Fine-mapping of a QTL segregating on pig chromosome 2 highlighted epistasis

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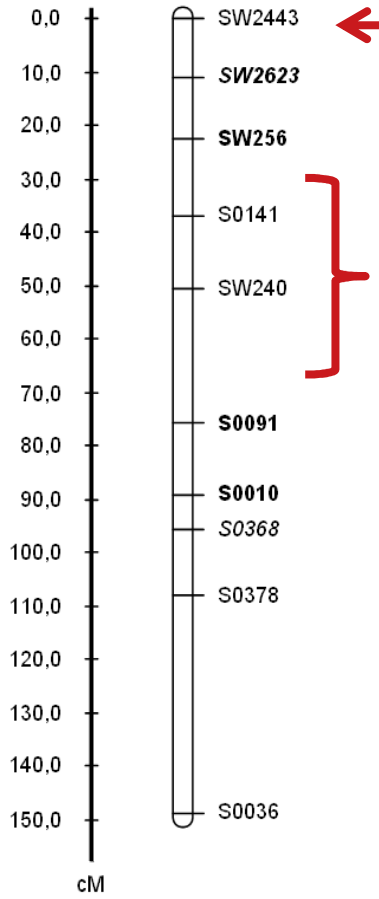
INRA

SSC2 and backfat thickness



IGF2 -intron3-G3072A (Van Laere *et al.*, 2003)

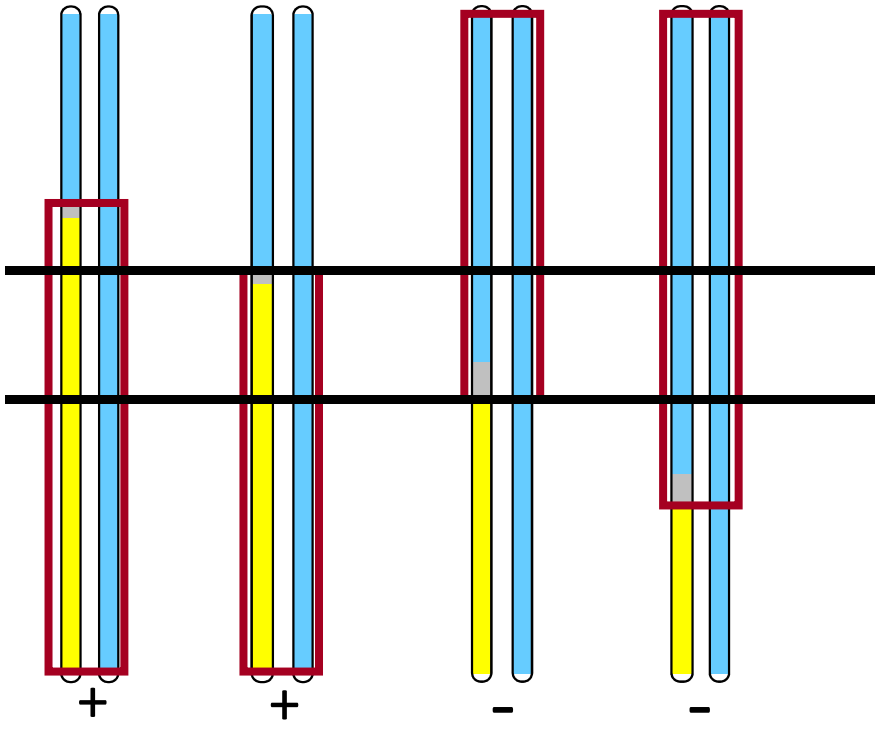
BUT not only explanation (Sanchez *et al.*, 2006)

Reports of other QTLs
(Lee *et al.*, 2003 ; Geldermann *et al.*, 2010 ; Tortereau *et al.*, 2011)

