Office hours

REVISED

- Fridays 12-1pm (zoom or Stewart Biology, N5/8)

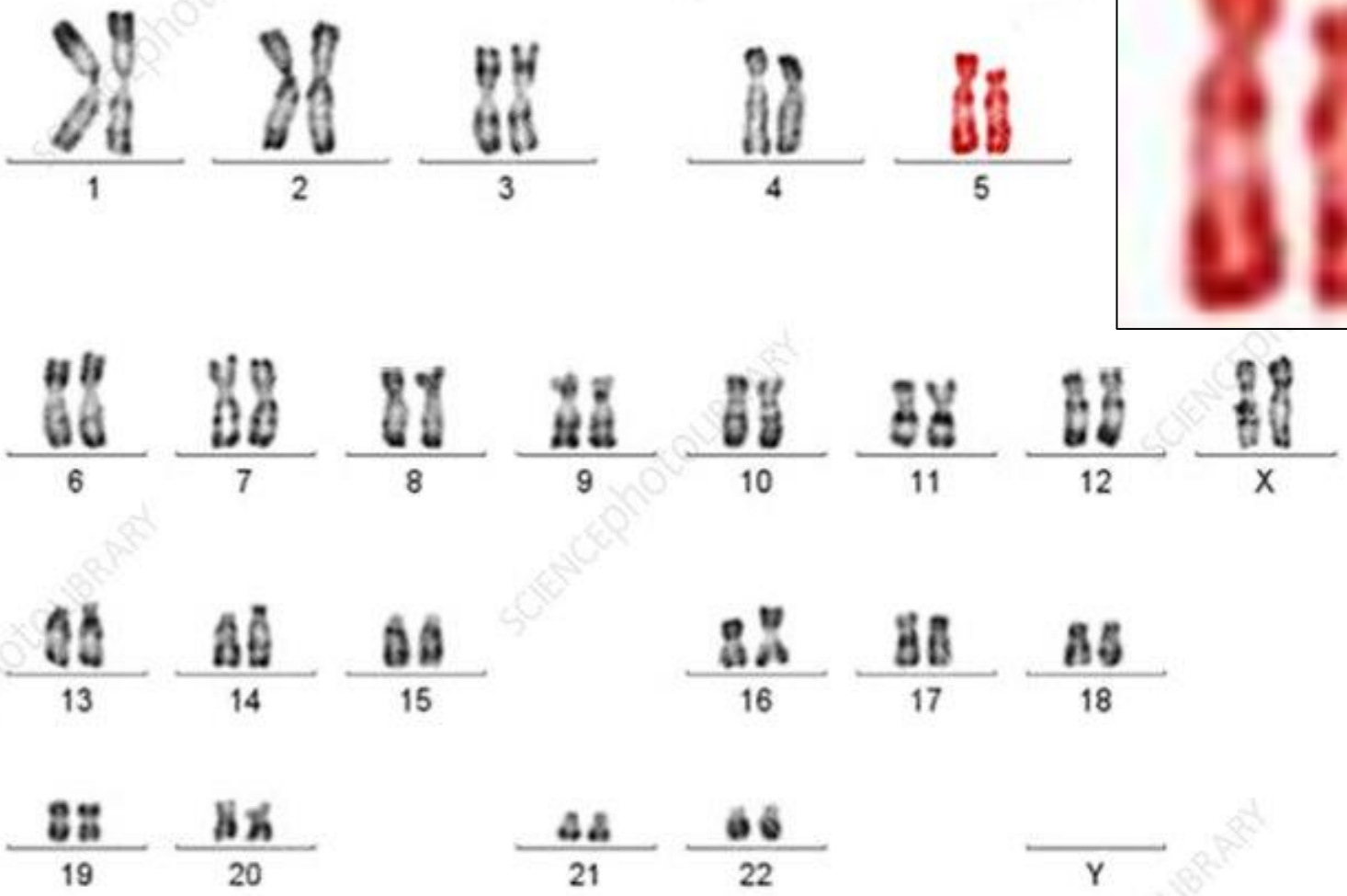
https://mcgill.zoom.us/j/81407275167?pwd=8Cgm0RPnWQRlOdaCNFyXnS3M8amQUj.1

- By appointment
- Before or after class, right here in Leacock 132

Large Scale Chromosomal Changes

Changes in Chromosome Structure

Cri-du-chat Syndrome



Cri-du-chat Syndrome

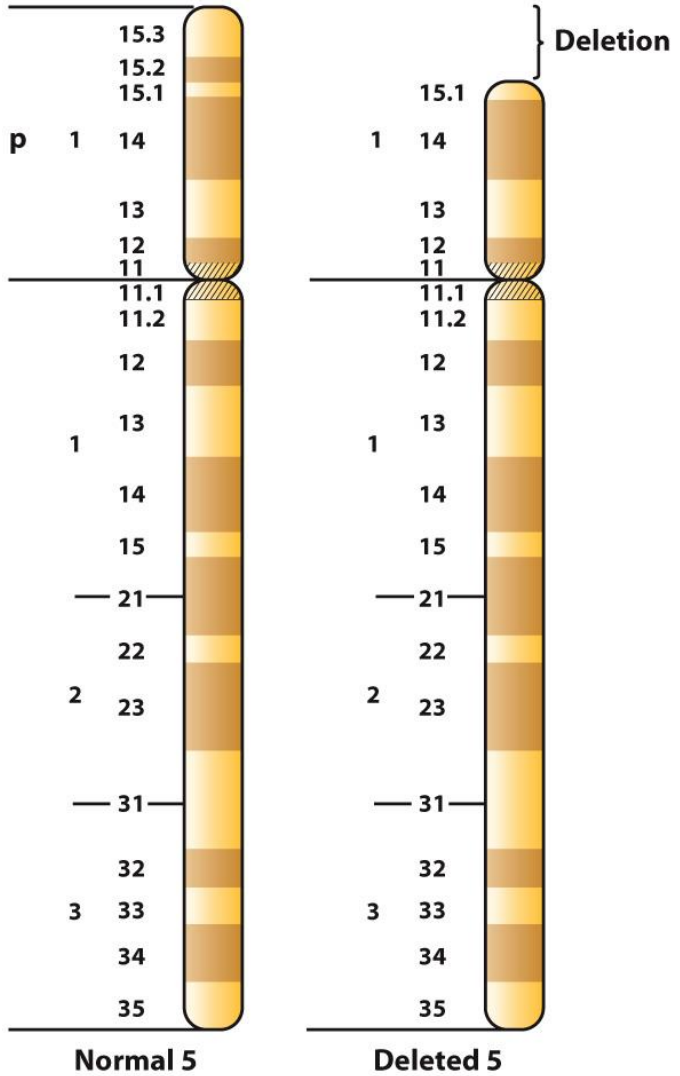


Figure 17-22
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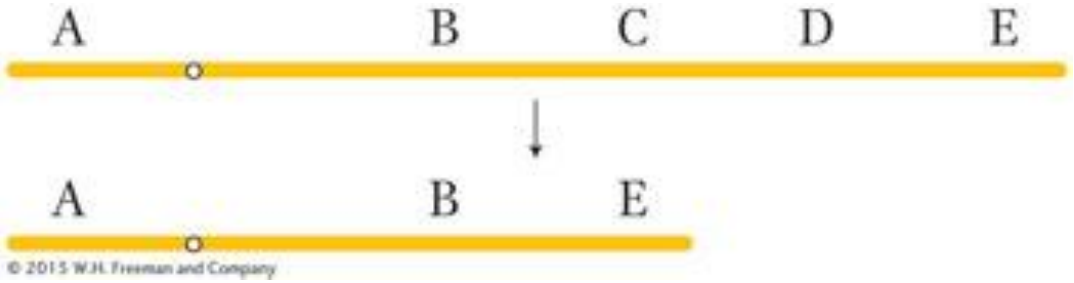
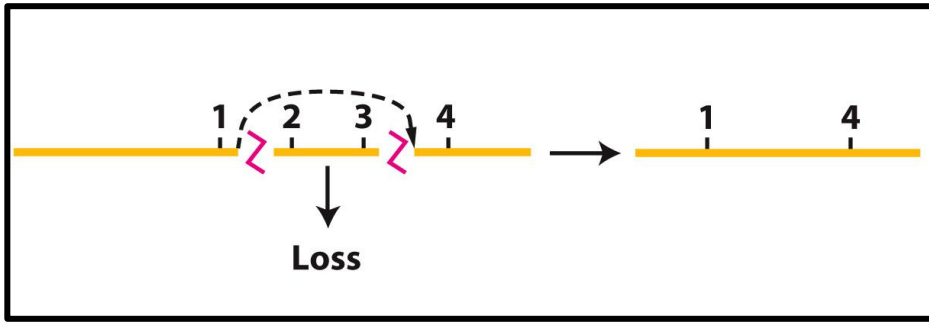
Chromosomal deletions and their possible causes



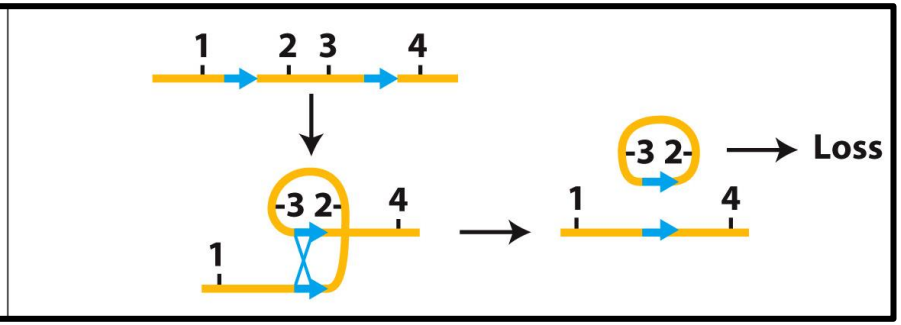
Can be large
Can be small

How would genes look on this diagram?

