



**HAL**  
open science

## Fine QTL mapping of pig QTL in France

Jean Pierre Bidanel, Denis Milan

► **To cite this version:**

Jean Pierre Bidanel, Denis Milan. Fine QTL mapping of pig QTL in France. France - Taiwan Seminar, Dec 2004, Tainan, Taiwan. hal-03364937

**HAL Id: hal-03364937**

**<https://hal.inrae.fr/hal-03364937>**

Submitted on 5 Oct 2021

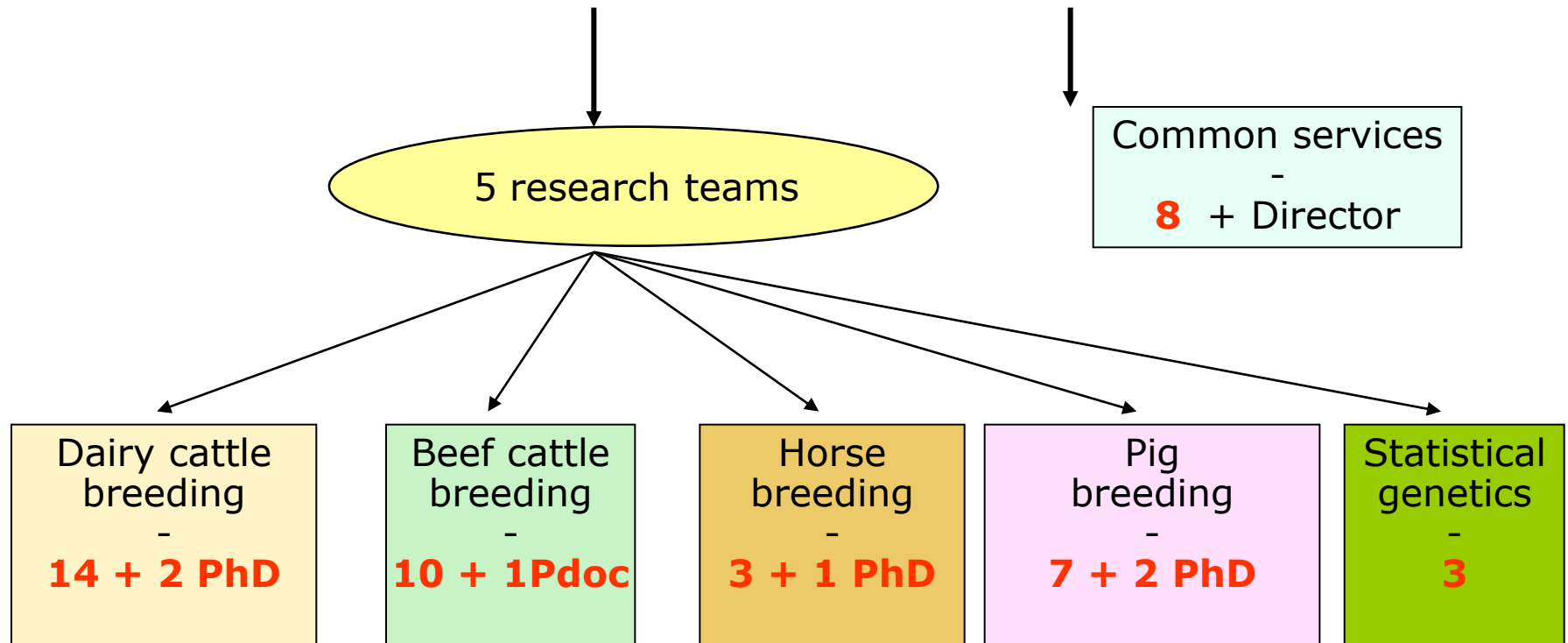
**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



# SGQA - Organisation

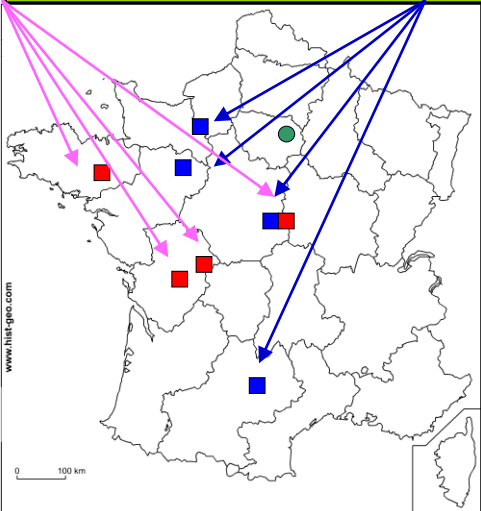
Staff : 51 (36 INRA permanent positions)



**SGQA**  
Research facilities & collaborations

**Station de Génétique  
quantitative et appliquée**

**8 experimental units**



■ UE bovine   ■ UE porcine   ● SGQA

**Staff : 76**  
Support : 245 k€ + salaries  
250 DC, 520 BC  
360 S, 2400 pig pl.

**1 service unit:  
(computing center)**

Management  
of national  
genetic  
databases

Work-  
stations,  
mainframe

**Genotyping laboratory  
Labogéna**

DNA  
banks

Geno-  
types

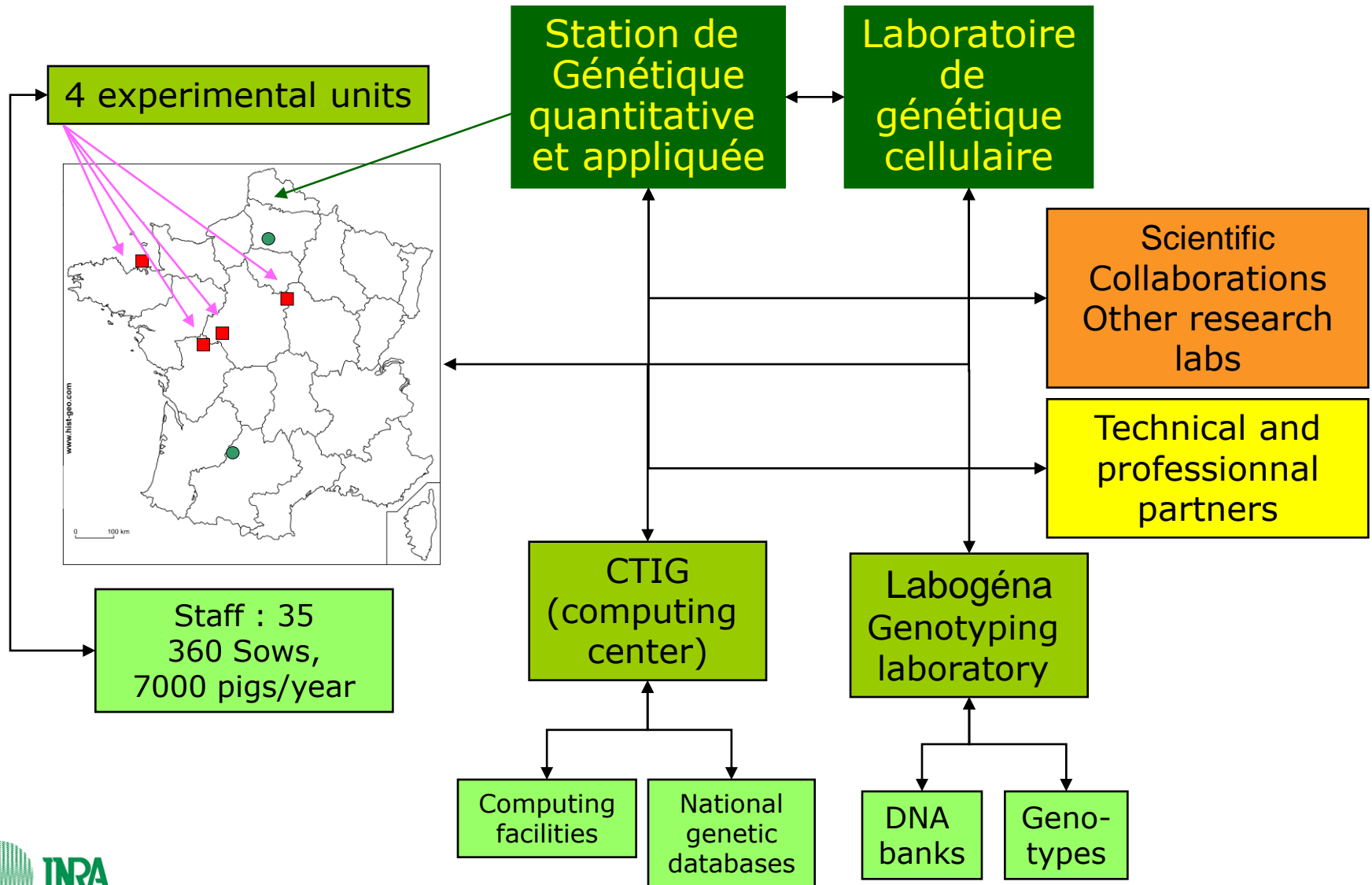
**Scientific  
Collaborations**  
SAGA  
LGC  
LGBC  
...