Confirmation, fine-mapping and description of its mode of segregation

Marker-assisted backcross design

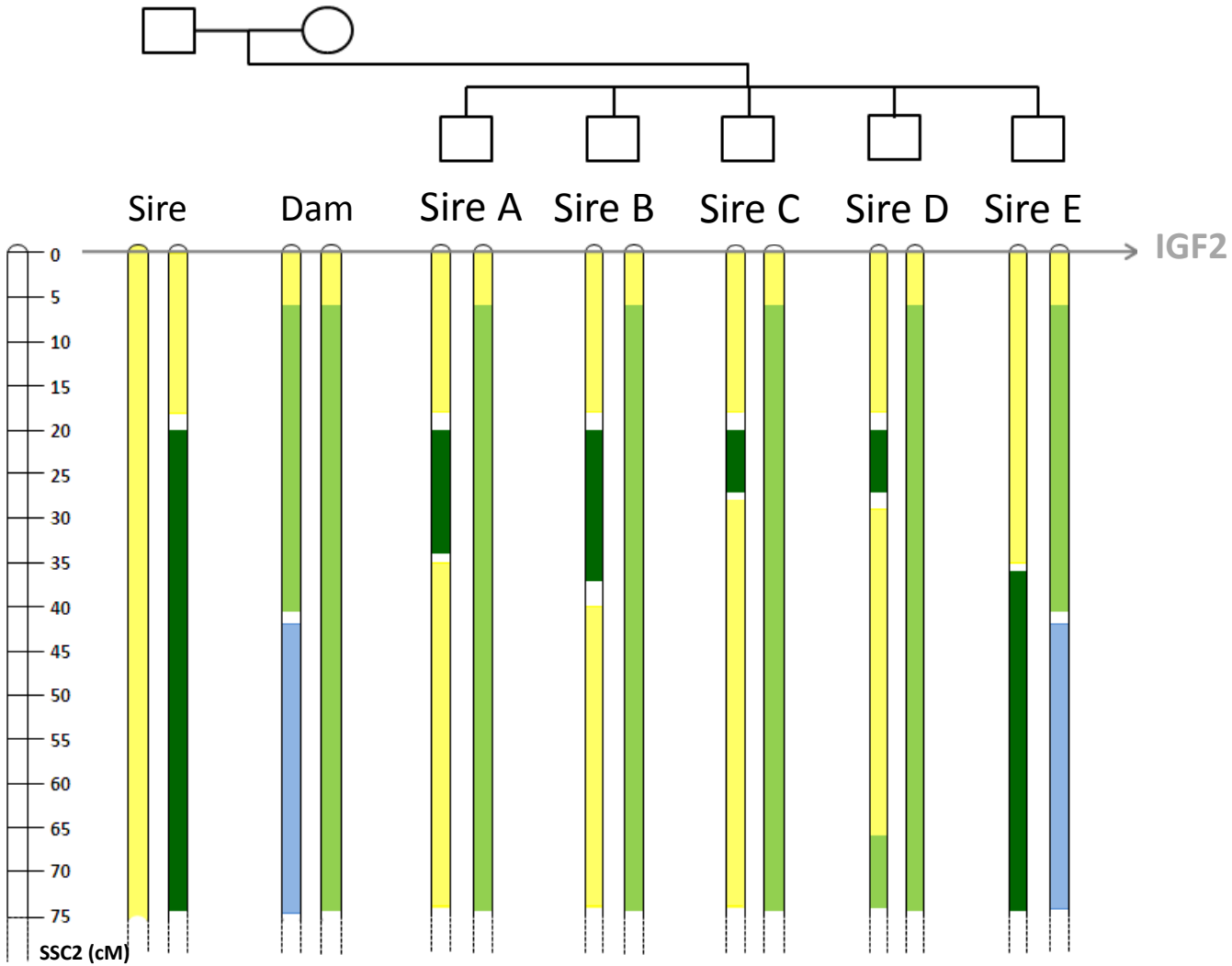
Creation of animals carrying different recombination points in the candidate region



Smaller QTL interval

QTL segregation

Tested sires



Only G/G animals, to avoid the segregation of the mutation

By construction :