Breakage and rejoining



Crossing over between repetitive DNA



Chromosomal deletions

example: possible origin of the Williams syndrome deletion

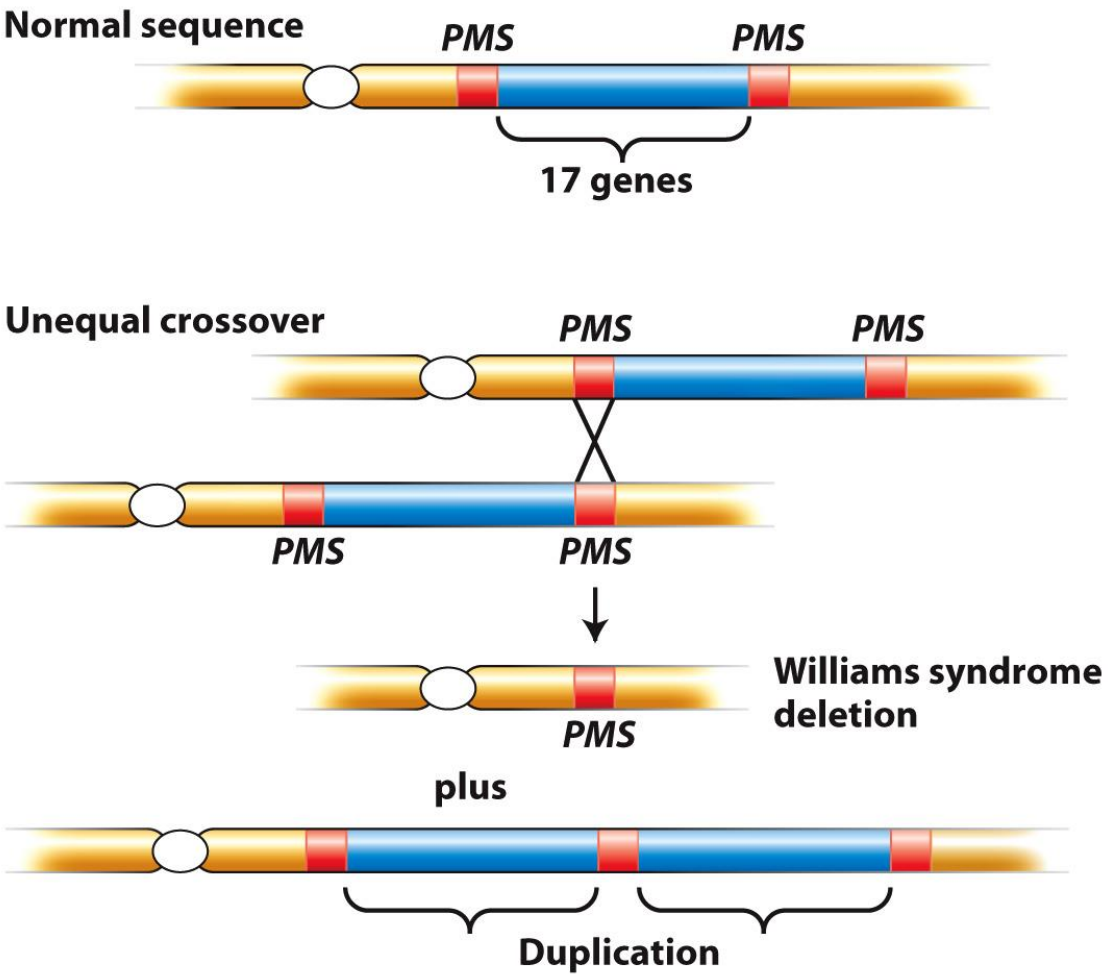


Figure 17-23
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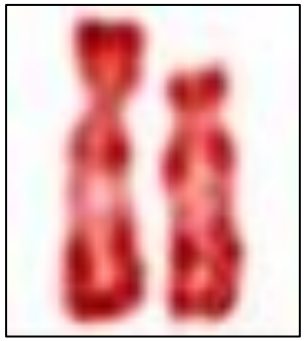
Williams syndrome is found at a frequency of about 1 in 10,000 people.

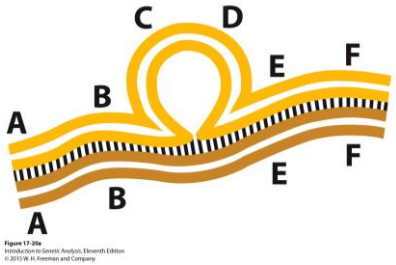
Among other traits, individuals often have pronounced musical or singing ability, as well as hyper-sociality.

The syndrome is almost always caused by a 1.5-Mb deletion on one homolog of chromosome 7, specifically at band 7q11.23.

How to detect chromosomal deletions

By observing their length or pairing



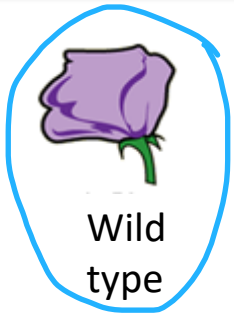


Deletion loop observed in paired homologous chromosomes

By doing a complementation test

Through DNA analysis using genomic techniques

Complementation test - concept



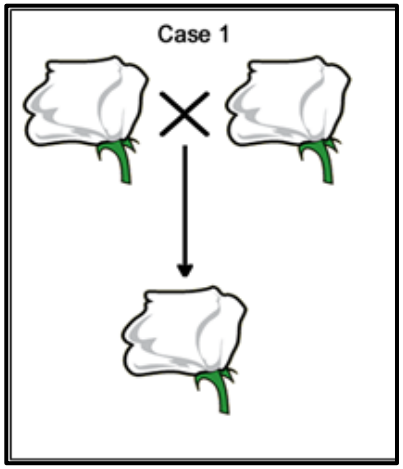
Wild type

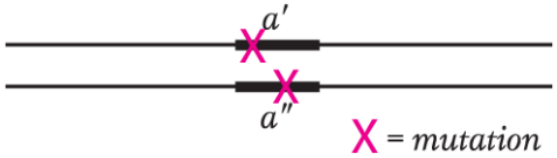
Mutant strain 1

Mutant strain 2

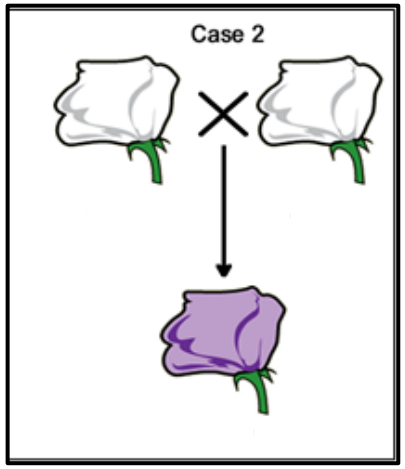
Do strain 1 and strain 2 have mutations in the same gene?

"fails to complement"

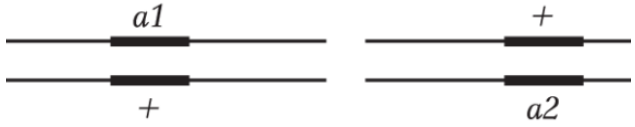




Interpretation: Strain 1 and strain 2 have mutations in the same gene



"complements"



Interpretation: Strain 1 and strain 2 have mutations in different genes

Testing for chromosomal deletions using complementation

Strain to be tested

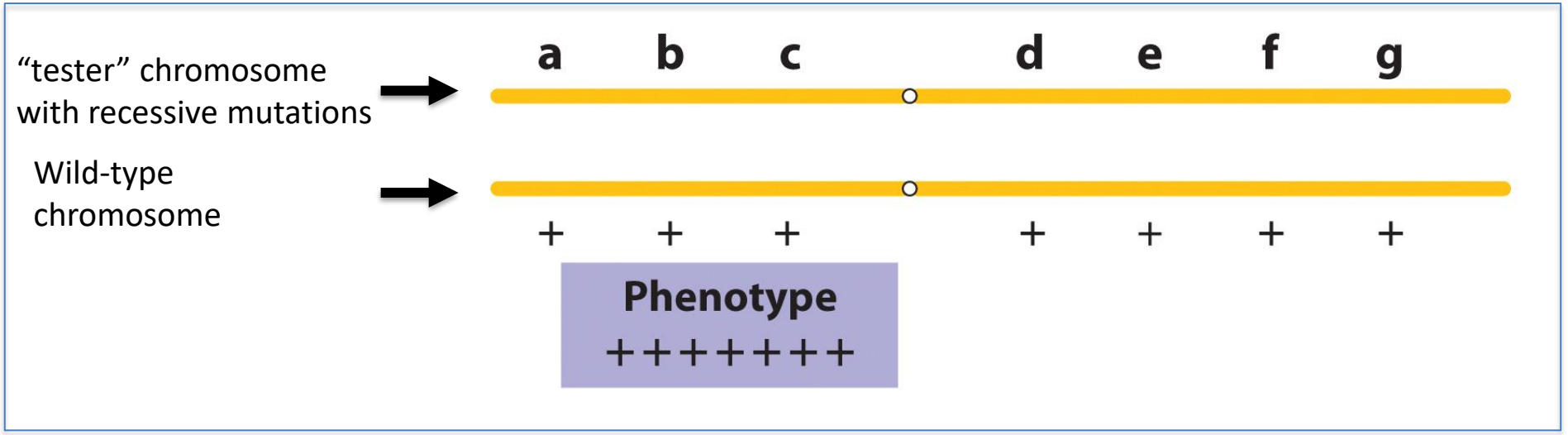
"tester" strain with multiple with recessive mutations

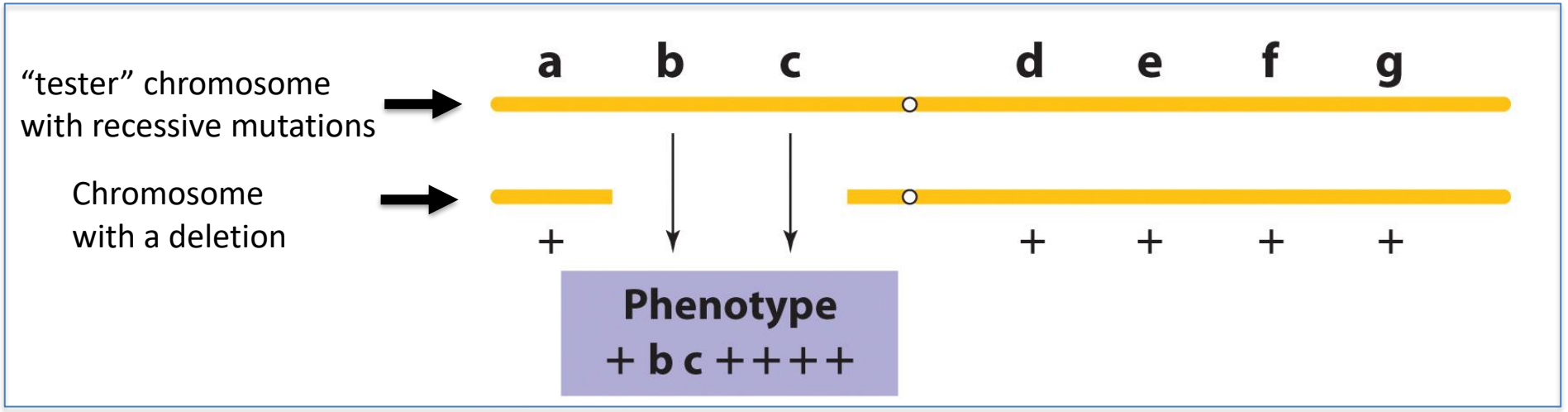
++++++/++++++ x abcdefg/abcdefg

++++++/abcdefg Phenotype?

