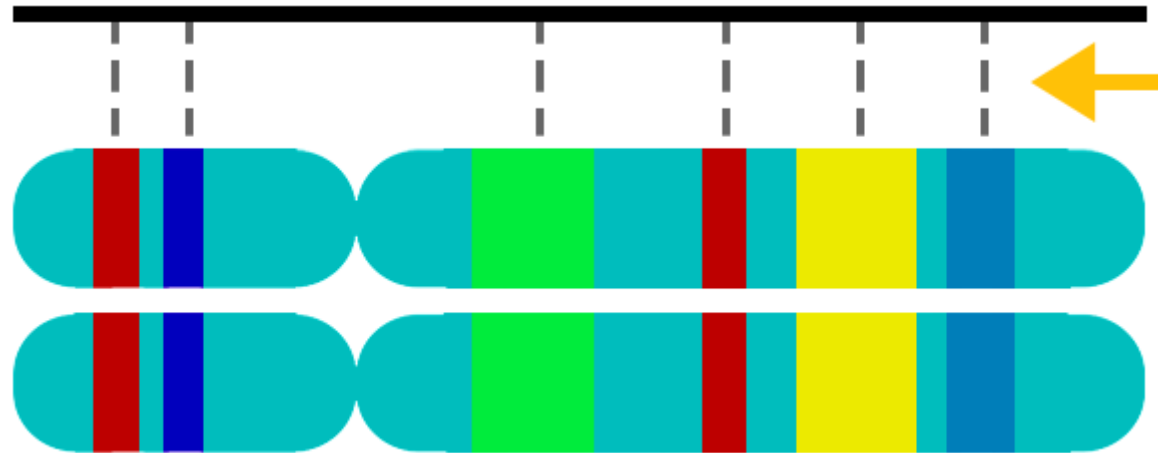
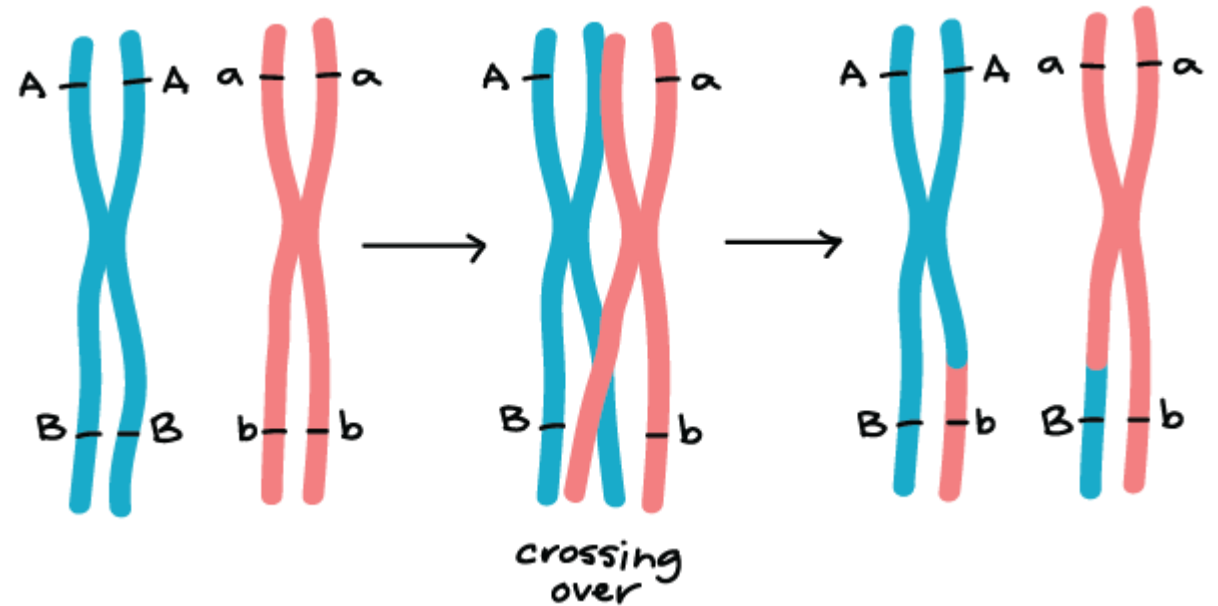
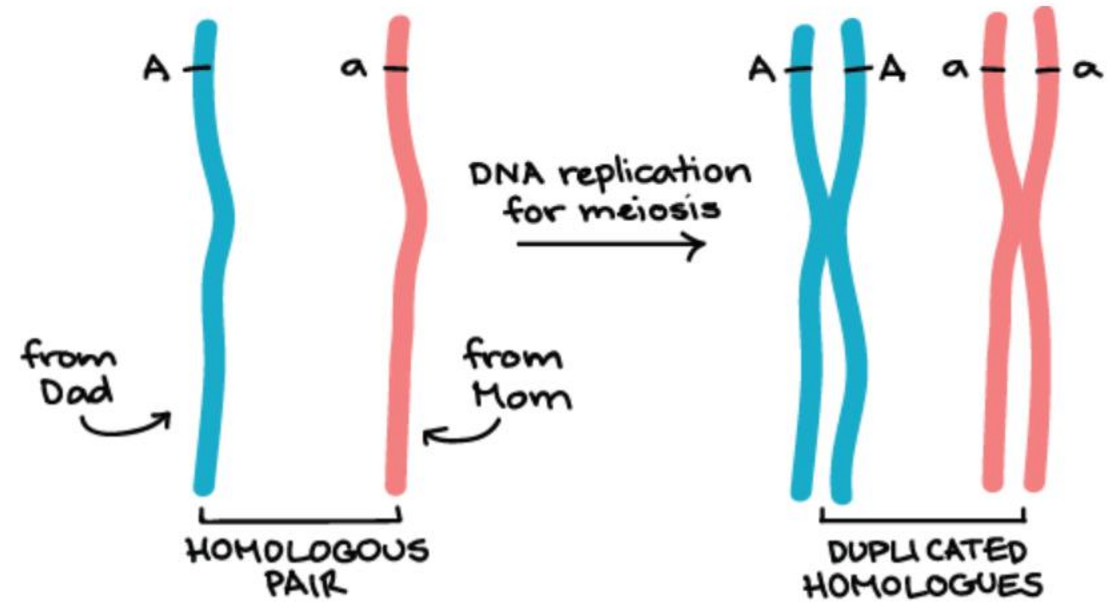


