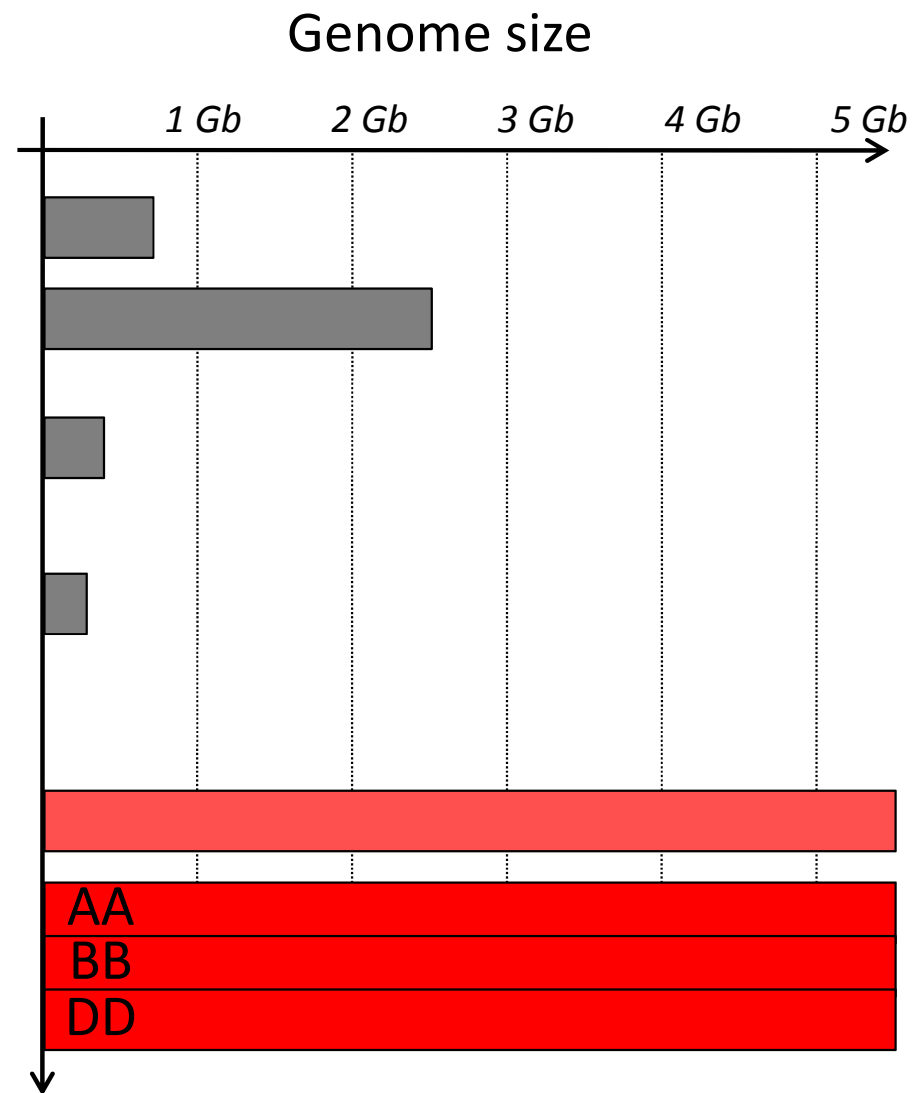
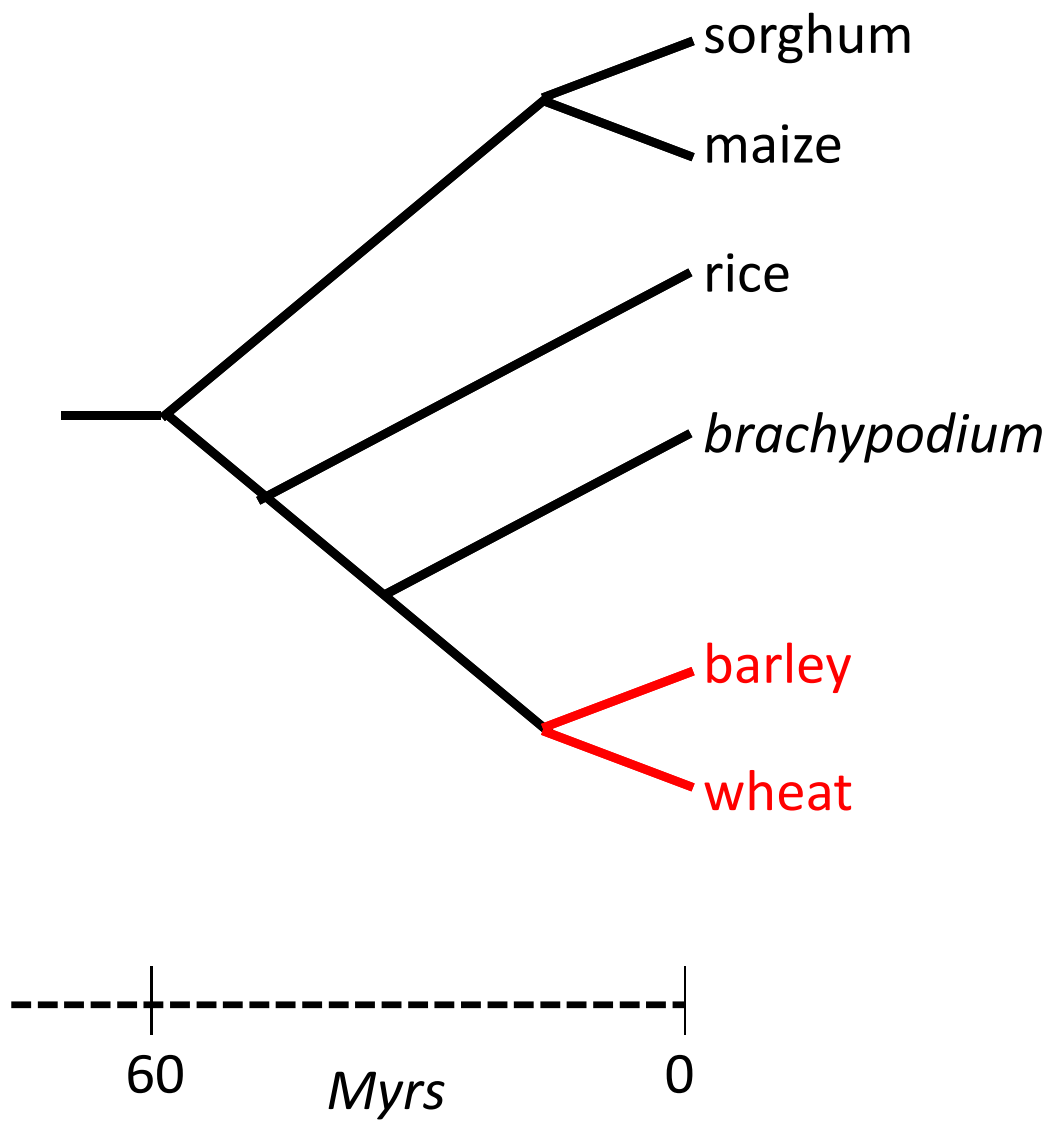
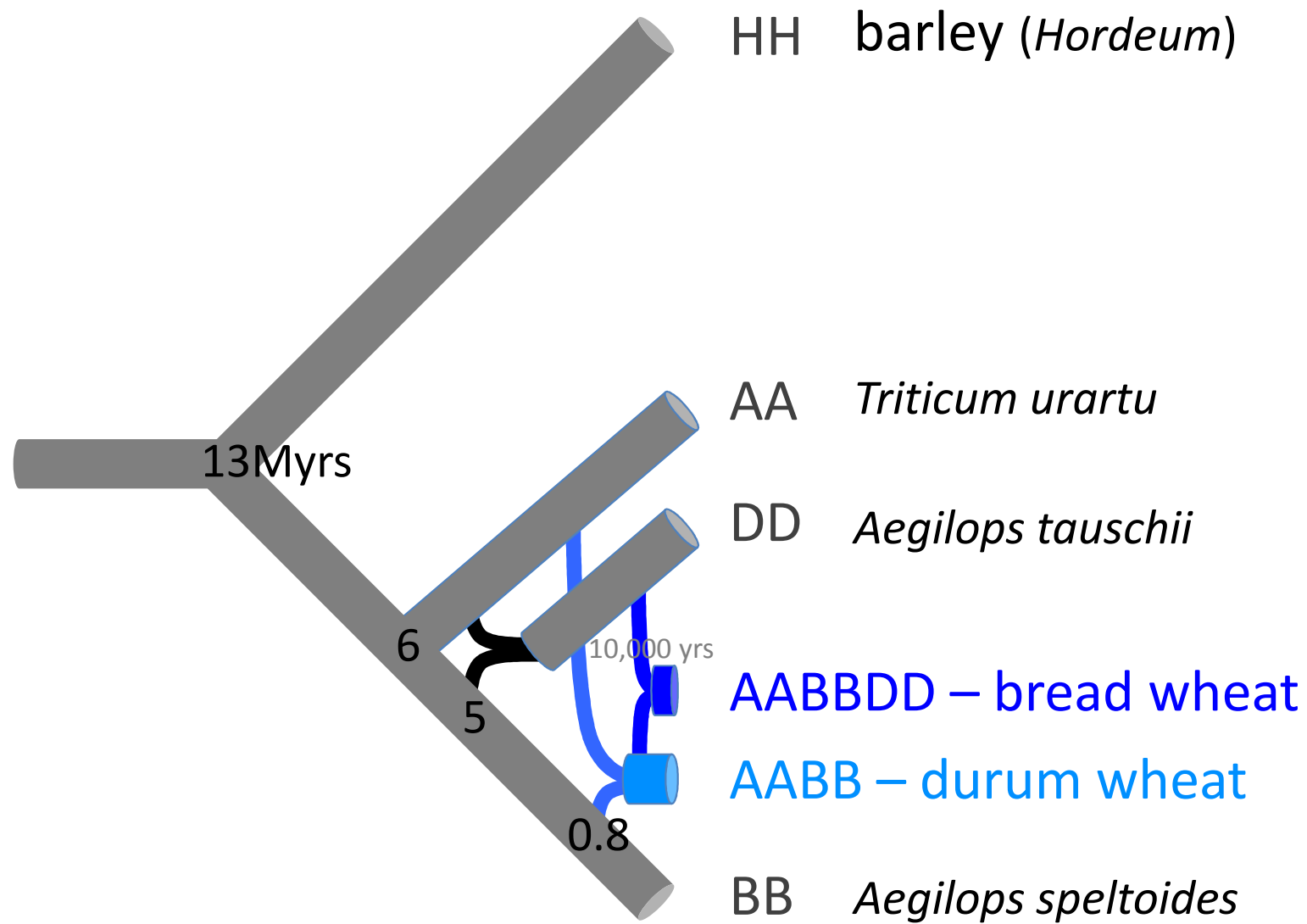