Detecting chromosomal deletions

complementation test



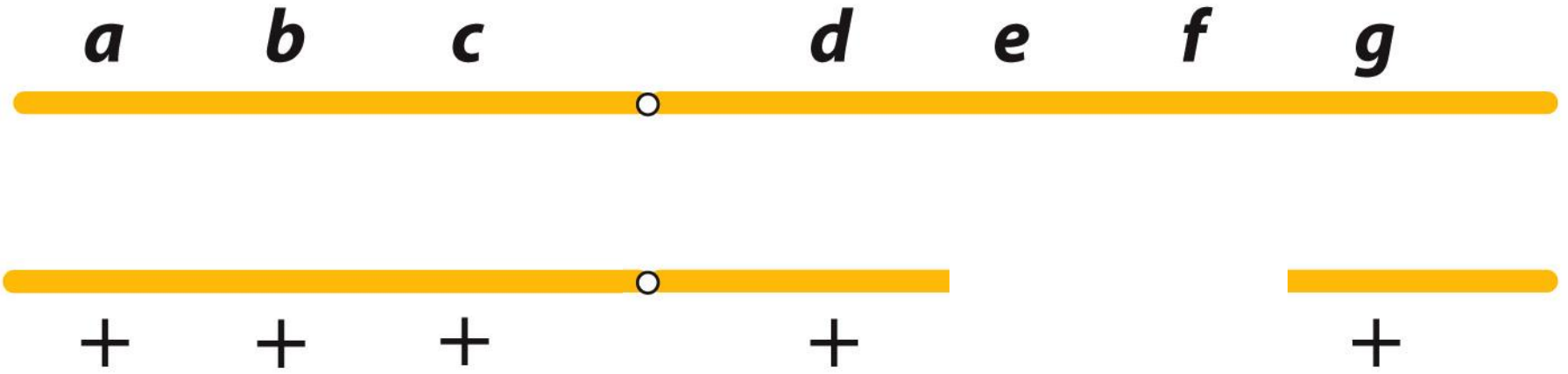


Using a complementation test to detect chromosomal deletions

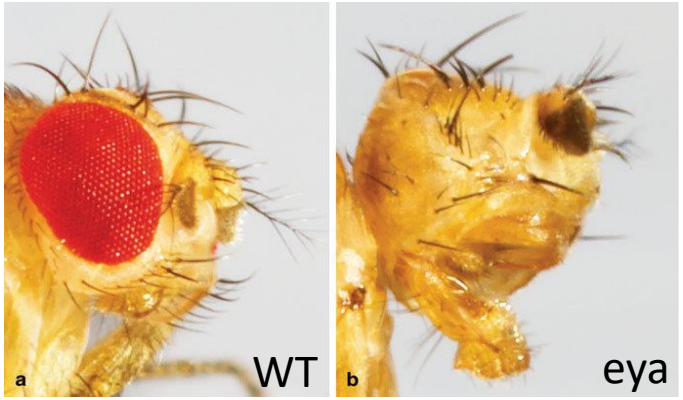
"unknown strain" x abcdefg/abcdefg

"unknown strain" /abcdefg

Phenotype: e f



Known deletions can be used to map a recessive mutant allele

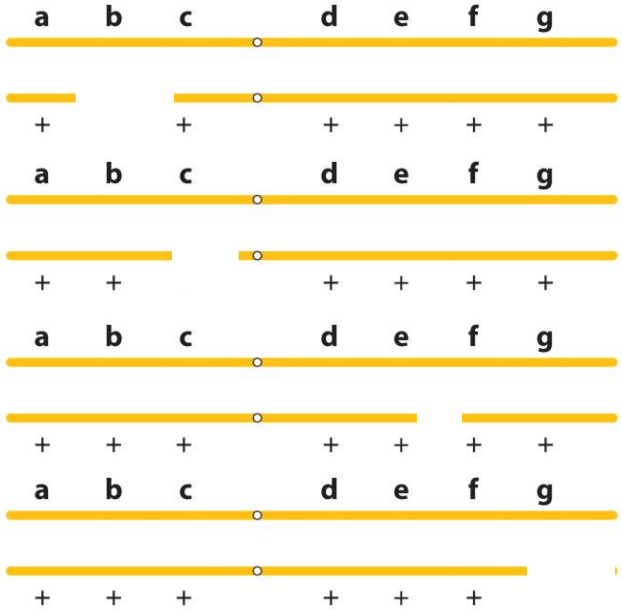


Example:

Flies homozygous for the “eya” (eyes absent) chromosome have no eyes.

Where is the mutated eya gene located?

Deletion mapping of the *eya* mutation: cross to known deletions and check F1 phenotype



phenotype: normal eyes

phenotype: normal eyes

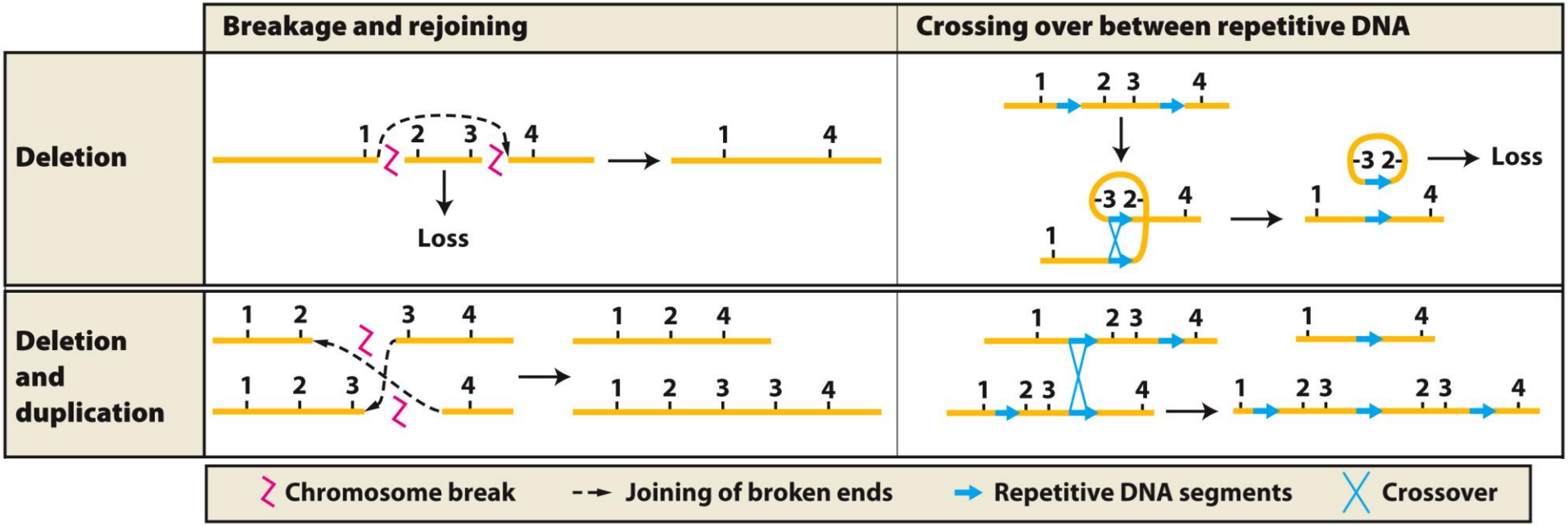
phenotype: no eyes

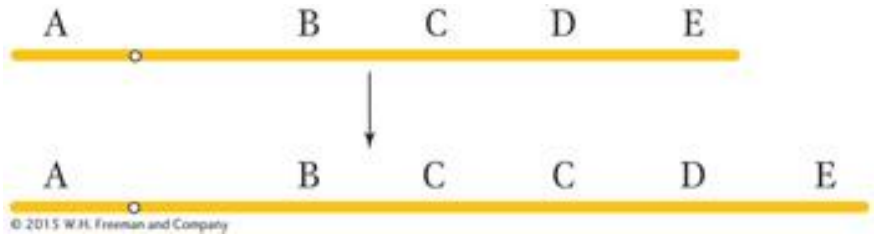
phenotype: normal eyes

This analysis identifies which region of the chromosome bears the *eya* mutation.

