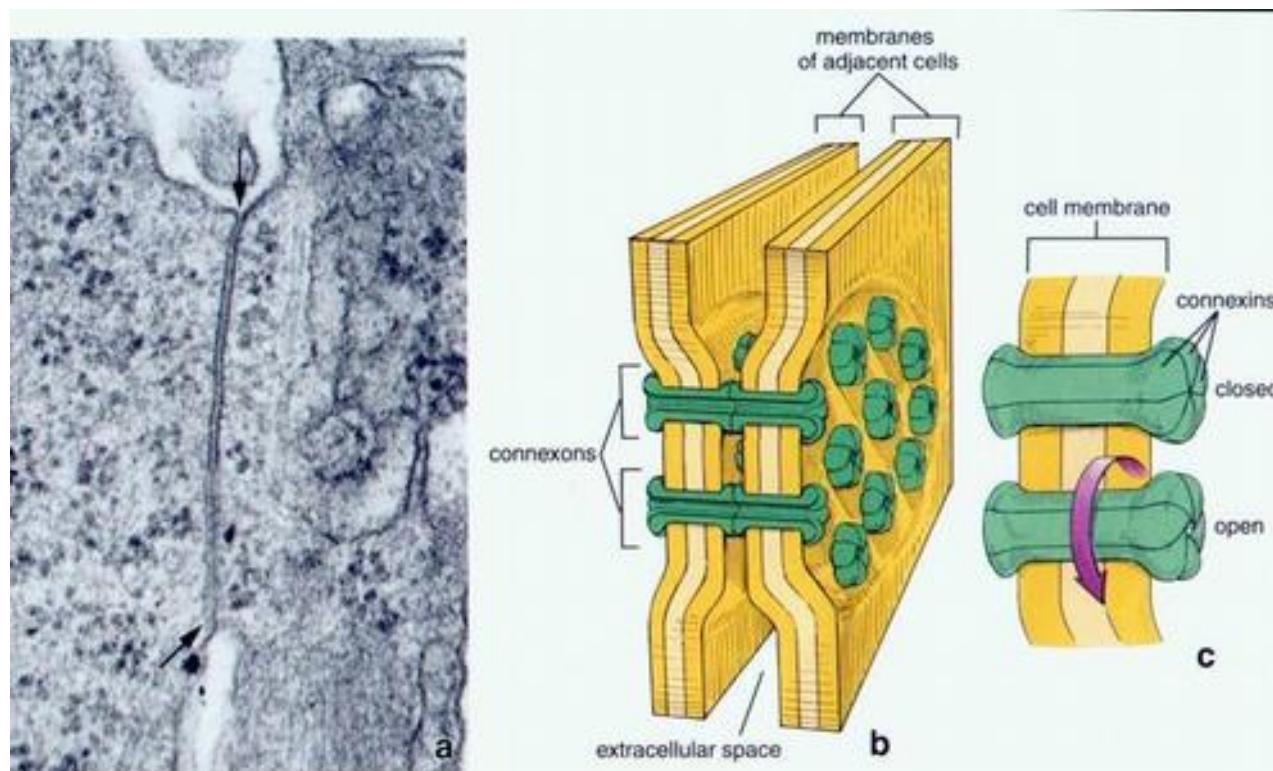
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*Examples: hearing loss*



## DFNB1A/B (*GJB2* and *GJB6*)

- Autosomal recessive
- 13q12.11
- *GJB2* (Gap junction beta-2; Connexin 26) and *GJB6* (Gap junction beta-6; Connexin 30)



Examples: hearing loss



## ***DFNB1A/B (GJB2 and GJB6)***

---

- Autosomal recessive
- 13q12.11
- *GJB2* (Gap junction beta-2; Connexin 26) and *GJB6* (Gap junction beta-6; Connexin 30)
- *GJB2*: ~90 mutations → **non-syndromic deafness**
  - other mutations: syndromes (skin + deafness)



## ***DFNB1A/B (GJB2 and GJB6)***

---

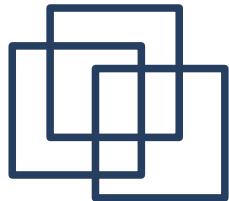
- Autosomal recessive
- 13q12.11
- *GJB2* (Gap junction beta-2; Connexin 26) and *GJB6* (Gap junction beta-6; Connexin 30)
- *GJB2*: ~90 mutations → **non-syndromic deafness**
  - other mutations: syndromes (skin + deafness)
- *GJB6*: some mutations → **non-syndromic deafness**
  - other mutations: skin disorders



## ***DFNB1A/B (GJB2 and GJB6)***

---

- Autosomal recessive
  - 13q12.11
  - *GJB2* (Gap junction beta-2; Connexin 26) and *GJB6* (Gap junction beta-6; Connexin 30)
  - *GJB2*: ~90 mutations → **non-syndromic deafness**
    - other mutations: syndromes (skin + deafness)
  - *GJB6*: some mutations → **non-syndromic deafness**
    - other mutations: skin disorders
- **potassium levels** in the inner ear?



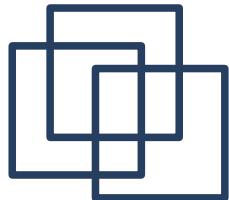
## ***DFNB3 (MYO15A)***

---

- Autosomal recessive
- 17p11.2

---

*Examples: hearing loss*



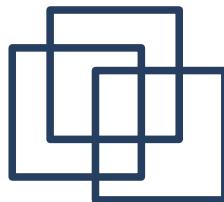
## ***DFNB3 (MYO15A)***

---

- Autosomal recessive
- 17p11.2
- *MYO15A* (unconventional myosin-15; myosin XVa)

---

*Examples: hearing loss*



## DFNB3 (MYO15A)

- Autosomal recessive
- 17p11.2
- *MYO15A* (unconventional myosin-15; myosin XVa)

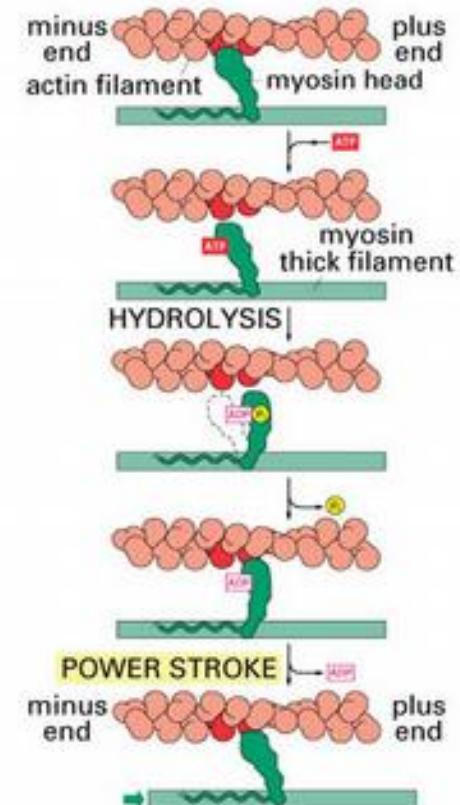
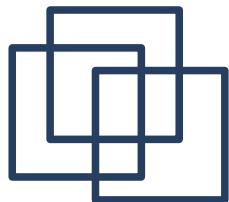