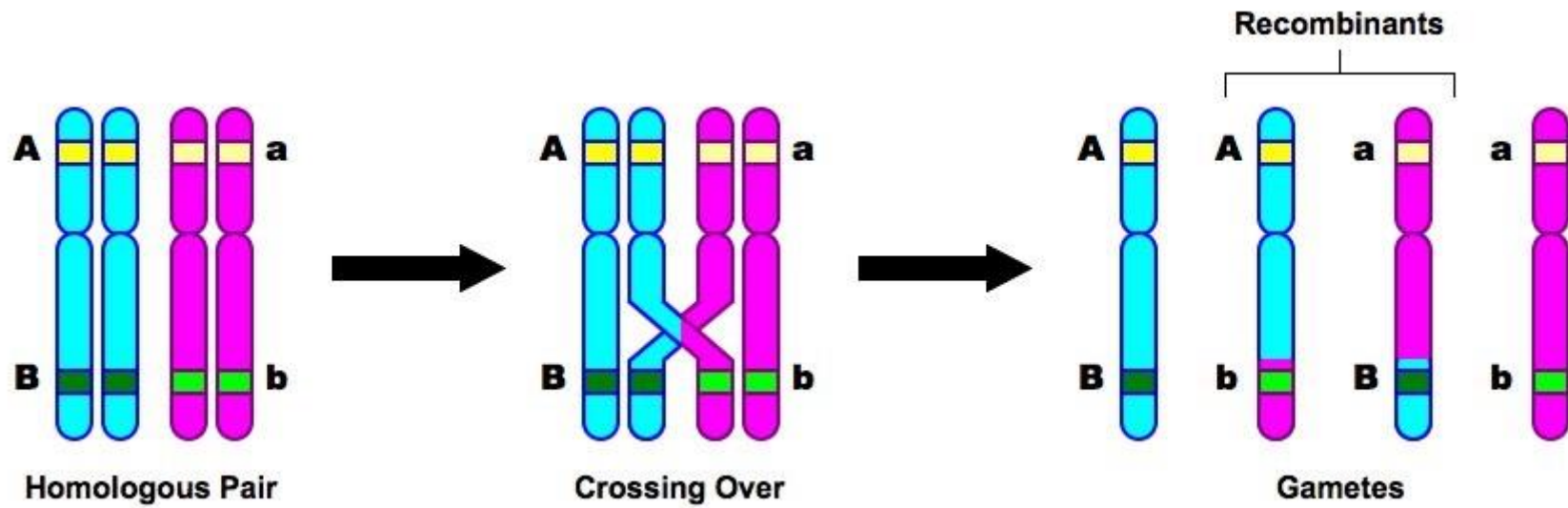
Linkage and Gene Mapping



Basics?

- **Homologous chromosomes** are paired chromosomes that carry the same genes, but may have different alleles of those genes
- One member of each homologous pair comes from an organism's mom, the other from its dad.
- **Crossing over:** homologous chromosomes randomly exchange matching fragments.