- A unique **IBD** MS haplotype

-Various LW haplotypes

Progeny-testing results

Progeny testing with LW females, about 100 offspring per sire

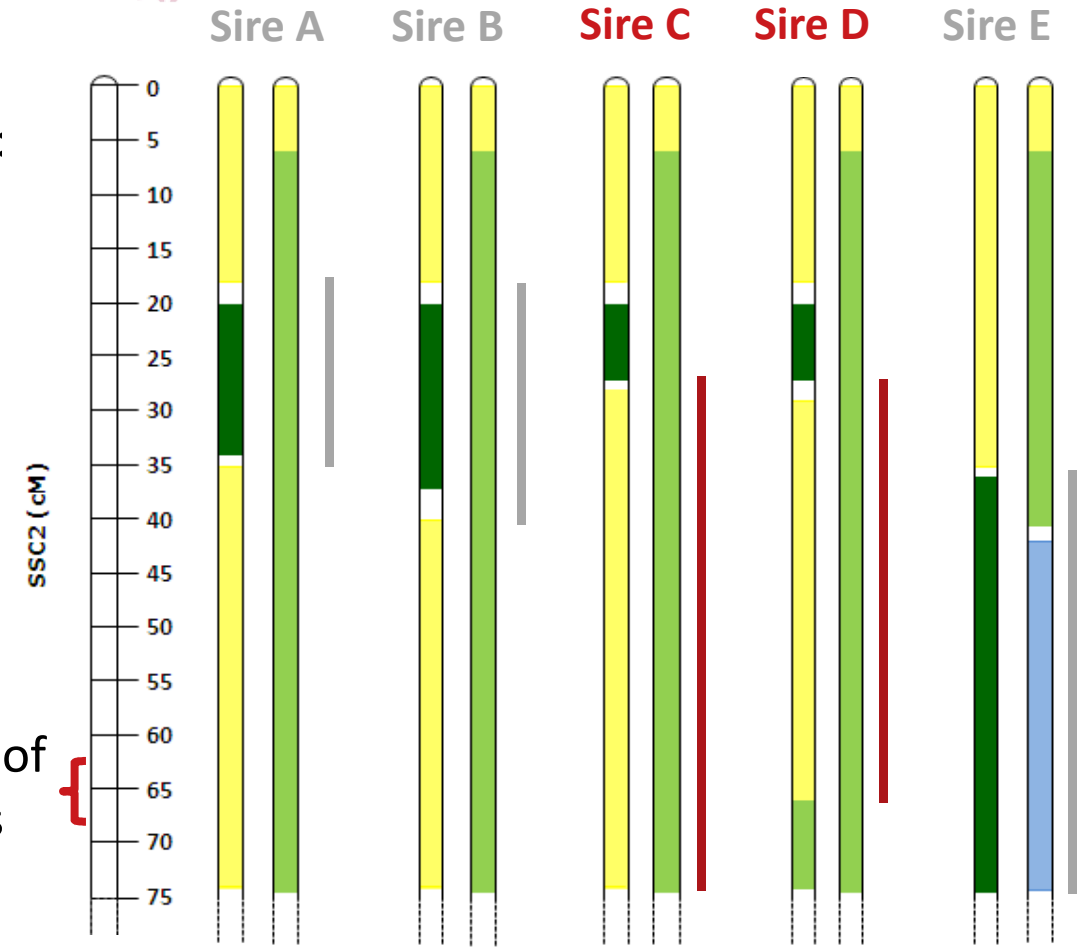
Results with US BFT measurements :