**Technical and  
professionnal  
partners**



# Pig QTL mapping at INRA

## Research facilities & collaborations



## □ Main collaborators

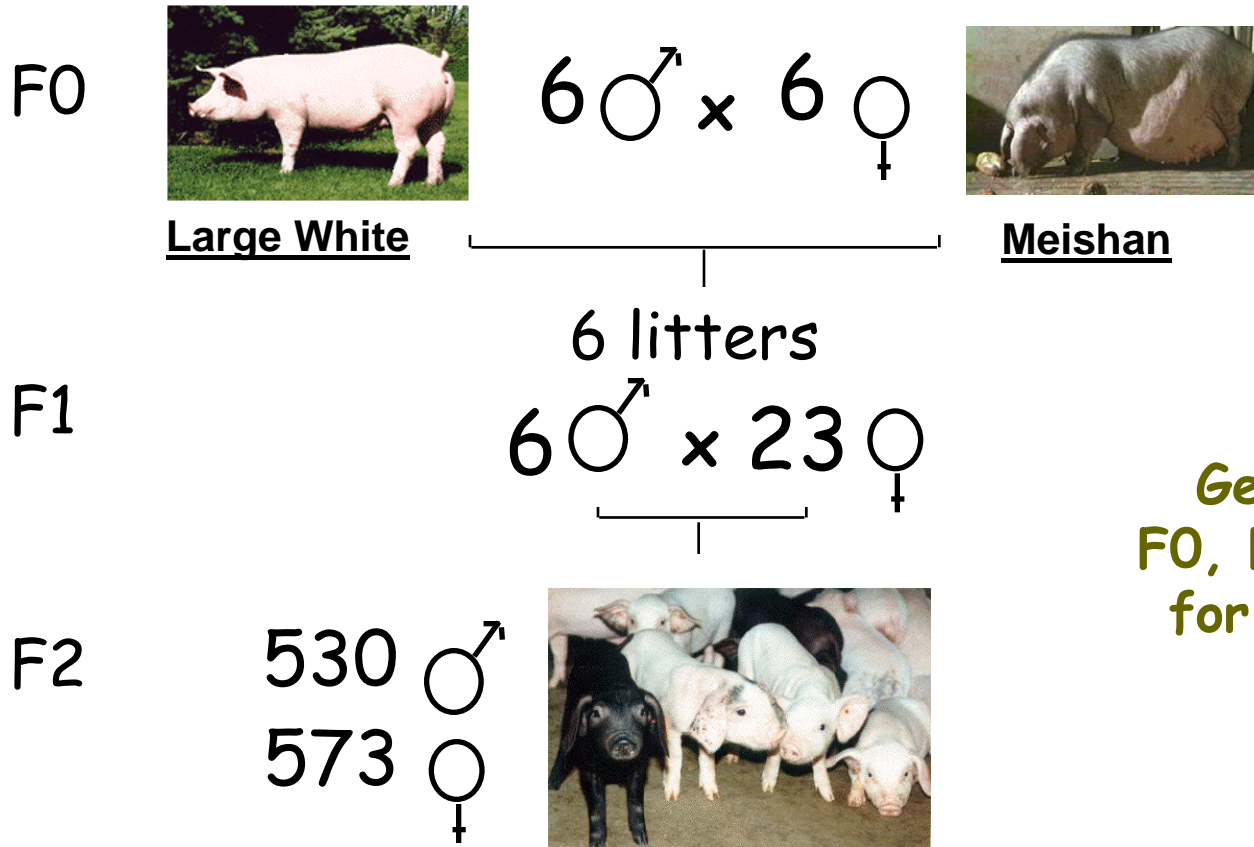
**J.P. Bidanel , D. Milan**, C. Chevalet, N. Woloszyn, F. Bourgeois, J.C. Caritez, J. Gruand, P. Le Roy, M. Bonneau, L. Lefaucheur, J. Mourot, A. Prunier, C. Désautés, P. Mormède, C. Renard, M. Vaiman, A. Robic, J. Gellin, L. Ollivier

## □ INRA research units

Station de Génétique Quantitative et Appliquée, Laboratoire de Génétique Cellulaire, Domaines expérimentaux du Magneraud et de Rouillé, Labogéna, Unité Mixte de Recherche sur le Veau et le Porc, Laboratoire de Radiobiologie et d'étude du génome, Laboratoire de Génétique du Stress

## □ Funded by :

European Union(Bridge, Biotech+)  
INRA incitative action "Structure of genomes"  
Animal Genetics Department  
Ministry of Research (GREG)