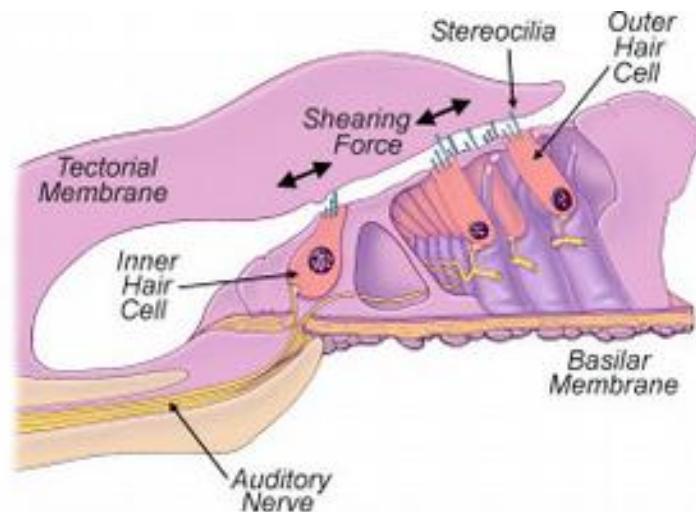
Figure 17-45 Essential Cell Biology, 2/e. (© 2004 Garland Science)

Examples: hearing loss



## DFNB3 (MYO15A)

- Autosomal recessive
- 17p11.2
- *MYO15A* (unconventional myosin-15; myosin XVa)  
→ stereocilia



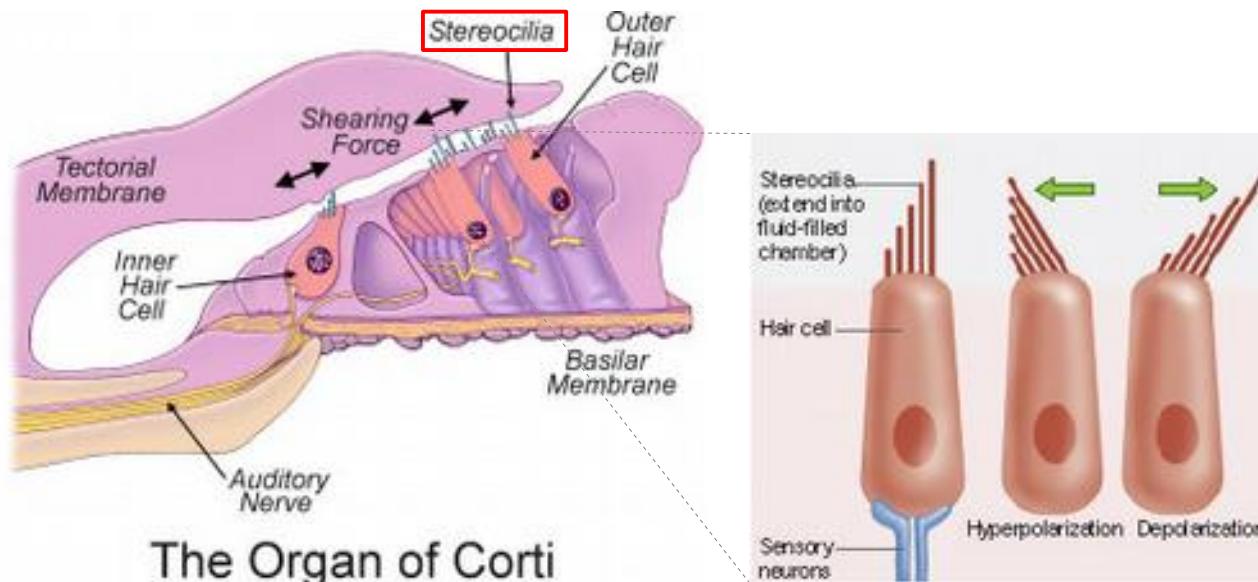
The Organ of Corti

Examples: hearing loss



## DFNB3 (MYO15A)

- Autosomal recessive
- 17p11.2
- *MYO15A* (unconventional myosin-15; myosin XVa)  
→ stereocilia

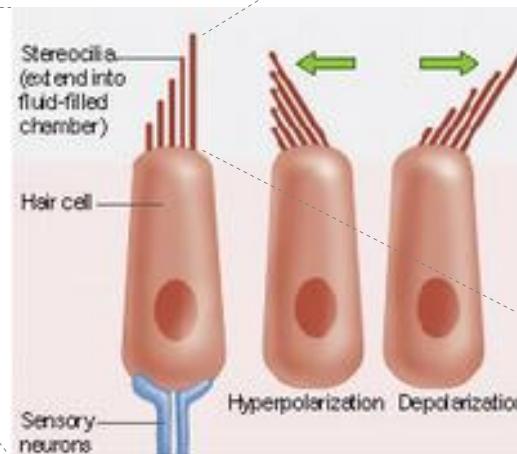
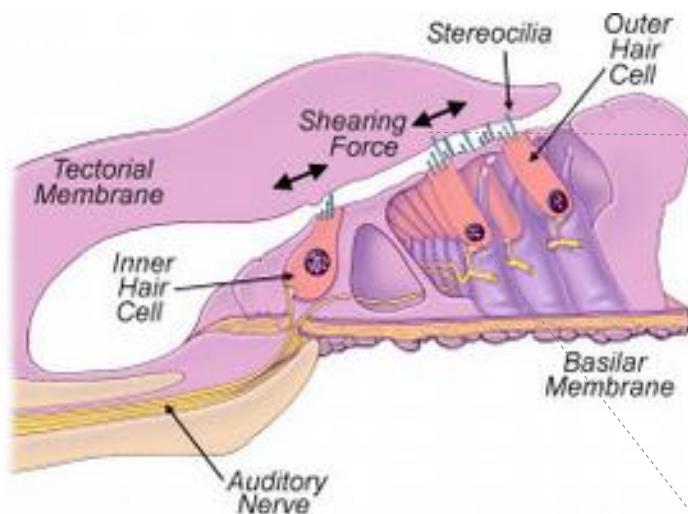


Examples: hearing loss

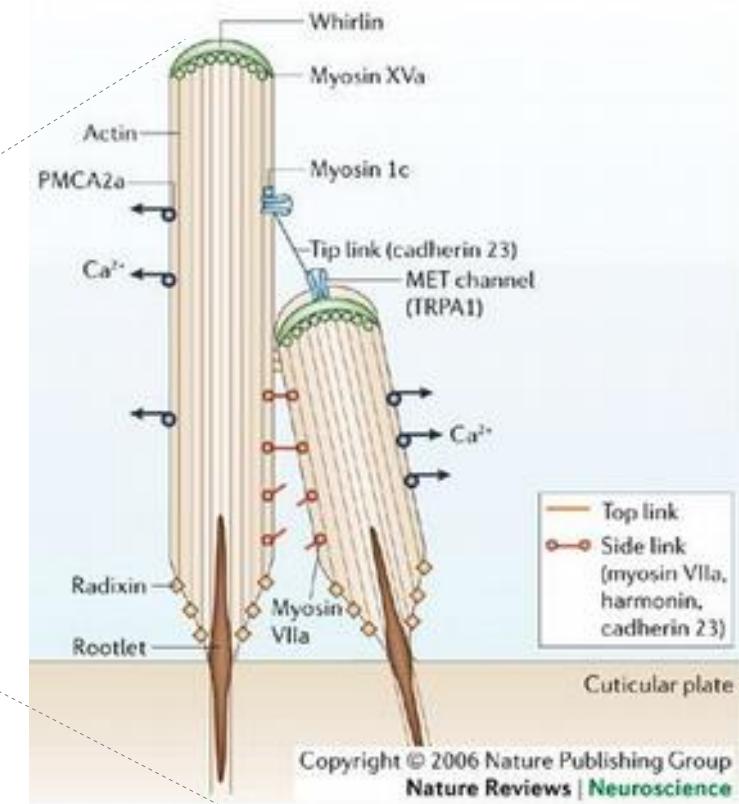


# DFNB3 (MYO15A)

- Autosomal recessive
- 17p11.2
- *MYO15A* (unconventional myosin-15; myosin XVa)  
→ stereocilia