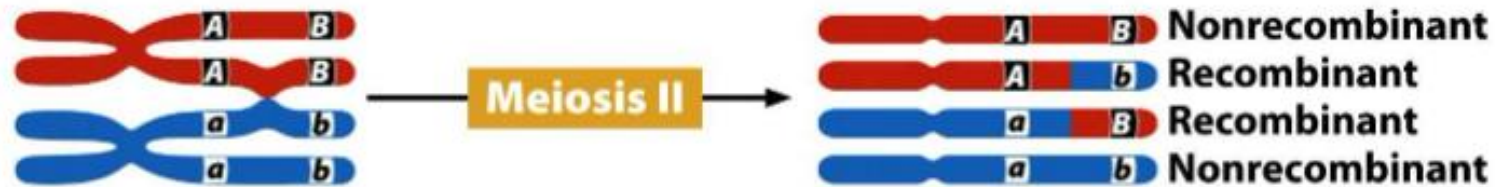


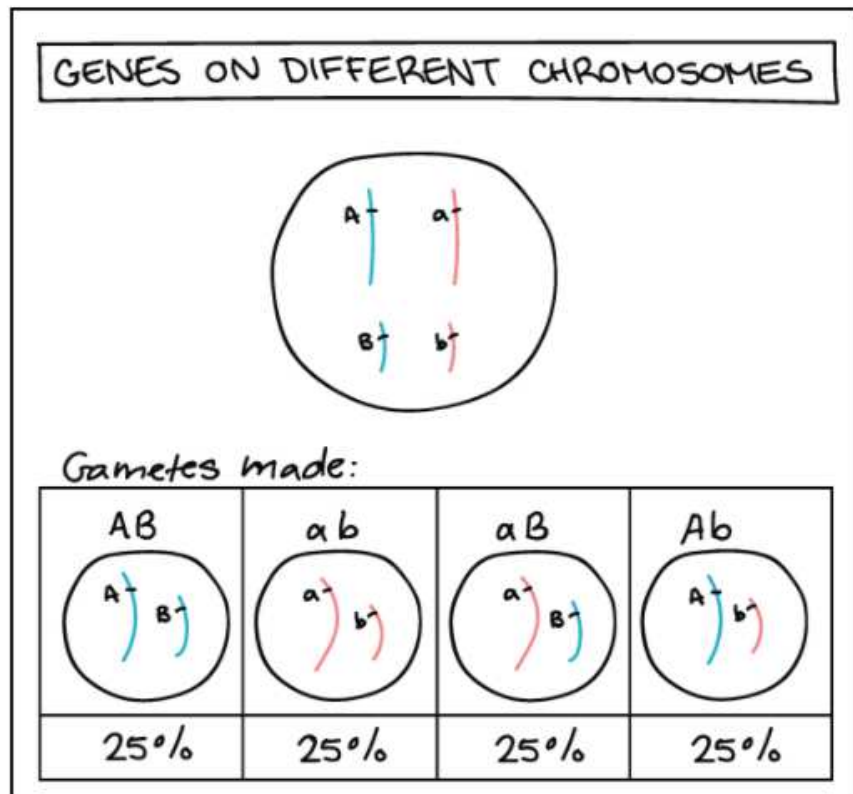


(a) No crossing over

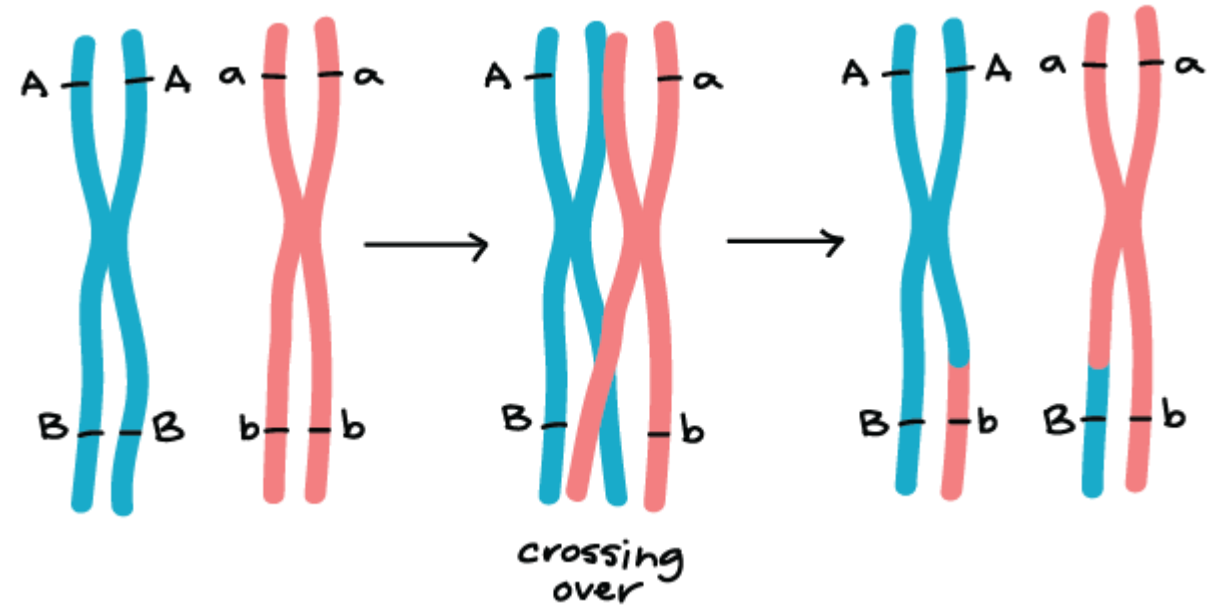
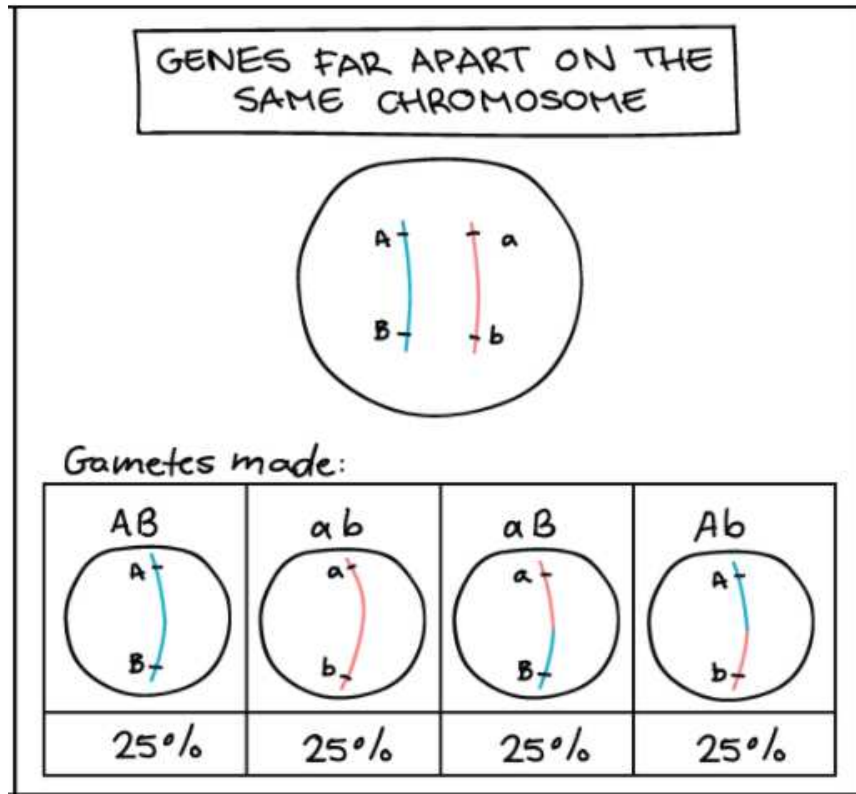


(b) Crossing over



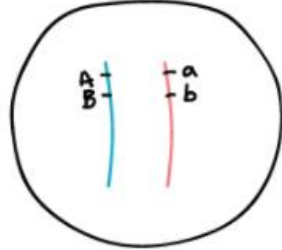


- When genes are on separate chromosomes, they **assort independently**. That is, when the genes go into gametes, the allele received for one gene doesn't affect the allele received for the other.
- Genes on separate chromosomes assort independently because of the random orientation of homologous chromosome pairs during meiosis.



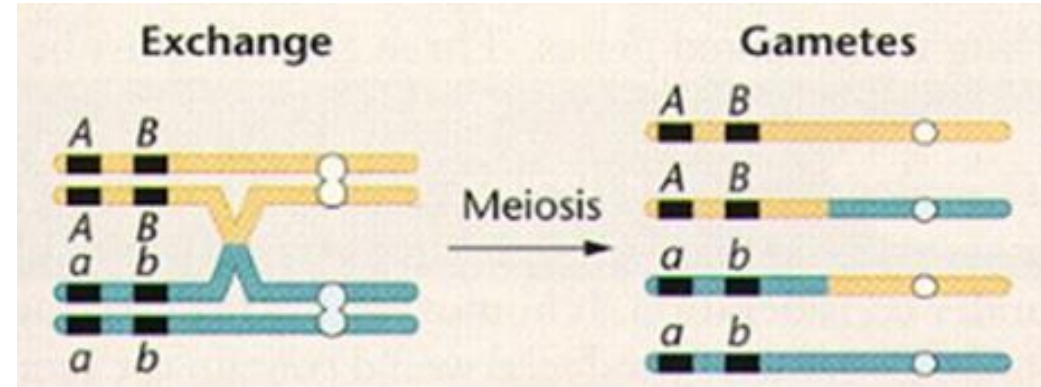
- When genes are on the same chromosome but very far apart, they assort independently due to **crossing over** (homologous recombination).