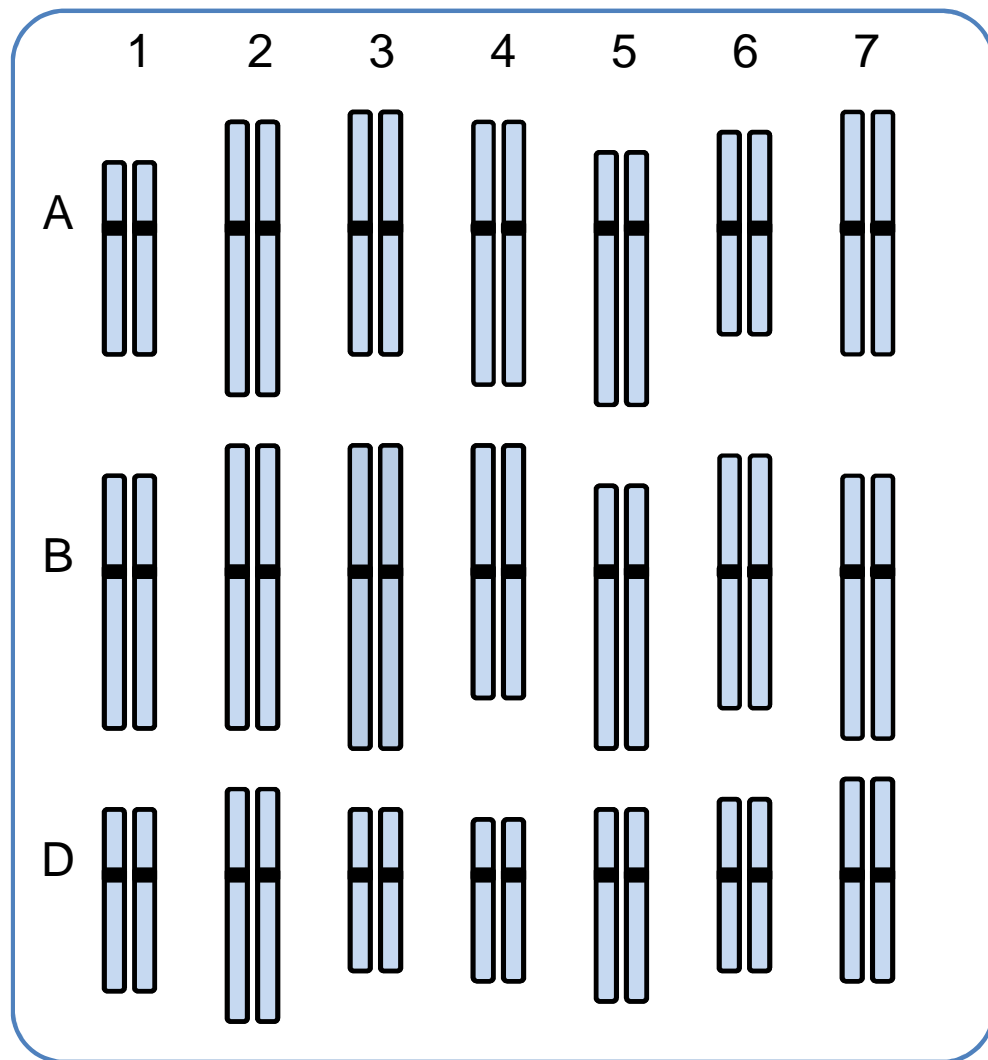
# Wheat Genome Sequencing Initiatives, Resources, Knowledge

