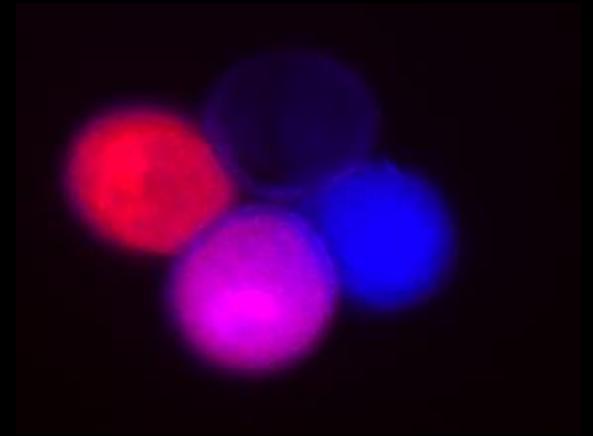
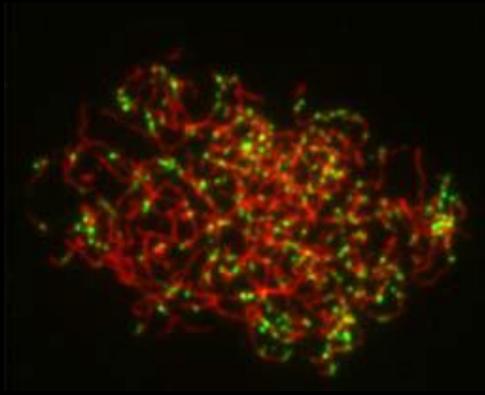


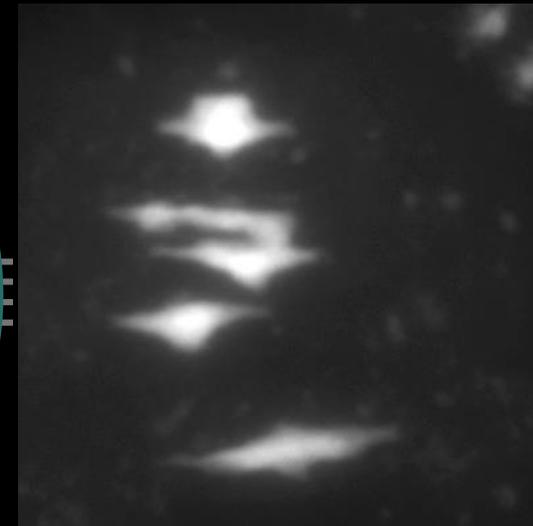
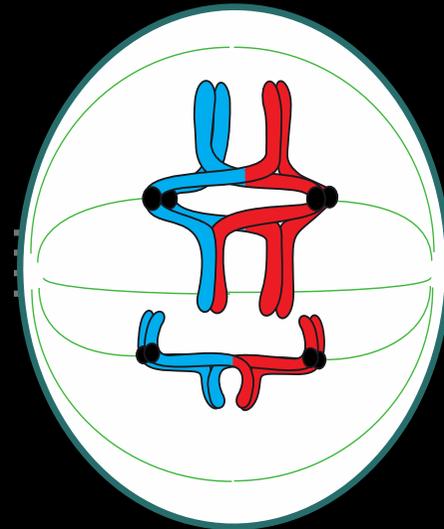
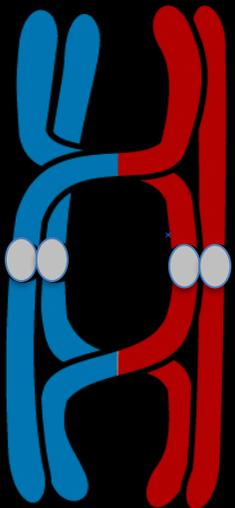
# Controlling meiotic recombination: To mix or not to mix



# Meiotic Crossovers

→ Crossovers generate genetic diversity among siblings

→ Crossovers are essential for accurate distribution of chromosomes at meiosis

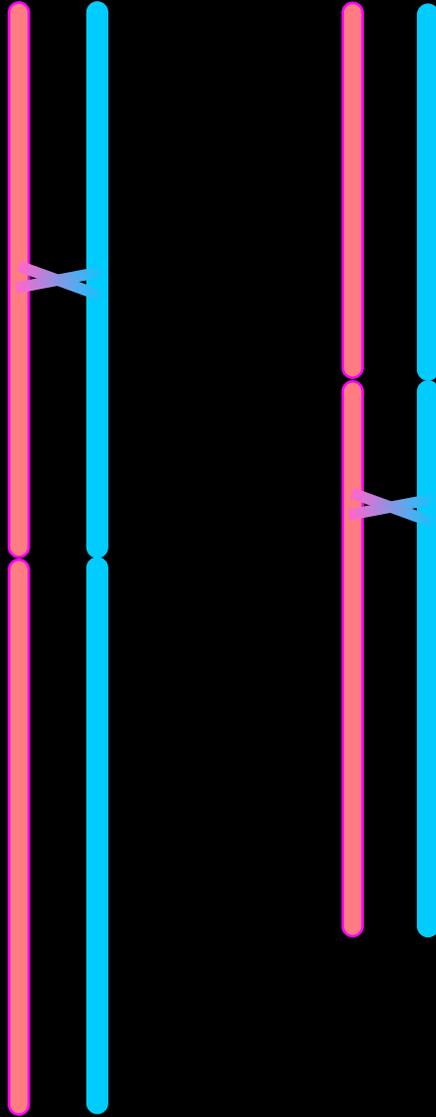


Crossover distribution is not random

# Crossover distribution is not random

1) Obligate  
crossover:

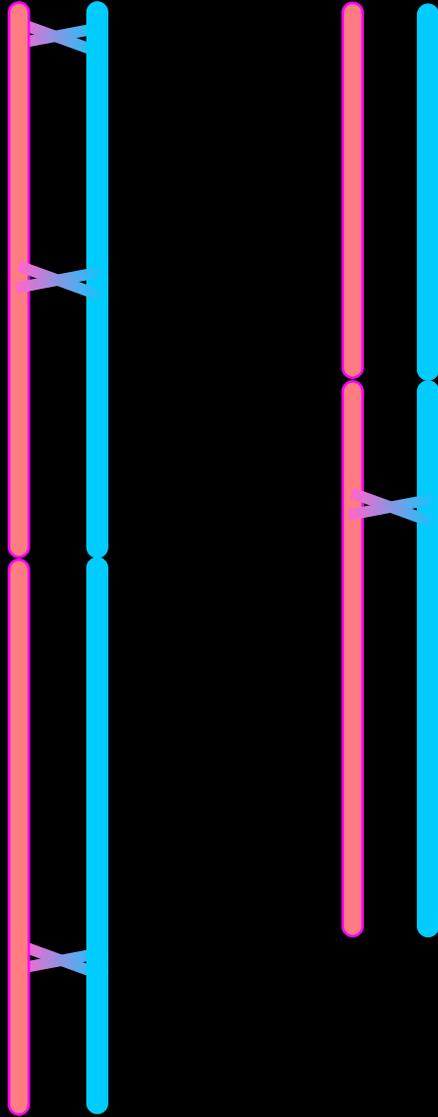
At least one per  
chromosome pair



# Crossover distribution is not random

2) Not numerous:

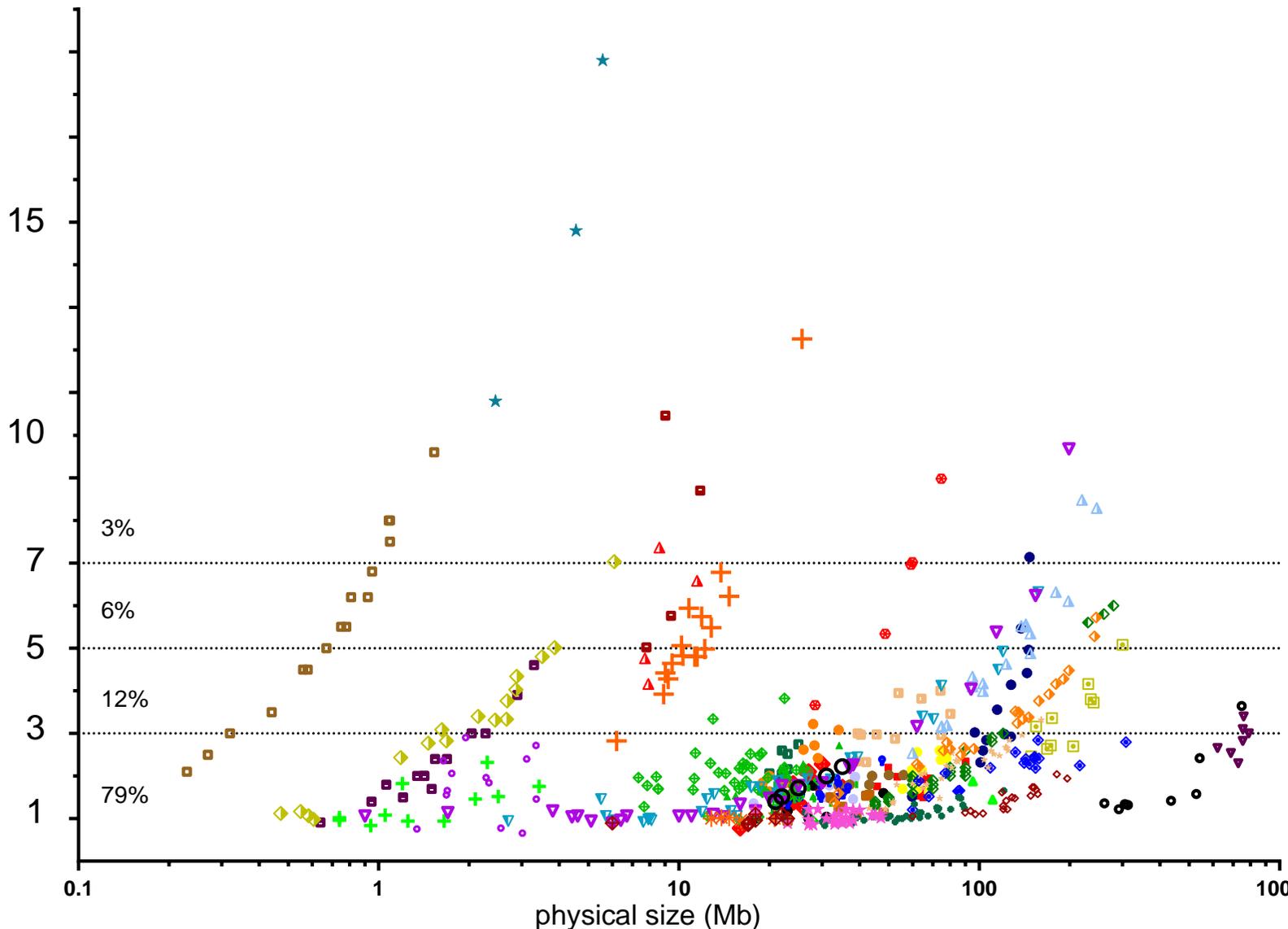
Typically 1 to 3 per chromosome pair



# Genetic (cM) vs physical size (Mb) of chromosomes from a range of species

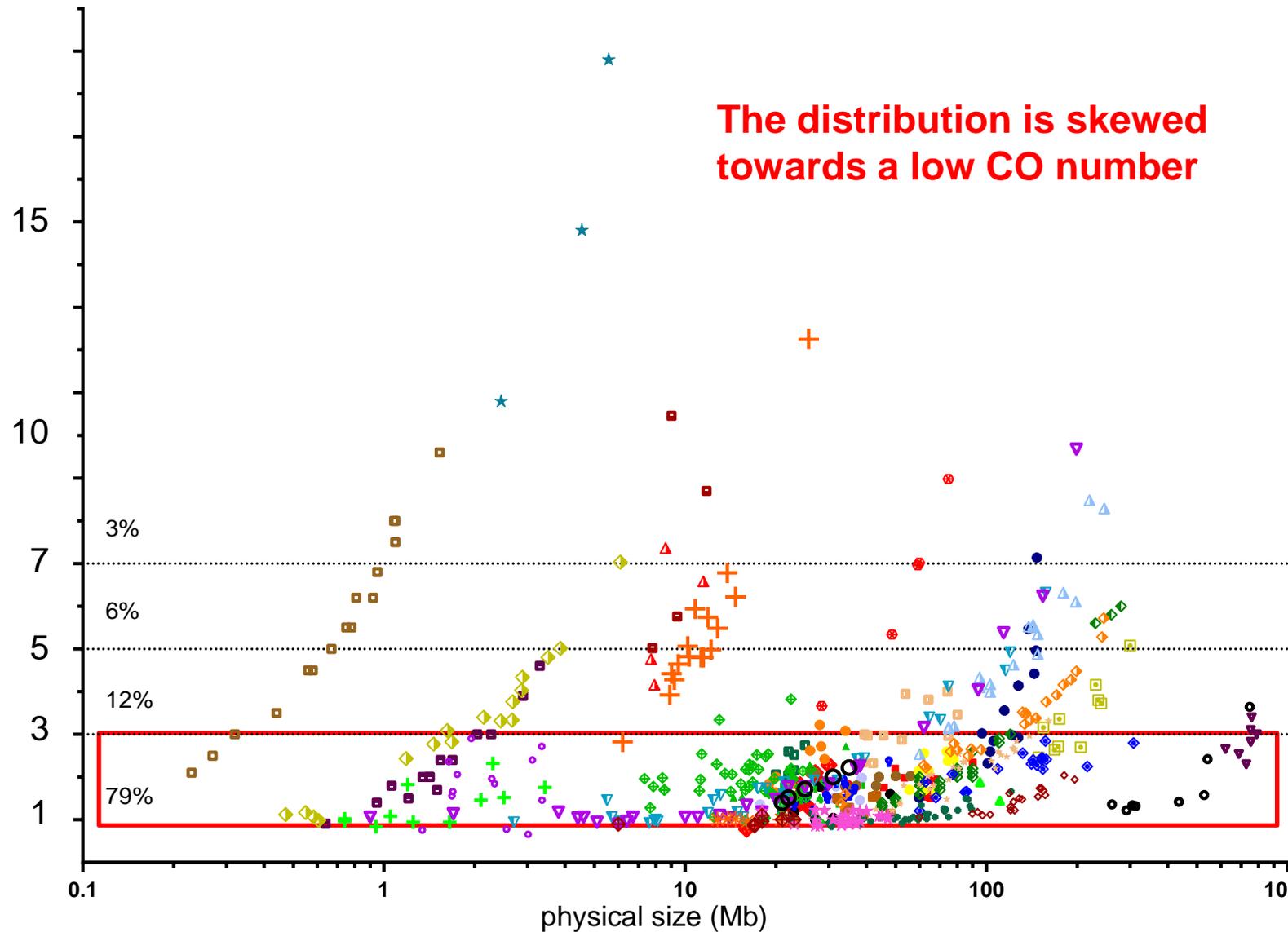
- *Arabidopsis thaliana*
- *Sorghum bicolor*
- *Eucalyptus grandis*
- *Medicago truncatula*
- *Brachypodium distachyon*
- *Cardamine hirsuta*
- *Corn Zea mays*
- *Apple Malus domestica*
- *wild strawberry Fragaria vesca*
- *Sugar Beet Beta vulgaris*
- *Chinese cabbage Brassica rapa*
- *Coton Gossypium arboreum*
- *Peach Prunus persica*
- ◆ *Capasella rubella*
- *Cacao Theobroma cacao*
- ◆ *Melon Cucumis melo*
- *Tomato Solanum lycopersicum*
- ▲ *Cucumber Cucumis sativus*
- ▼ *Barley Hordeum vulgare*
- ★ *Fission yeast Schizosaccharomyces Pombe*
- *Budding yeast Saccharomyces cerevisiae*
- *Button mushroom Agaricus bisporus*
- *Fusarium graminearum*
- ▲ *Fusarium Gibberella zeae*
- ◆ *Zyloseptoria tritici*
- ▼ *chicken Gallus gallus domesticus*
- ◆ *Human Homo sapiens*
- *Oposum Monodelphis domestica*
- ◆ *Mouse Mus Musculus*
- *Dog Canis familiaris*
- *Pig Sus scrofa*
- *Cattle Bos taurus*
- ▲ *Cat Felis catus*
- ◆ *Soay sheep Ovis aries*
- ▼ *Flycatcher*
- ◆ *Carp Cyprinus carpio*
- ★ *mangrove killifish Kryptolebias marmoratus*
- ★ *Caenorhabditis elegans*
- ★ *Honey bee Apis mellifera*
- ▲ *Anopheles gambiae*
- *Trypanosoma brucei*
- *Plasmodium falciparum*

Crossovers  
per meiosis



# Genetic (cM) vs physical size (Mb) of chromosomes from a range of species

Crossovers  
per meiosis

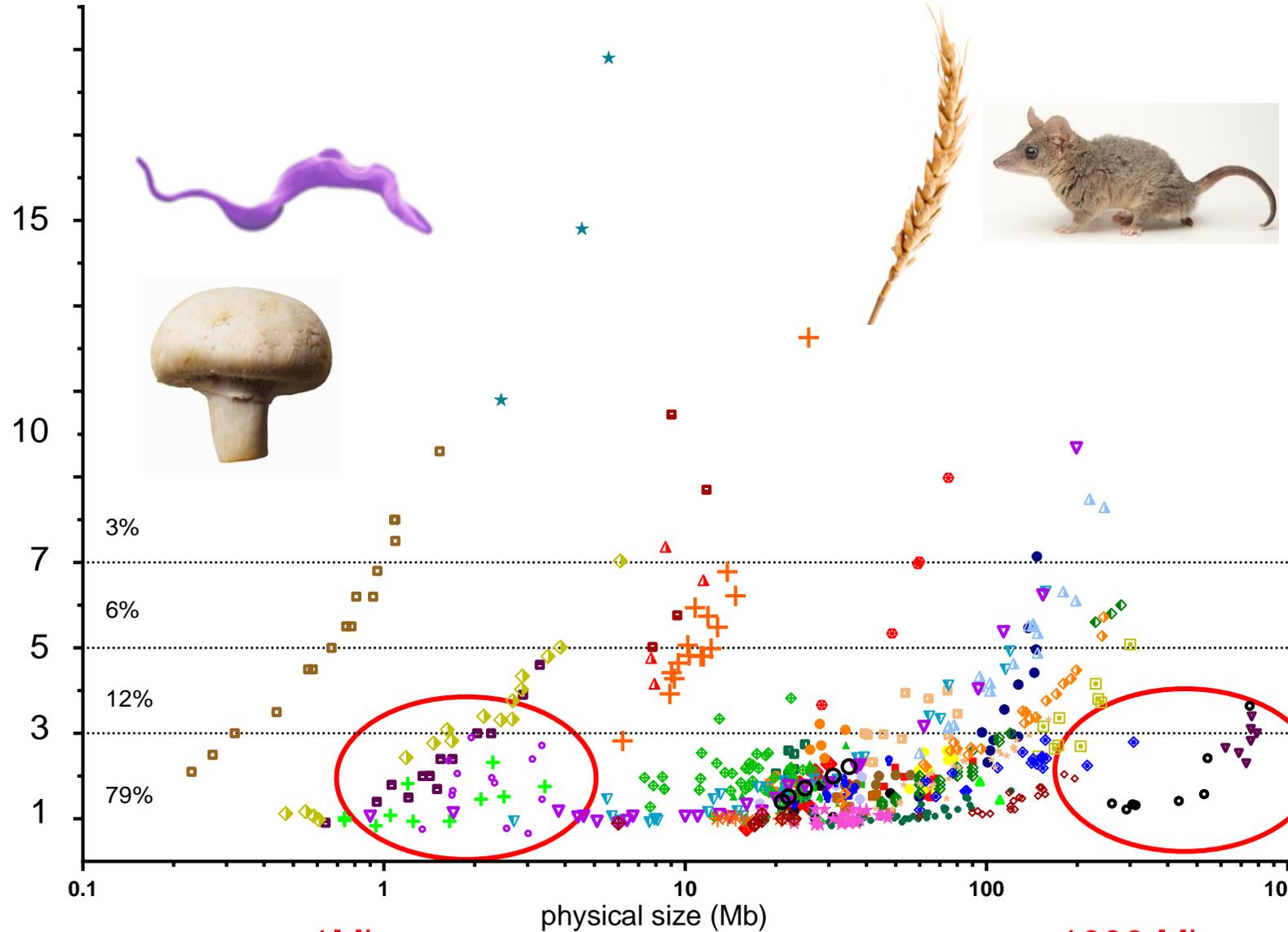


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- Anopheles gambiae
- *Trypanosoma brucei*
- Plasmodium falciparum