Chromosomal Rearrangements:

Duplications

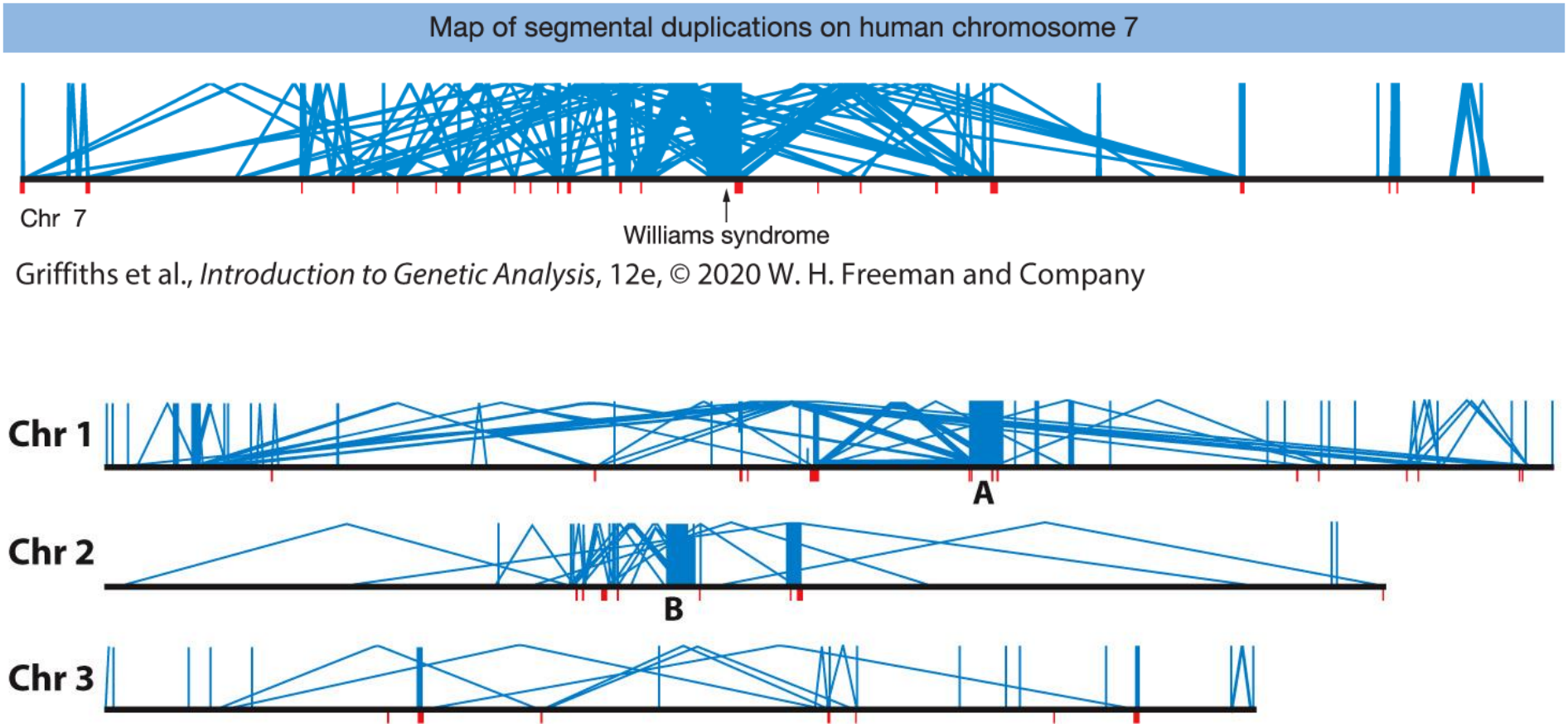




large duplications are called “segmental duplications”

Chromosomal duplications

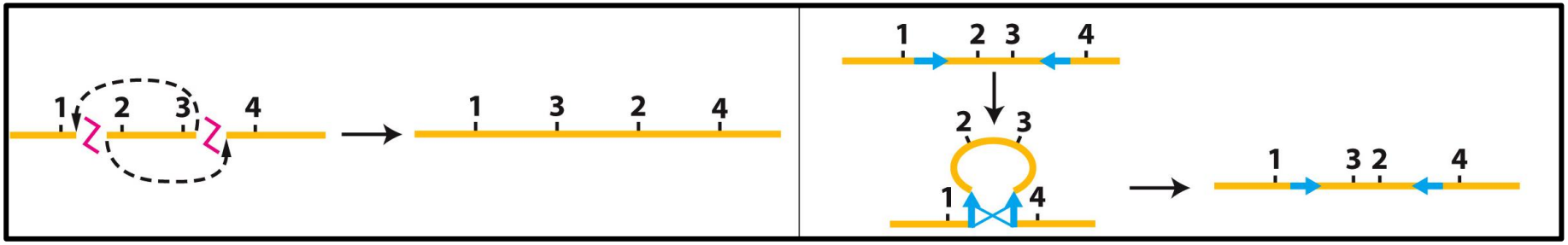
Map of segmental duplications in the human genome

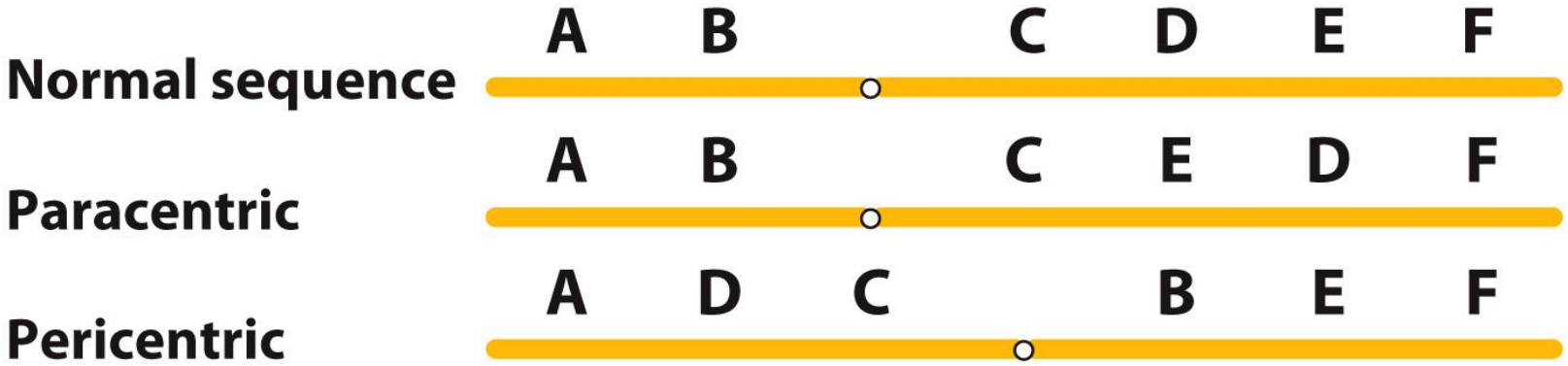


Think Break

Chromosomal Rearrangements:

Inversions





Unnumbered 17 p642
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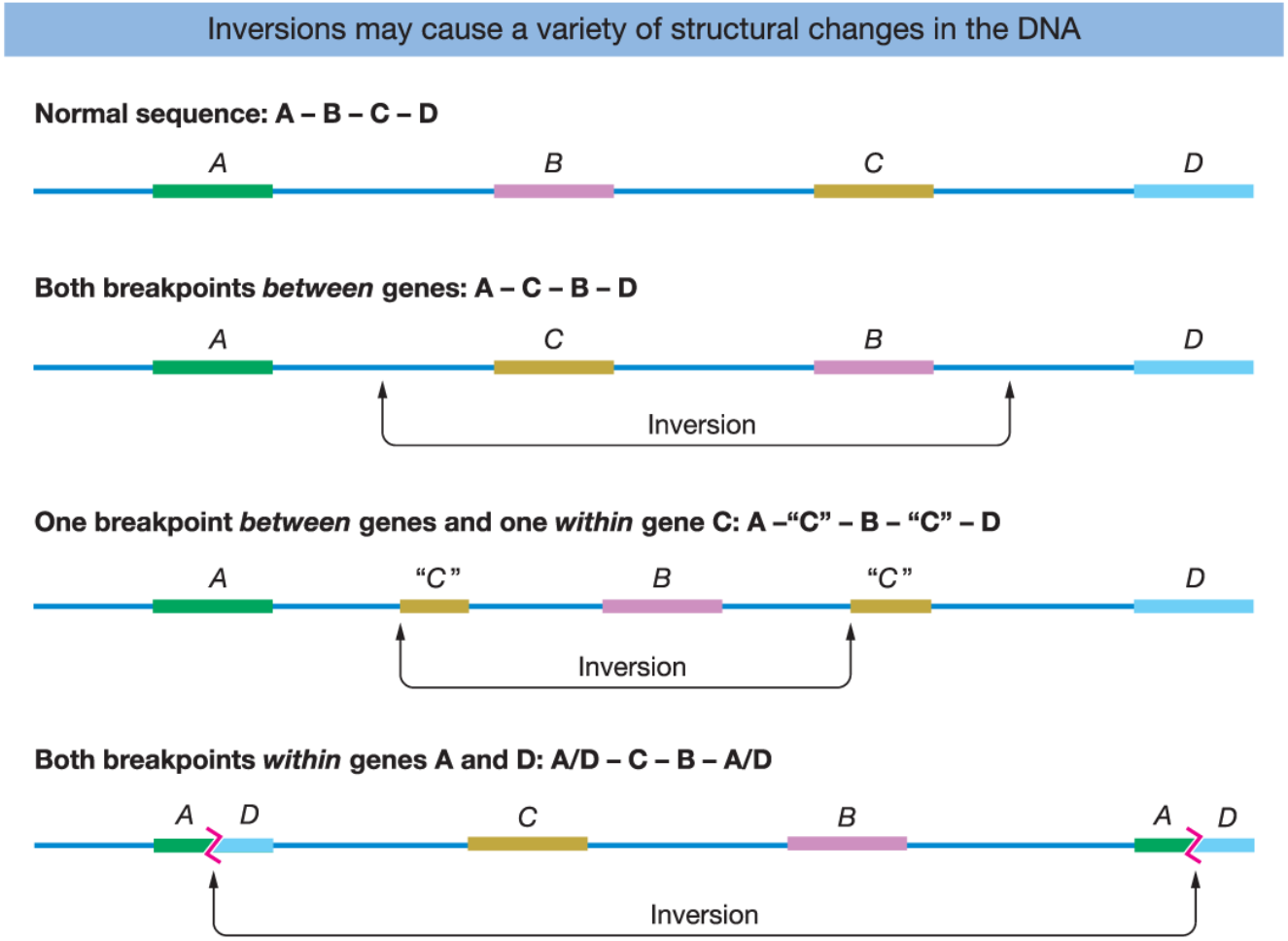
Chromosomal inversions