Frédéric CHOULET



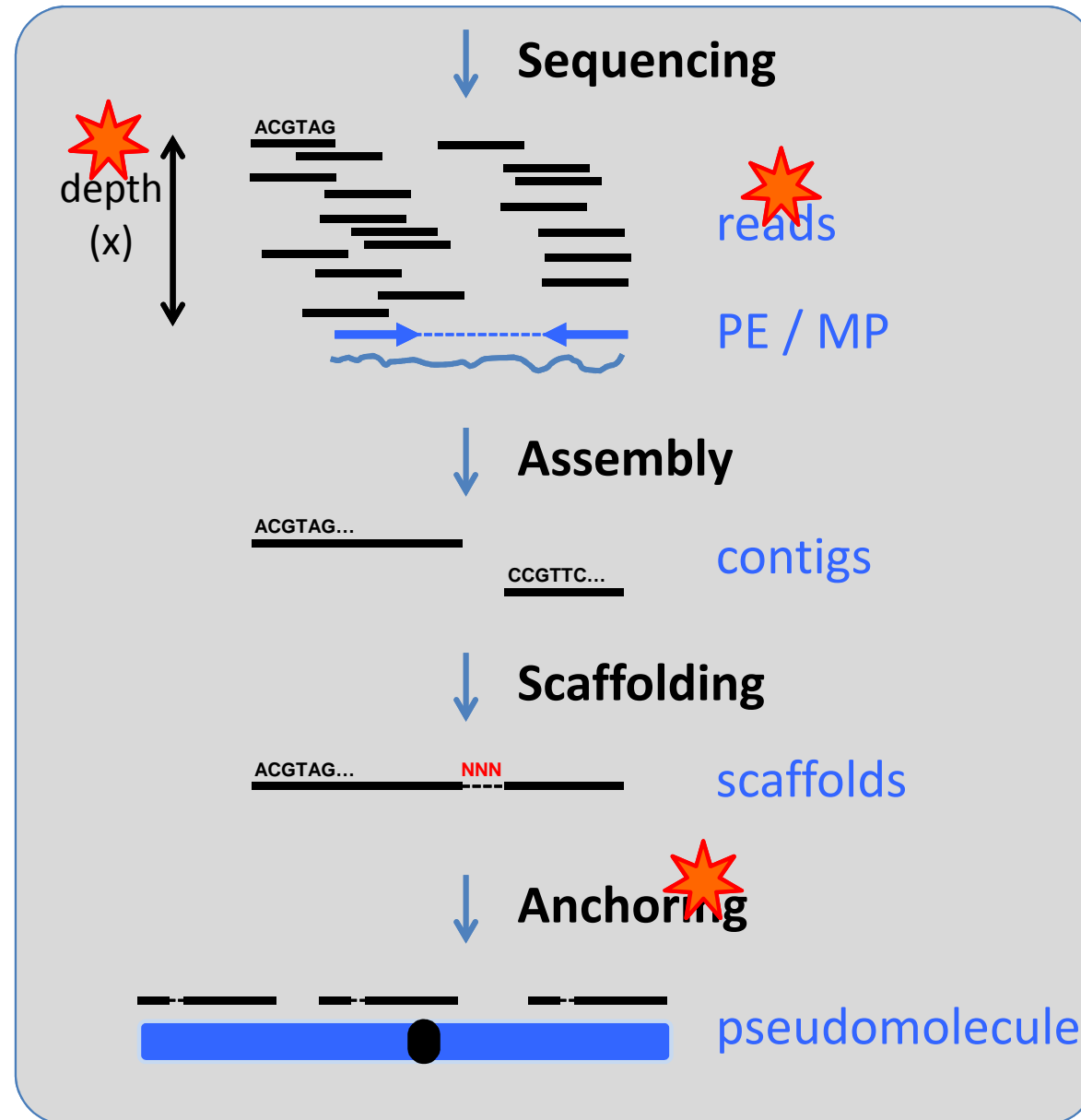








WGS

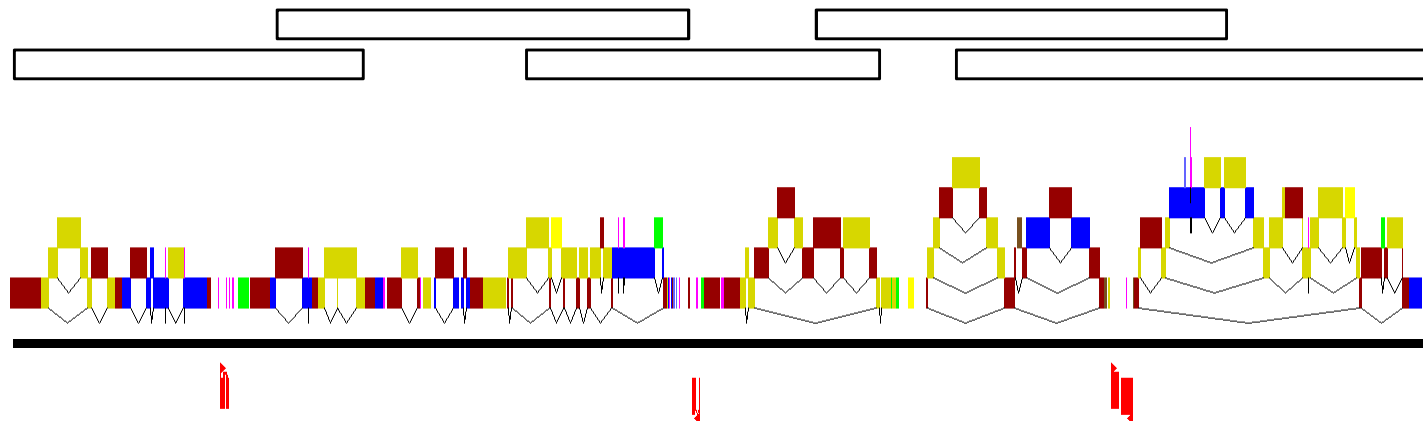




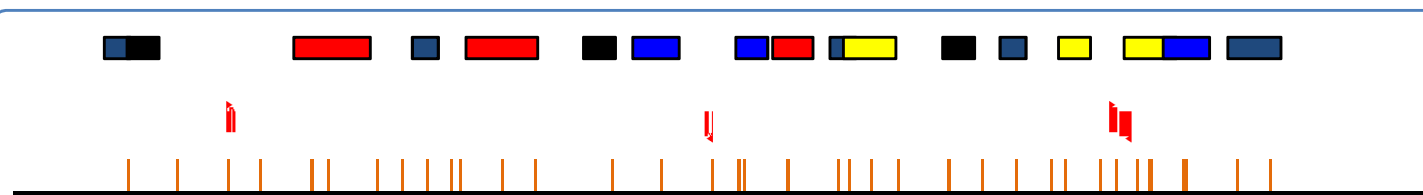
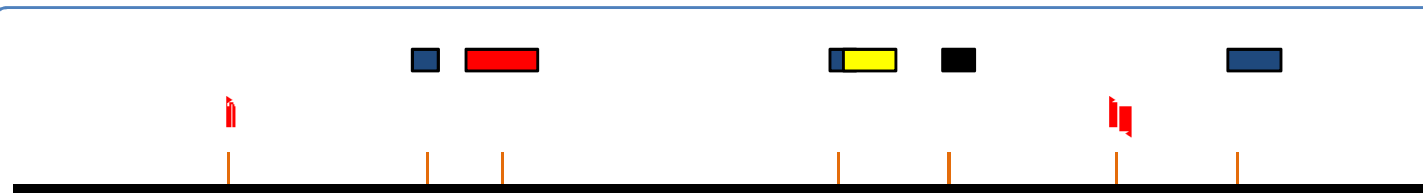
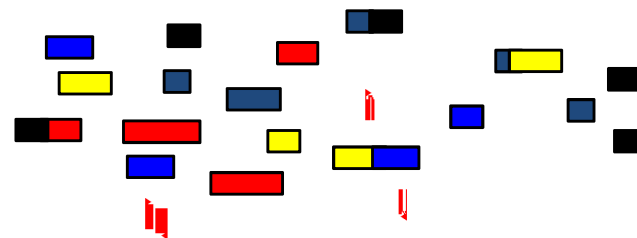
- reduce the complexity (*repeat-level*)
  - transcriptome (ESTs, RNASeq...)
  - methyl-filtration, high  $C_0t$ , ... exome capture
  - diploids
  - chromosome sorting
  - BACs



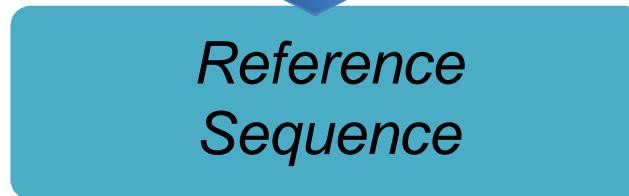
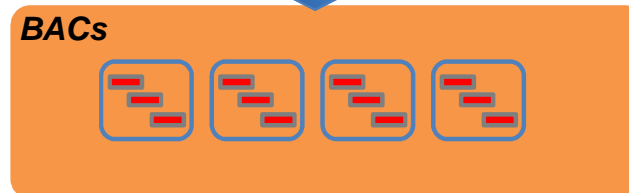
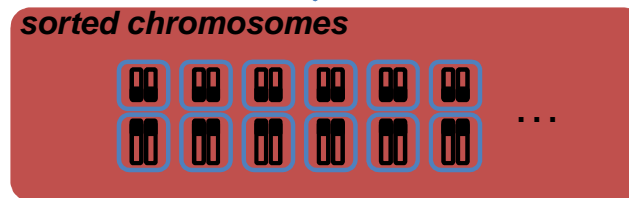
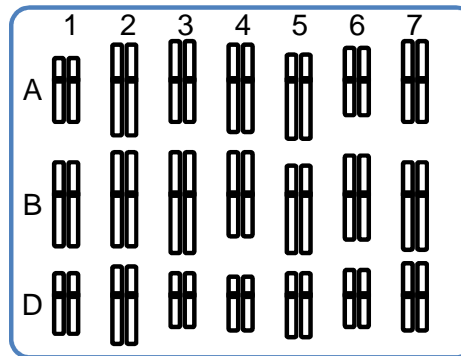
**BAC-based**