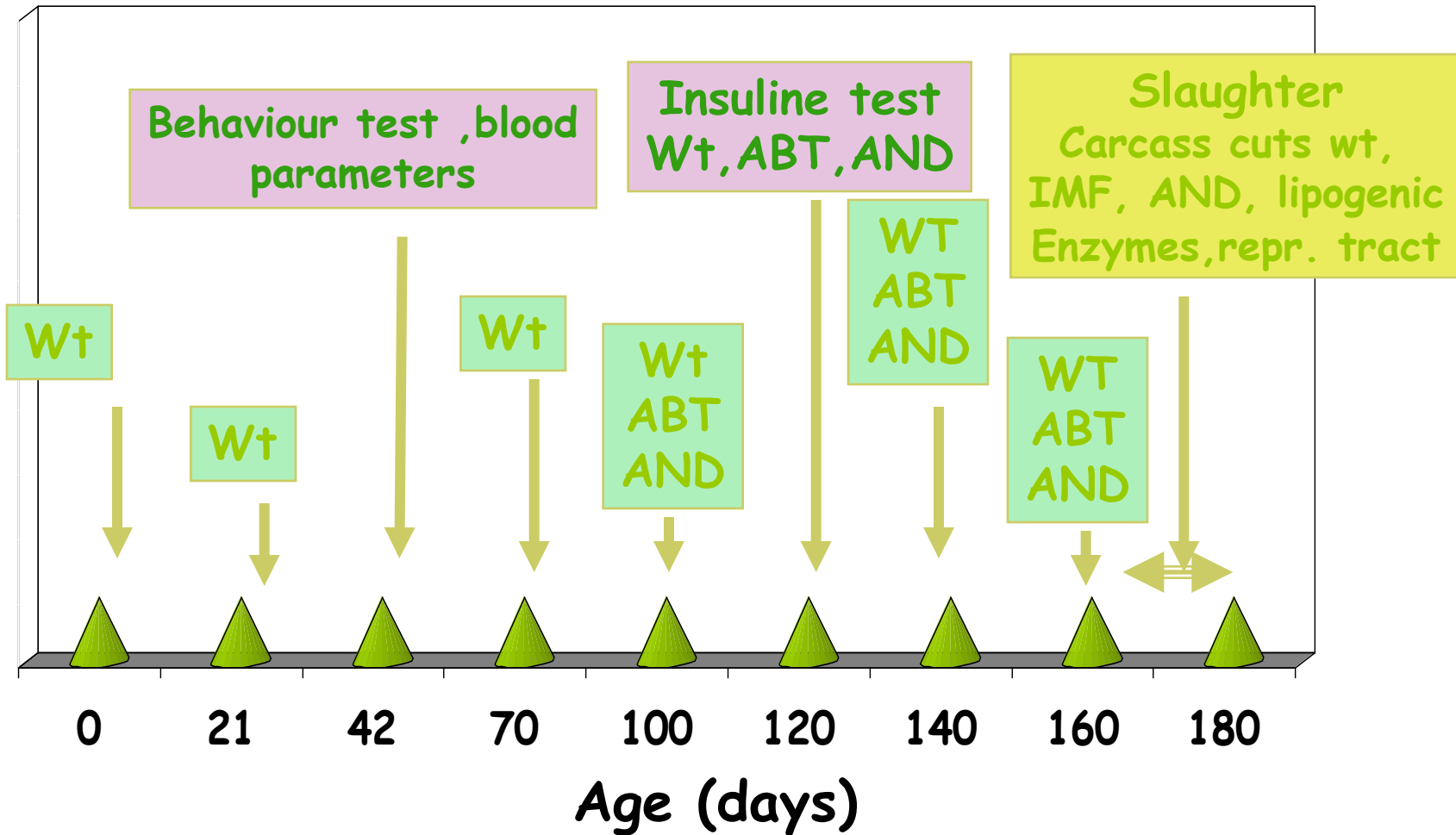


Genotyping of  
F0, F1, F2 animals  
for 137 markers

# Traits measured - males



# PORQTL

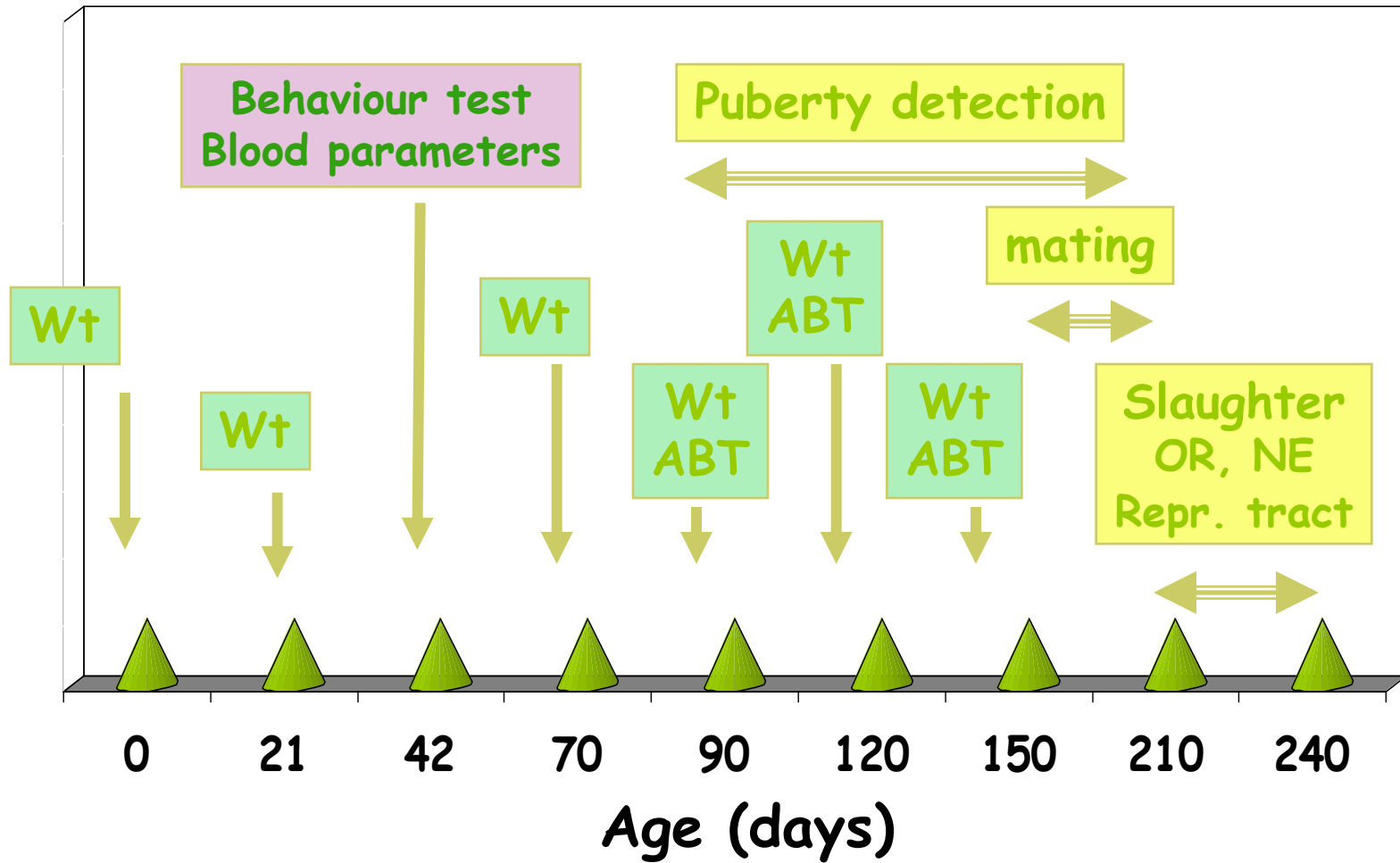




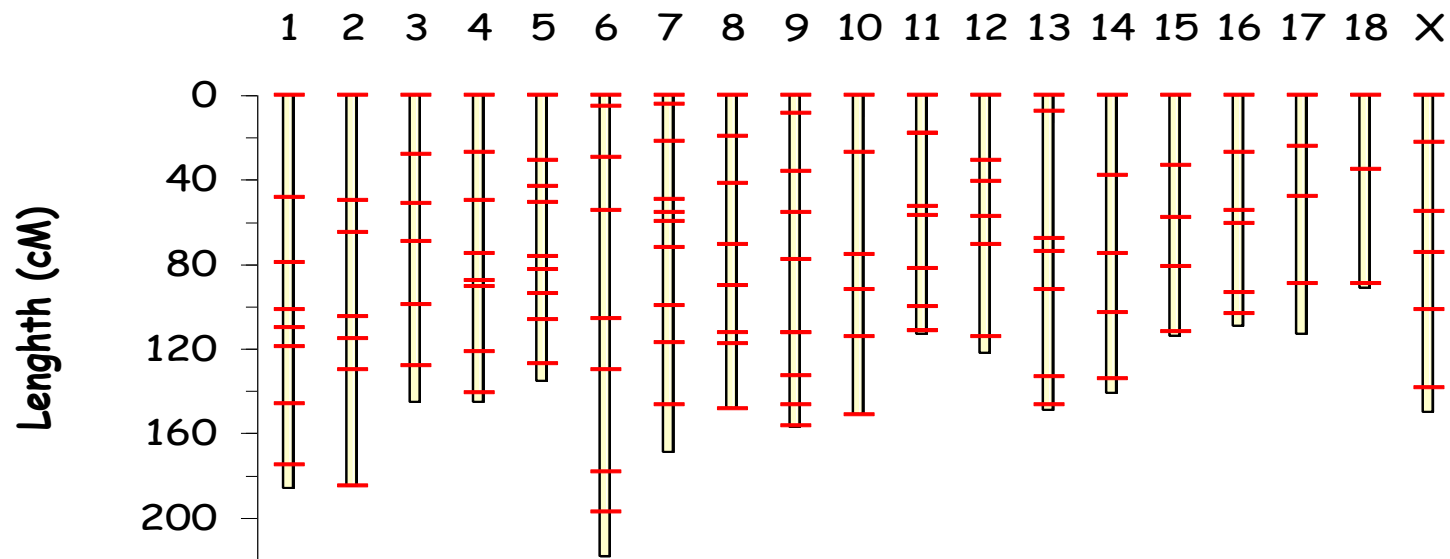
# Traits measured - females



# PORQTL



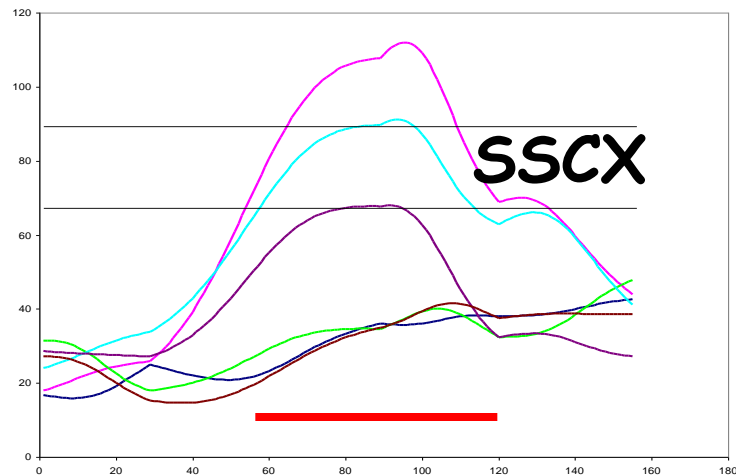
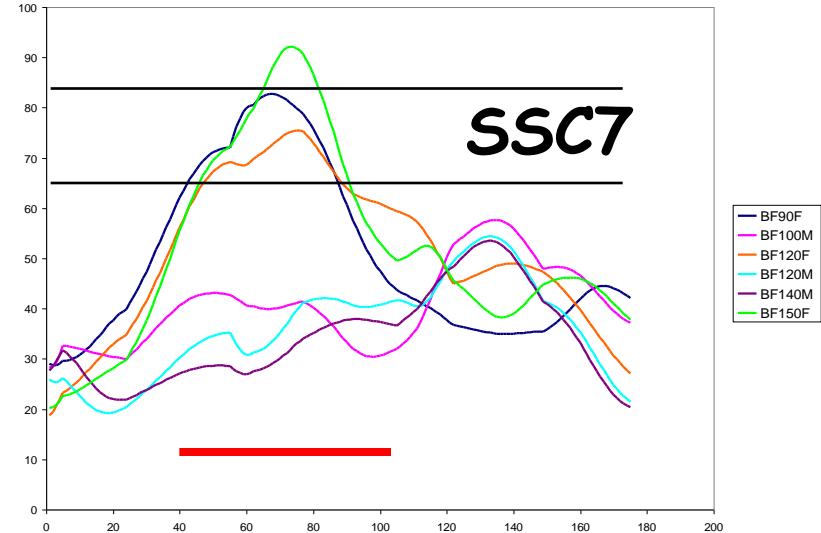
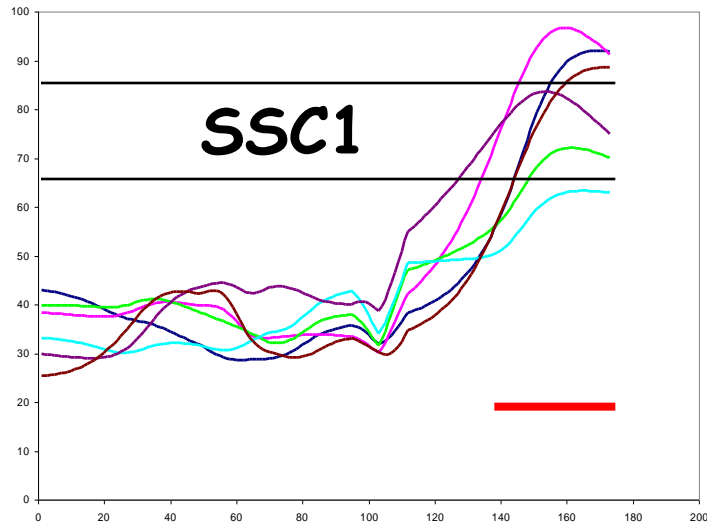
- Panel of 136 microsatellite markers + SLA
- Genotyping on automated sequencers
- Map built using Crimap software