GENES CLOSE TOGETHER ON THE SAME CHROMOSOME



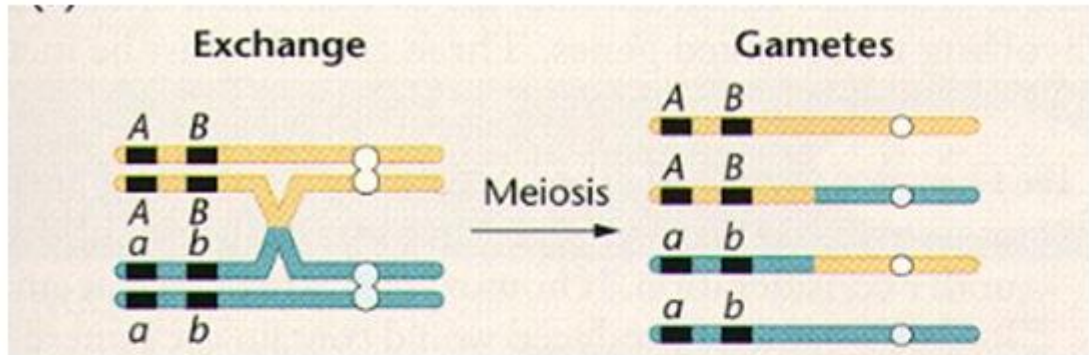
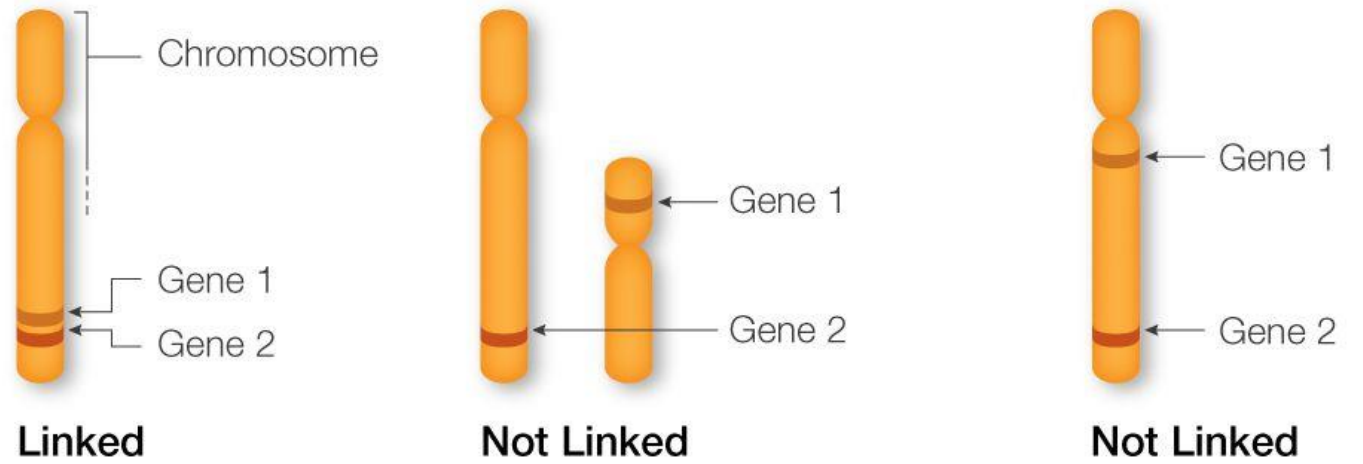
Gametes made:

AB	Ab	aB	ab
48%	2%	2%	48%



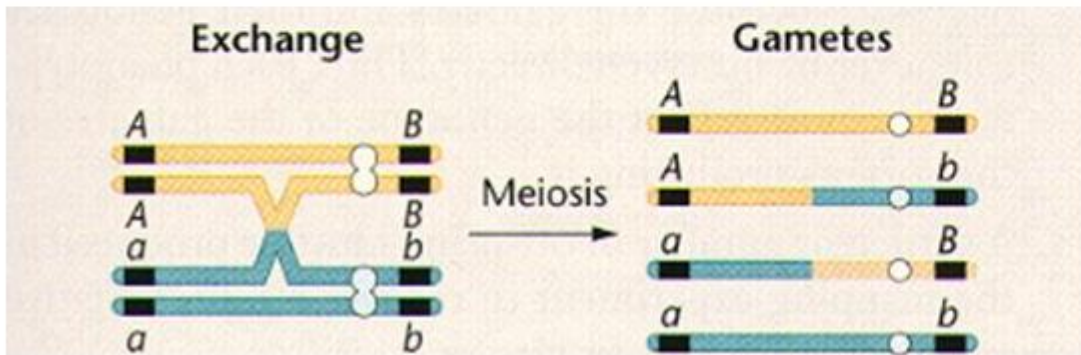
- When genes are very close together on the same chromosome, crossing over still occurs, but the outcome (in terms of gamete types produced) is different.
- Instead of assorting independently, the genes tend to "stick together" during meiosis. That is, the alleles of the genes that are already together on a chromosome will tend to be passed as a unit to gametes.

- **Linked genes:** when two genes are so close together that they cannot be separated during crossing over



if closely linked:
cross-overs less likely to occur between A&B

Linkage



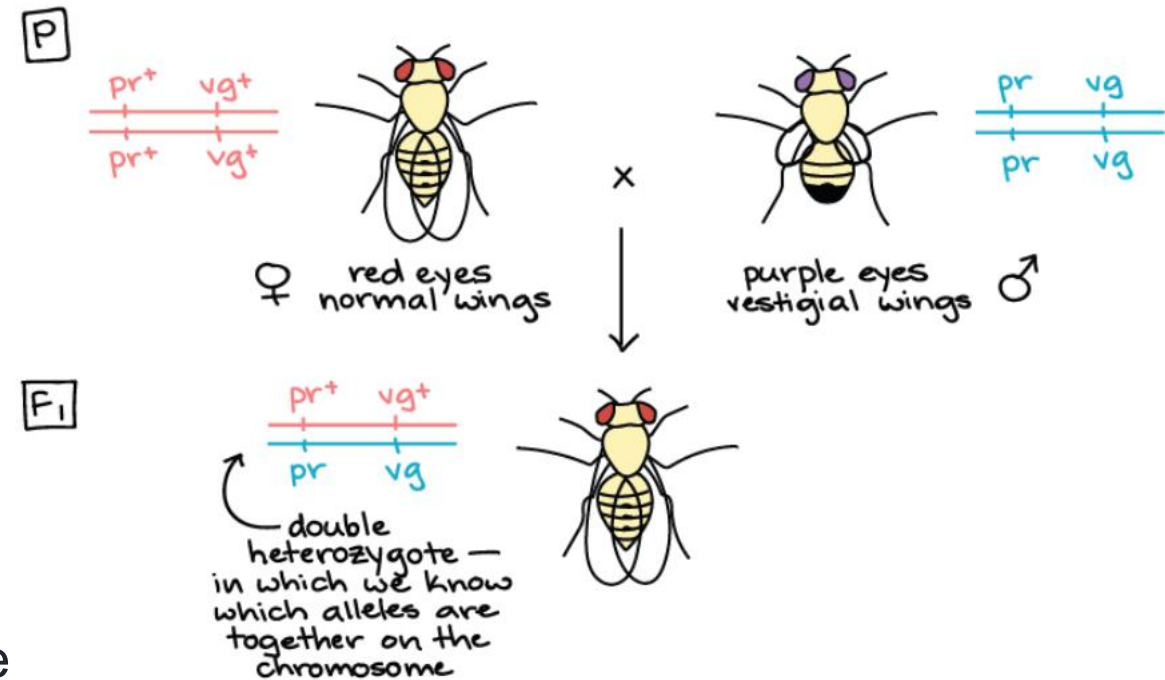
if farther apart:
cross-overs more likely to occur between A&B

Finding recombination frequency

Let's suppose we are interested in seeing whether two genes in the fruit fly (*Drosophila*) are linked to each other, and if so, how tightly linked they are.