**WGS**



**POPSeq**





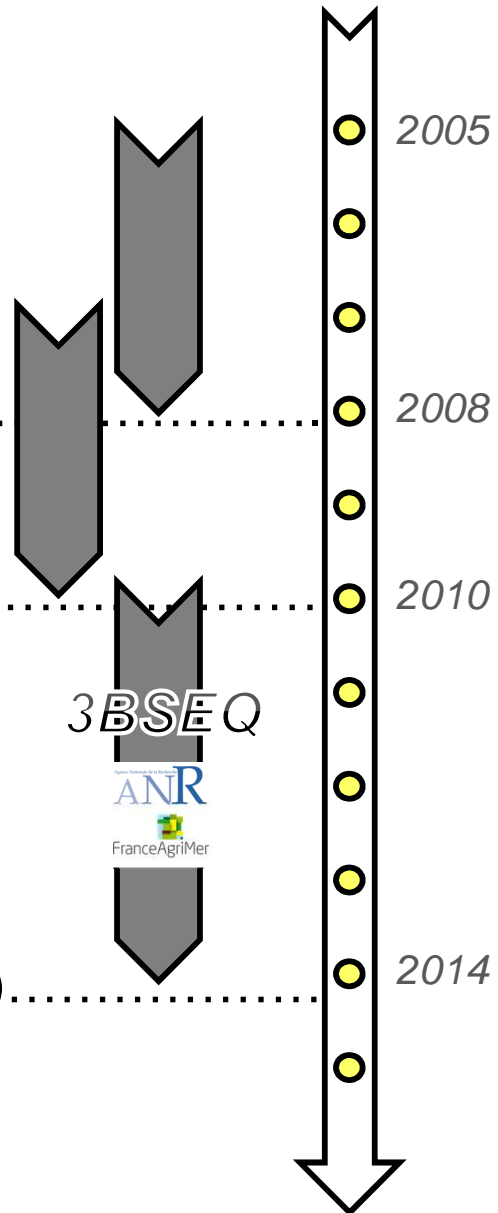


## BAC-based

○ 1<sup>st</sup> physical map (3B).

○ seq pilot project.....

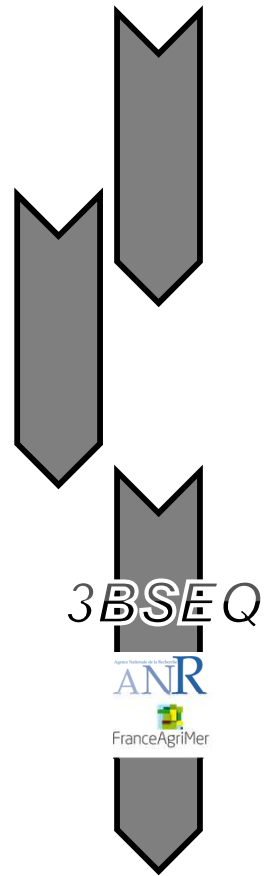
○ 1<sup>st</sup> reference seq (3B).....





BAC-based

WGS



2005

2008

2010

2014



UK, AABBD *Brenchley et al. Nature 2012*



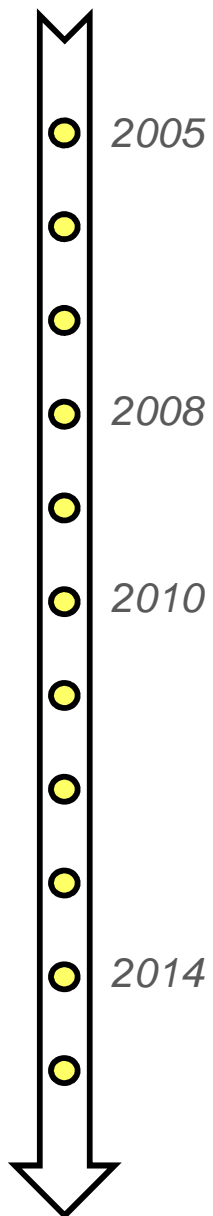
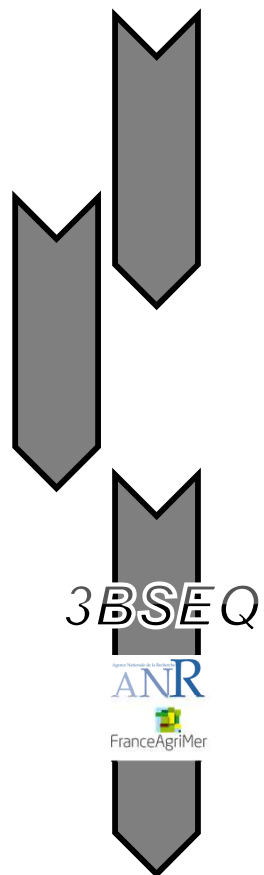
BGI, AA + DD *Ling et al. Nature 2013*  
*Jia et al. Nature 2013*



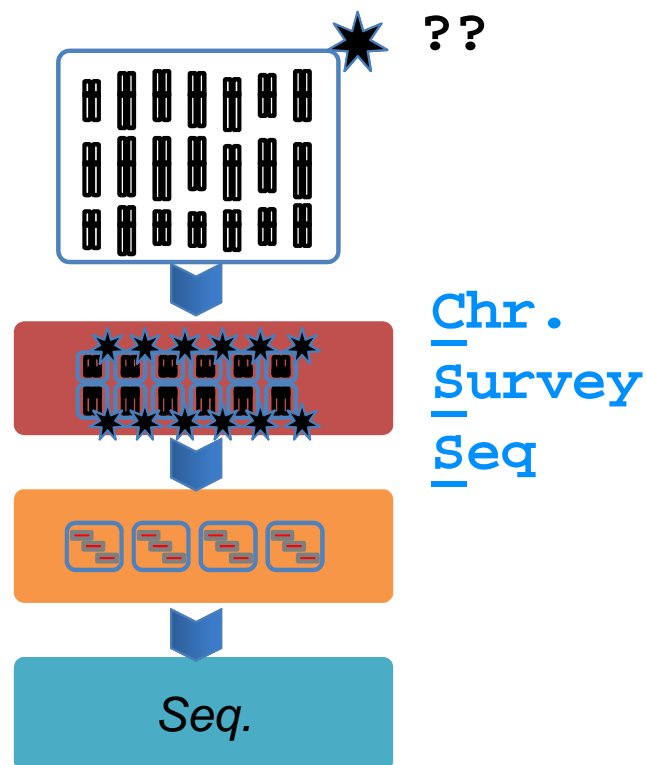
JGI, AABBD *Chapman et al. Genom Biol 2015*