- 3 to 12 markers / chromosome
- Average marker interval : 22 cM

# Results : example - backfat thickness

# PORQTL



Low accuracy of QTL position

# QTL fine mapping

---

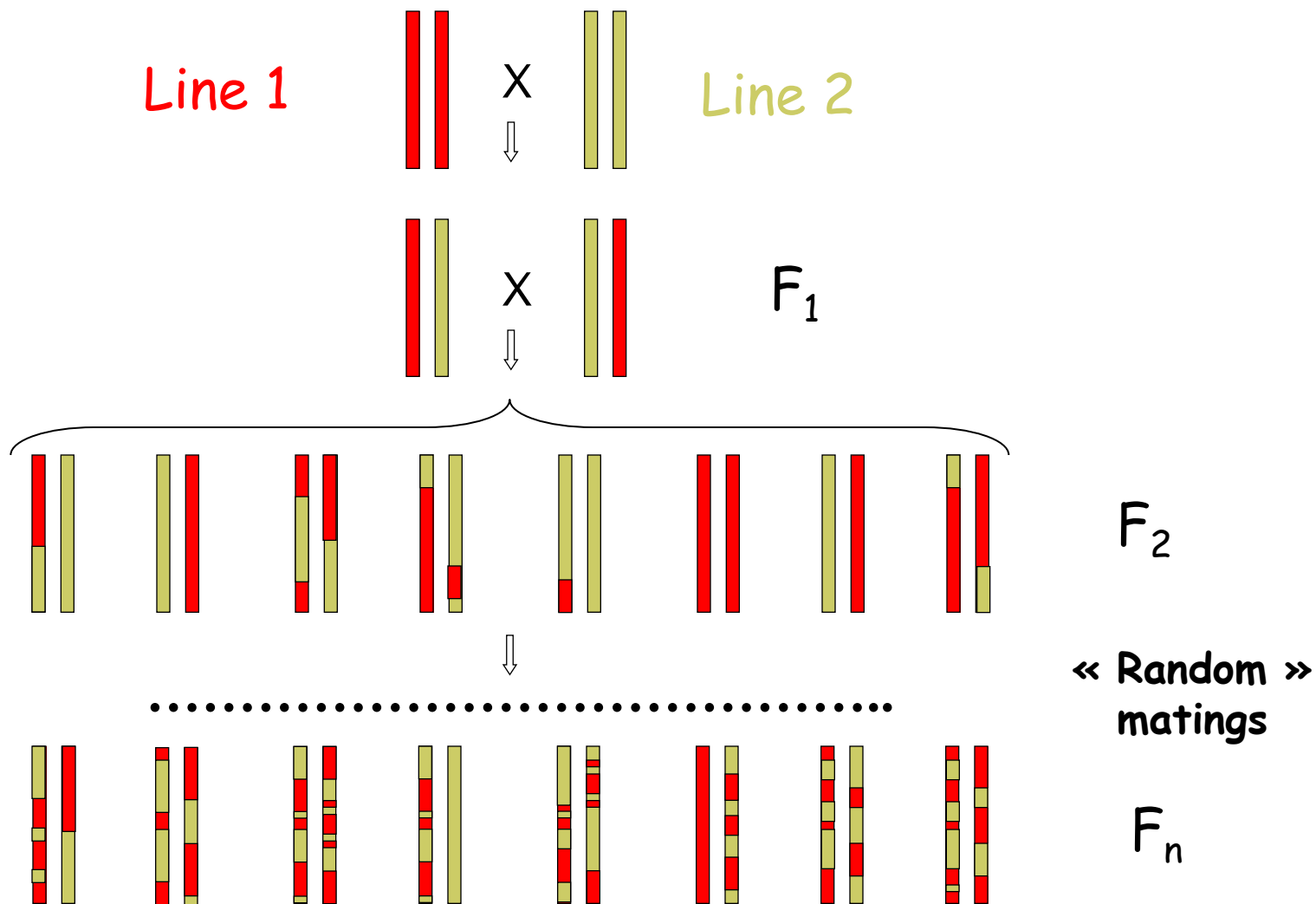
Many experimental designs available in plants and mice ...

- Recombinant inbred lines
- Recombinant inbred segregation test
- Selective phenotyping
- Interval specific congenic strains
- ...

... but only some of them can be used for farm animals

- Advanced intercross lines
- Recombinant progeny testing

# Advanced Intercrossed Lines (AIL)



# Advanced Intercrossed Lines (AIL)

---

- Characteristics

- 1 individual = « Mosaic » of genome fragments from founder populations

- Interests

- Increase in genome « length »

$$c_t = \frac{1 - (1 - c_1)^{t-2} (1 - 2c_1)}{2}$$

Generation  $\nearrow$   $c_t$   $\nwarrow$  Recombinaison rate

- Can be used for non inbred populations

# Advanced Intercrossed Lines (AIL)

---

## Synthetic breeds can be used as AIL

Readily available material in many livestock species:

### **Cattle**

Zebu x cattle: Brangus, St Gertrudis, ...

INRA 95

### **Sheep**

INRA401 = Romanov x Berrichon du Cher

### **Pigs, rabbits**

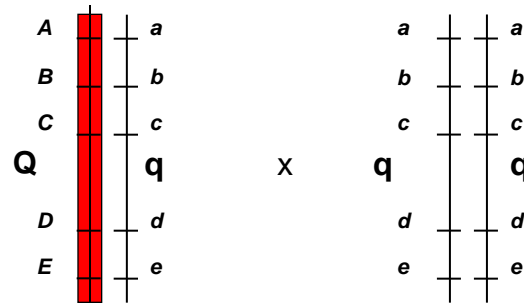
Laconie = Pietrain x LW x Hampshire

Tiameslan = Meishan x Laconie

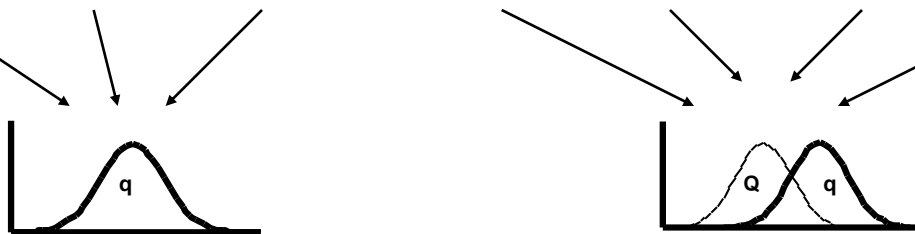
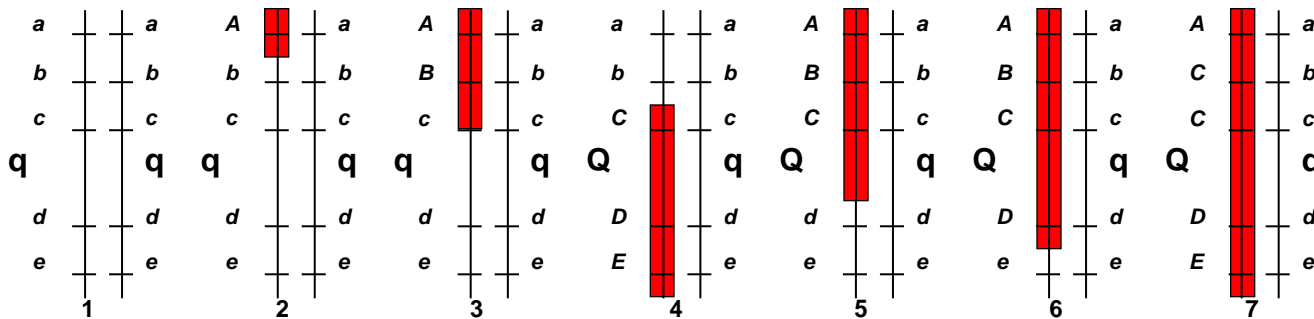
Taizumu = Meishan x Large White