The Organ of Corti

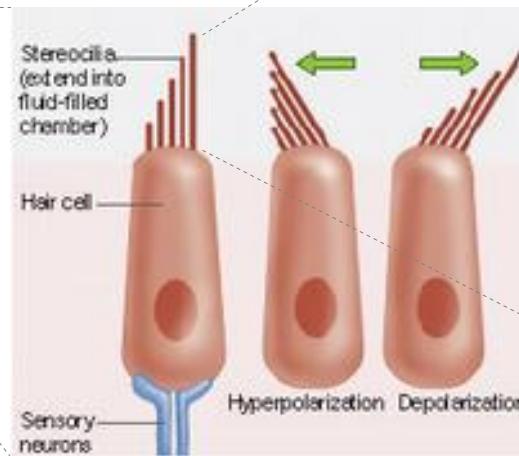
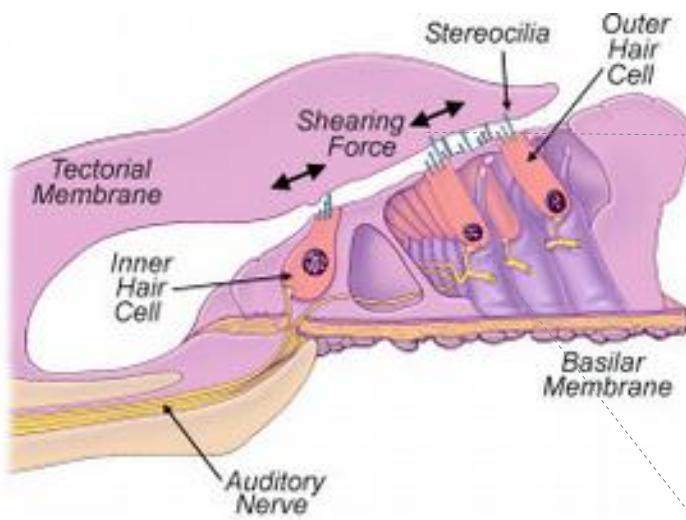


Examples: hearing loss

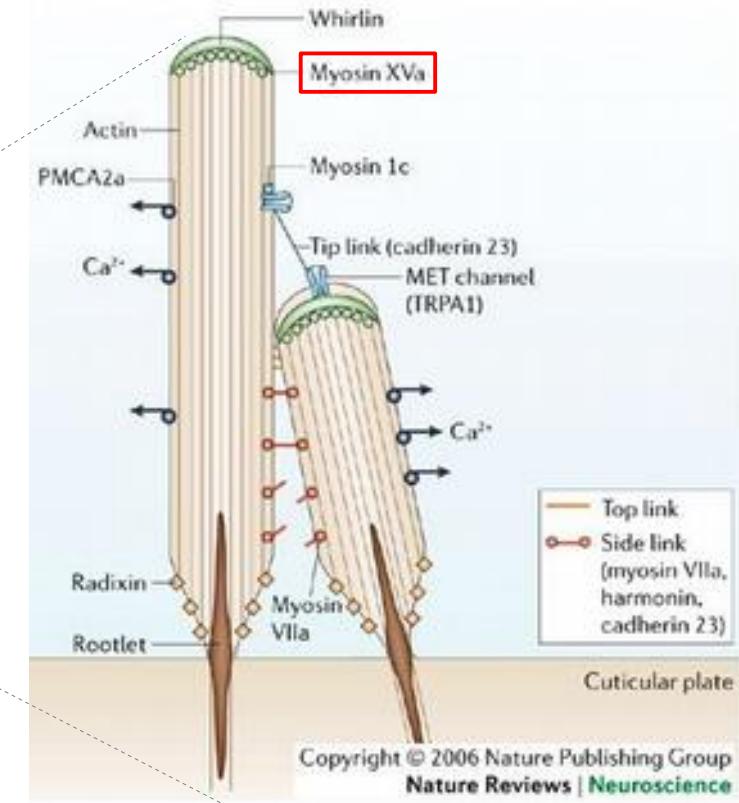


# DFNB3 (MYO15A)

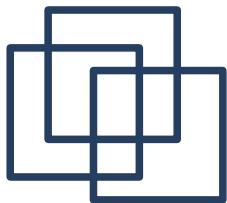
- Autosomal recessive
- 17p11.2
- *MYO15A* (unconventional myosin-15; myosin XVa)  
→ stereocilia



The Organ of Corti

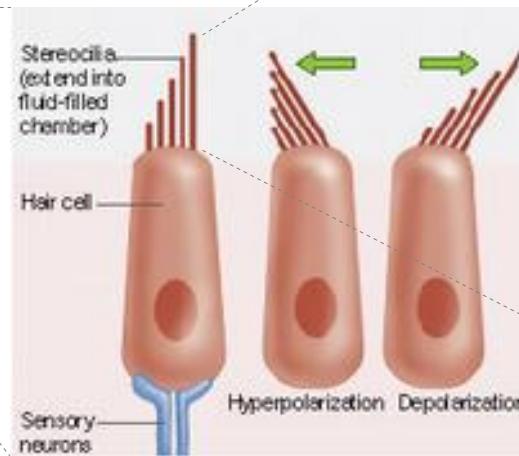
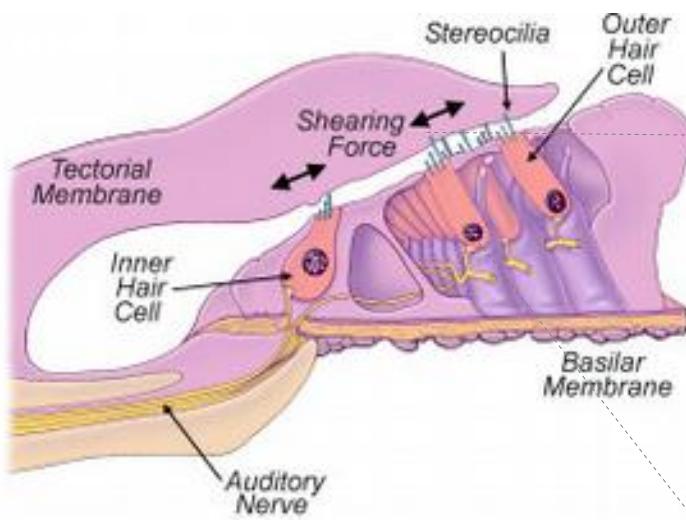


Examples: hearing loss

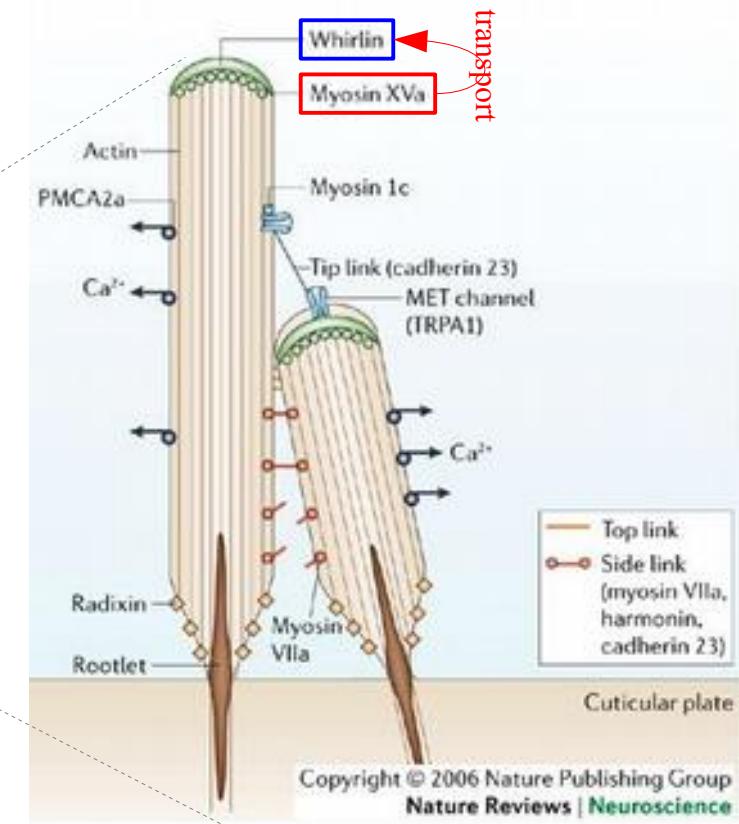


# DFNB3 (MYO15A)

- Autosomal recessive
- 17p11.2
- *MYO15A* (unconventional myosin-15; myosin XVa)  
→ stereocilia