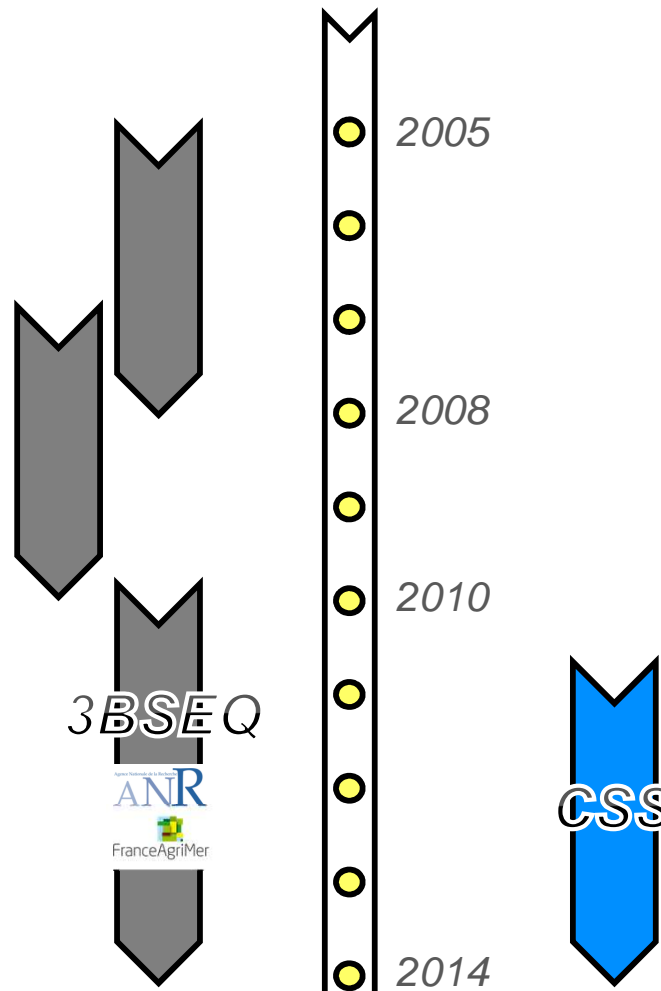


BAC-based



WGS





○ Choulet et al. *Science* 2014



○ IWGSC *Science* 2014

○ Marcussen et al. *Science* 2014

○ Pfeiffer et al. *Science* 2014

○ Daron et al. *Genom Biol* 2014

○ Pingault et al. *Genom Biol* 2015



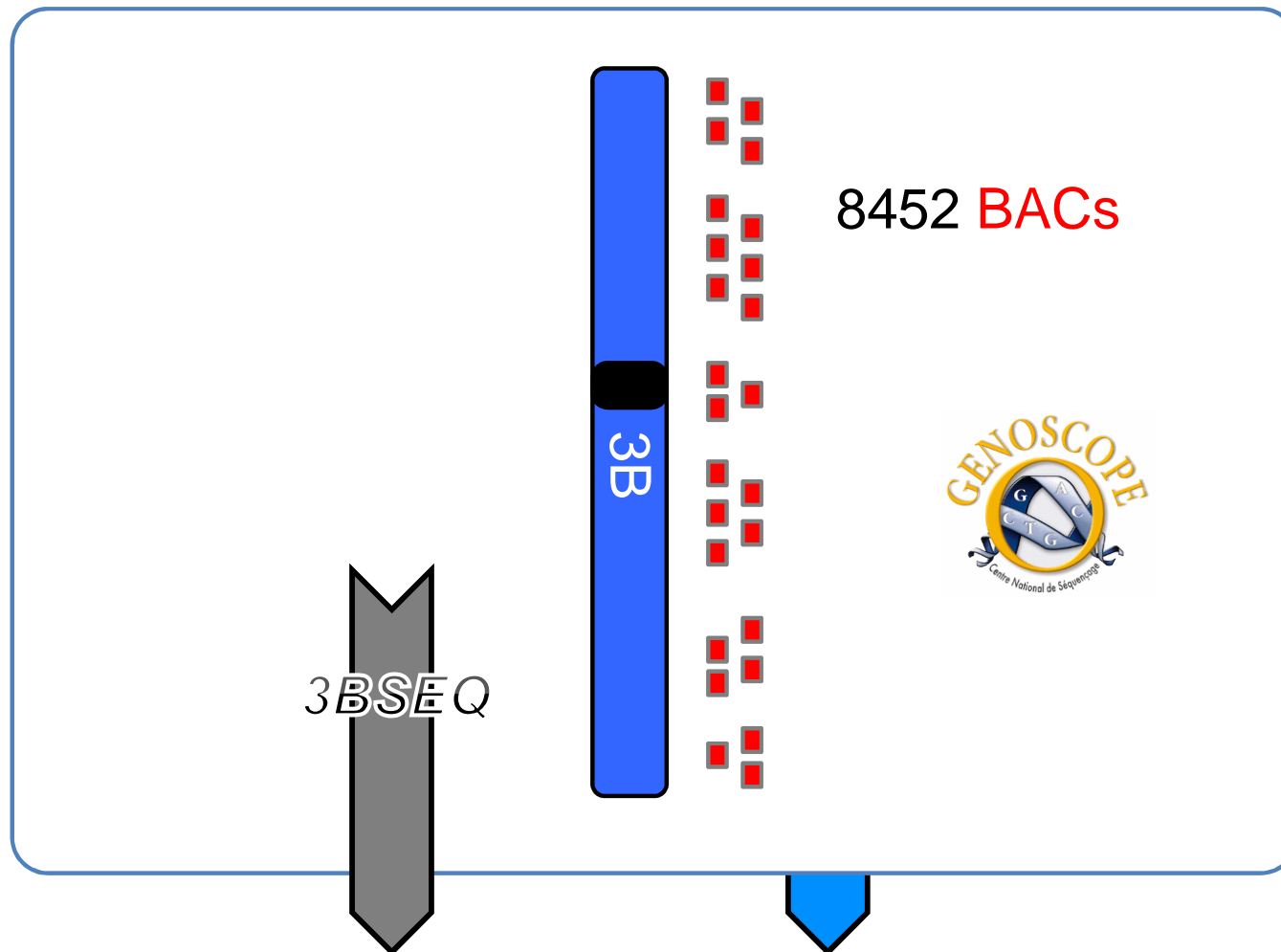
❑ Resources

- 1 draft seq / chromosome arm
- **10 Gb - 10 M** contigs (N50: 2.4 kb)
- **124,000** genes
- **75,000** genes anchored