Crossovers  
per meiosis



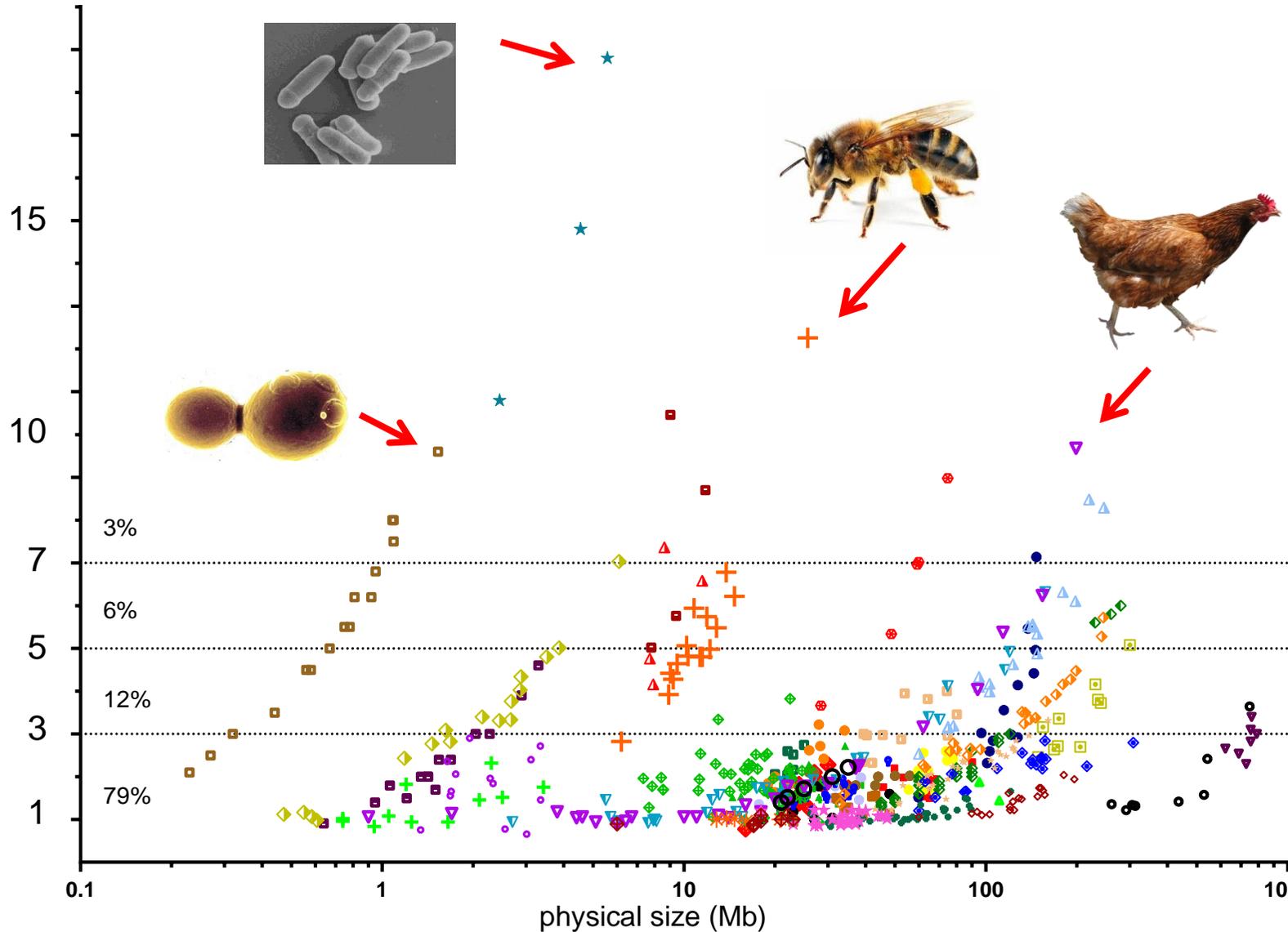
~1Mbase

~1000 Mbases

# Genetic (cM) vs physical size (Mb) of chromosomes from a range of species

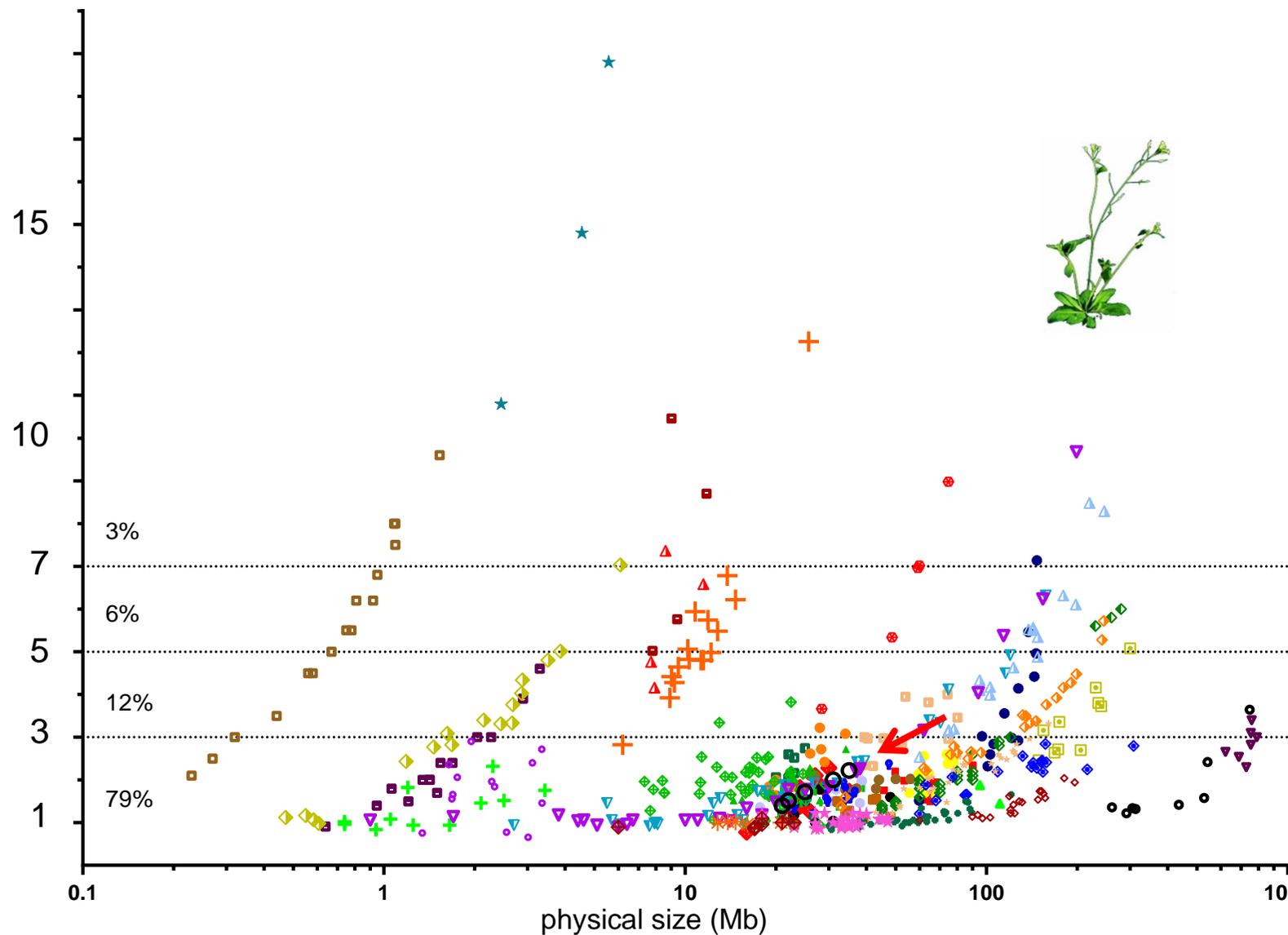
- *Arabidopsis thaliana*
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- Honey bee *Apis mellifera*
- ▲ Anopheles gambiae
- *Trypanosoma brucei*
- Plasmodium falciparum

Crossovers  
per meiosis



# Genetic (cM) vs physical size (Mb) of chromosomes from a range of species

Crossovers  
per meiosis

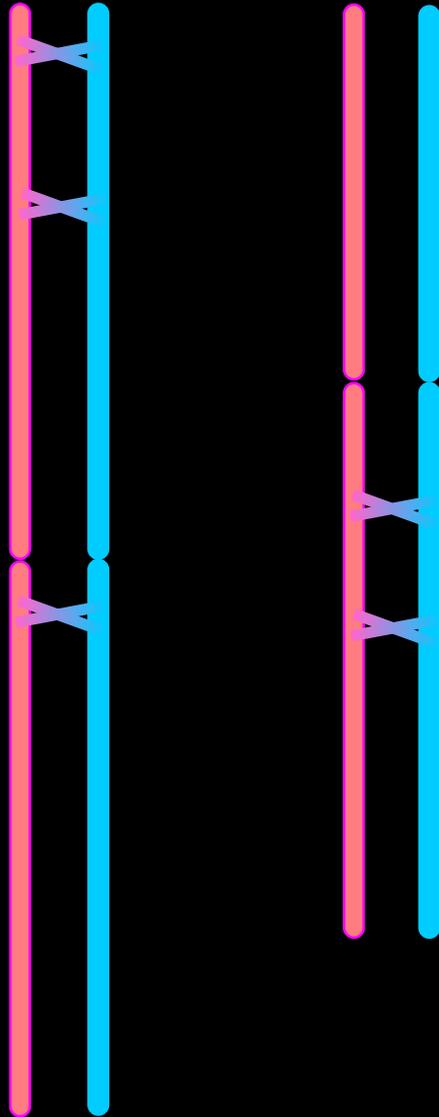


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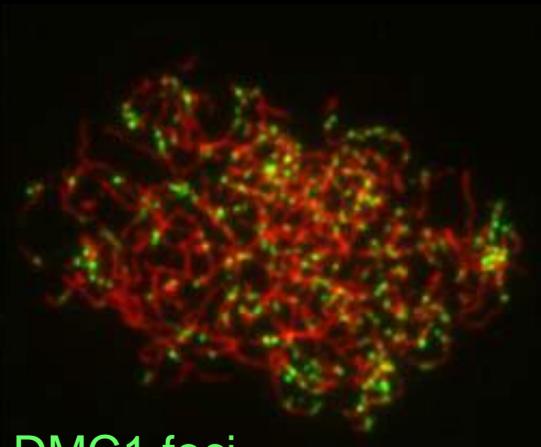
# Crossover distribution is not random

3) crossover interference:

Crossovers tend to be away from each others



# Precursors largely excess crossovers



DMC1 foci

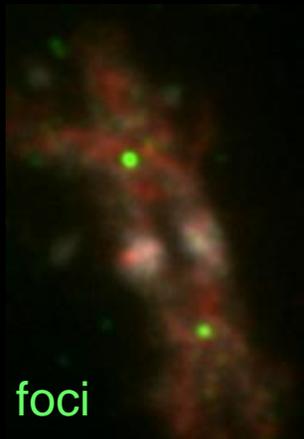
**Double Strand Breaks**  
(~200)



**Non-Crossover repair**

**Class I COs**  
(~9)  
(Interfering)

**Class II COs**  
(~1)  
(Non interfering)



MLH1 foci



- Crossover number is very low in most species
- molecular precursors largely outnumber crossovers

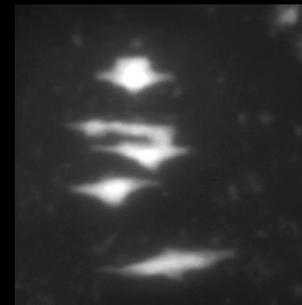
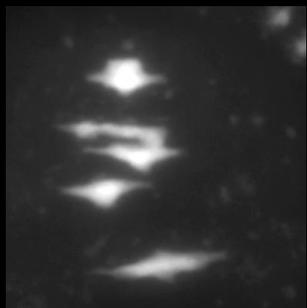
*What limits crossover formation?*

Looking for anti-crossover factors

**Wild-type**

***zmm* mutant**

***Supressors ?***



*zmm*<sup>-/-</sup> (T-DNA)

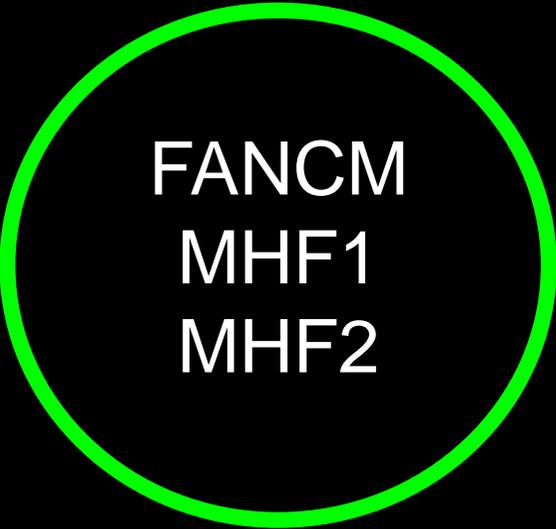


*gene?*<sup>-/-</sup> (EMS)