Consequences: somatic



No genes disrupted

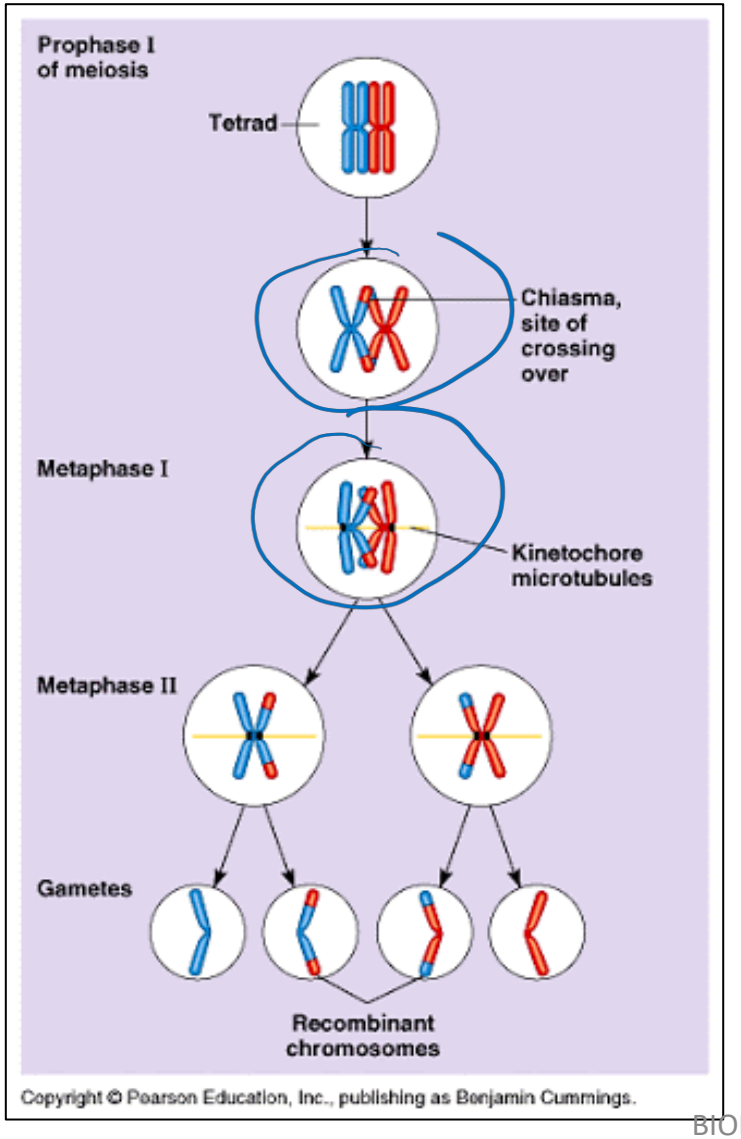
Gene C disrupted

A/D gene fusion

Griffiths et al., *Introduction to Genetic Analysis*, 12e, © 2020 W. H. Freeman and Company