### **Creole livestock**

# Recombinant progeny testing (RPT)



- Selection of recombinant individuals
- Progeny test





# Recombinant progeny testing (RPT)

---

- Interests

- **Sequential design:**

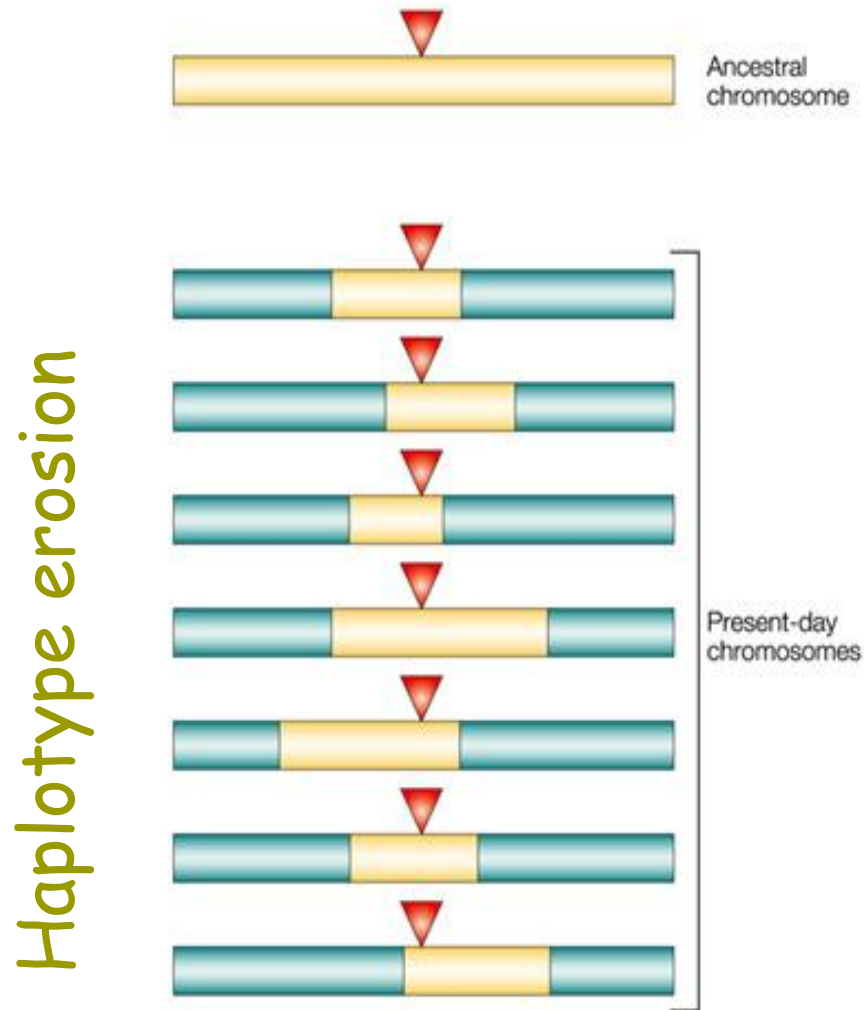
- allows the QTL mapping interval to be progressively reduced

- **Can be used in noninbred populations**

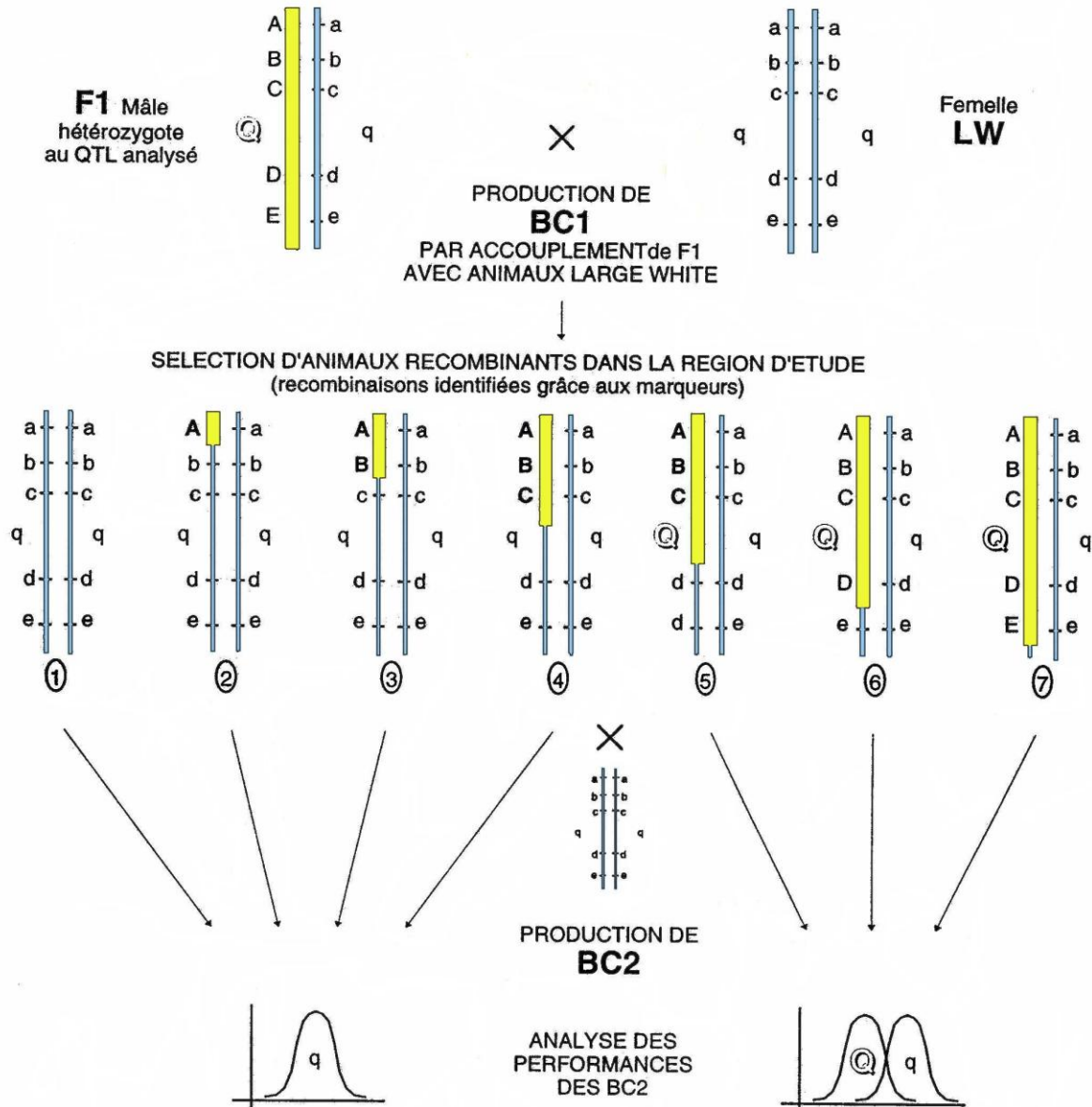
- Disadvantage

- Important number of individuals to be phenotyped and genotyped

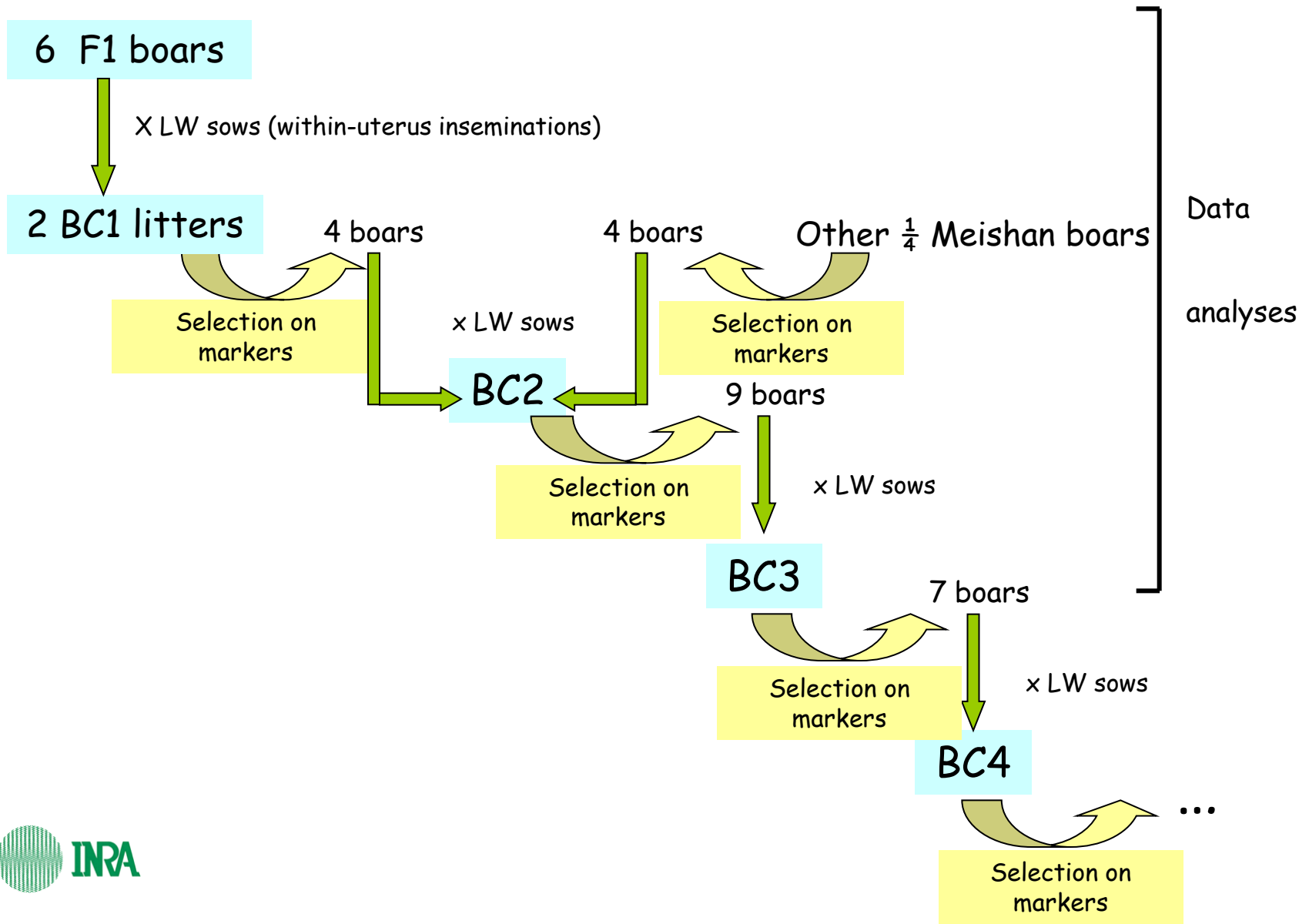
# Use of linkage disequilibrium / « historical » recombinations