The Organ of Corti

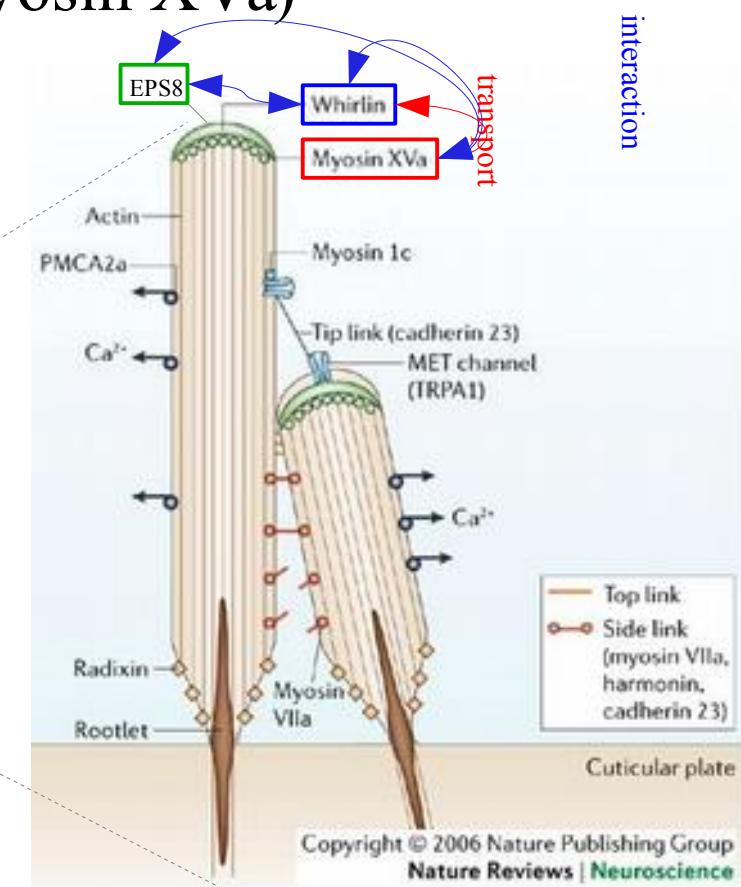
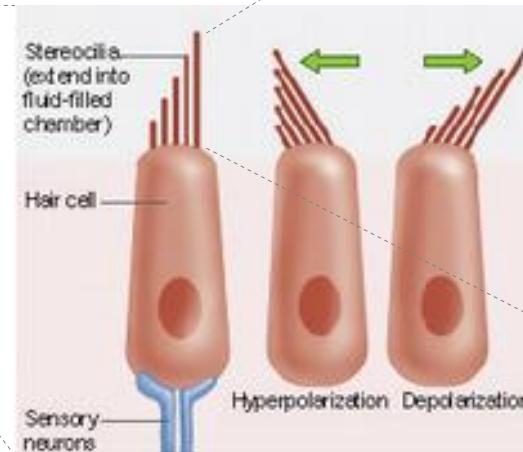
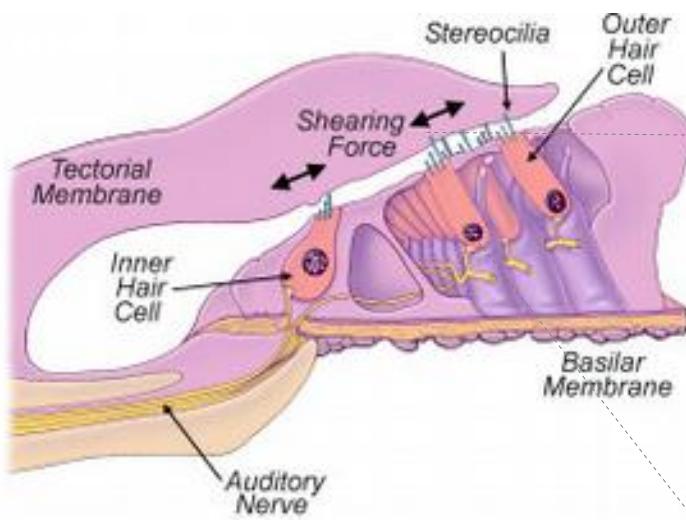


Examples: hearing loss

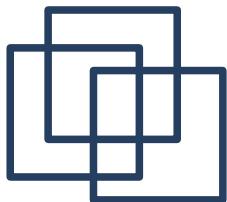


# DFNB3 (MYO15A)

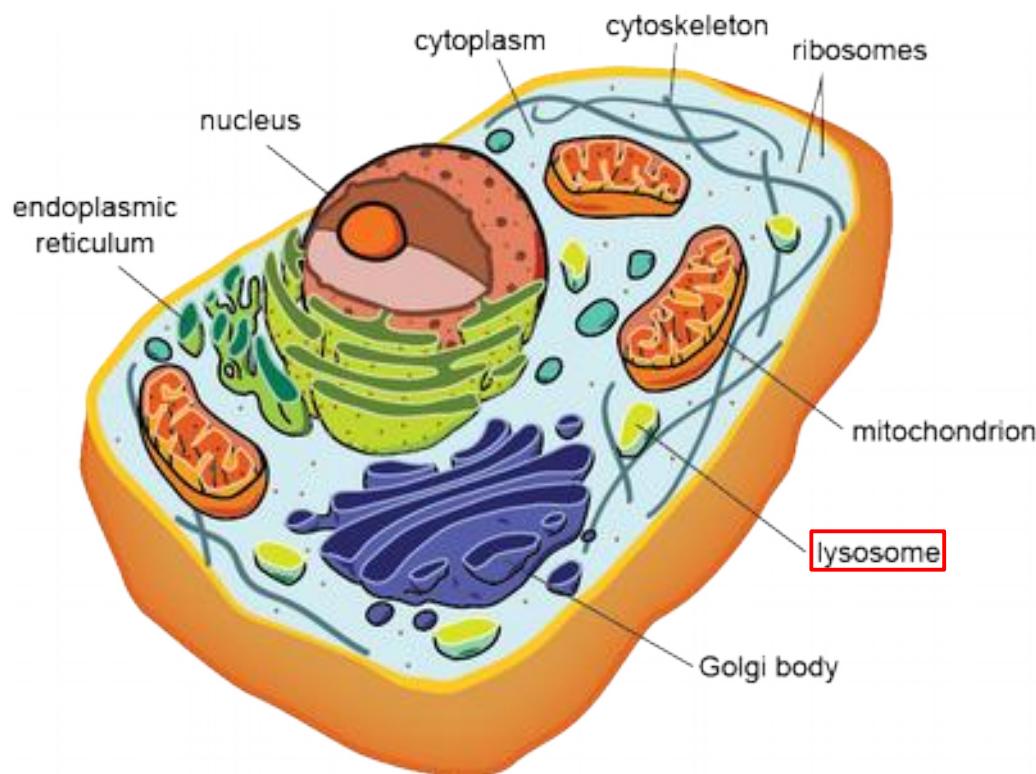
- Autosomal recessive
- 17p11.2
- *MYO15A* (unconventional myosin-15; myosin XVa)  
→ stereocilia