Chromosomal inversions

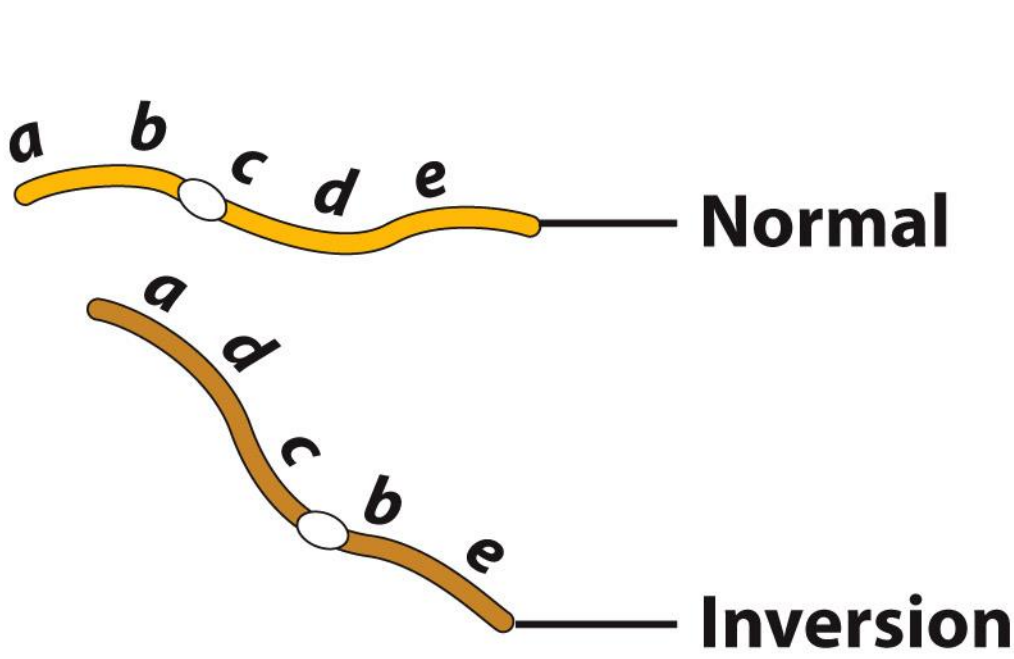
Consequences: germline



Reminder: recombination occurs during meiosis I

Chromosomal inversions

Effects on chromosome behavior during meiosis



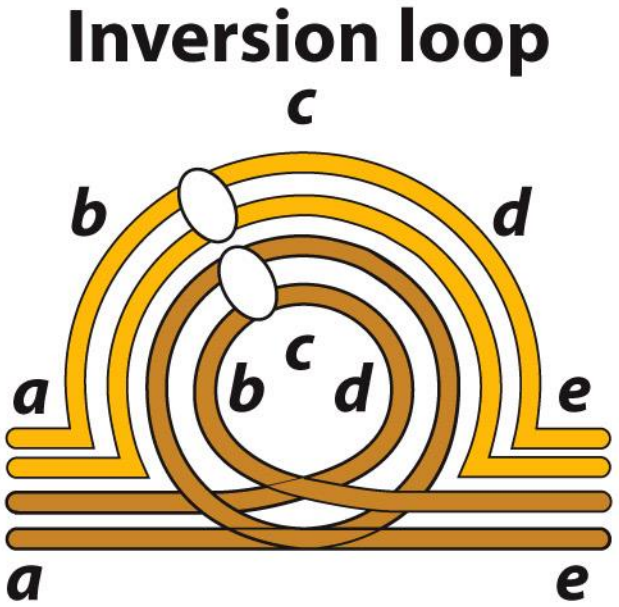


Figure 17-27
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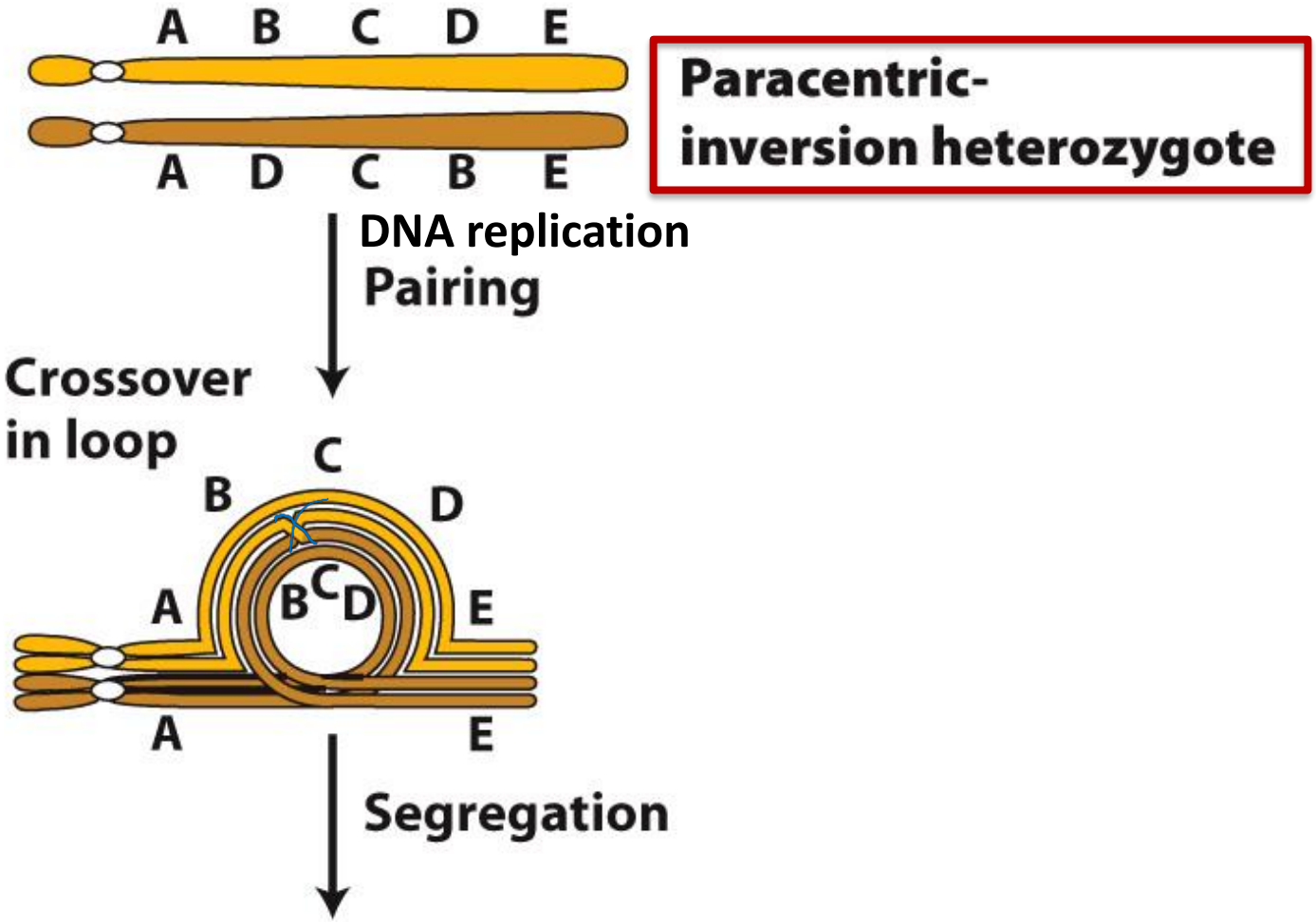
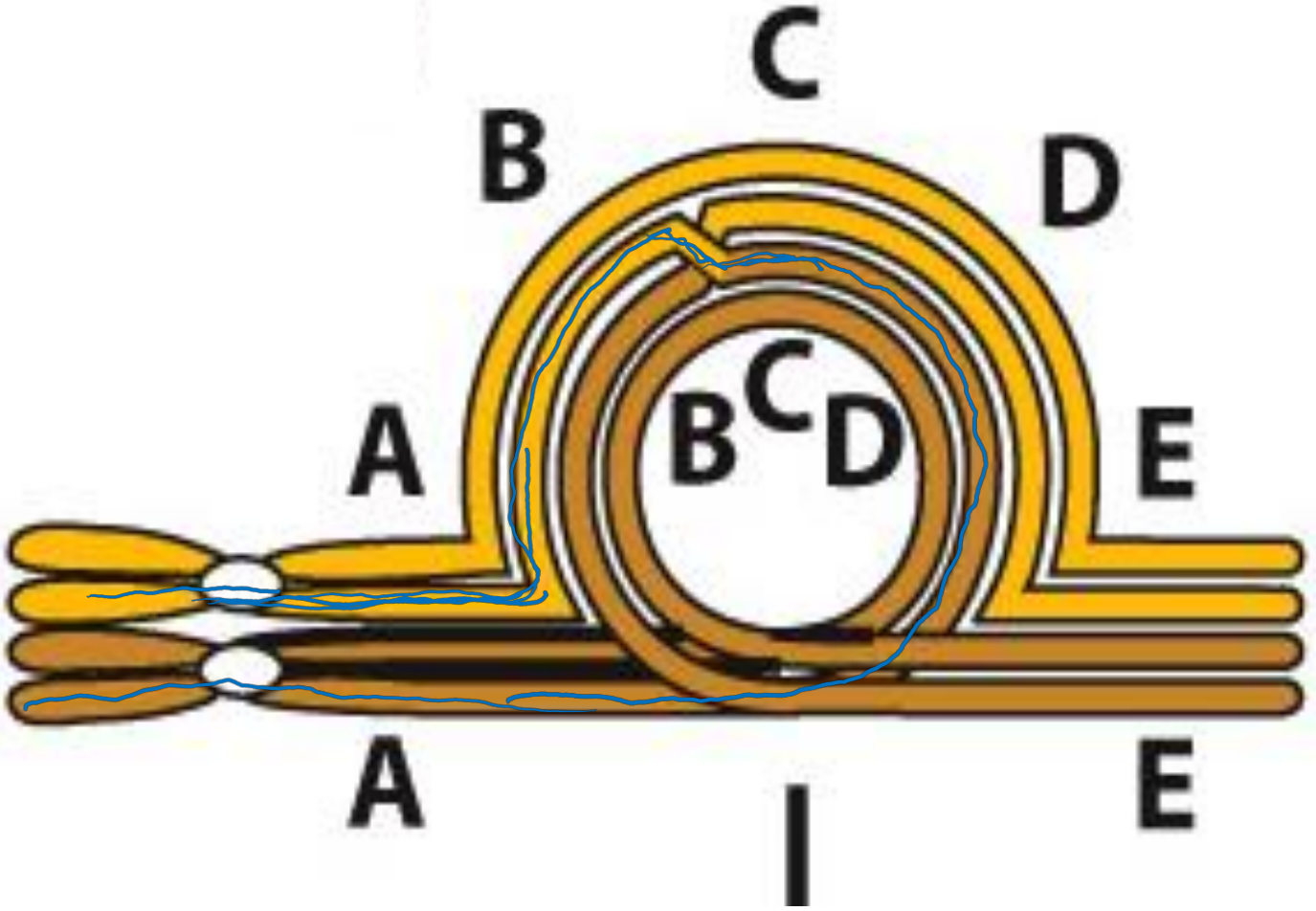
Chromosomal inversions

Effects on chromosome behavior during meiosis



Chromosomal inversions

Consequences: germline



Crossing over in a paracentric inversion heterozygote → dicentric chromosome

Paracentric inversions → deletions

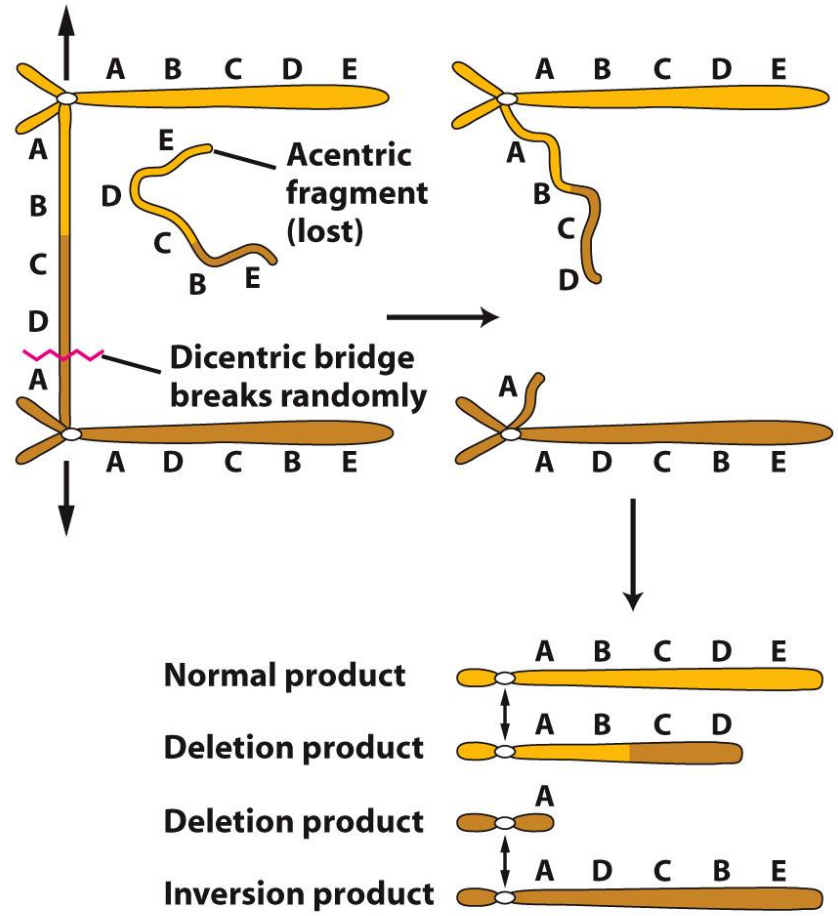


Figure 17-28 part 2
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Crossing over in a paracentric inversion heterozygote → dicentric chromosome → breakage → loss of acentric fragment and products with major deletions

Pericentric inversions → duplications and deletions

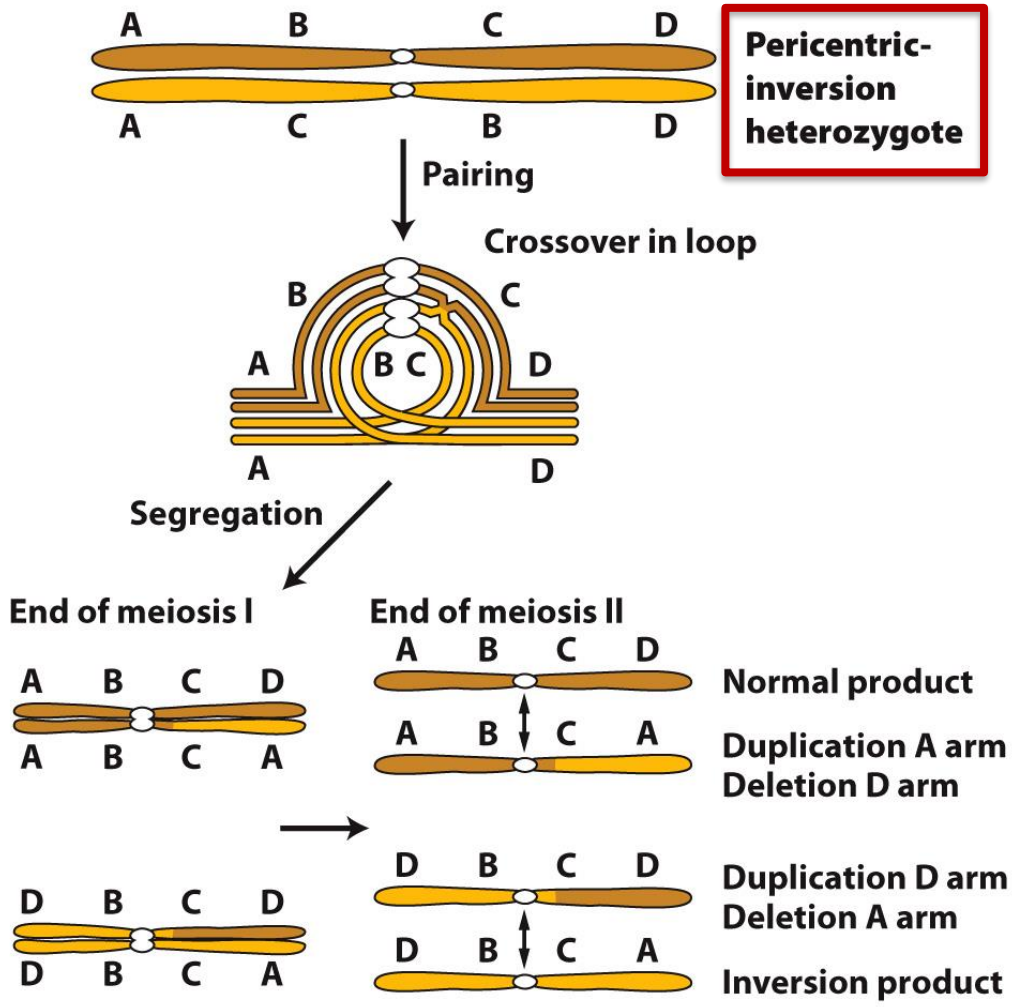

Figure 17-29
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Crossing over in a pericentric inversion heterozygote → products with major deletions