# Fine mapping of QTL using backcrosses



# Fine mapping through successive generations of backcrosses



# Traits measured

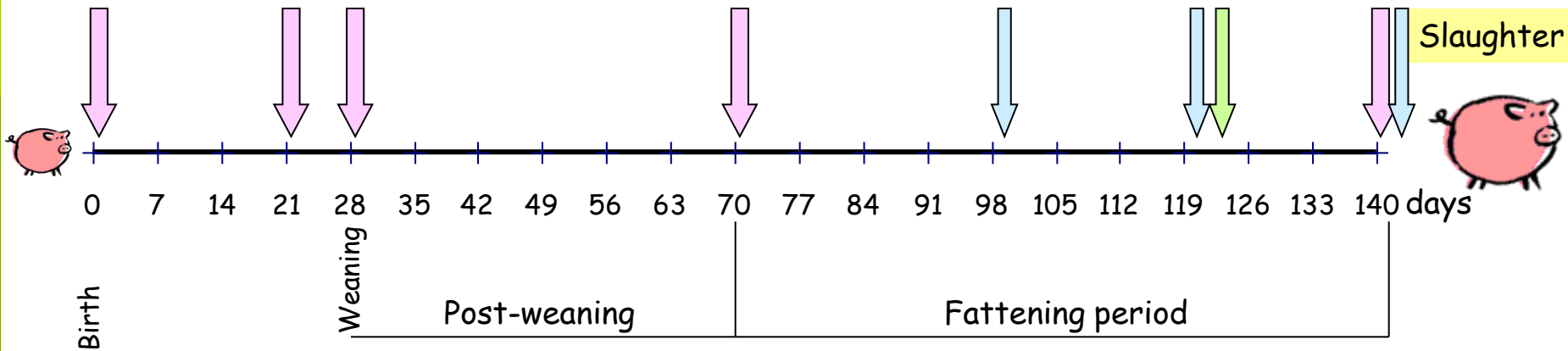
Weights

US backfat thickness

Biopsies of fat (androstenone) and muscle (IMF)

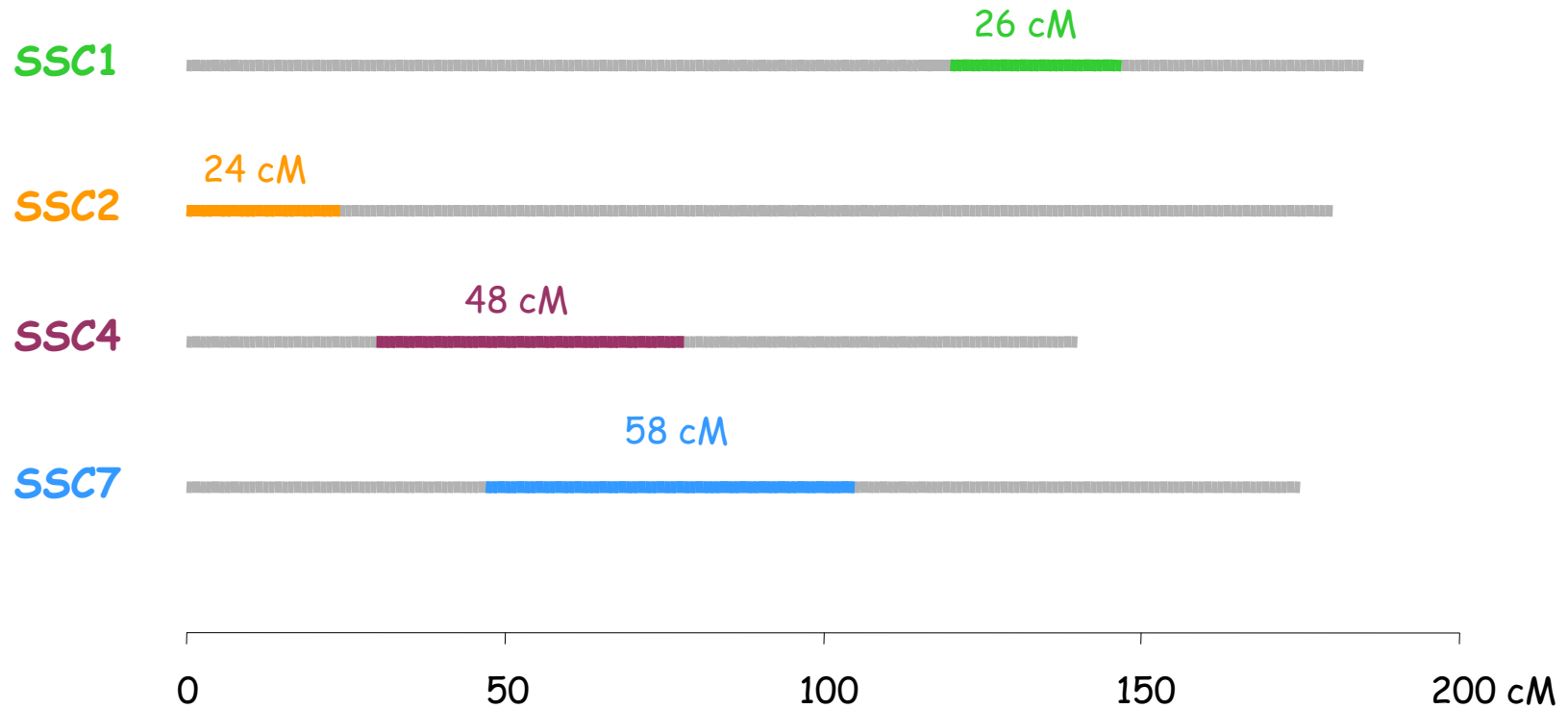
At slaughter:

- Carcass cuts weights
- Carcass fat and lean depths
- pH 24h of Adductor femoris, Gluteus superficialis, Longissimus dorsi, semi membranosus, semi spinalis
- Wetting time of Gluteus superficialis
- Reflectance ( $L^*$   $a^*$   $b^*$ ) of Gluteus superficialis



# Chromosomal regions investigated

---



# Example : SSC2

---

0 24 cM



991377

991373

**BC1**

## SSC2: progeny testing of BC1 boars

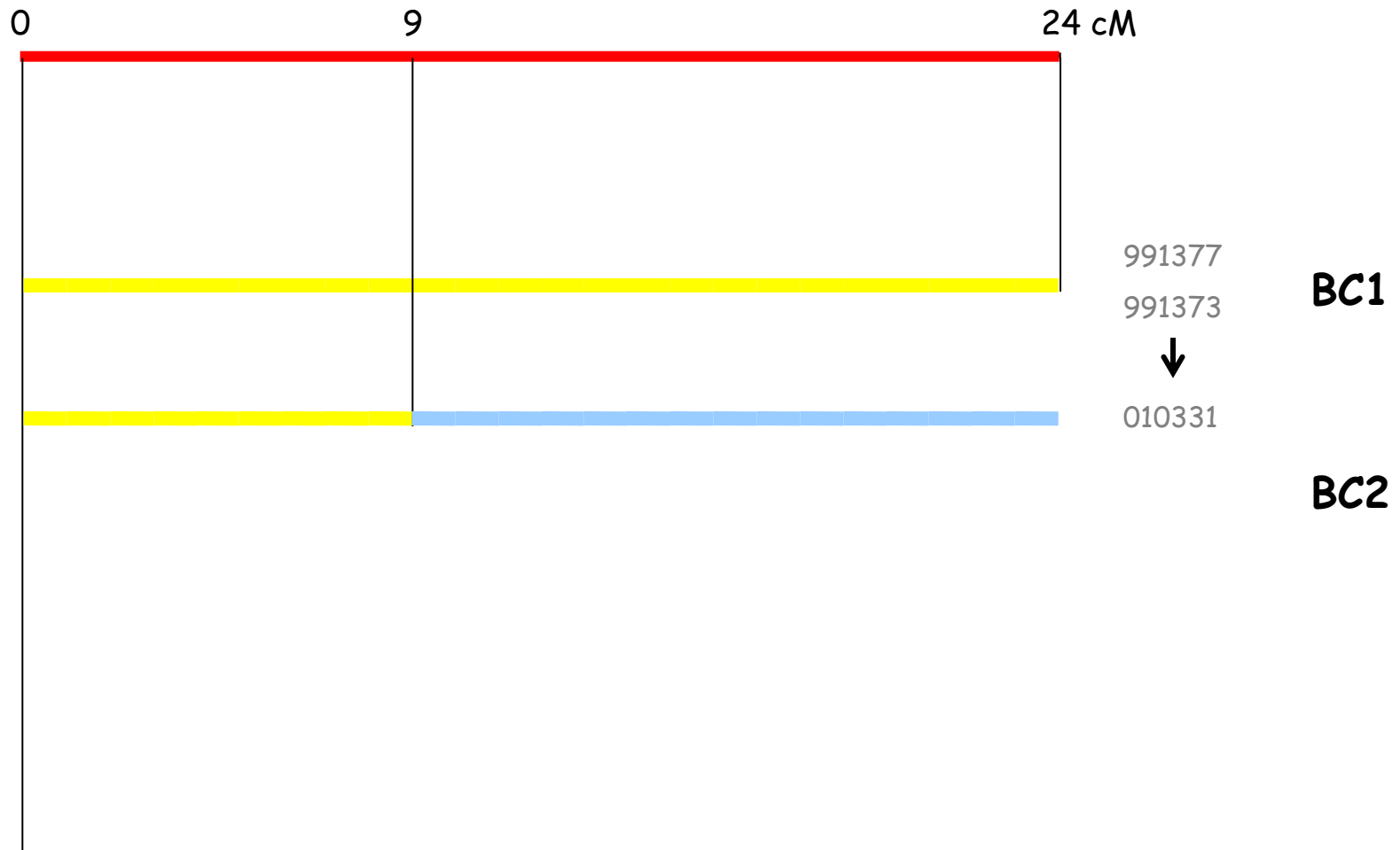
---

Generation	Boar	Growth	Carcass composition	Meat quality
BC1	991373	**	***	*
	991377	*	***	*