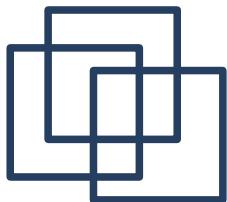
Examples: hearing loss



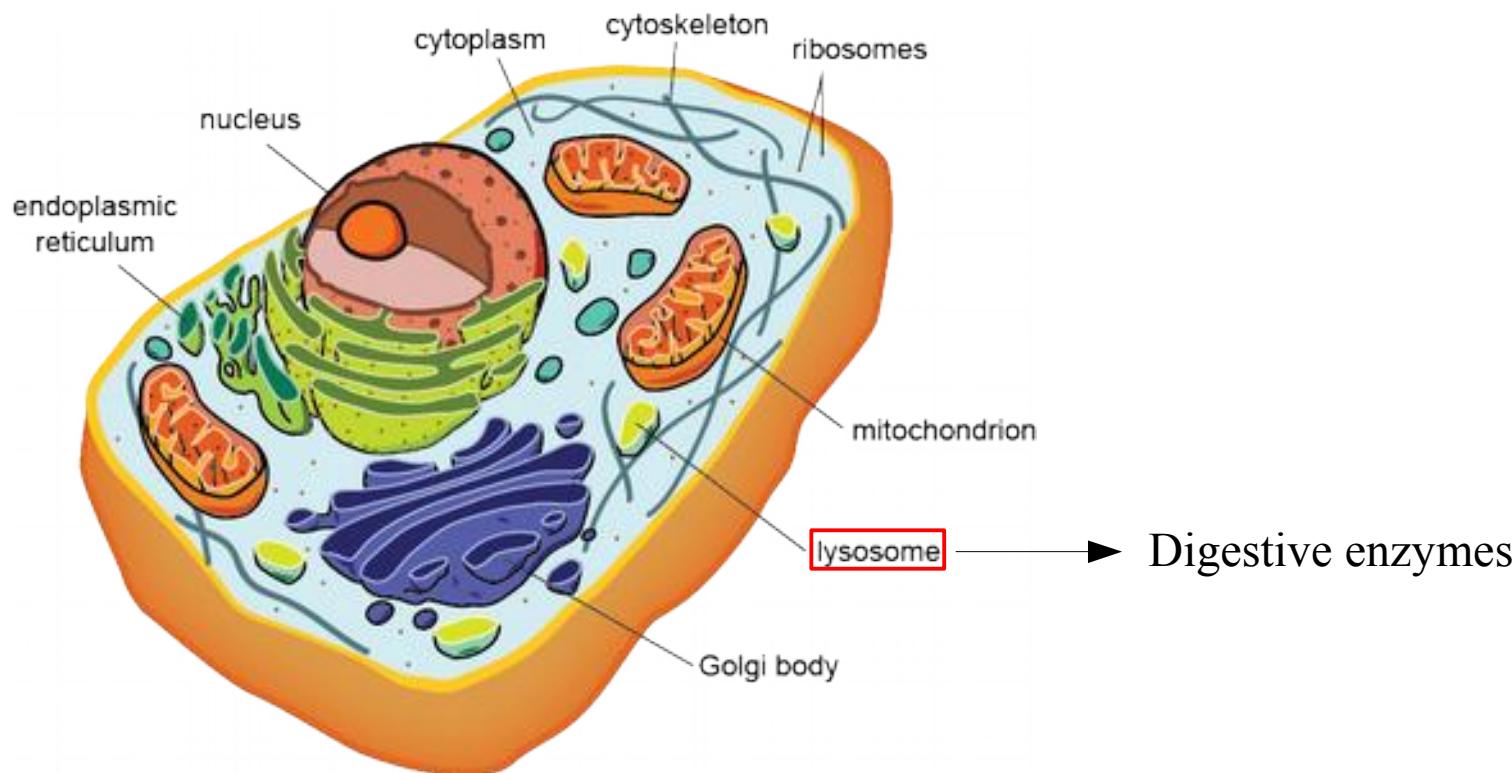
## Some examples: *stuttering*



Examples: *stuttering*



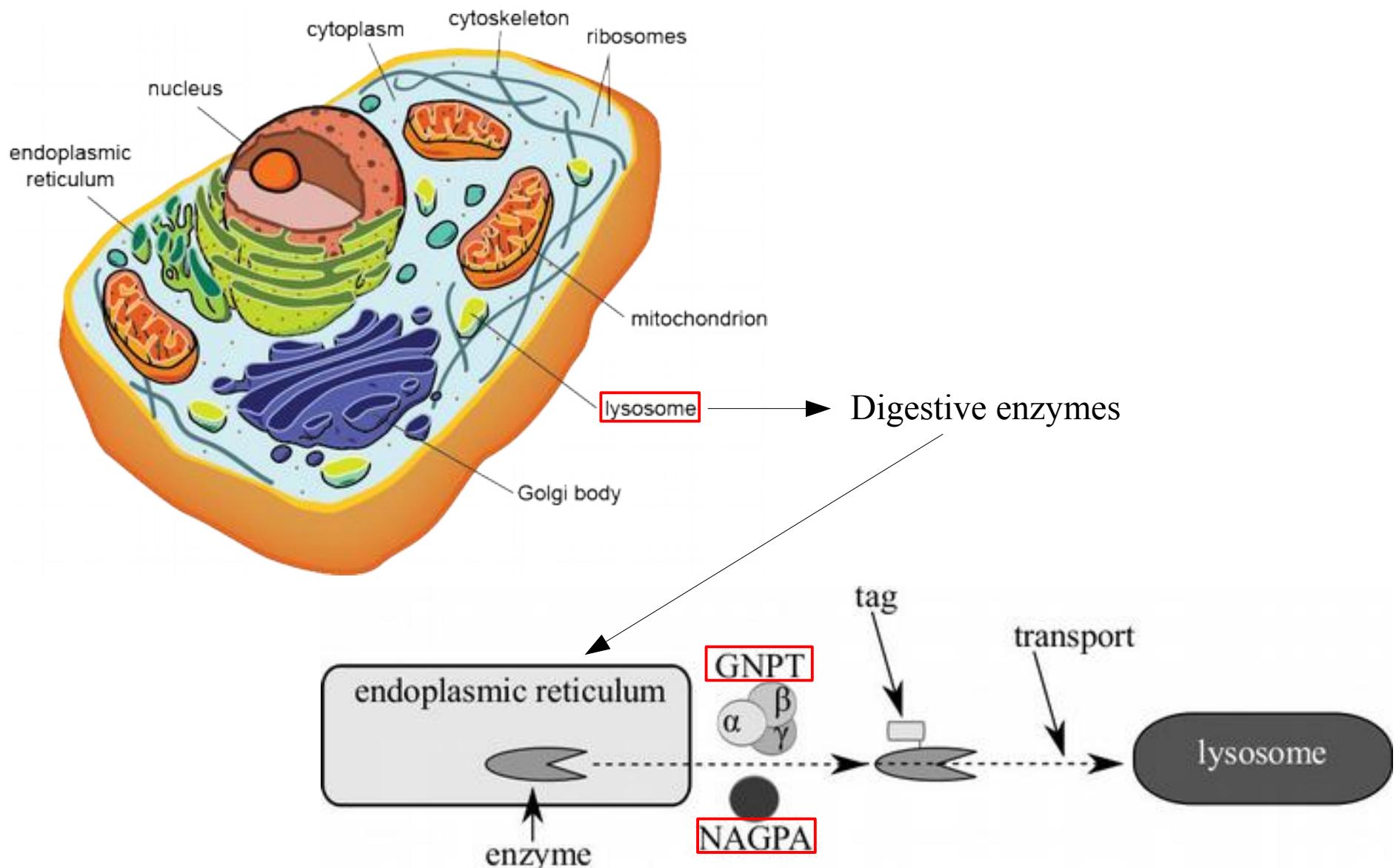
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Examples: *stuttering*