Think Break

Effect on frequency of recombinant progeny

Example from Drosophila
dp: dumpy
cn: cinnabar
45 map units apart

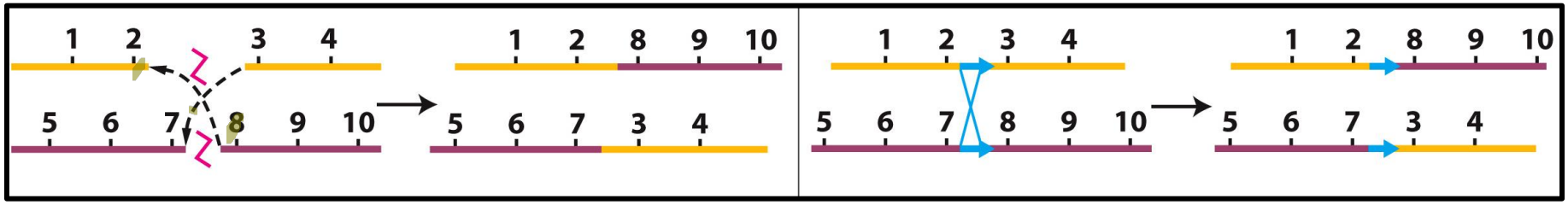
+ +/+ + x *dp cn/dp cn*

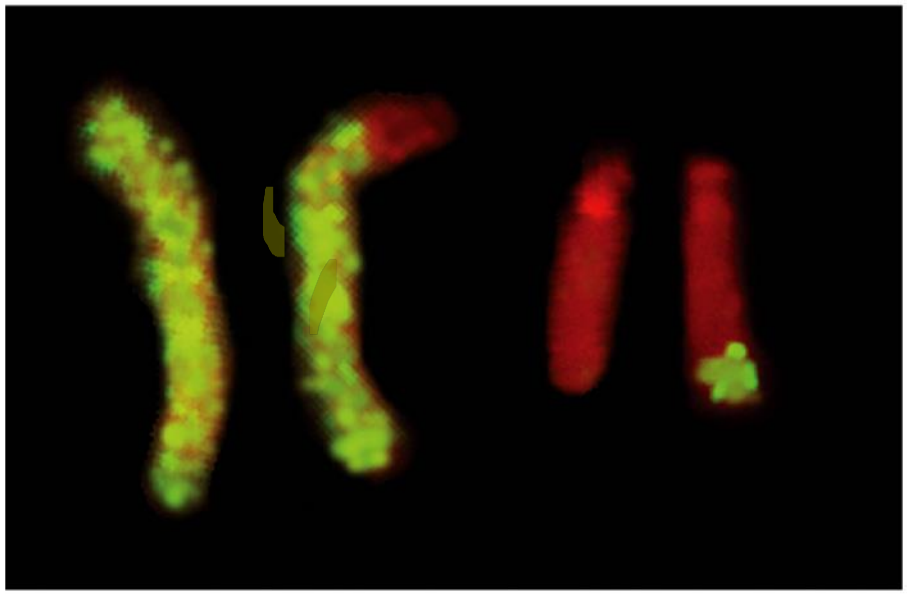
+ +/dp cn x *dp cn/dp cn* F1

250	wild type	*+ +/dp cn*	
246	dumpy cinnabar	*dp cn/dp cn*	F2
5	dumpy	*dp +/dp cn*	
7	cinnabar	*+ cn/dp cn*	

Expect 45% recombinant progeny

Chromosomal translocations





Chapter 17 Opener
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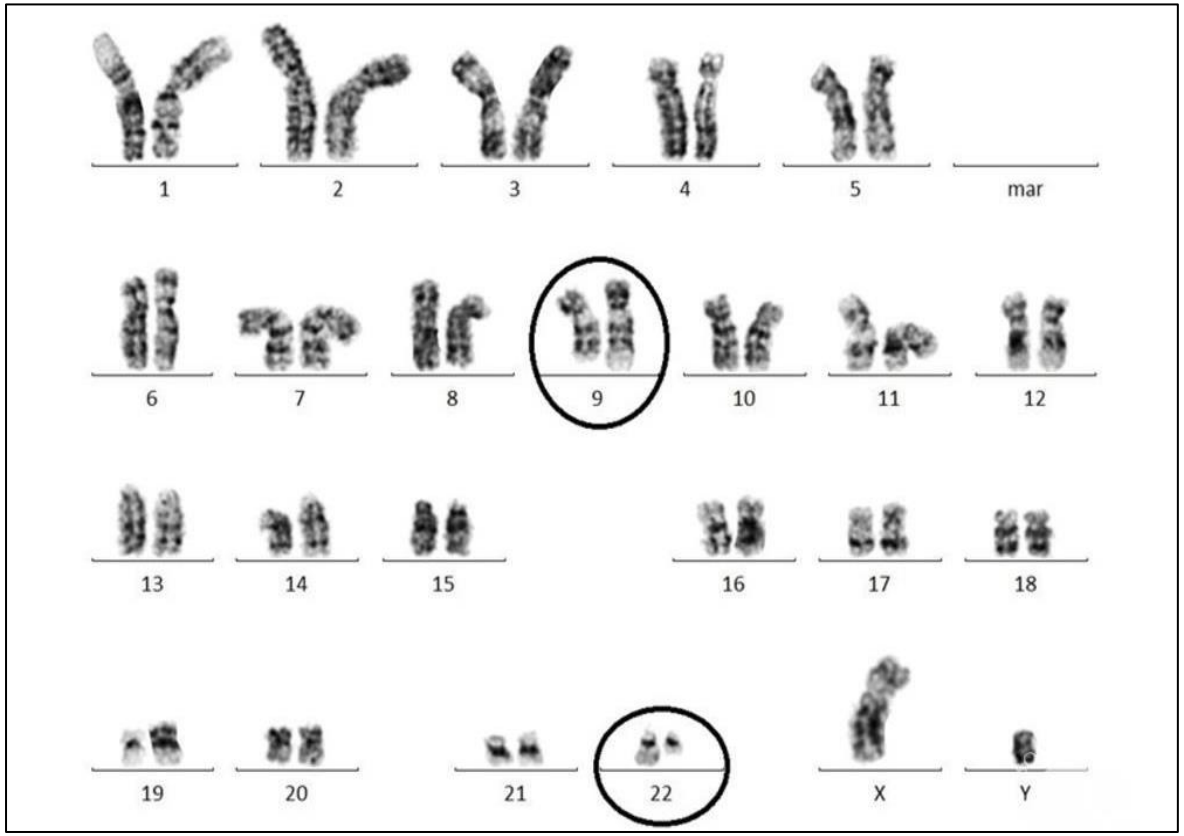
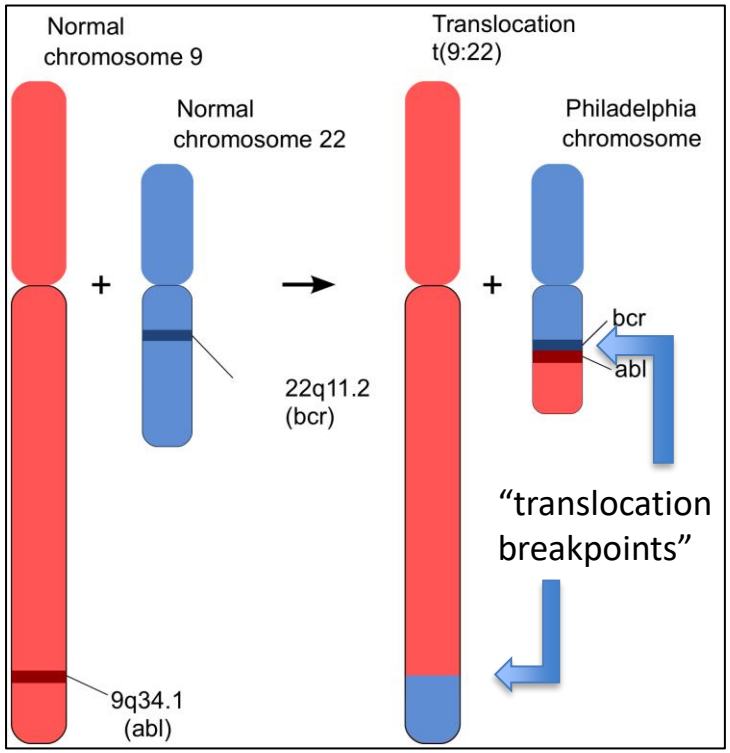
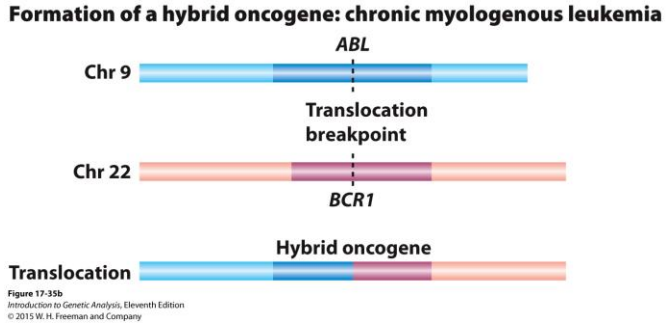
Addenbrookes Hospital/Science Source