NS: non significant - \*  $P < 0.05$  - \*\*  $P < 0.01$  - \*\*\*  $P < 0.001$   
(at the chromosome level)



# Example : SSC2



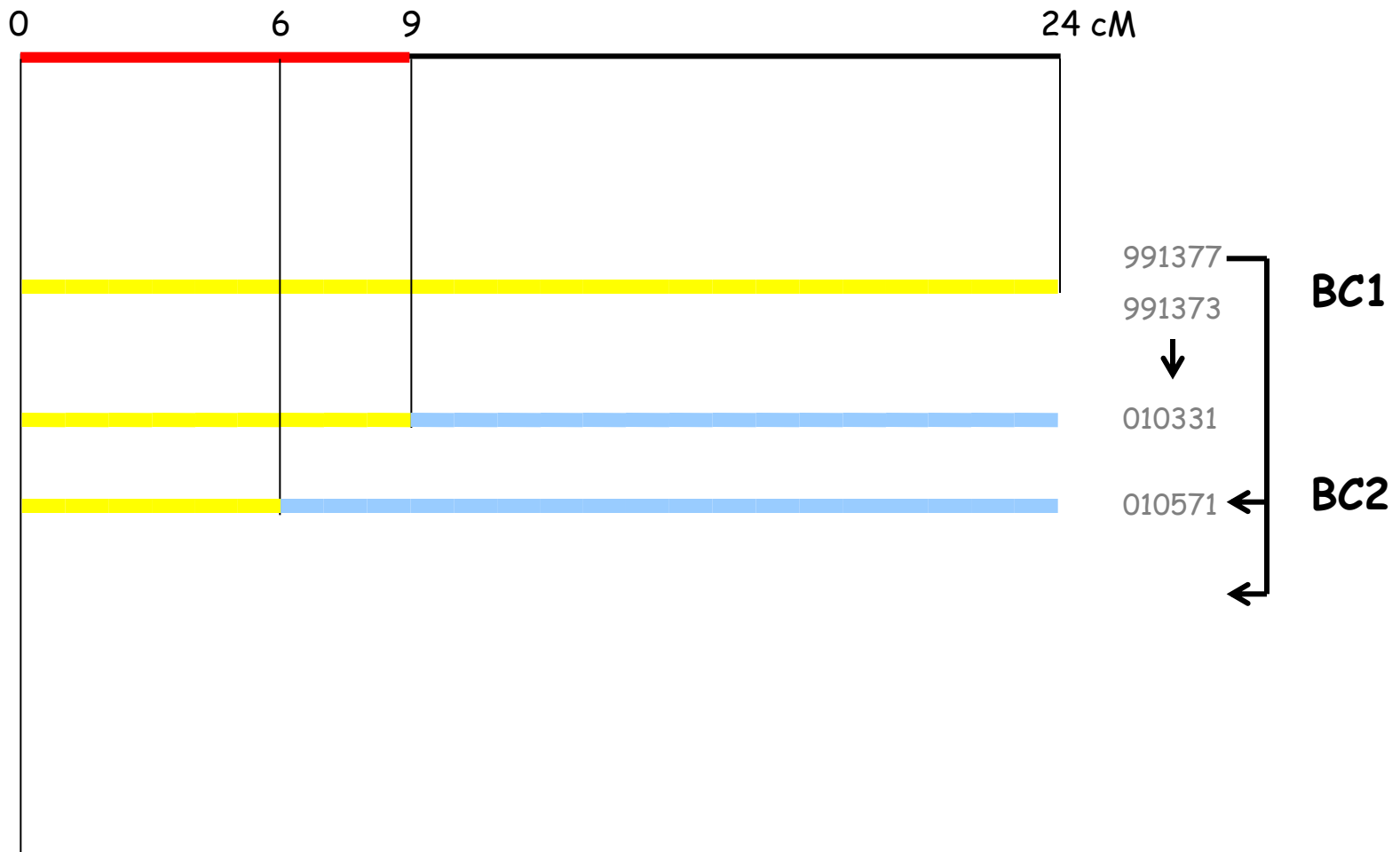
## SSC2: progeny testing of BC2 boars

---

Generation	Boar	Growth	Carcass composition	Meat quality
BC1	991373	**	***	*
	991377	*	***	*
BC2	010331	**	***	NS

NS: non significant - \*  $P < 0.05$  - \*\*  $P < 0.01$  - \*\*\*  $P < 0.001$   
(at the chromosome level)

# Exemple : SSC2



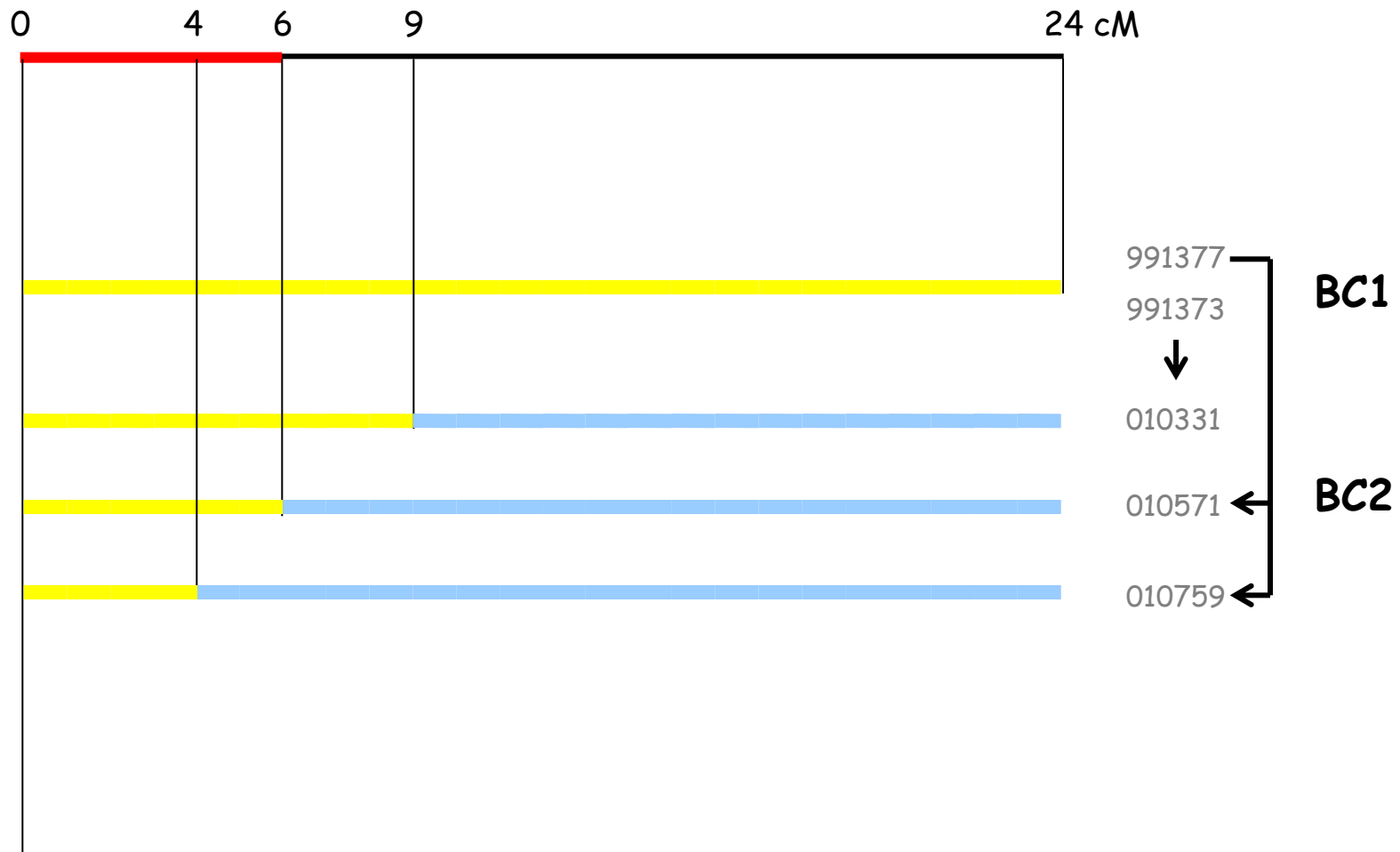
## SSC2: progeny testing of BC2 boars

---

Generation	Boar	Growth	Carcass composition	Meat quality
BC1	991373	**	***	*
	991377	*	***	*
BC2	010331	**	***	NS
	010571	***	***	*