## Some examples: *stuttering*

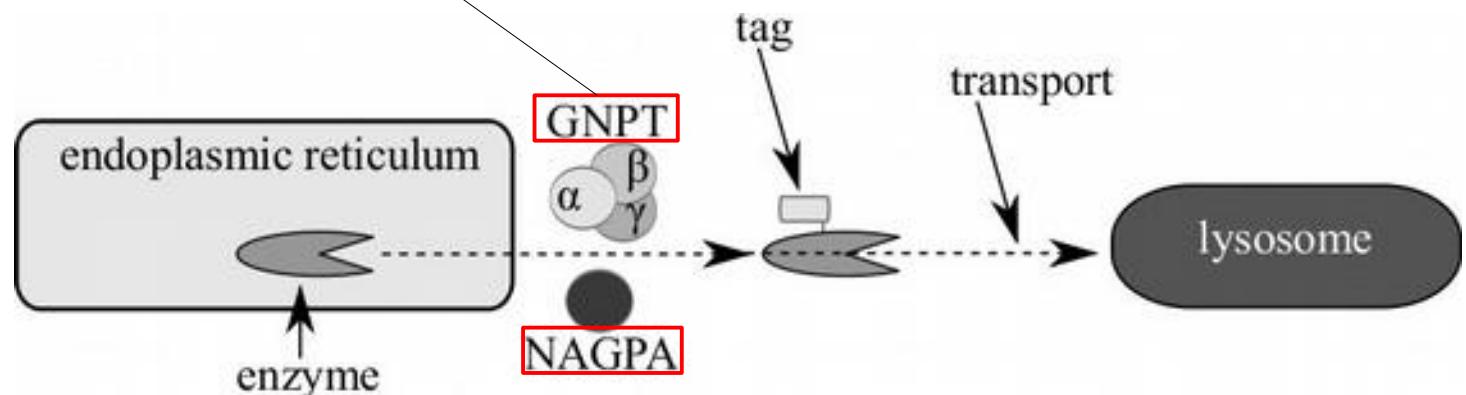


Examples: *stuttering*

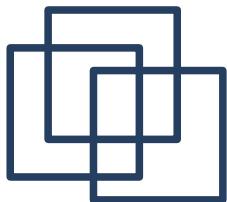


## Some examples: *stuttering*

**GNPT** → 3 subunits ( $\alpha$ ,  $\beta$ , and  $\gamma$ )



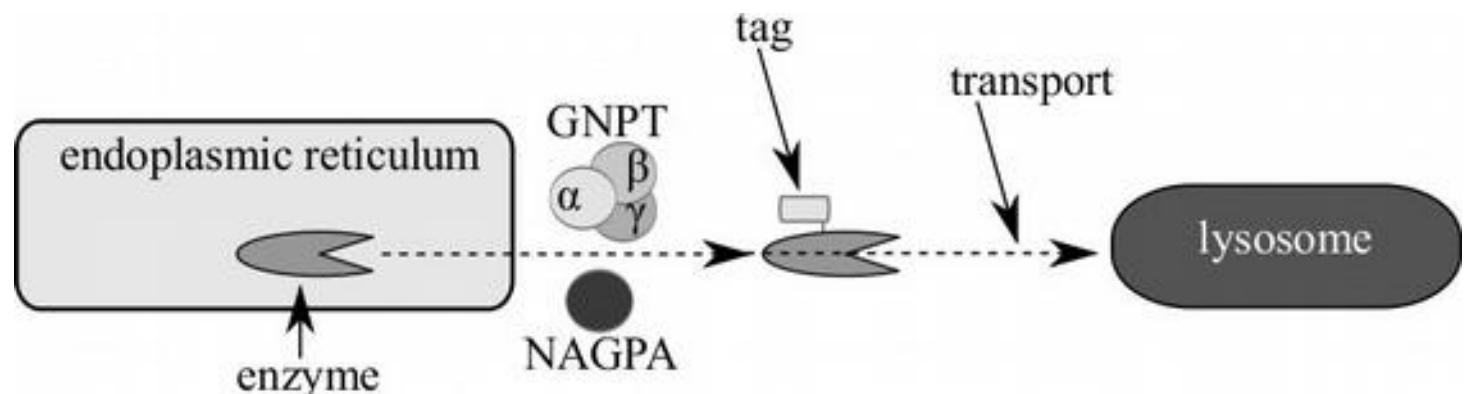
*Examples: stuttering*



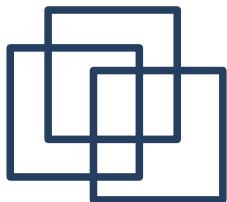
## Some examples: *stuttering*

**GNPT** → 3 subunits ( $\alpha$ ,  $\beta$ , and  $\gamma$ )

*GNPTAB* (chr 12)

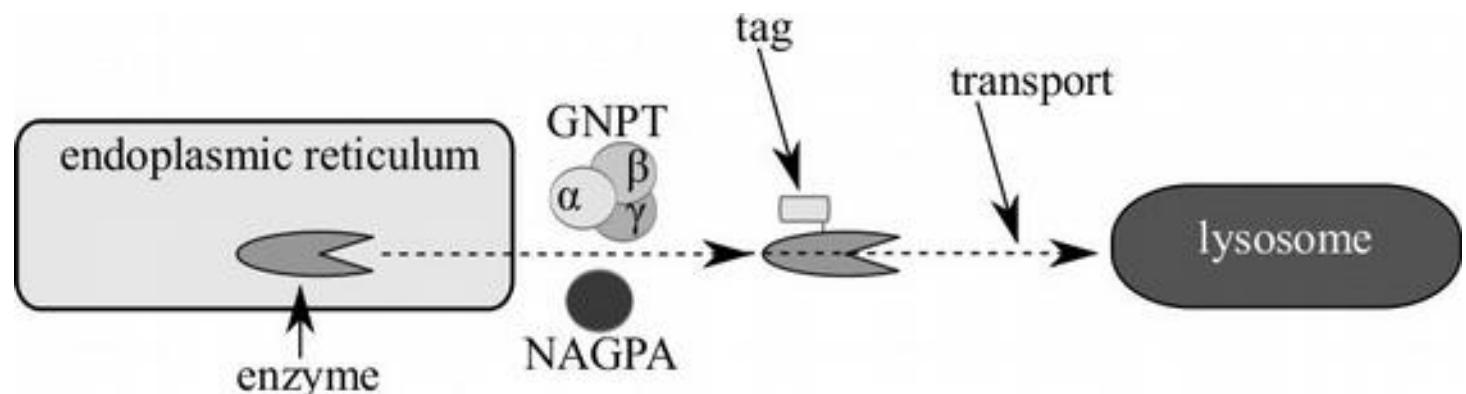


Examples: *stuttering*



## Some examples: *stuttering*

*GNPTG* (chr 16)  
↑  
 $\text{GNPT} \rightarrow 3 \text{ subunits } (\alpha, \beta, \text{ and } \gamma)$   
*GNPTAB* (chr 12)