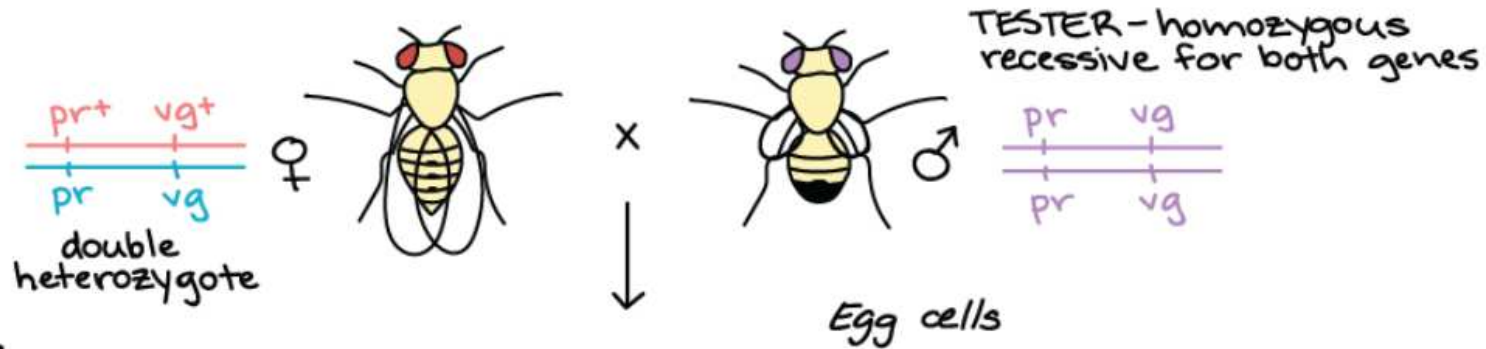
In our example, the genes are:

- The *purple* gene, with a dominant pr^+ allele that specifies normal, red eyes and a recessive pr allele that specifies purple eyes.
- The *vestigial* gene, with a dominant vg^+ allele that specifies normal, long wings and a recessive vg allele that specifies short, "vestigial" wings.

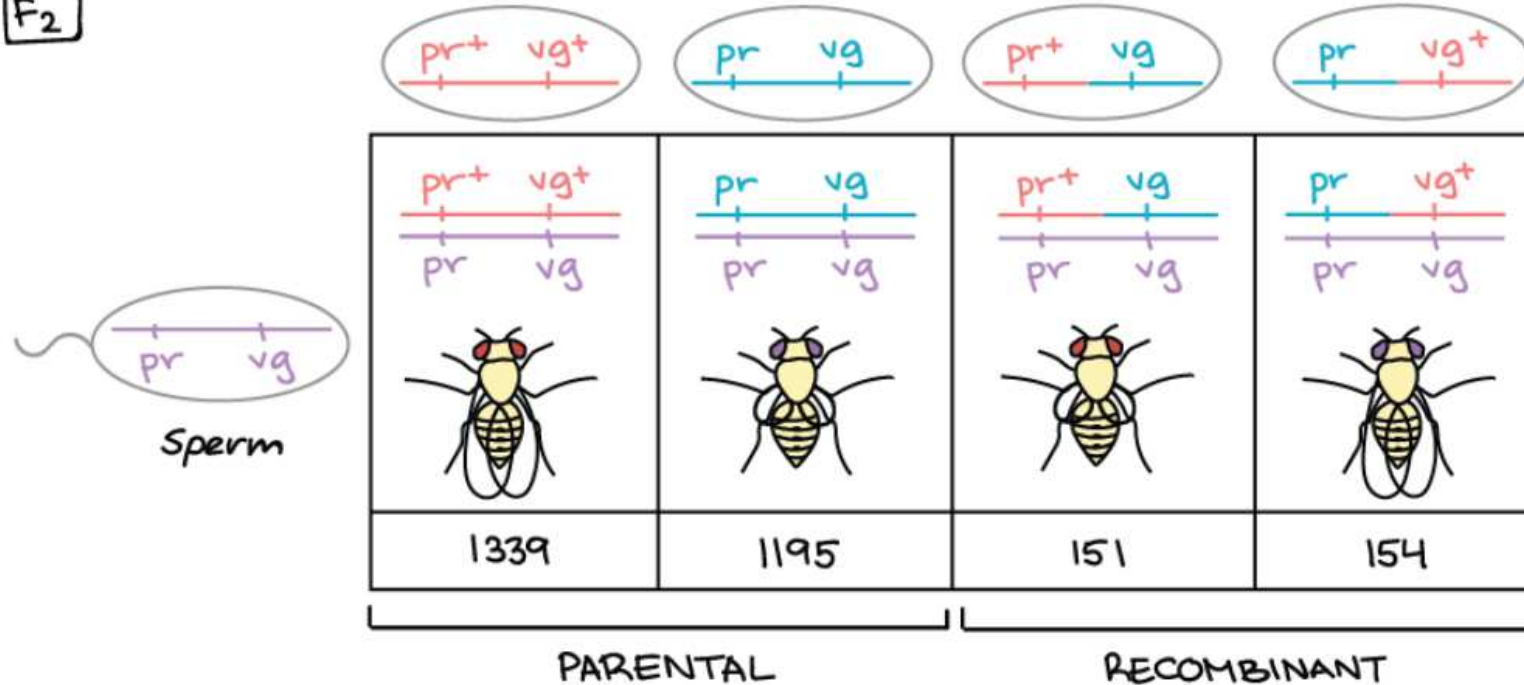


Finding recombination frequency

F₁



F₂



Finding recombination frequency

- Recombination frequency = distance between genes (map distance)
- In linkage maps, distances expressed as centimorgans or map units rather than recombination frequencies
- There's a direct relationship among these values: 1% recombination frequency is equivalent to 1 **centimorgan** or 1 map unit

$$\text{Recombination frequency (RF)} = \frac{\text{Recombinants}}{\text{Total offspring}} \times 100\%$$

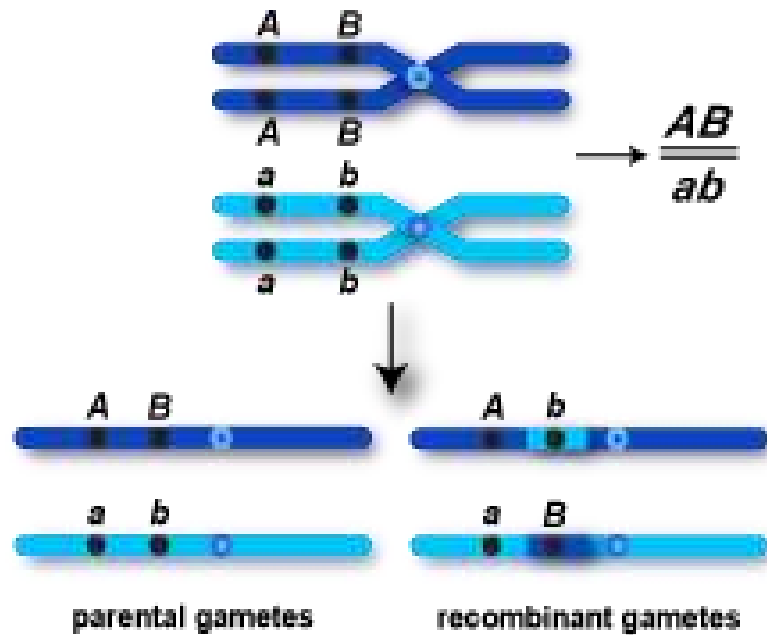
So, for the cross above, we can write our equation as follows:

$$\text{RF} = \frac{151 + 154}{1339 + 1195 + 151 + 154} \times 100\% = 10.7\%$$

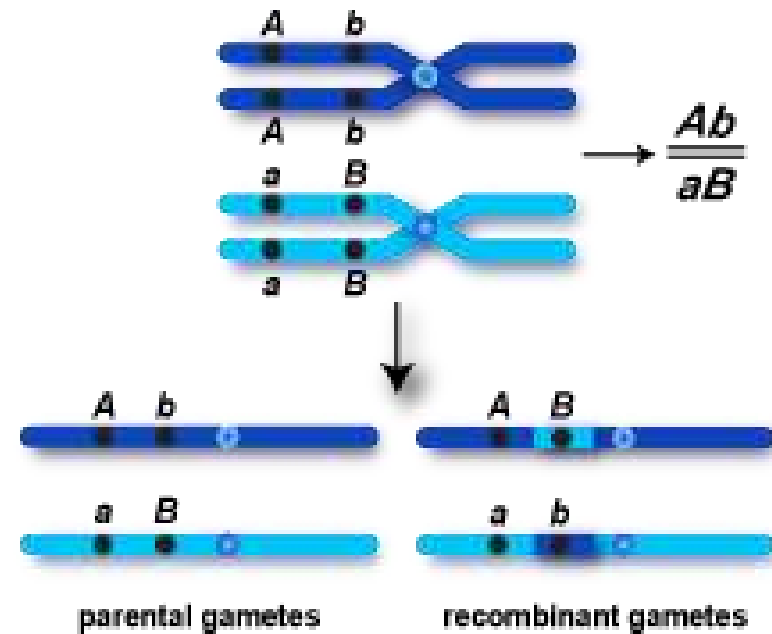
The recombination frequency between the *purple* and *vestigial* genes is 10.7%.

CIS and TRANS configuration

**CIS configuration
(coupling)**



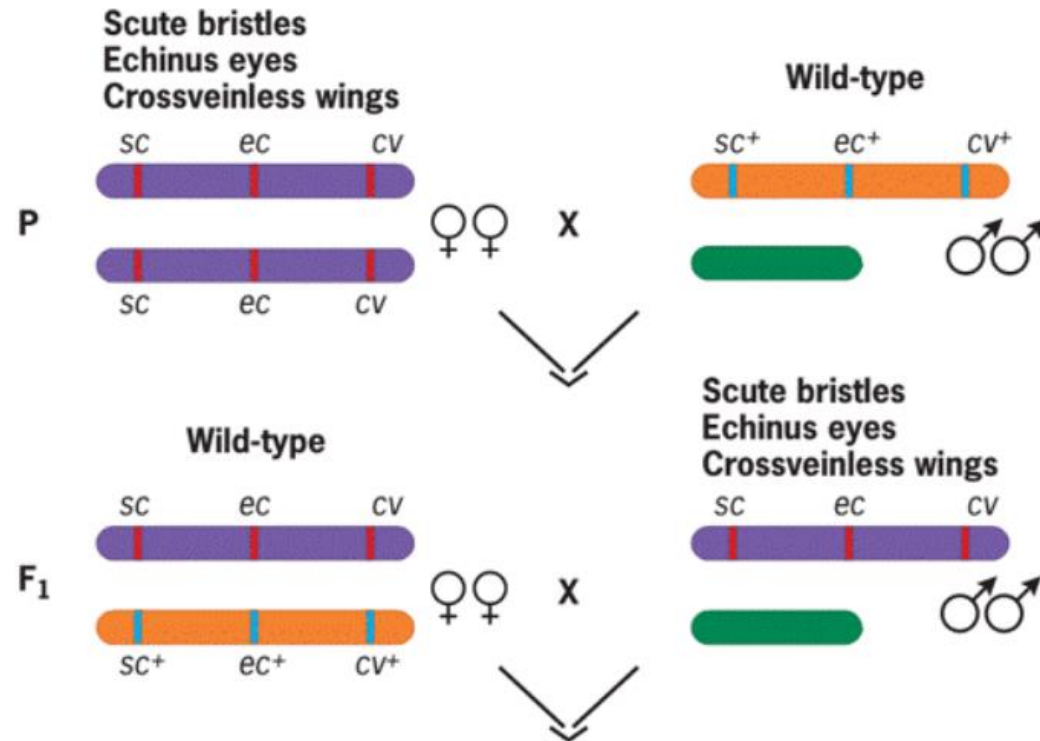
**TRANS configuration
(repulsion)**

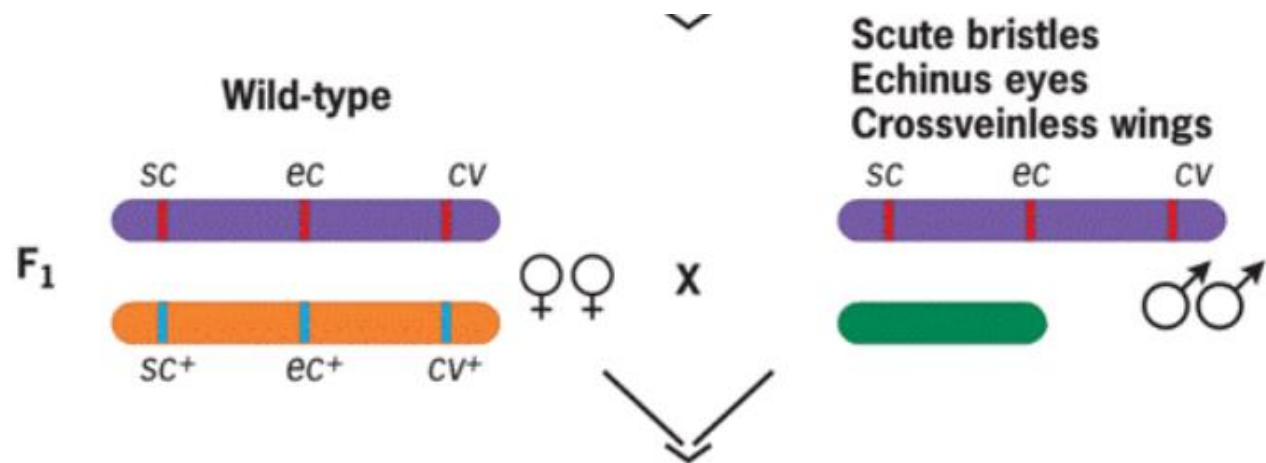


Three point test cross

Three point test cross in *Drosophila*:

- Wild-type Male *Drosophila* was crossed with female *Drosophila* homozygous for three recessive X-linked mutations—**scute (sc)** bristles, **echinus (ec)** eyes, and **crossveinless (cv)** wings to obtain F1 progeny.
- Wild Male *Drosophila* = (sc^+ , ec^+ , cv^+)
- Mutated female *Drosophila* = (sc , ec , cv)