Chromosomal translocations

somatic consequences





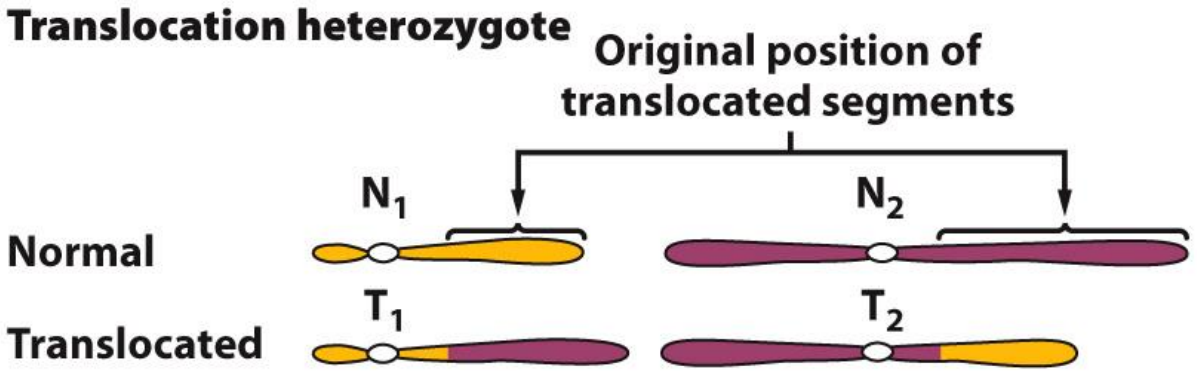


First chromosome abnormality linked with a specific human cancer

Chromosomal translocations

somatic consequences

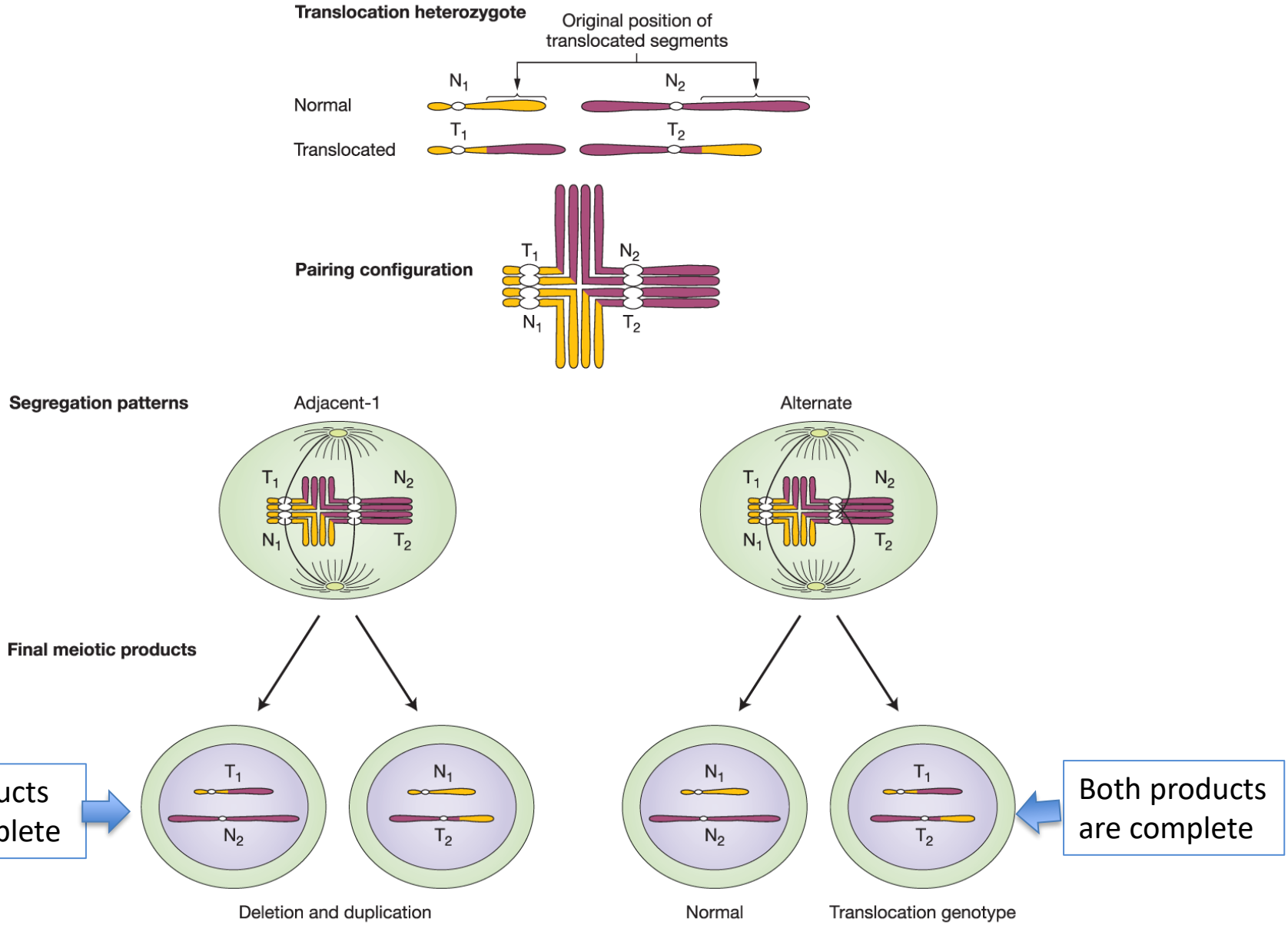
balanced translocations:



What phenotype would you predict for an individual with this translocation?

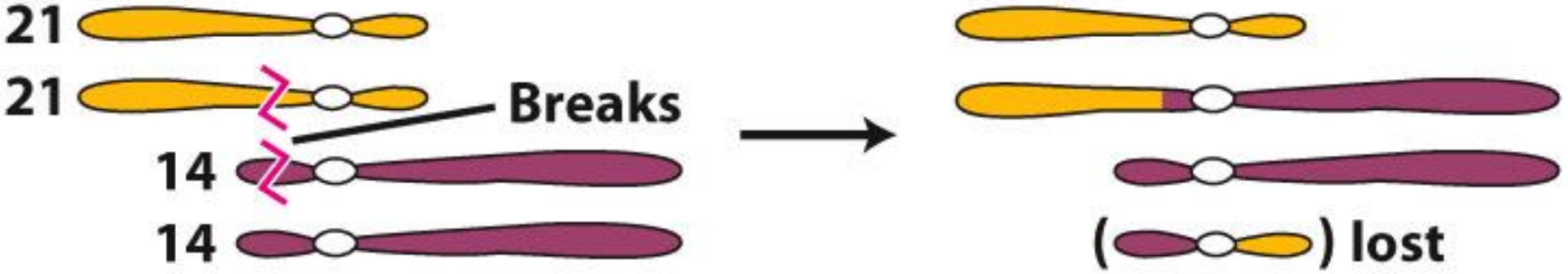
Balanced translocations and meiosis

two segregation patterns in a reciprocal-translocation heterozygote



Consequences of balanced translocations

Robertsonian translocations

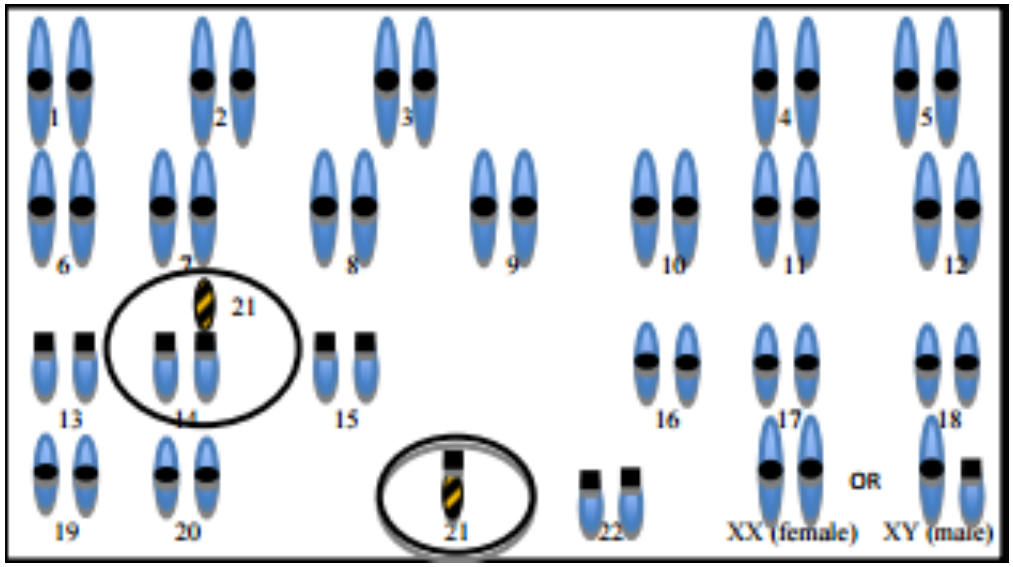


A type of balanced translocation

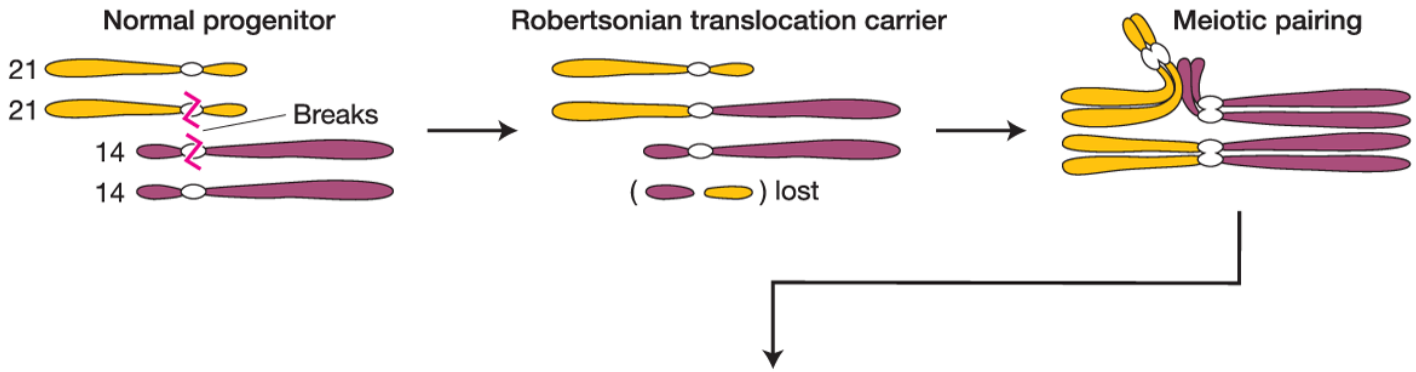
Can involve any of the acrocentric chromosomes: 13, 14, 15, 21, or 22

Frequency: 1/1000 babies

Phenotype usually normal



A balanced Robertsonian translocation resulting in inheritance of trisomy 21 (Down's Syndrome)



Segregation during meiosis → 6 possible gametes

A balanced Robertsonian translocation resulting in inheritance of trisomy 21 (Down's Syndrome)