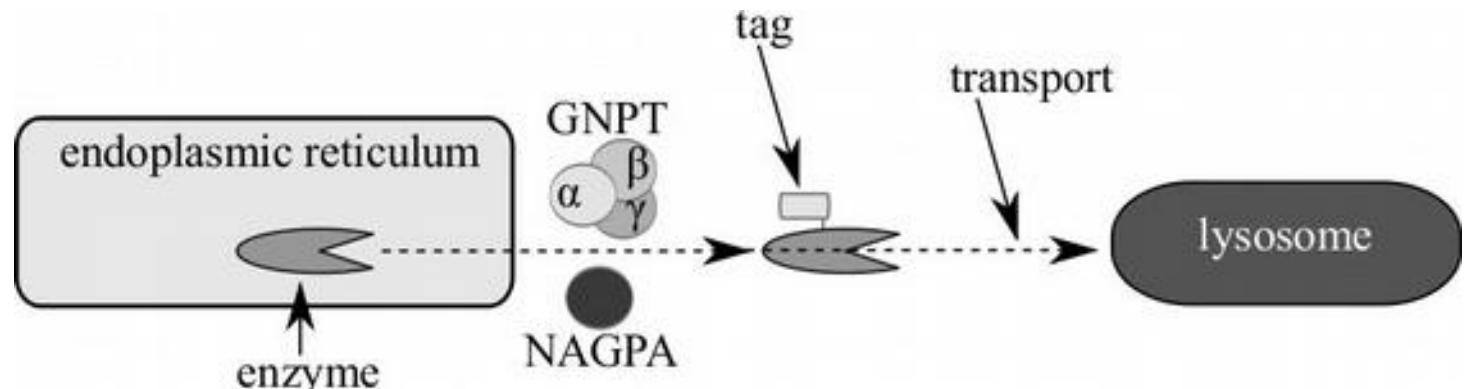
Examples: *stuttering*



## Some examples: *stuttering*

*GNPTG* (chr 16)  
↑  
 $\text{GNPT} \rightarrow 3 \text{ subunits } (\alpha, \beta, \text{ and } \gamma)$   
*GNPTAB* (chr 12)

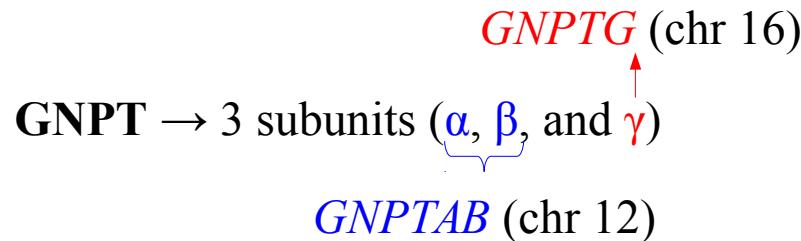
Genome-wide linkage in many Pakistani families → mutation in *GNPTAB*



Examples: *stuttering*

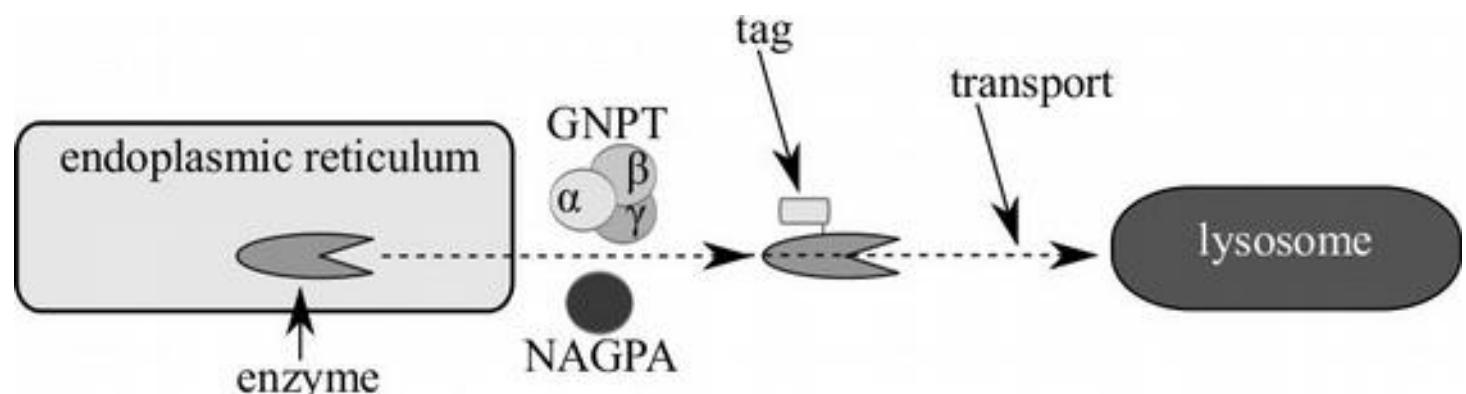


## Some examples: *stuttering*



Genome-wide linkage in many Pakistani families → mutation in *GNPTAB*

+ → identification of mutations in *GNPTG* and *NAGPA*



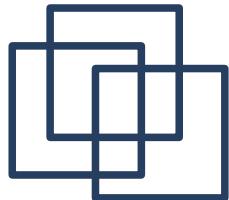
Examples: *stuttering*



## Some examples: *dyslexia*

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- Linkage in a Finnish family with severe dyslexia



## Some examples: *dyslexia*

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- Linkage in a Finnish family with severe dyslexia +
- Non-related patient



## Some examples: *dyslexia*

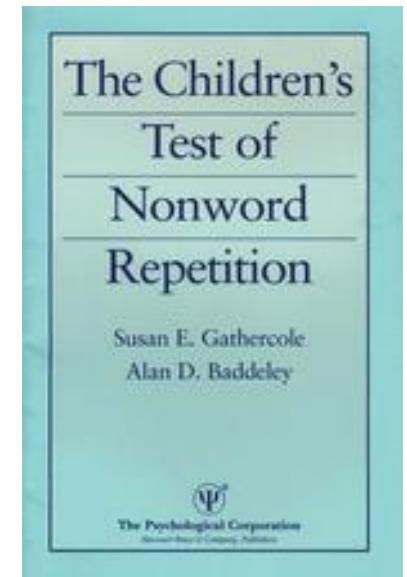
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- Linkage in a Finnish family with severe dyslexia +
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→ *ROBO1* gene on chromosome 3



## Some examples: dyslexia

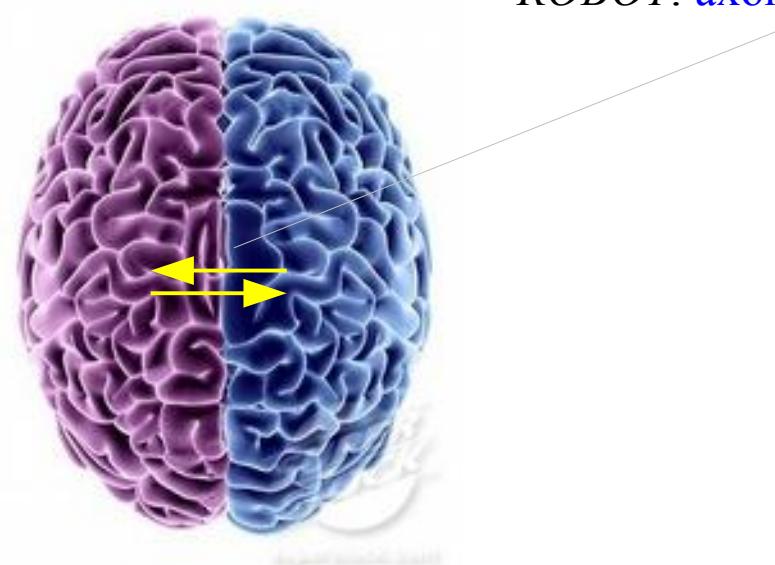
- Linkage in a Finnish family with severe dyslexia +
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→ *ROBO1* gene on chromosome 3
- Association with NWR in normal population