<i>Class</i>	<i>Phenotype</i>	<i>Genotype of maternally inherited X chromosome</i>			<i>Number observed</i>
1	Scute, echinus, crossveinless	sc	ec	cv	1158
2	Wild-type	sc ⁺	ec ⁺	cv ⁺	1455
3	Scute	sc	ec ⁺	cv ⁺	163
4	Echinus, crossveinless	sc ⁺	ec	cv	130
5	Scute, echinus	sc	ec	cv ⁺	192
6	Crossveinless	sc ⁺	ec ⁺	cv	148
7	Scute, crossveinless	sc	ec ⁺	cv	1
8	Echinus	sc ⁺	ec	cv ⁺	1
				Total:	3248

F₂

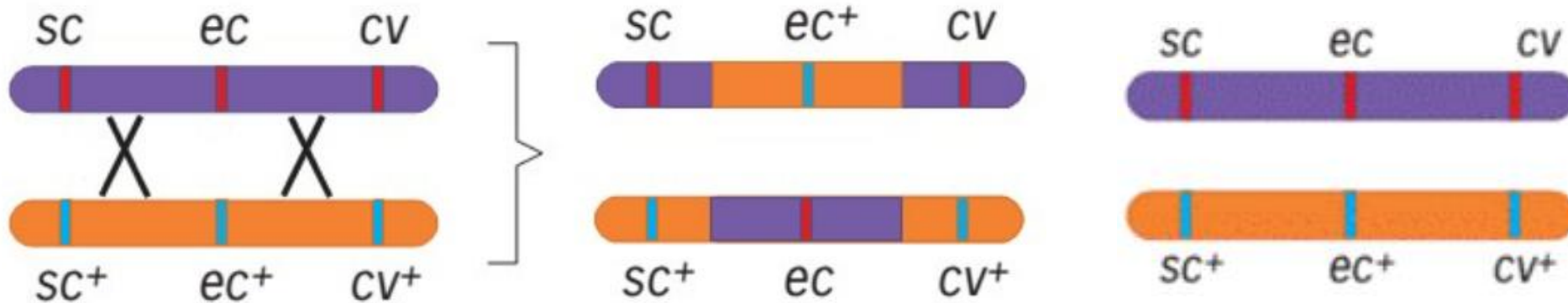
Class	Phenotype	Genotype of maternally inherited X chromosome			Number observed
1	Scute, echinus, crossveinless	sc	ec	cv	1158
2	Wild-type	sc ⁺	ec ⁺	cv ⁺	1455
3	Scute	sc	ec ⁺	cv ⁺	163
4	Echinus, crossveinless	sc ⁺	ec	cv	130
5	Scute, echinus	sc	ec	cv ⁺	192
6	Crossveinless	sc ⁺	ec ⁺	cv	148
7	Scute, crossveinless	sc	ec ⁺	cv	1
8	Echinus	sc ⁺	ec	cv ⁺	1
				Total:	3248

There are three possible gene orders :

1. *sc—ec—cv*

2. *ec—sc—cv*

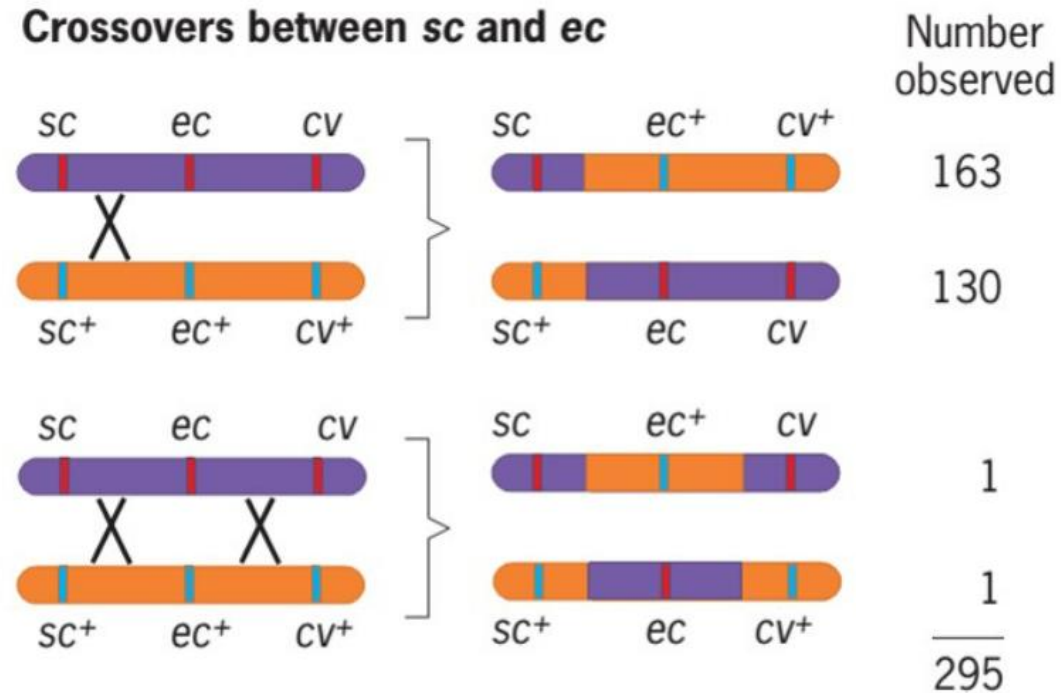
3. *ec—cv—sc*



F₂

Class	Phenotype	Genotype of maternally inherited X chromosome			Number observed
1	Scute, echinus, crossveinless	sc	ec	cv	1158
2	Wild-type	sc ⁺	ec ⁺	cv ⁺	1455
3	Scute	sc	ec ⁺	cv ⁺	163
4	Echinus, crossveinless	sc ⁺	ec	cv	130
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6	Crossveinless	sc ⁺	ec ⁺	cv	148
7	Scute, crossveinless	sc	ec ⁺	cv	1
8	Echinus	sc ⁺	ec	cv ⁺	1
				Total:	3248