# *Anti-crossover screen summary*

- 7000 lines screened
- 8 genes characterized so far
- 3 pathways



FANCM  
MHF1  
MHF2

The FANCONI pathway

Crismani et al, Science 2012  
Girard et al, NAR 2014



RECQ4/BLM  
TOP3 $\alpha$   
RMI1

The BTR pathway

Séguéla et al, PNAS 2015  
Séguéla et al, NAR 2016



FIGL1  
FLIP

The FIDGETIN pathway

Girard et al, PLoS Genetics 2015  
Fernandes et al, unpublished

# Class II crossovers are specifically increased in all these mutants



Double Strand Breaks



Non-Crossover repair

ZMM

MUS81

Class I COs

Class II COs



Double Strand Breaks



Non-Crossover repair

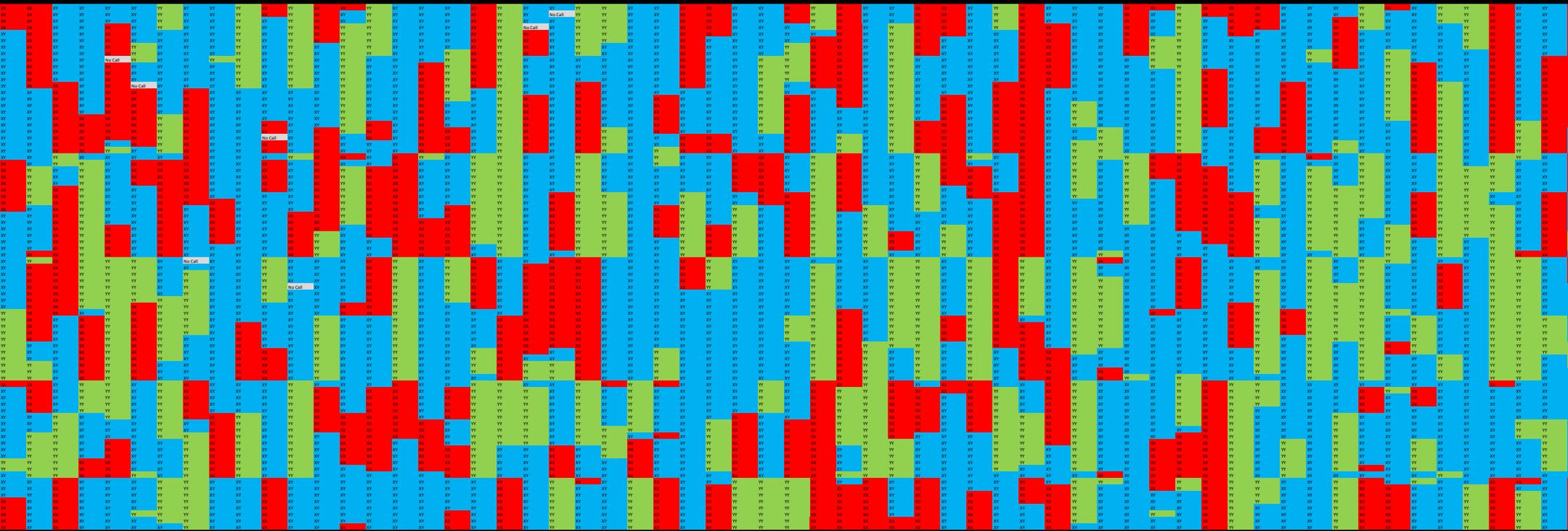
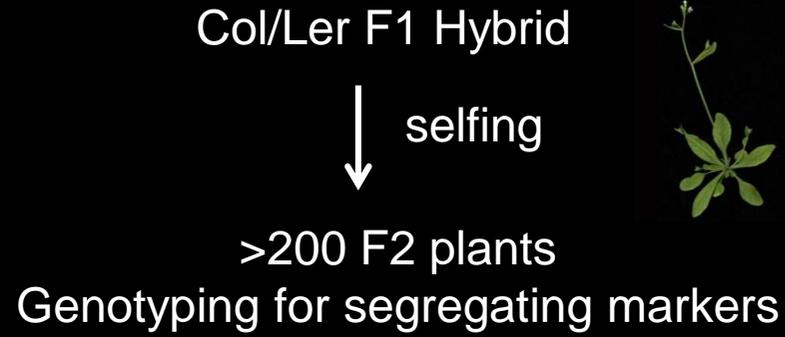
ZMM

MUS81

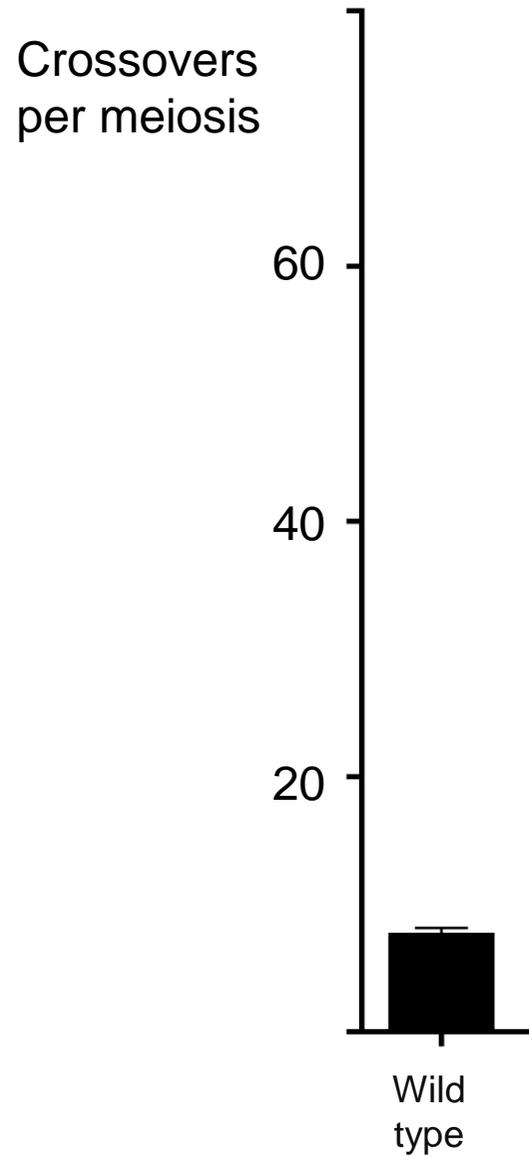
Class I COs

Class II COs

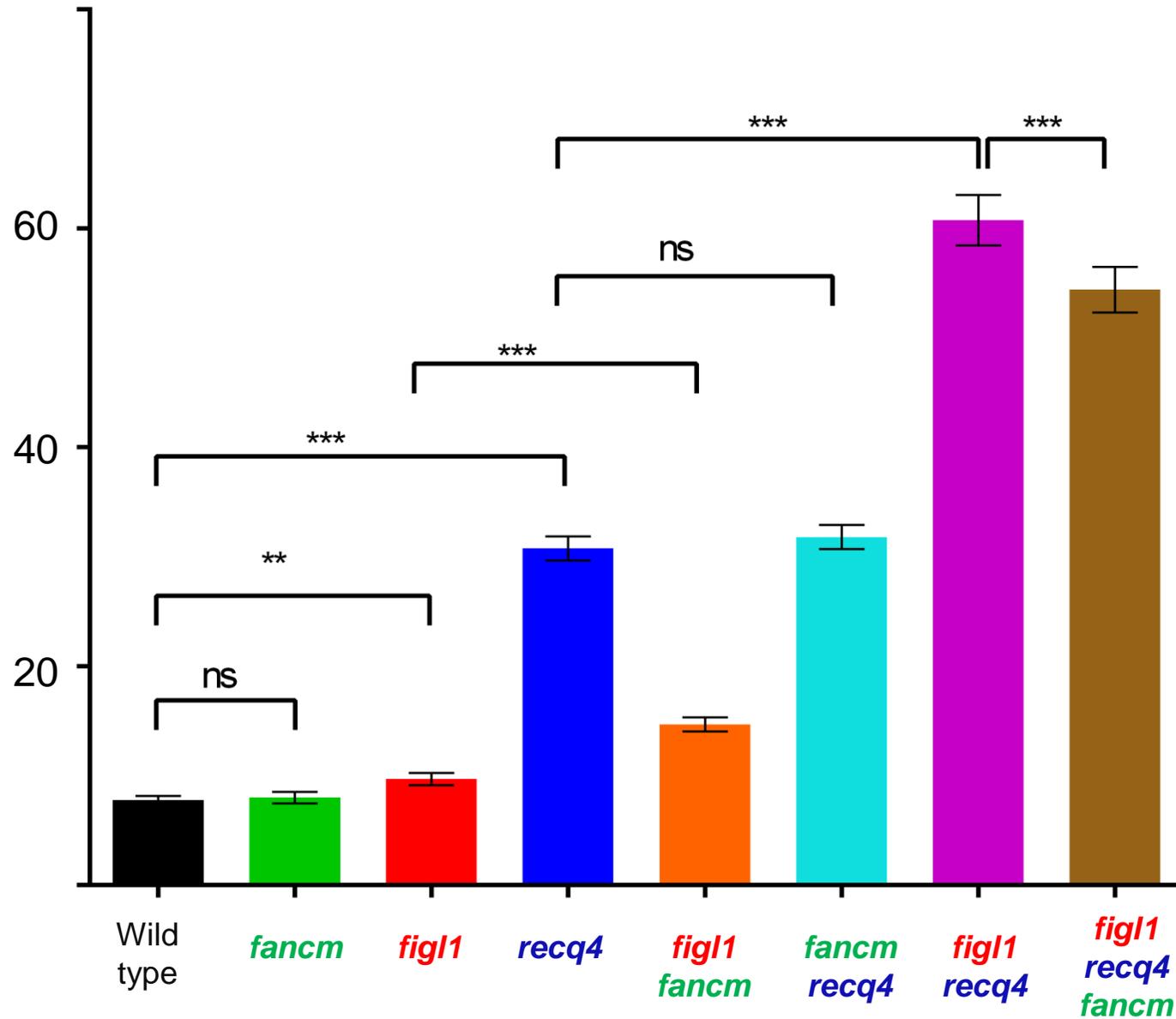
# Genome wide analysis of recombination in single and multi-mutants