❑ Main Results

- Gene loss--
- SSD++
- Dominance--
- A-B-D tree

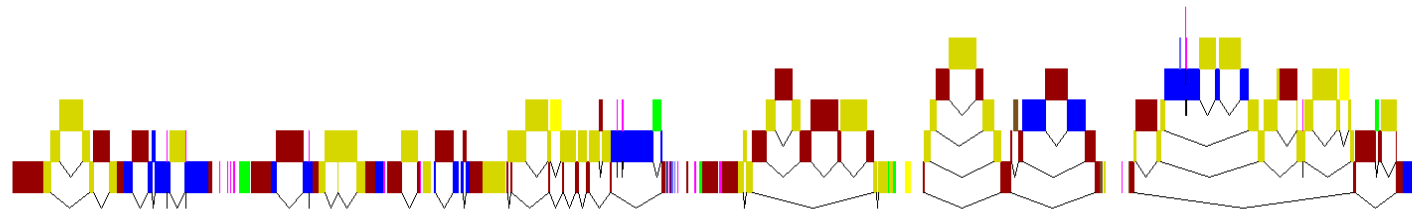




○ Choulet et al. Science 2014

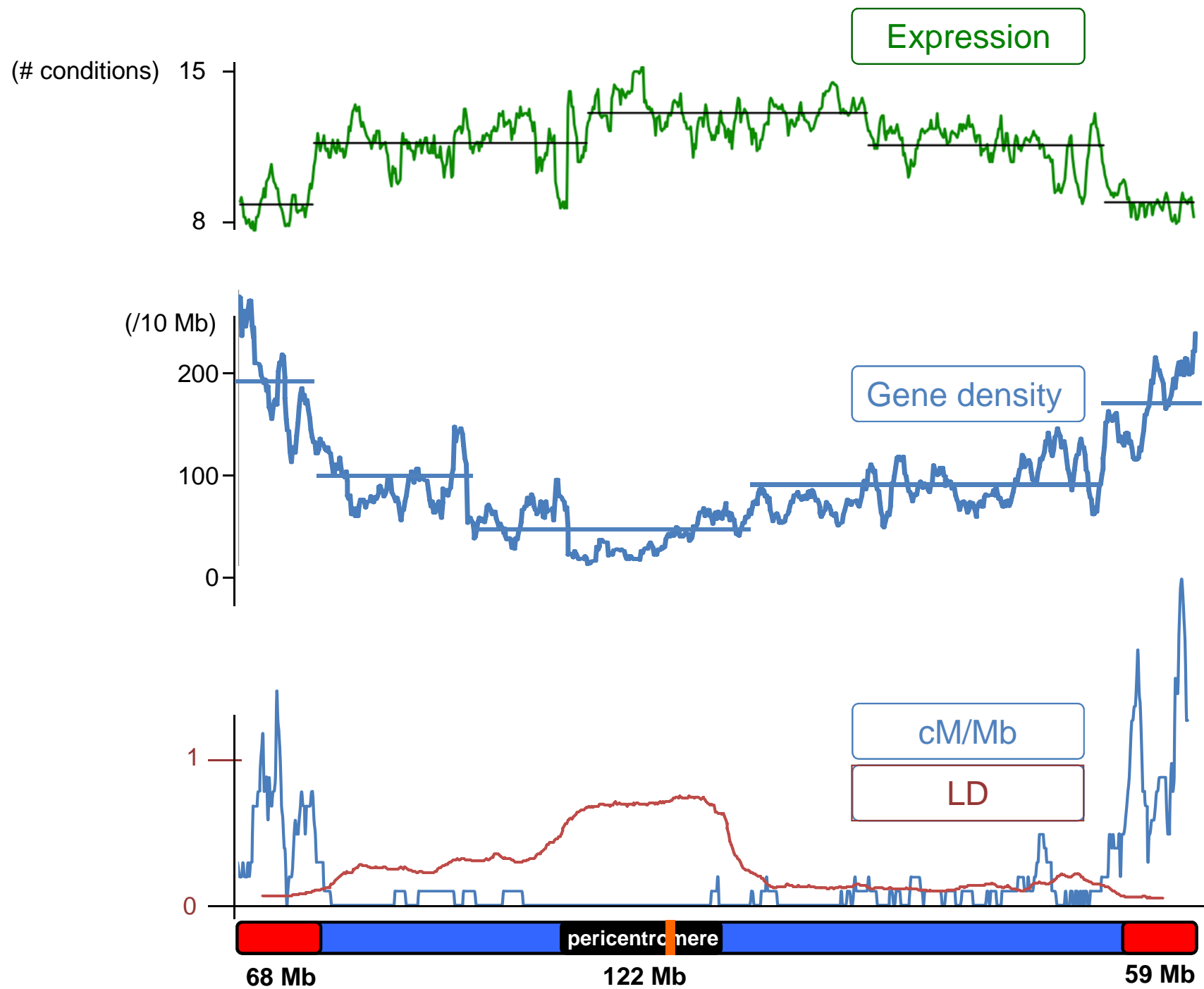
86%

7,264  
+2,692



774 Mb

3B  
pseudomolecule

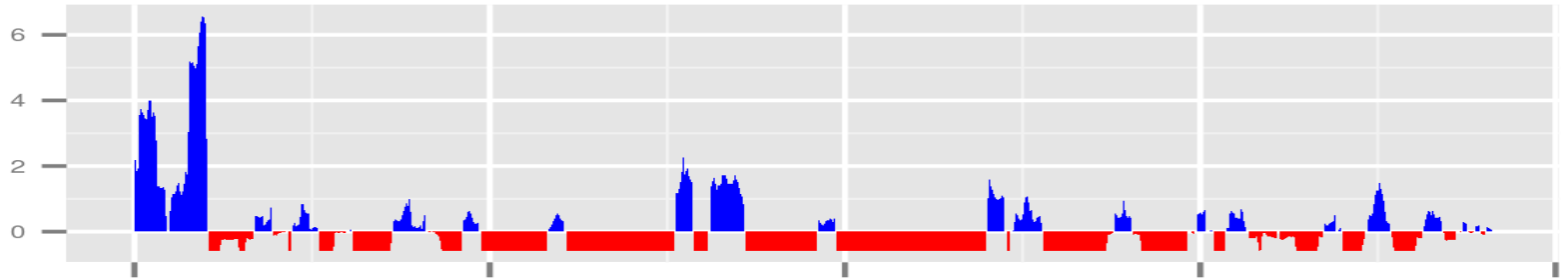
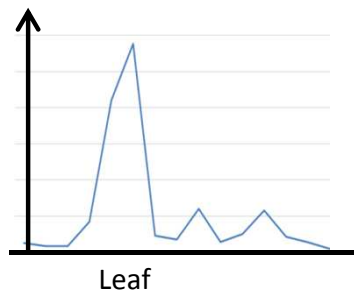
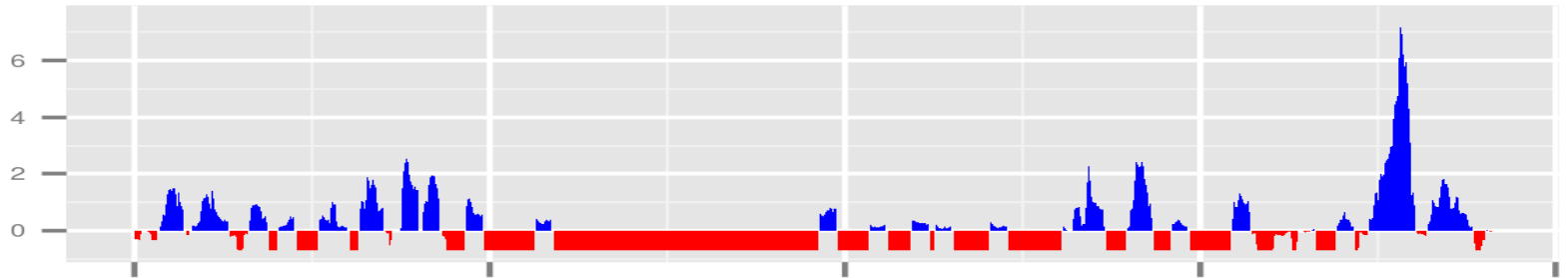
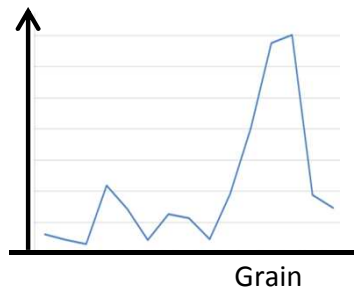
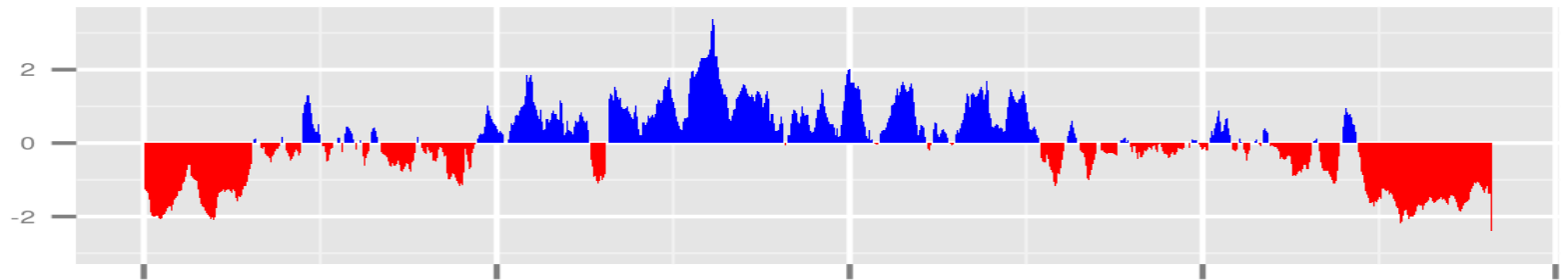
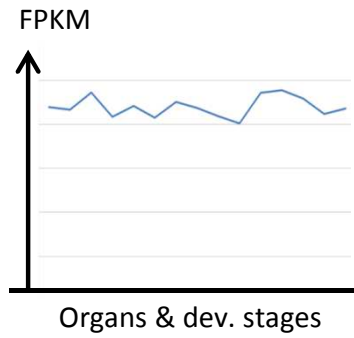