Crossovers between sc and ec

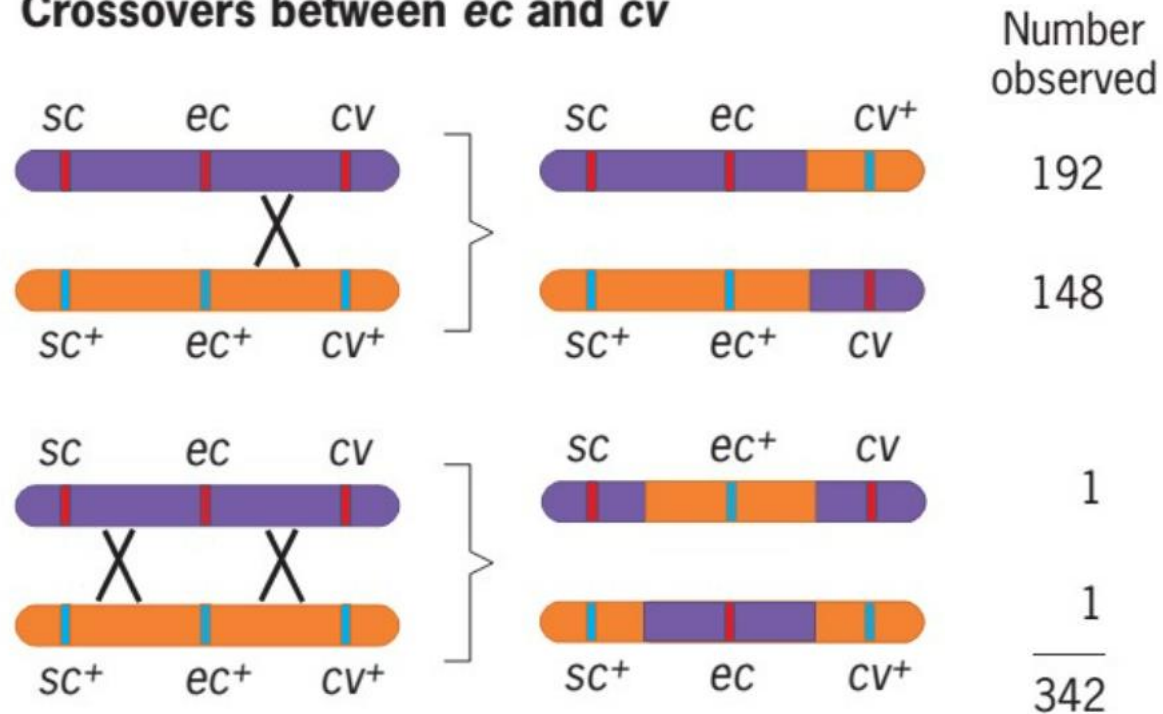


$$\text{Map distance} = \frac{295}{3248} \times 100 = 9.1 \text{ centiMorgans}$$

F₂

Class	Phenotype	Genotype of maternally inherited X chromosome			Number observed
1	Scute, echinus, crossveinless	sc	ec	cv	1158
2	Wild-type	sc ⁺	ec ⁺	cv ⁺	1455
3	Scute	sc	ec ⁺	cv ⁺	163
4	Echinus, crossveinless	sc ⁺	ec	cv	130
5	Scute, echinus	sc	ec	cv ⁺	192
6	Crossveinless	sc ⁺	ec ⁺	cv	148
7	Scute, crossveinless	sc	ec ⁺	cv	1
8	Echinus	sc ⁺	ec	cv ⁺	1
				Total:	3248

Crossovers between *ec* and *cv*



$$\text{Map distance} = \frac{342}{3248} \times 100 = 10.5 \text{ centiMorgans}$$

Total map distance:

- Combining the data for the two regions, the map is ***sc—9.1— ec—10.5— cv***
- Thus map distances between ***sc*** and ***cv*** = 9.1 cM + 10.5 cM = 19.6 cM

Question

[CSIR NET DEC 2017]

In *Drosophila*, Bar eye (B) is a dominant mutation while miniature wing (m) and yellow body colour (y) are recessive mutations. Heterozygous females for these mutations were crossed to normal eyed miniature winged and yellow body coloured males. Assume the following progeny was obtained:

Phenotypes	Number
$B^+ m^+ y^+$	30
$B m y^+$	25
$B m^+ y^+$	165
$B^+ m y^+$	120
$B m y$	20
$B^+ m y$	185
$B m^+ y$	110
$B^+ m^+ y$	45

Based on the result obtained, the order of genes will be:

- A. $B m y$
- B. $m B y$

The genetic distance between B and y will be:

- C. 40 cM
- D. 17.1 cM

The correct combination answer is

- a) A and C
- b) B and C
- c) A and D
- d) B and D

Step 1: Finding Parental and Double crossovers; Gene order

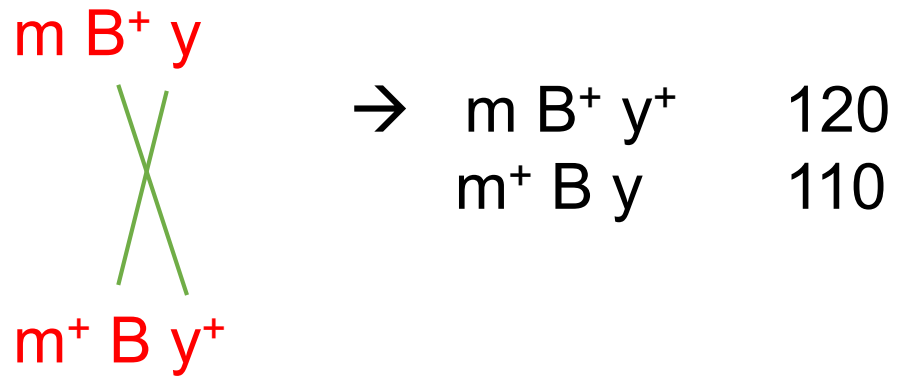
$B m^+ y^+$ $B^+ m y$
 $B^T m^+ y^+ / B m y^+ / B m y$
 $B \times m^+ \times y^+$
 $B^+ m y$
 $B m y^+$
 $B^+ m^+ y$

...the following prog

Phenotypes	Number
$B^+ m^+ y^+$	30
$B m y^+$	25
$B m^+ y^+$	165
$B^+ m y^+$	120
$B m y$	20
$B^+ m y$	185
$B m^+ y$	110
$B^+ m^+ y$	45

$\checkmark B^T m^+ y^+ / B m y^+ / \checkmark B m y$
 $m^+ B y^+$
 $X \quad X$
 $m B^+ y$
 $B^+ B^+ y^+$
 $B B^+ y^+$

Step 2: Finding Single crossovers; Distance between B and y



Phenotypes	Number
$B^+ m^+ y^+$	30
$B m y^+$	25
$B m^+ y^+$	165
$B^+ m y^+$	120
$B m y$	20
$B^+ m y$	185
$B m^+ y$	110
$B^+ m^+ y$	45

Distance bet B and y: $120+110+30+20/700 \times 100 = 280/700 \times 100 = 40 \text{ cM}$

Step 3: Finding Single crossovers; Distance between m and B

m B⁺ y



m⁺ B y⁺

→ m B y⁺ 25
m⁺ B⁺ y 45

Phenotypes	Number
<i>B⁺ m⁺ y⁺</i>	30
<i>B m y⁺</i>	25
<i>B m⁺ y⁺</i>	165
<i>B⁺ m y⁺</i>	120
<i>B m y</i>	20
<i>B⁺ m y</i>	185
<i>B m⁺ y</i>	110
<i>B⁺ m⁺ y</i>	45

Distance bet m and B: $25+45+30+20/700 \times 100 = 120/700 \times 100 = 17.14 \text{ cM}$