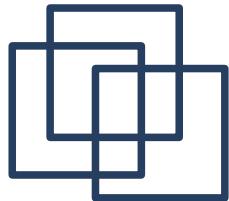


## Some examples: dyslexia

- Linkage in a Finnish family with severe dyslexia +
- Non-related patient  
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- Association with NWR in normal population



*ROBO1*: axonal midline crossing



# Conclusions

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- Just at the beginning



## Conclusions

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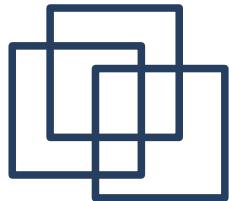
- Just at the beginning
- Already some genes known  
→ complex and fascinating mechanisms



## Conclusions

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  - complex and fascinating mechanisms
- “molecular windows” into the genetic architecture



## Conclusions

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- Already some genes known
  - complex and fascinating mechanisms
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- Varied **methodology**, multiple **complementary** approaches



## Conclusions

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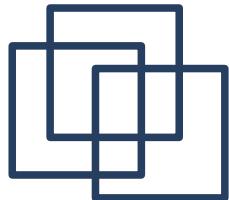
- Just at the beginning
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- More work:
  - (endo-)phenotyping (language scholars!)



## Conclusions

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- Already some genes known
  - complex and fascinating mechanisms
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  - large samples (association)
  - **pedigrees** (linkage)



## Conclusions

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- Just at the beginning
- Already some genes known
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  - large samples (association)
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**Thanks to:** Alejandrina Cristia, Sarah Graham, Steve Levinson

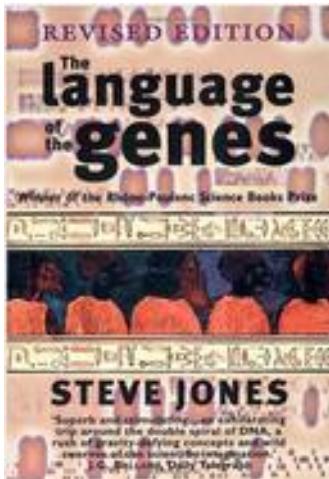
**Funding:** Netherlands Organisation for Scientific Research ( NWO) Vidi grant 276-70-022

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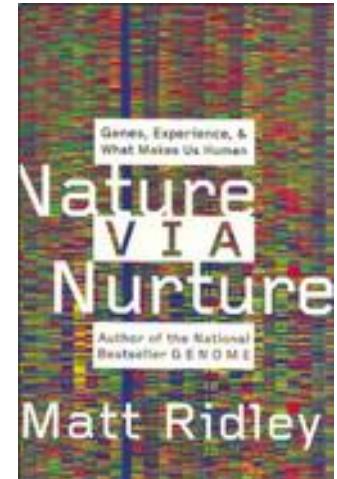


# Suggested reading

- General books:

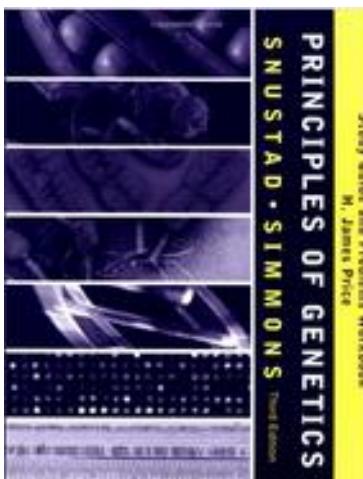


Jones, Steve (2000). *The language of the genes*. London: Flamingo.

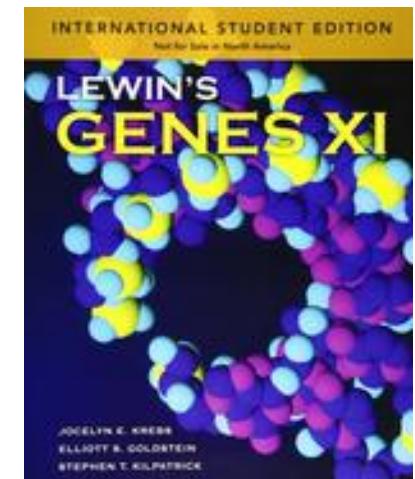


Ridley, M. (2004). *Nature via nurture: genes, experience and what makes us human*. London: Harper Perennial.

- Introductions to genetics:



Snustad, D. P., & Simmons, M. J. (2010). *Principles of genetics*. John Wiley & Sons, Inc.



Krebs, J. E., Kilpatrick, S. T., & Goldstein, E. S. (2013). *Lewin's Genes XI*. Jones and Bartlett Publishers, Inc.



## Suggested reading

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- **Heritability:**

Visscher, P. M., Hill, W. G., & Wray, N. R. (2008). Heritability in the genomics era—concepts and misconceptions. *Nat Rev Genet* **9**:255–266. doi:10.1038/nrg2322

Charney, E. (2012). Behavior genetics and postgenomics. *Behavioral and Brain Sciences* **35**:331–358. doi:10.1017/S0140525X11002226

Stromswold, K. (2001). The Heritability of Language: A Review and Metaanalysis of Twin, Adoption, and Linkage Studies. *Language* **77**:647–723.

- **Linkage:**

Dawn Teare, M., & Barrett, J. H. (2005). Genetic linkage studies. *The Lancet* **366**:1036–1044. doi:10.1016/S0140-6736(05)67382-5

- **Association:**

Hirschhorn, J. N., & Daly, M. J. (2005). Genome-wide association studies for common diseases and complex traits. *Nature Reviews Genetics* **6**:95–108. doi:10.1038/nrg1521

Balding, D. J. (2006). A tutorial on statistical methods for population association studies. *Nature Reviews Genetics* **7**:781–791. doi:10.1038/nrg1916



## Suggested reading

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- **Sequencing:**

Deriziotis, P., & Fisher, S. E. (2013). Neurogenomics of speech and language disorders: the road ahead. *Genome biology* **14**:204. doi:10.1186/gb-2013-14-4-204

O'Roak, B. J., Deriziotis, P., Lee, C., Vives, L., Schwartz, J. J., Girirajan, S., ... Eichler, E. E. (2011). Exome sequencing in sporadic autism spectrum disorders identifies severe de novo mutations. *Nature genetics* **43**:585–589. doi:10.1038/ng.835

- **Genetics of language:**

Graham, S. A., & Fisher, S. E. (2013). Decoding the genetics of speech and language. *Current Opinion in Neurobiology* **23**:43-51. doi:10.1016/j.conb.2012.11.006

Kang, C., & Drayna, D. (2011). Genetics of speech and language disorders. *Ann rev genomics hum genet* **12**:145–164. doi:10.1146/annurev-genom-090810-183119

Smith, S. D., Grigorenko, E., Willcutt, E., Pennington, B. F., Olson, R. K., & DeFries, J. C. (2010). Etiologies and molecular mechanisms of communication disorders. *Journal of developmental and behavioral pediatrics* **31**, 555–563. doi:10.1097/DBP.0b013e3181ee3d9e

Bishop, D. V. M. (2009). Genes, cognition, and communication: insights from neurodevelopmental disorders. *Ann N Y Acad Sci* **1156**:1–18. doi:10.1111/j.1749-6632.2009.04419.x

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