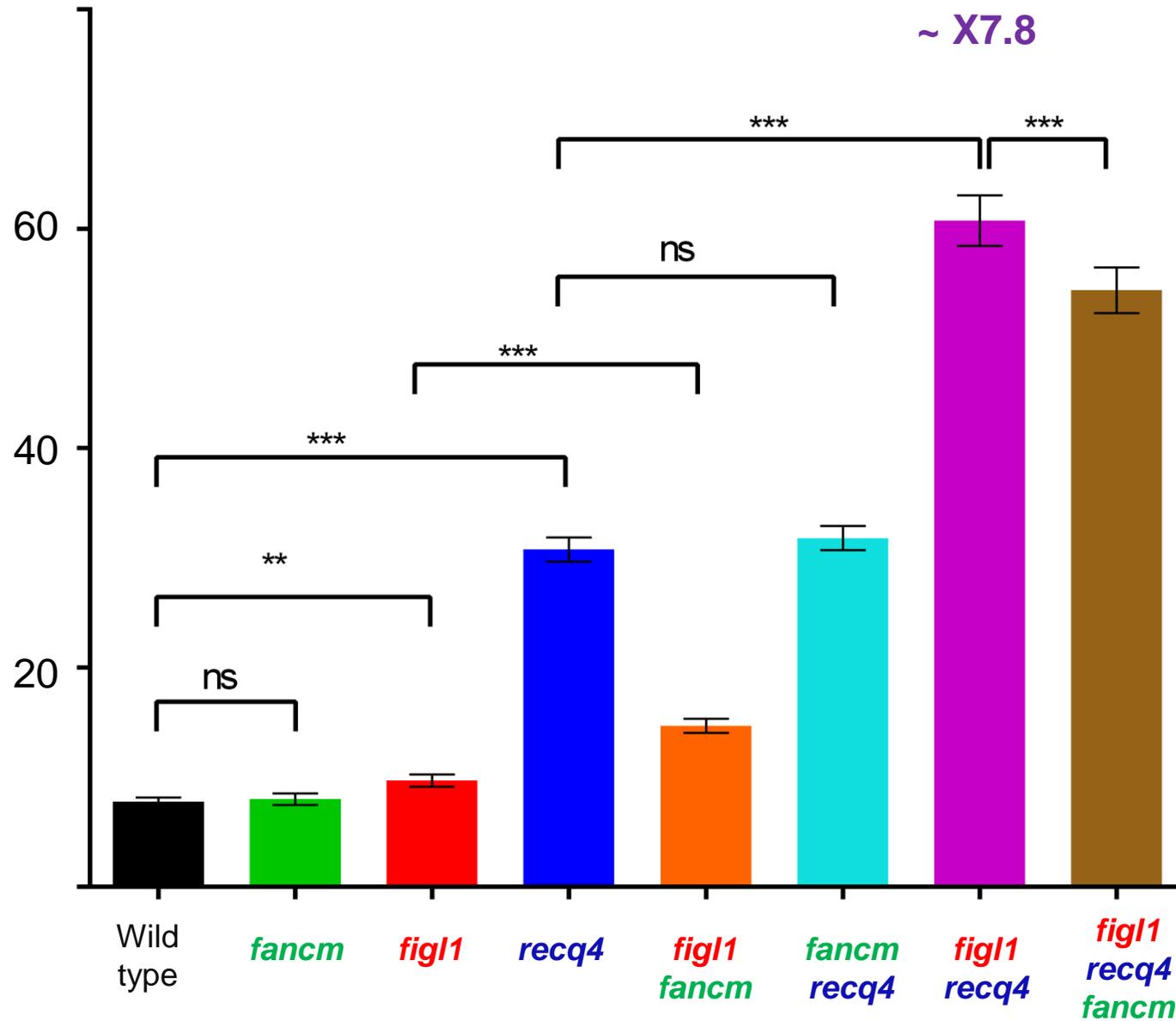
# Genome wide analysis of recombination in single and multi-mutants



# Genome wide analysis of recombination in single and multi-mutants

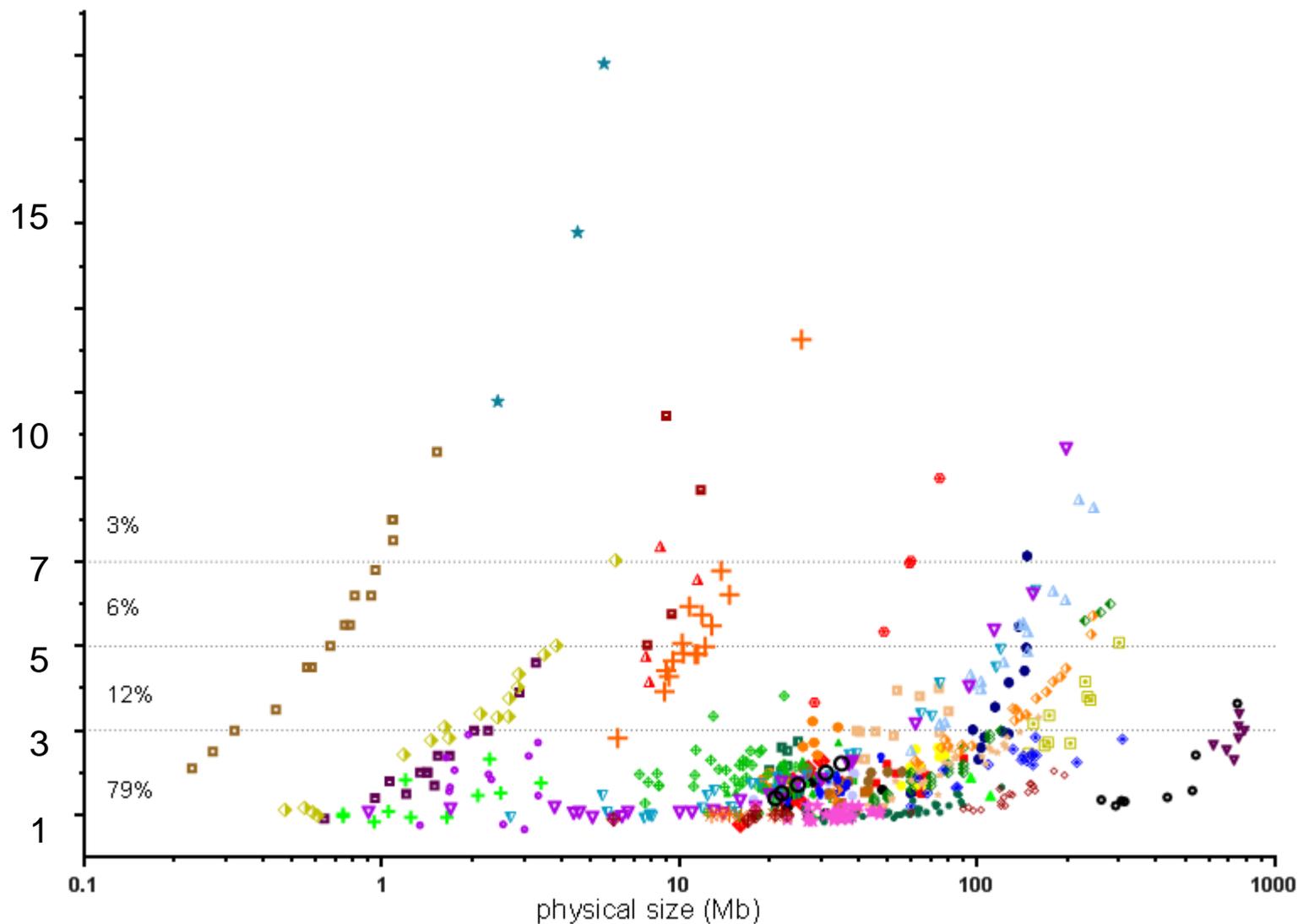


# Genome wide analysis of recombination in single and multi-mutants



# Genetic (cM) vs physical size (Mb) of chromosomes from in a range of species

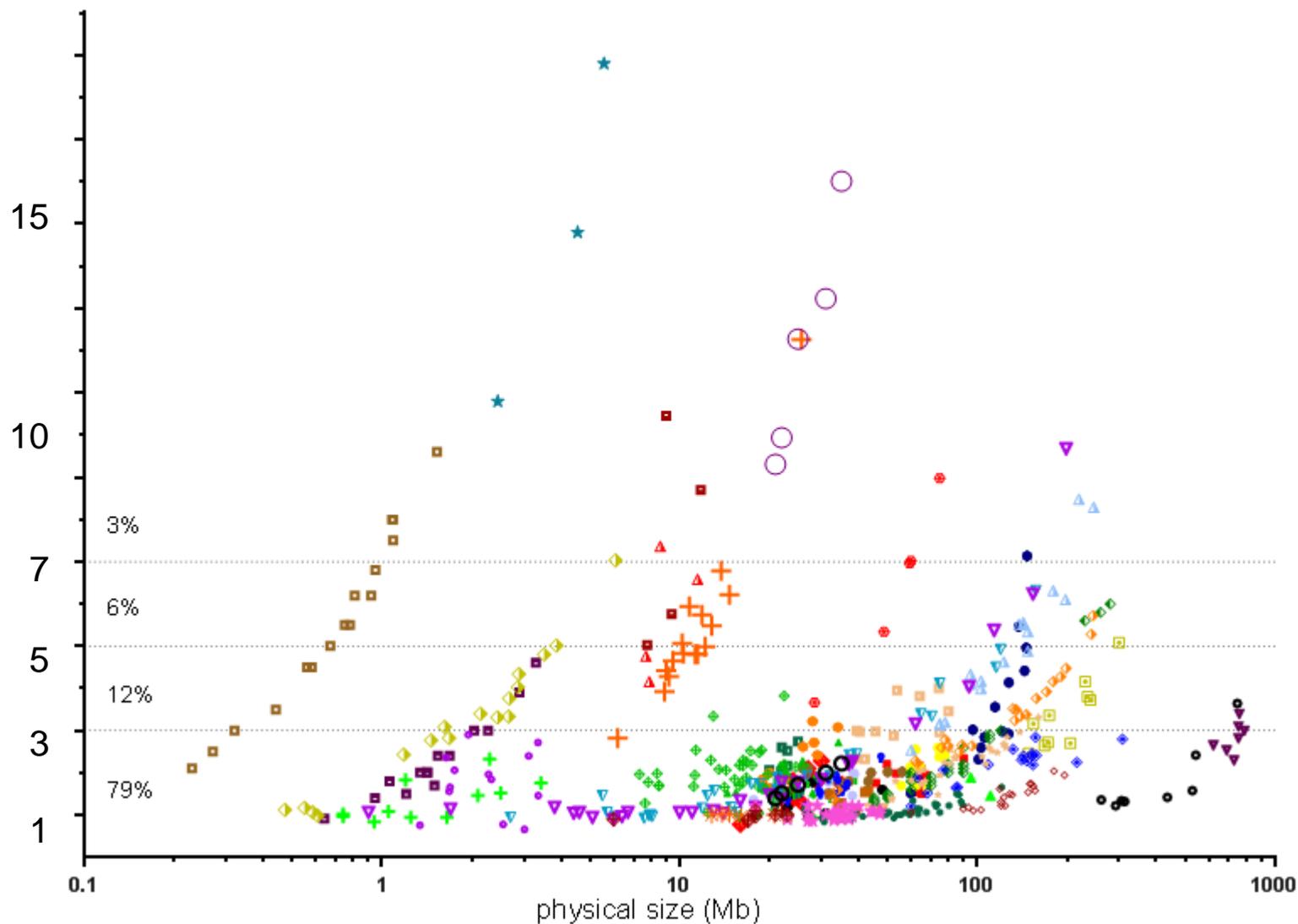
Crossovers  
per meiosis



- *Arabidopsis thaliana*
- *Sorghum bicolor*
- *Eucalyptus grandis*
- *Medicago truncatula*
- *Brachypodium distachyon*
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# Genetic (cM) vs physical size (Mb) of chromosomes from in a range of species