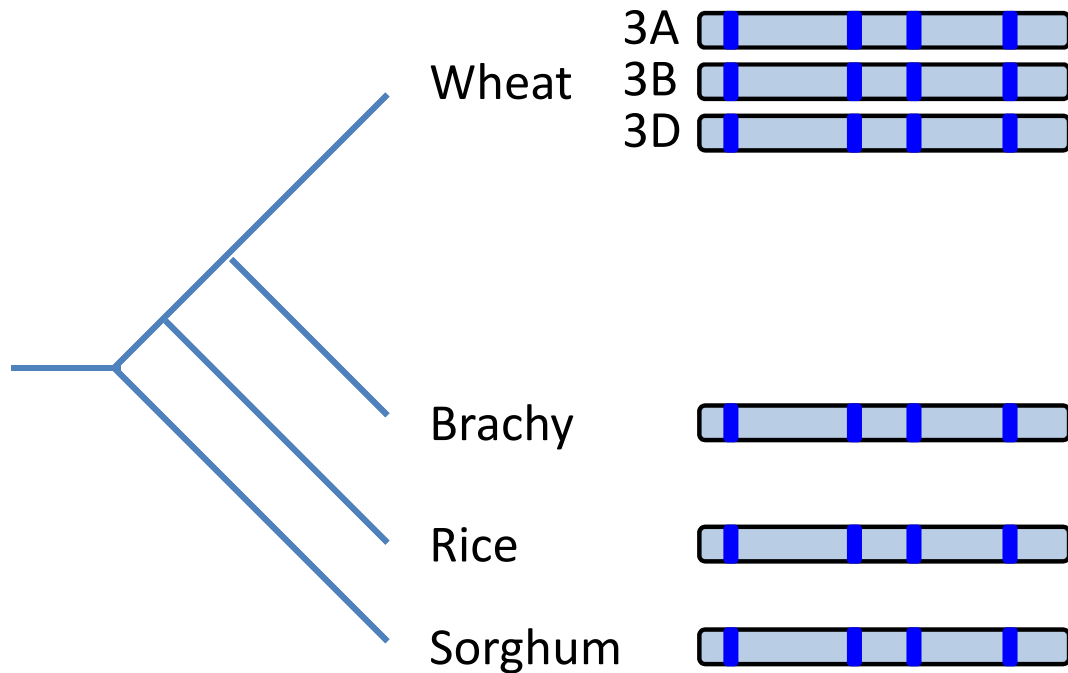
- 171 resistance genes

79%

21%



# □ Gene loss vs gene retention?



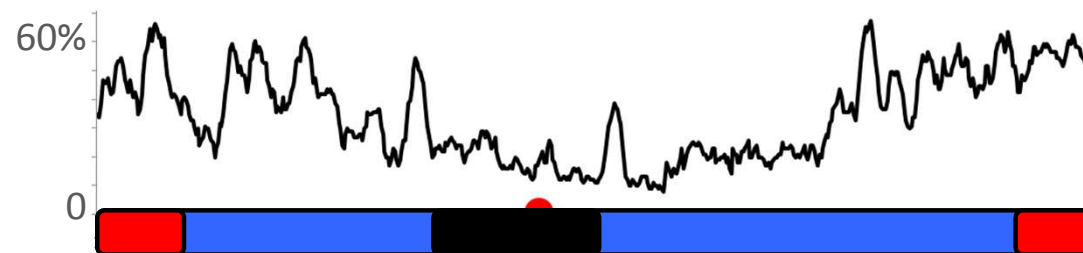
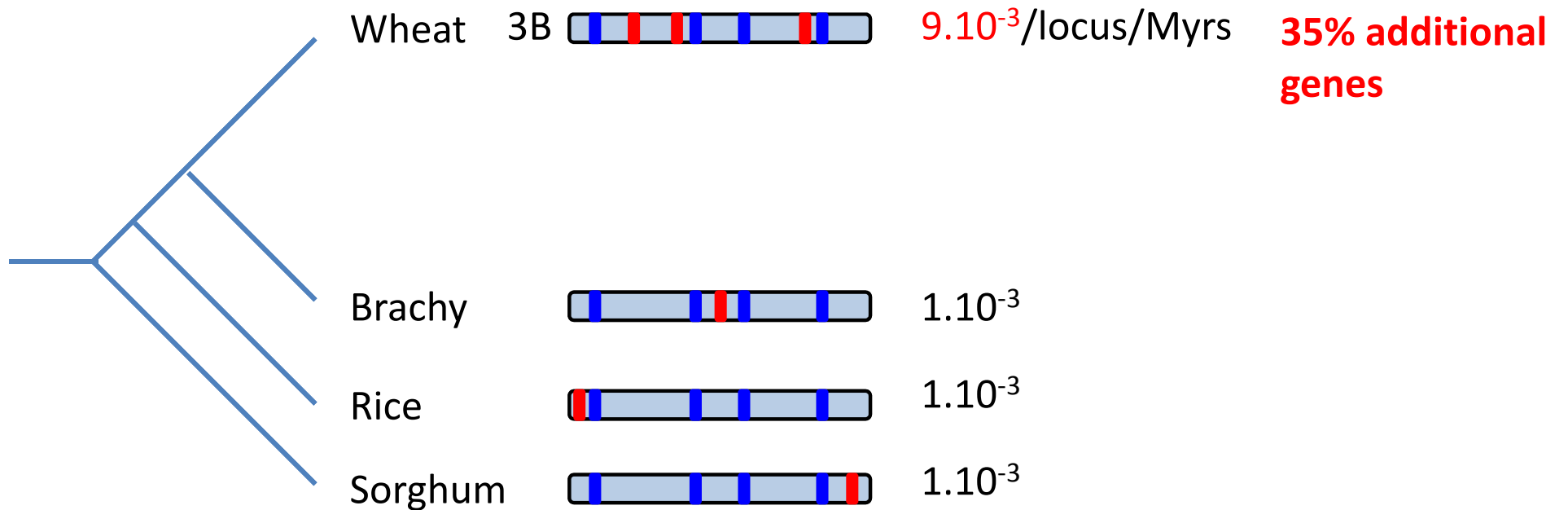
- **94%** expected genes found

limited gene loss

- **41%** homeologs differentially expressed

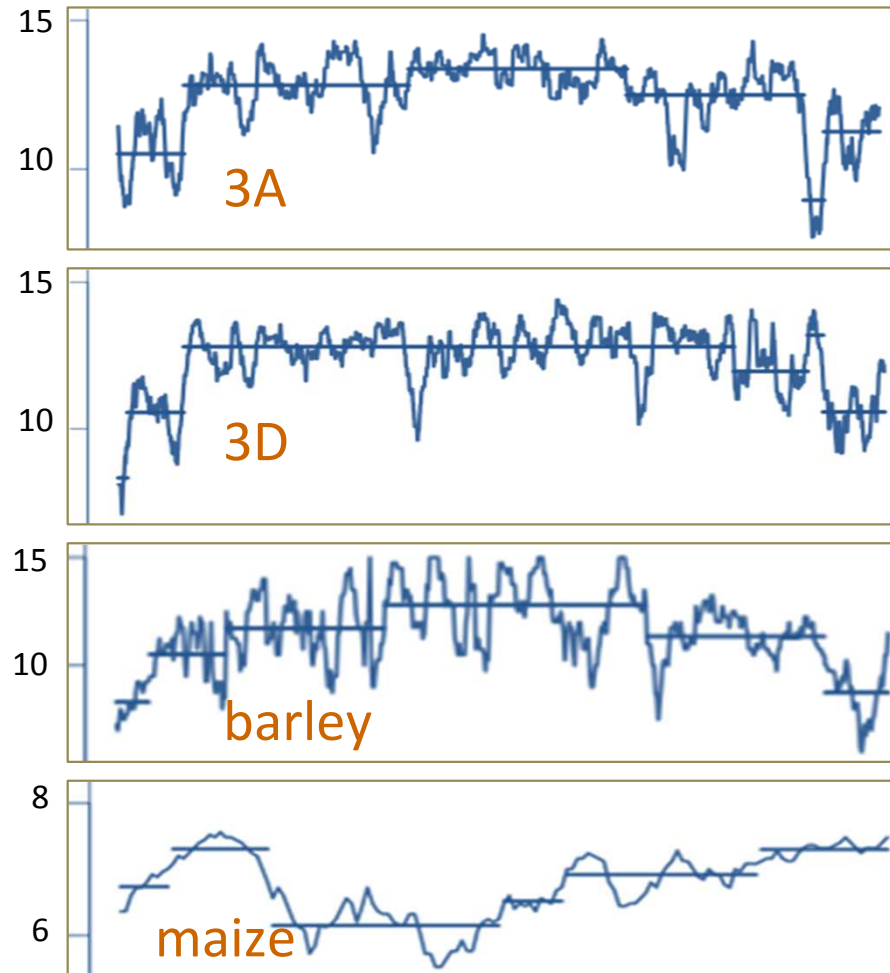
subfunctionalization of  
redundant genes