NS: non significant - \*  $P < 0.05$  - \*\*  $P < 0.01$  - \*\*\*  $P < 0.001$   
(at the chromosome level)

# Exemple : SSC2



## SSC2: progeny testing of BC2 boars

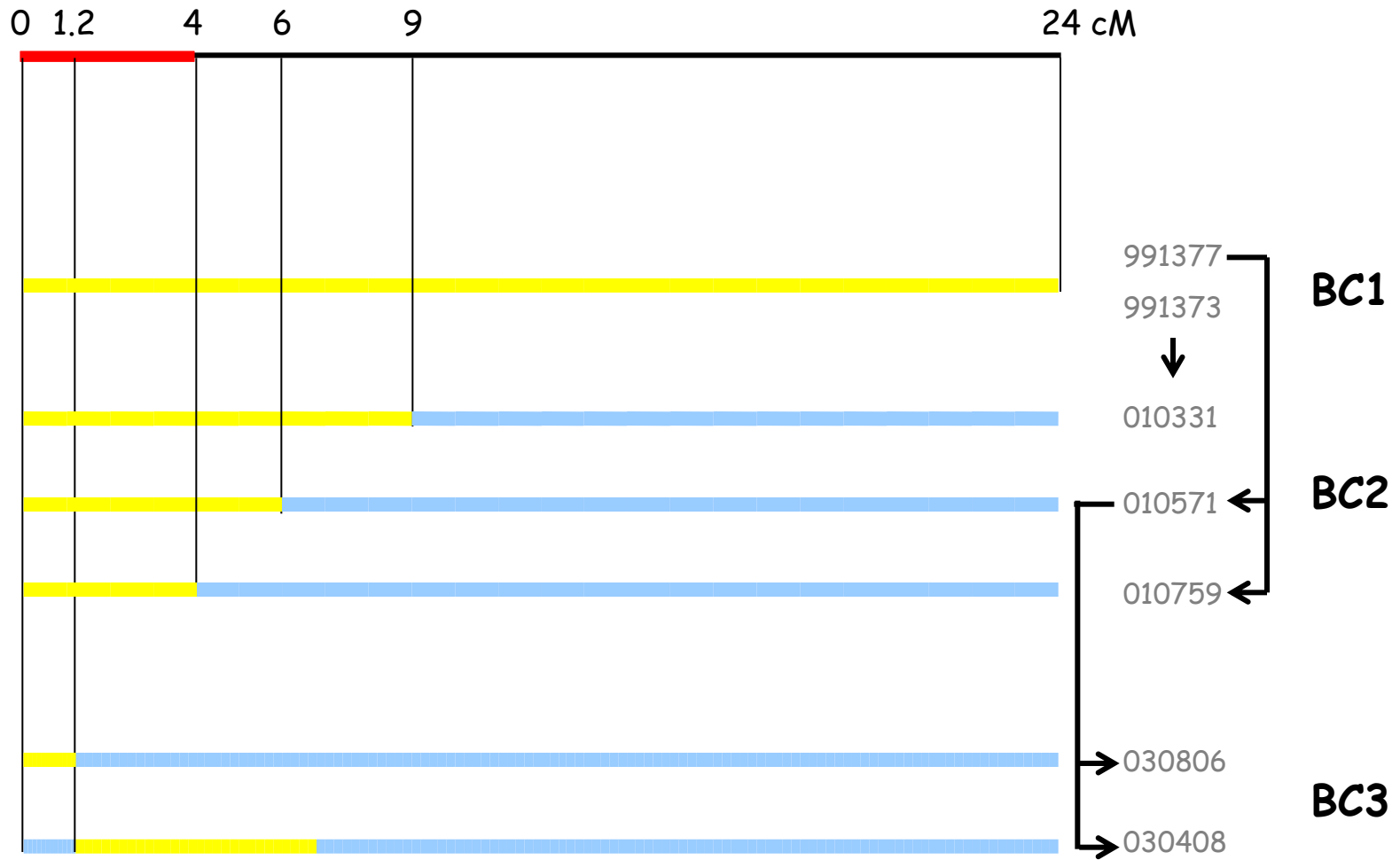
---

Generation	Boar	Growth	Carcass composition	Meat quality
BC1	991373	**	***	*
	991377	*	***	*
BC2	010331	**	***	NS
	010571	***	***	*
	010759	NS	***	**

NS: non significant - \*  $P < 0.05$  - \*\*  $P < 0.01$  - \*\*\*  $P < 0.001$

(at the chromosome level)

# Exemple : SSC2



# Conclusion (fine mapping)

---

Mapping interval has been reduced to : **SSC2** : 4 cM

**SSC7** : 6 cM

For **SSC1** & **SSC4**: BC2 boars will be analysed soon

→ Much work remain to be done

Other traits:


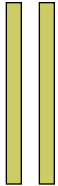
**IMF**

**ANDROSTENONE**: fat samples remain to be analysed

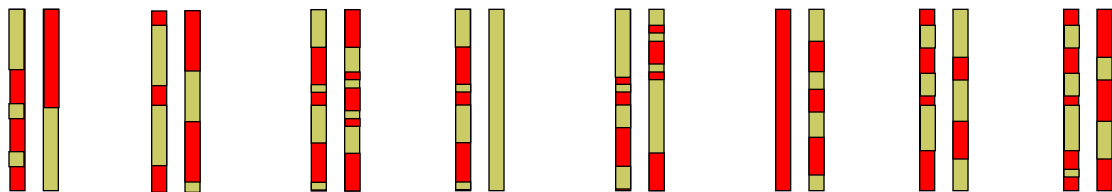
Additional analyses: Transcriptome  
SSC2 imprinting



# Use of « historical » recombinations

Founder individual  X  Line 2

•  
•  
•  
•



« Random »  
matings

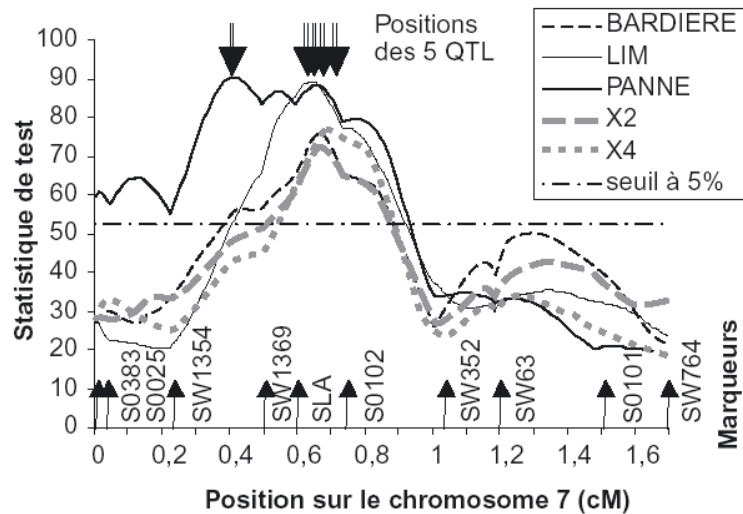
$F_n$

- Development of methods and a software for QTL primary detection => QTLMAP software
  - Analysis of half-sib (HS) and mixtures of half and full-sib families (HFS)
    - HS well suited for dairy cattle data
      - Extended to take into account the information of maternal grand-sires
    - HFS well suited for pig data
      - Within – population or in crosses between divergent lines
      - No assumption concerning the fixation of QTL alleles in parental populations
      - Compute the probability of different possible phases
      - Heterogeneity of sire family variances can be accounted for (e.g. when another QTL is segregating)

=> QTLMAP available upon request

- Multiple trait – multiple QTL (Gilbert, 2003)
  - Use of discriminant analysis in order to reduce the number of parameters
    - Increases detection power
    - Different models (pleiotropic vs linked QTL)
  - Implemented in QTLMAP software
- Traits with specific distribution (Moreno, 2003)
  - Discrete traits, survival traits
  - Implemented in QTLMAP software
- Use of population linkage disequilibrium
  - Development of a software based on the method developed by Meuwissen and Goddard
  - Comparing different methods :
    - Meuwissen and Goddard
    - Fernando et al.
  - Applications to fine mapping in dairy cattle and pigs

# Multiple trait / QTL : an example on SSC7



**Figure 1** - Résultats des analyses "unicaractère" et "uniQTL"

**Tableau 5** - Synthèse des résultats : positions et effets additifs<sup>1</sup> des 5 QTL détectés

Caractères Position (cM)	BARDIERE	PANNE	X2	X4	LIM
66	-0,58				
0	-0,22				
66		-0,59			0,83
18			-0,27	-0,28	
68			-0,32	-0,36	

<sup>1</sup> En unité d'écart type phénotypique

Gilbert et al (2004)