Crossovers  
per meiosis



- *Arabidopsis thaliana*
- *Arabidopsis thaliana recq4 fig11*
- *Sorghum bicolor*
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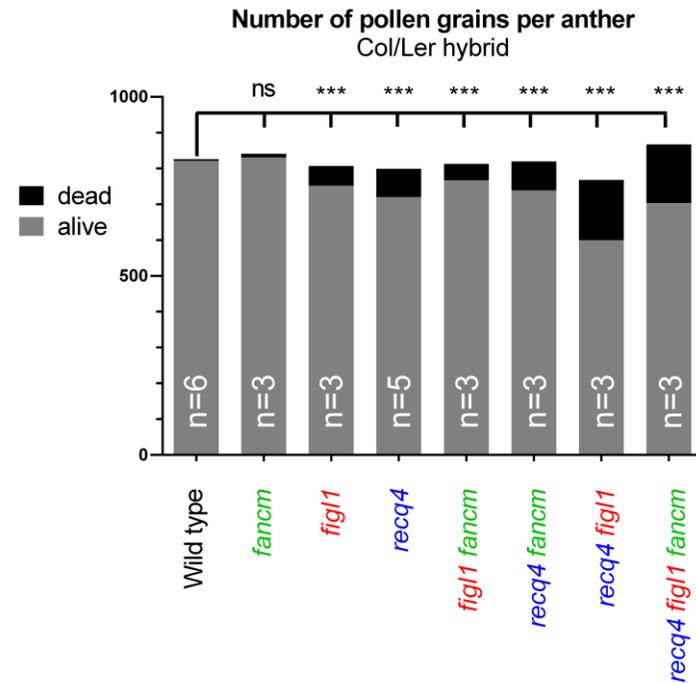
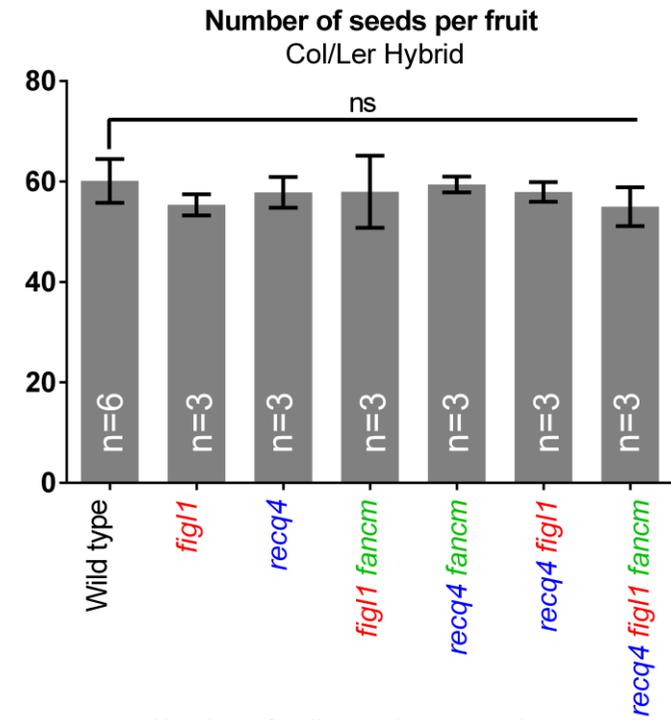
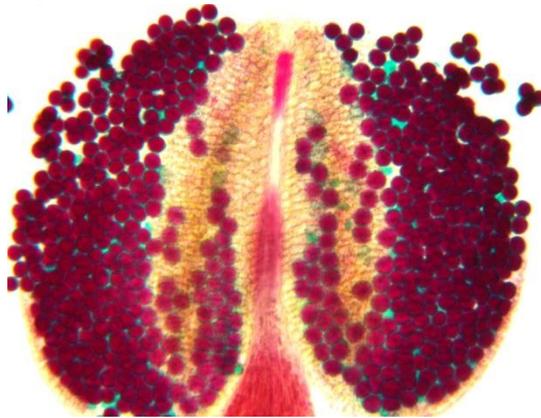
# Fertility in these Hyper-recombinant Mutants ?



Wild type



*recq4*  
*figl1*

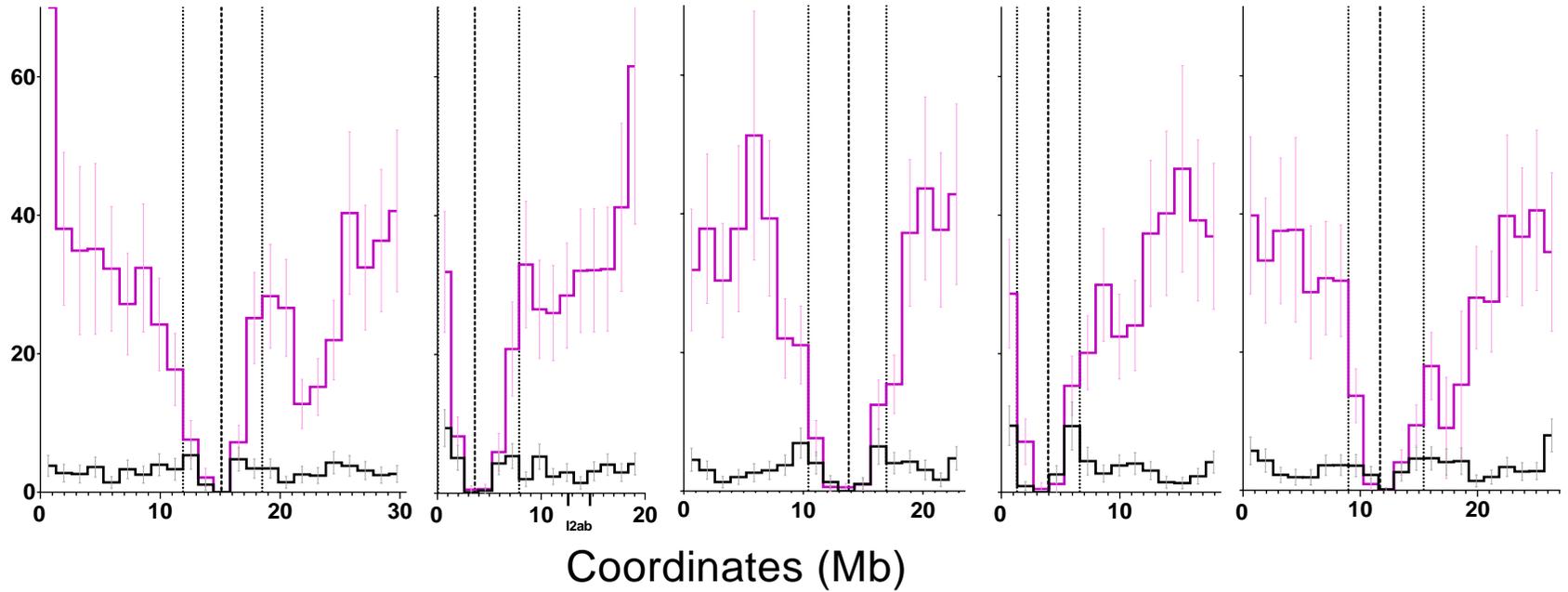


# Recombination frequency along chromosomes

recombination  
(cM/mb +/- 95% CI)

*recq4*  
*fig1*

— Wild  
type

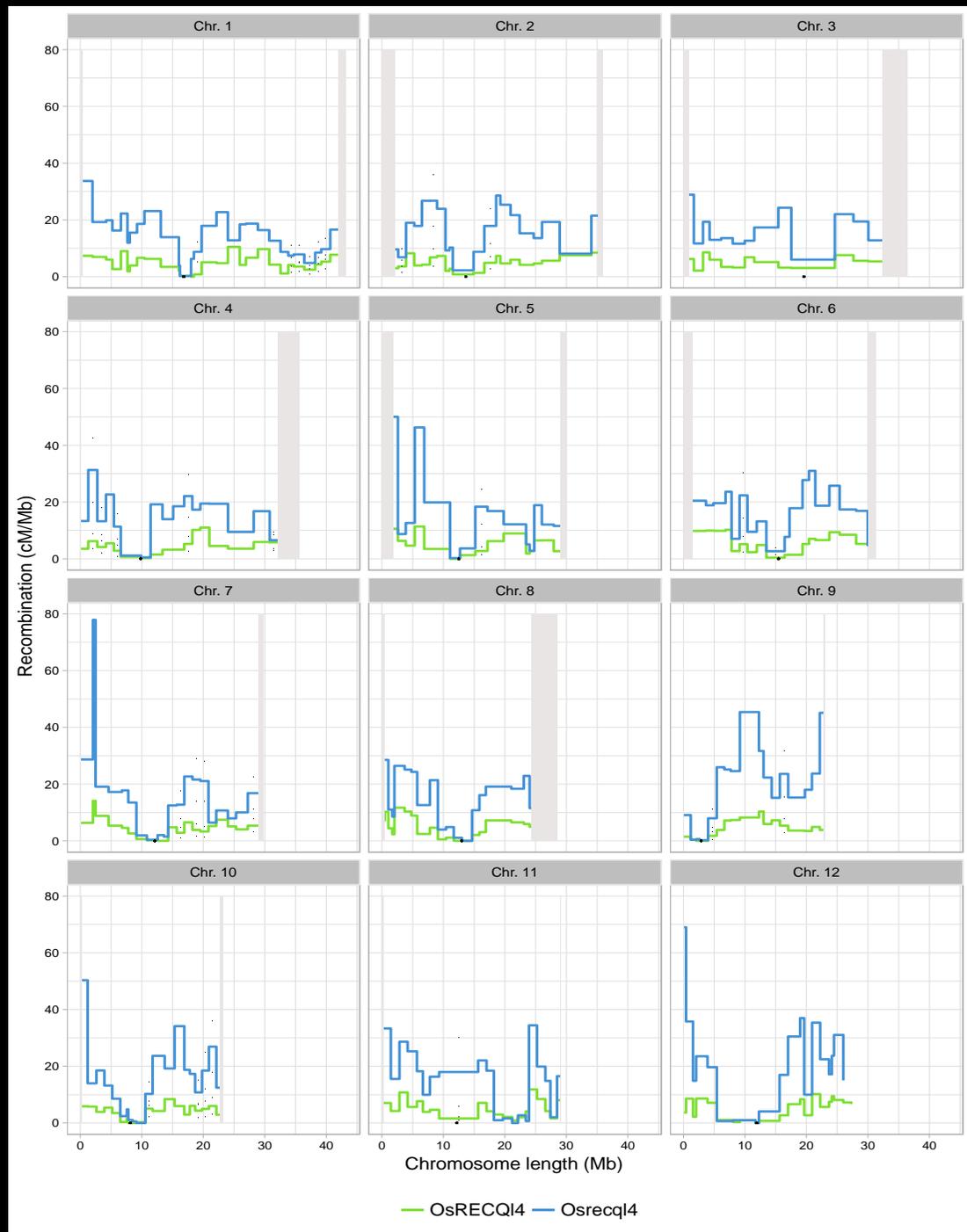


Transfer to crops

# Transfer to crops



*recq4* compared to wild type  
rice: x 3.3



## CONCLUSIONS for « to mix »

- Meiotic crossovers can be largely increased (x7.8 genome wide)
  - Potential great tool for plant breeding
  - But no effect in peri-centromeres
  - Why having so few crossovers in most species?