- 2 segregating sires

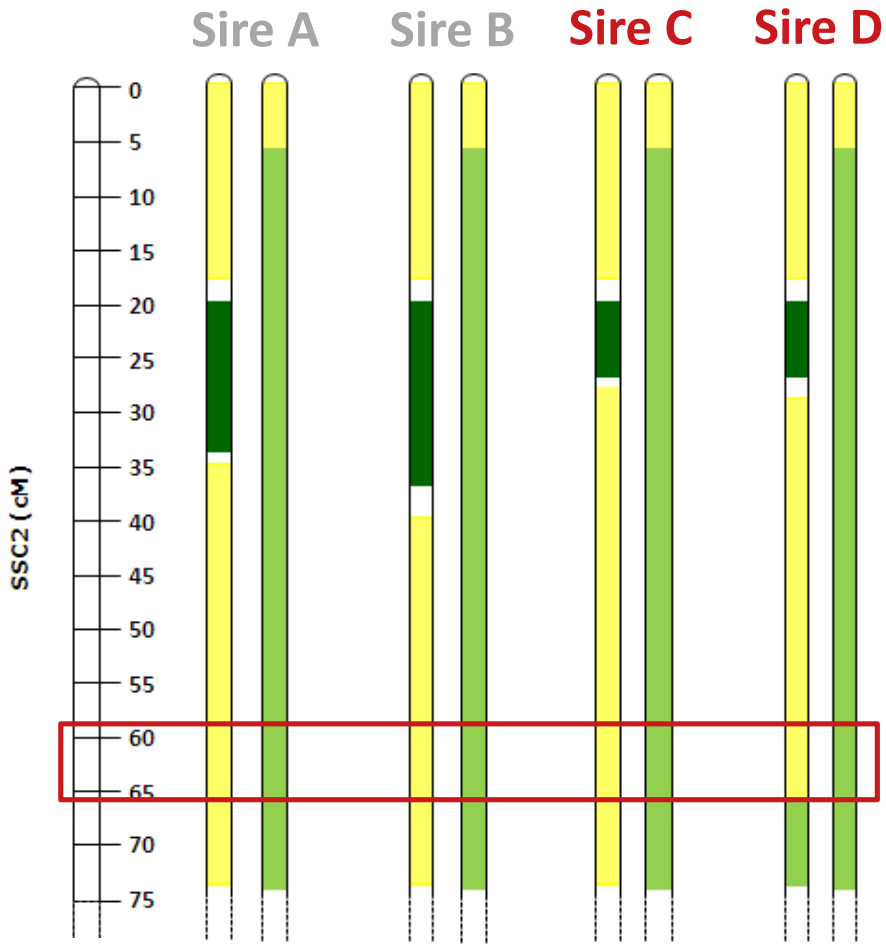
-3 non-segregating sires

No overlapping region ...

Most likely position of the detected QTLs



Full-sibs with identical contrasts



At the most likely position: same contrasts between two IBD haplotypes

Interaction with another locus in the genome

Whole genome scan

Genotyping of 578 microsatellites covering all the autosomes and SSCX

Selection of candidate microsatellites :

	Interaction candidate region			Genotype		
	Marker	Chromosome	Position	All1	All2	
Sire A	S0155	1	95	4	2	Excluded
Sire B	S0155	1	95	4	2	
Sire C	S0155	1	95	4	1	
Sire D	S0155	1	95	4	2	
Sire A	SW2551	1	96	1	1	No informative
Sire B	SW2551	1	96	1	1	
Sire C	SW2551	1	96	1	1	
Sire D	SW2551	1	96	1	1	
Sire A	SW2512	1	144	9	10	Identical genotypes
Sire B	SW2512	1	144	9	10	
Sire C	SW2512	1	144	7	10	Identical genotypes
Sire D	SW2512	1	144	7	10	