# □ Evolution



# □ 3B specific vs common pattern?

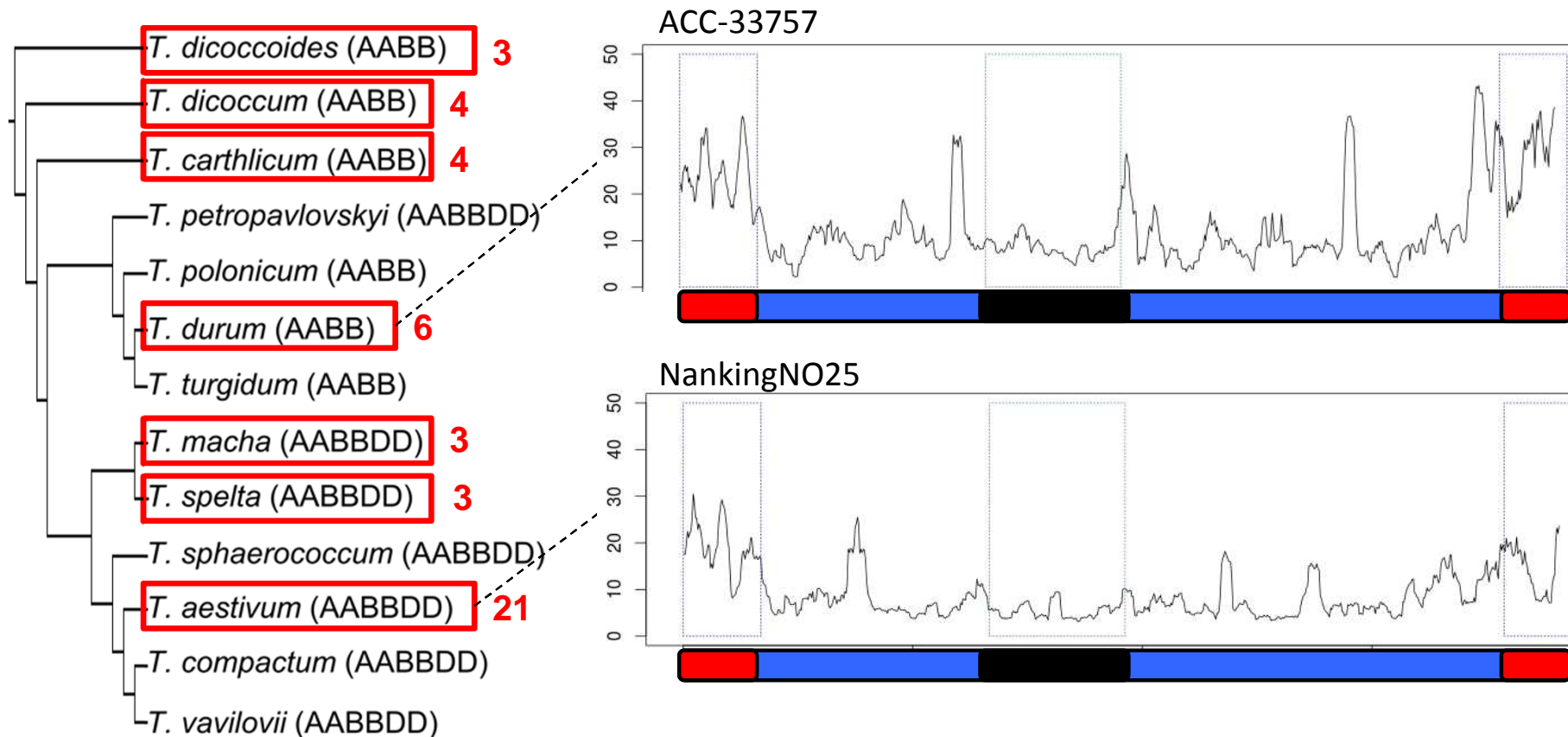
Expression breadth



# □ Current research

## □ Structural variations, core and pan-genome

- Hélène Rimbert
- Emeric Dyonmant
- Josquin Daron



# ❑ Current research

## ❑ Structural variations, core and pan-genome

- *Hélène Rimbert*
- *Emeric Dynomant*
- *Josquin Daron*

## ❑ landscape of Epigenetic marks

- *Aurélie Evrard*
- *Hélène Rimbert*
- *Jonathan Kitt*

# Public resources

Gene  
models

2012	U Liverpool, UK	WGS	Cs	OGA
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depth: 5x

2012	DOE JGI, US	WGS	AA	24,879
------	-------------	-----	----	--------

- [http://plants.ensembl.org/Triticum\\_aestivum/](http://plants.ensembl.org/Triticum_aestivum/)
- <http://wheat-urgi.versailles.inra.fr/>

2014	IWGSC	chr-by-chr	Cs	124,201
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chr-based

	GDEC/Génoscope	3B-pseudomol	Cs	7,264
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BAC-based

2015	DOE-JGI, US	WGS	W7984	-
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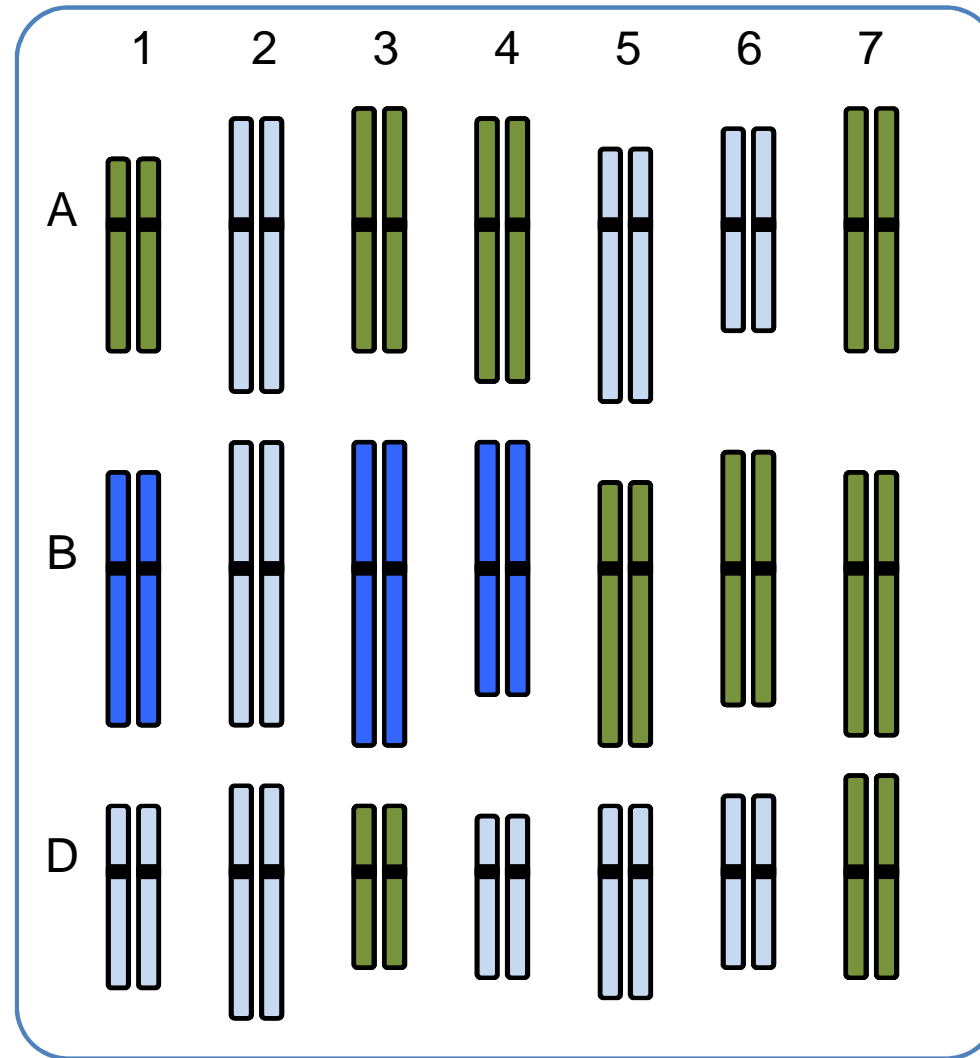
POPSeq

25 M SNP

7 Gb anchored

+RNASeq +Resequencing data

# Where we are





# Thanks

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## **GDEC**

Etienne Paux  
Josquin Daron  
Lise Pingault  
Natasha Glover  
Aurélie Evrard  
Hélène Rimbert  
Emeric Dynomant  
Jonathan Kitt  
Philippe Leroy  
Nicolas Guilhot  
Aurélien Bernard  
Sébastien Theil  
Nelly Cubizolles  
Elodie Rey  
Pierre Sourdille & GeCO  
François Balfourier & CRB  
Charles Poncet & GENTYANE  
Catherine Feuillet

**CEA-IG-Génoscope**

**INRA URGI**

**INRA CNRGV**

**INRA BIA**

**IEB**

**VIB**

**TGAC**

**MIPS/IBIS**