*not To Mix:  
towards apomixis*

# Apomixis

(clonal reproduction through seeds)

- Relatively common in the plant kingdom



Erigeron



*Taraxacum*



*Heracium*



*Tripsacum*



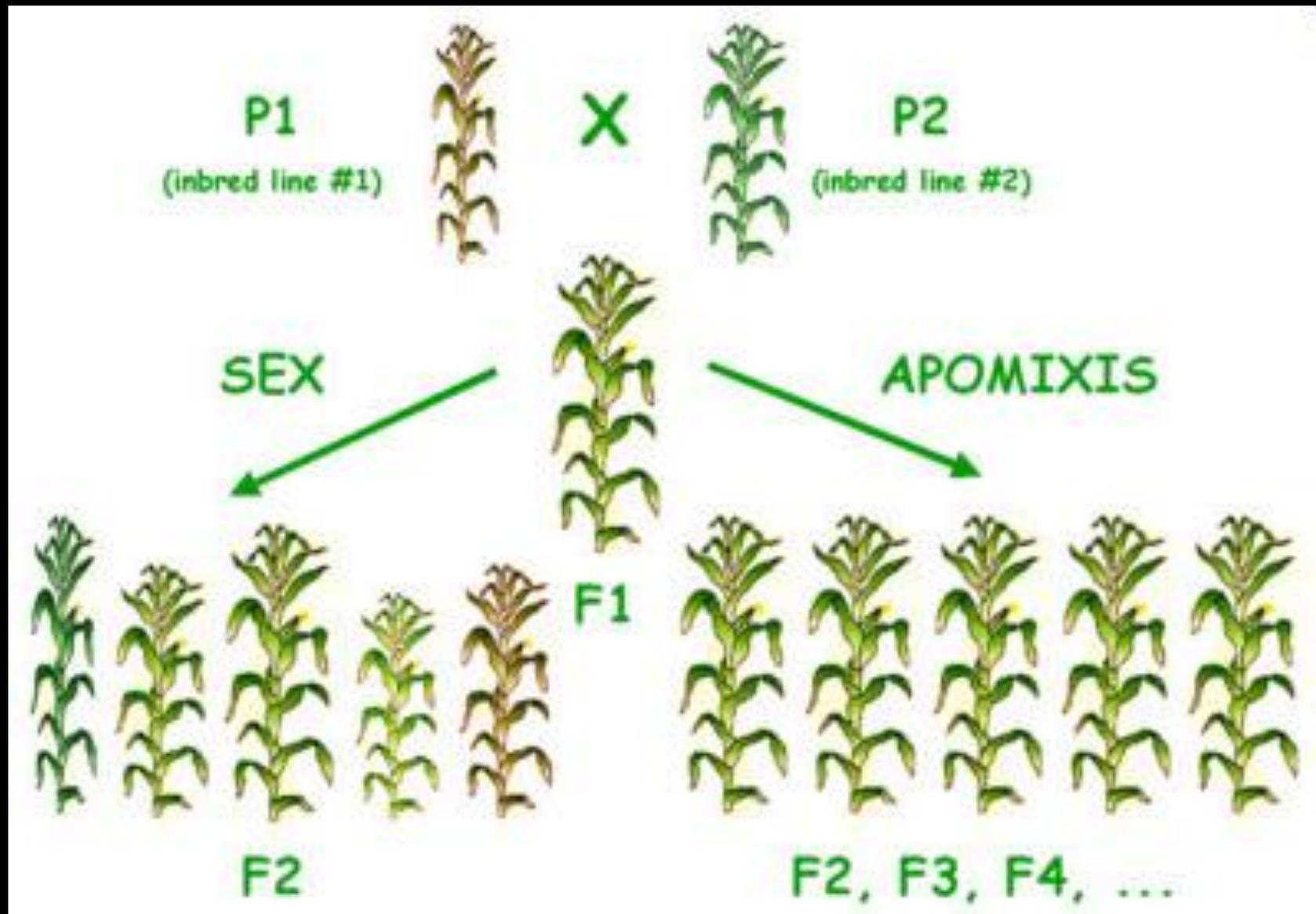
*Boechera*



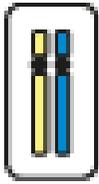
Ranunculus

- Absent in crops

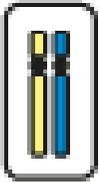
- Its introduction in crops has potential revolutionary application



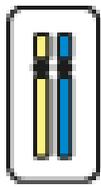
Hybrid parent



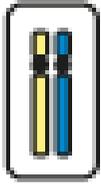
Clonal embryo



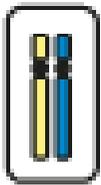
Hybrid parent



Clonal diploid  
gamete



Clonal embryo



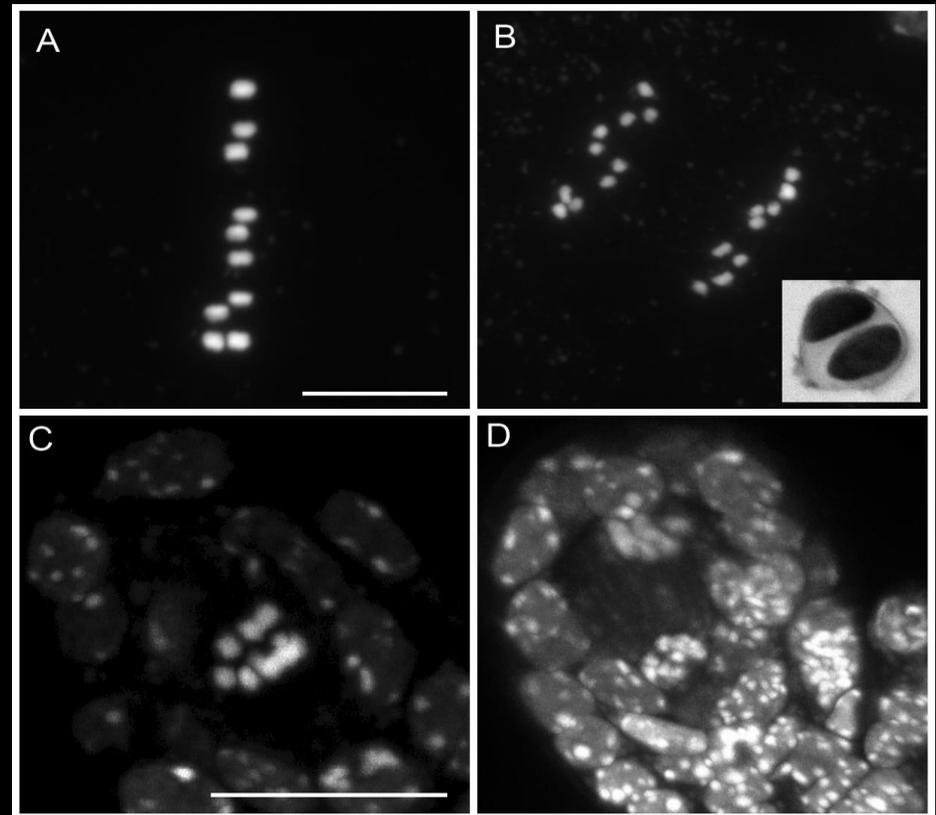
# The combination of three mutations turn meiosis into mitosis

- Recombination
- Two rounds of chromosome segregation
- Co-segregation of sister chromatids at division I



*MiMe*  
(*spo11/rec8/osd1*)

male



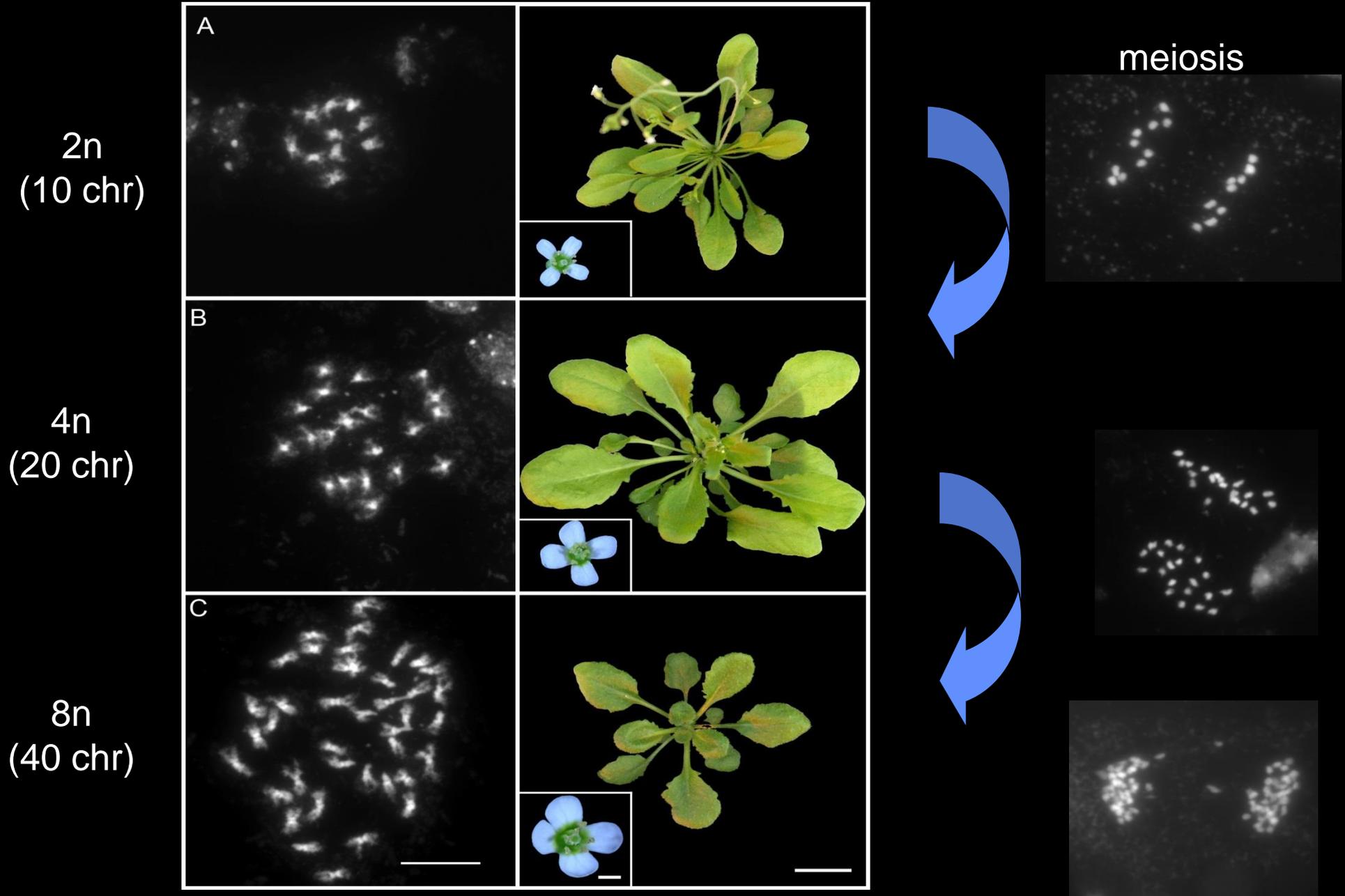
Female

100% clonal gametes

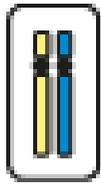
d'Erfurth et al, Plos Biol 2009.

d'erfurth, Cromer et al, Plos genet 2010

# Doubling of ploidy at each generation in the *MiMe* line

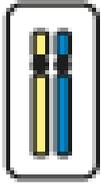


Hybrid parent

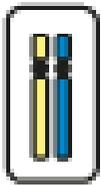


*MiMe*

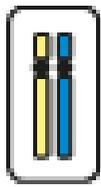
Clonal diploid  
gamete



Clonal embryo

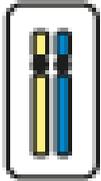


Hybrid parent

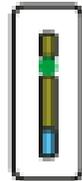


*MiMe*

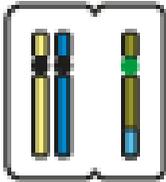
Clonal diploid gamete



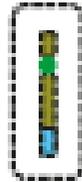
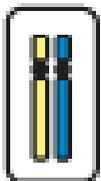
*GEM* Gamete



Fertilization



Clonal embryo



LETTERS

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## Haploid plants produced by centromere-mediated genome elimination

Maruthachalam Ravi<sup>1</sup> & Simon W. L. Chan<sup>1</sup>

**Simon Chan**

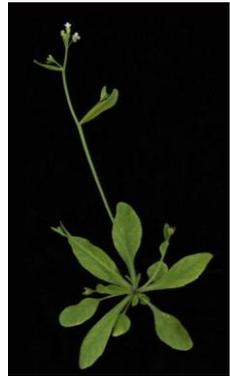
Ravi et al, Nature, 2010

cross (♀ x ♂)	Seeds per siliqua	Germination rate (%)	Total plants analysed	Hybrid diploid* (%)	Triploid (%)	Aneuploid (%)	Clones* (%)
<i>MiMe</i> x <i>GEM</i>	15	92	156	0.6	13	53	34
<i>GEM</i> x <i>MiMe</i>	23	0.5	12	0	25	33	42
cloned <i>MiMe</i> x <i>GEM</i>	14	91	79	1.3	20	54	24



*MiMe*♀ x *GEM*♂

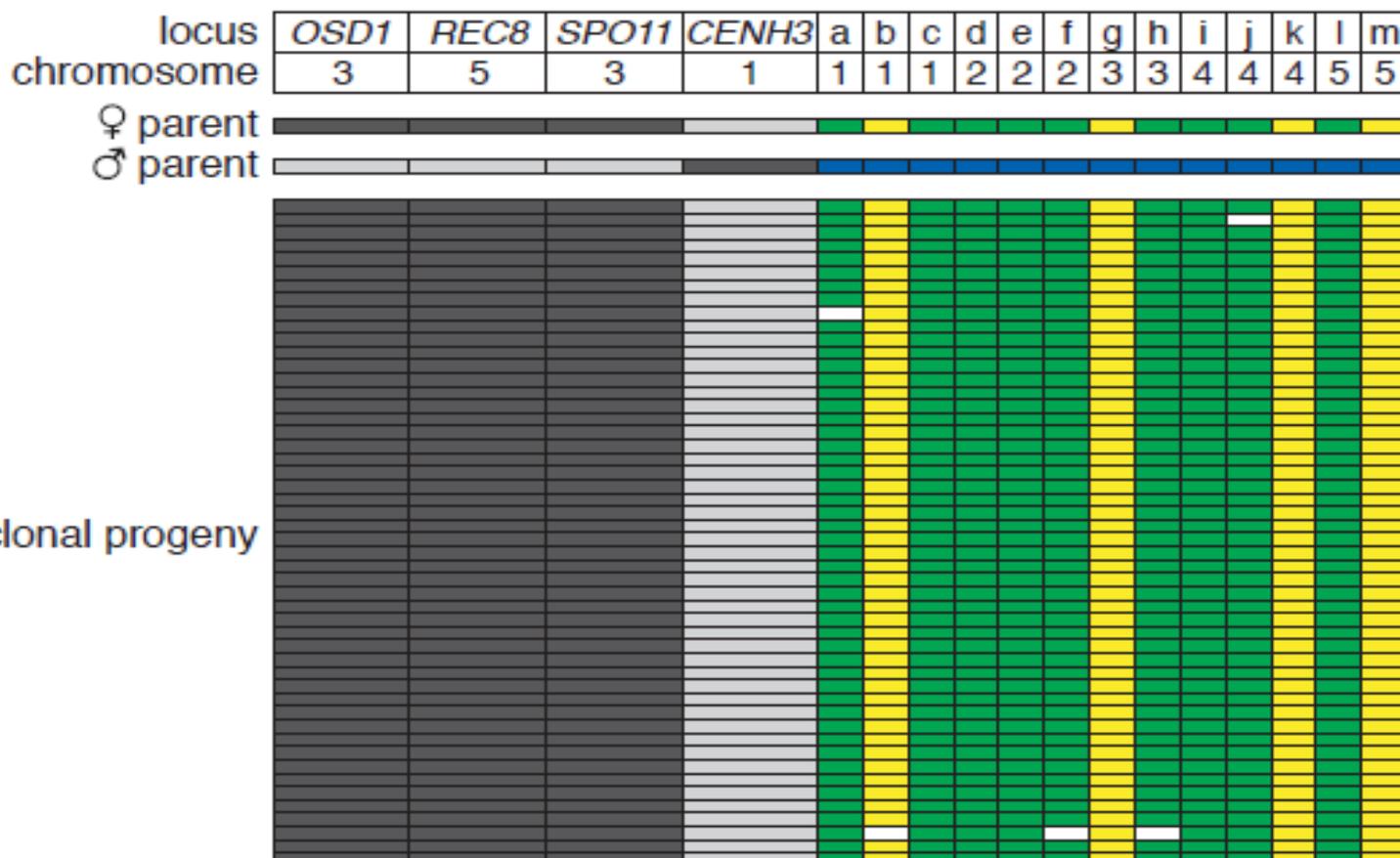
locus	<i>OSD1</i>	<i>REC8</i>	<i>SPO11</i>	<i>CENH3</i>	a	b	c	d	e	f	g	h	i	j	k	l	m
chromosome	3	5	3	1	1	1	1	2	2	2	3	3	4	4	4	5	5
♀ parent	[Color bar representing maternal genome]																
♂ parent	[Color bar representing paternal genome]																



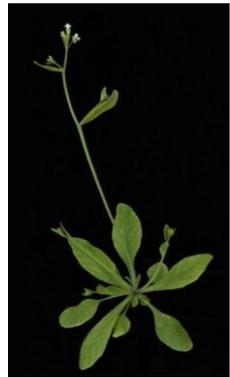
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*MiMe*♀ x *GEM*♂



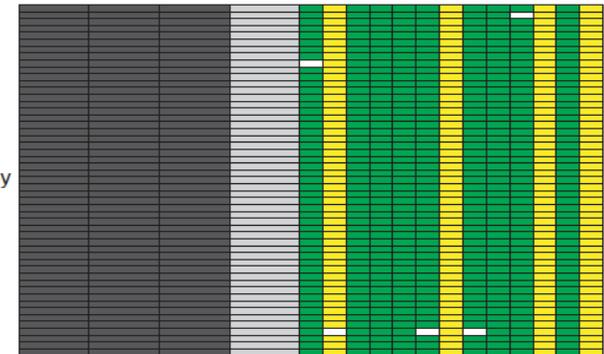
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*MiMe*♀ x *GEM*♂

locus	<i>OSD1</i>	<i>REC8</i>	<i>SPO11</i>	<i>CENH3</i>	a	b	c	d	e	f	g	h	i	j	k	l	m
chromosome	3	5	3	1	1	1	1	2	2	2	3	3	4	4	4	5	5
♀ parent	[Genetic marker bands]																
♂ parent	[Genetic marker bands]																

2n clonal progeny

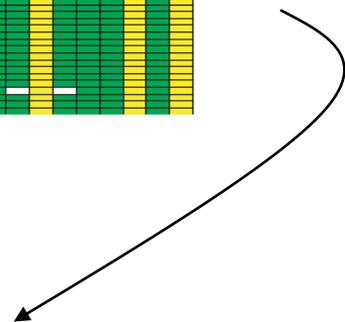
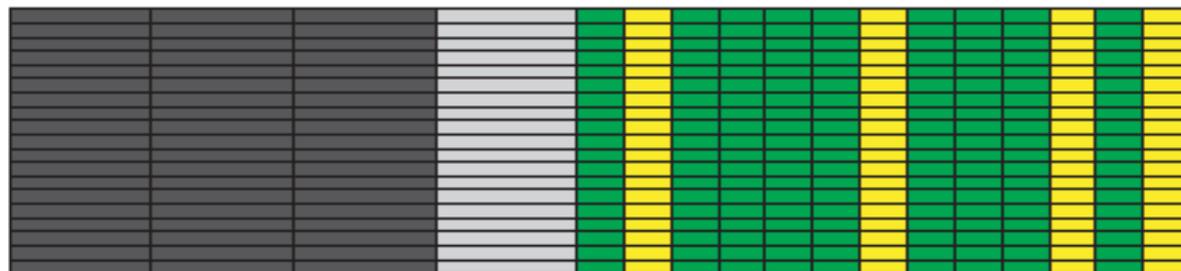


cloned *MiMe*♀ x *GEM*♂

locus	<i>OSD1</i>	<i>REC8</i>	<i>SPO11</i>	<i>CENH3</i>	a	b	c	d	e	f	g	h	i	j	k	l	m
chromosome	3	5	3	1	1	1	1	2	2	2	3	3	4	4	4	5	5

♀ parent	[Genetic marker bands]																
♂ parent	[Genetic marker bands]																

2n clonal progeny





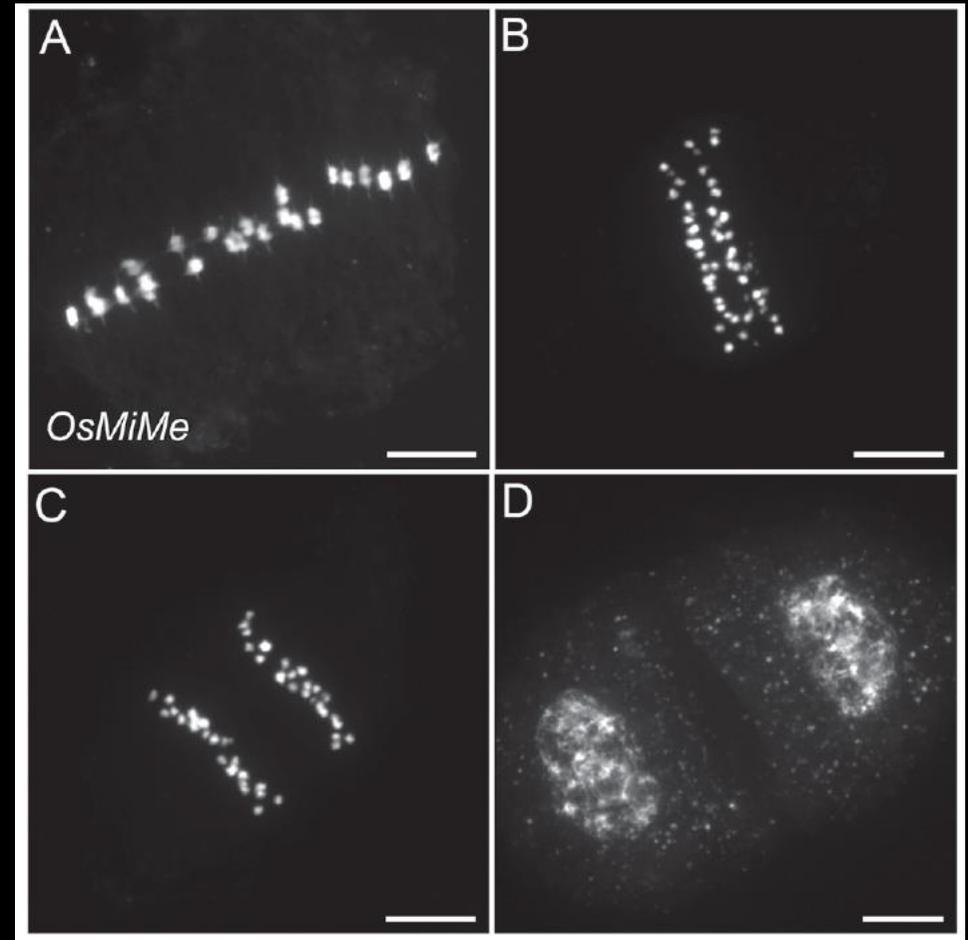
Mitosis instead of Meiosis  
+ Cross with the genome elimination line

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= Clonal seeds !



# The combination of the same three mutations turn meiosis into mitosis in rice



## CONCLUSIONS for « not to mix »

- It is possible to engineer clonal reproduction through seeds
- Some limitations remains
  - Frequency of clonal seeds
  - Induction of embryogenesis in crops



THANKS!



INRA Versailles  
Meiotic Mechanism Team

To mix

Not to mix

Mathilde Séguéla-Arnaud  
Joiselle Fernandes  
Chloé Girard  
Wayne Crismani  
*et al*

Isabelle d'Erfurth  
Sylvie Jolivet  
Laurence Cromer  
*et al*



CIRAD Montpellier  
UMR AGAP

Delphine Mieulet  
Emmanuel Guiderdoni