Different genotypes

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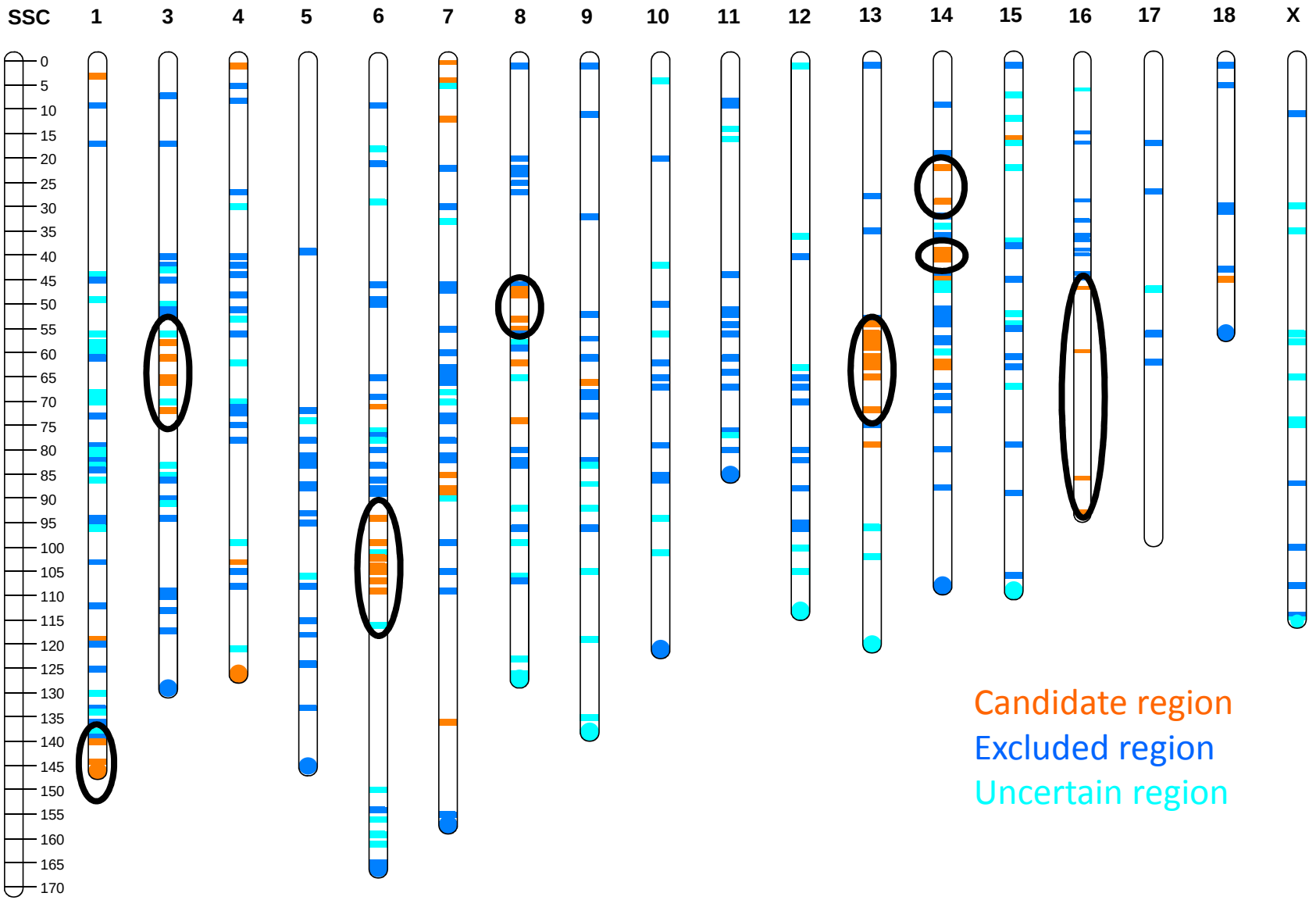
Different genotypes

Candidate regions



Detection of interactions

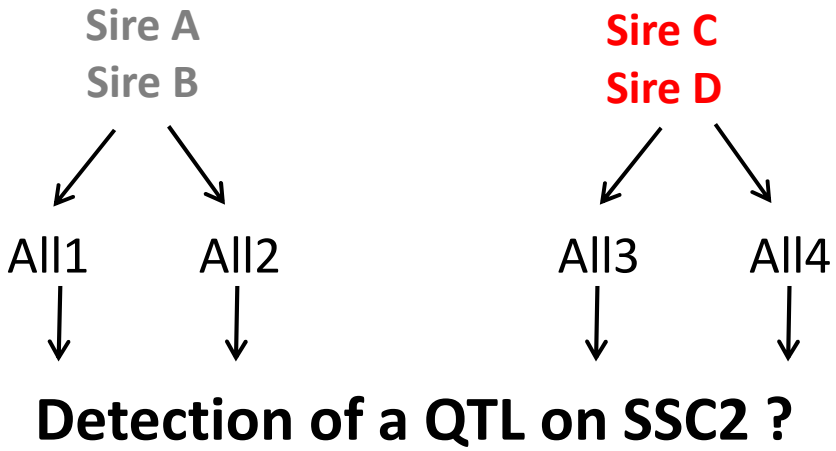
Selection of 1 or 2 microsatellite per candidate region

Genotyping of all the offspring of the 4 sires

Interaction analysis :

group of sires

alleles at the candidate interacting region

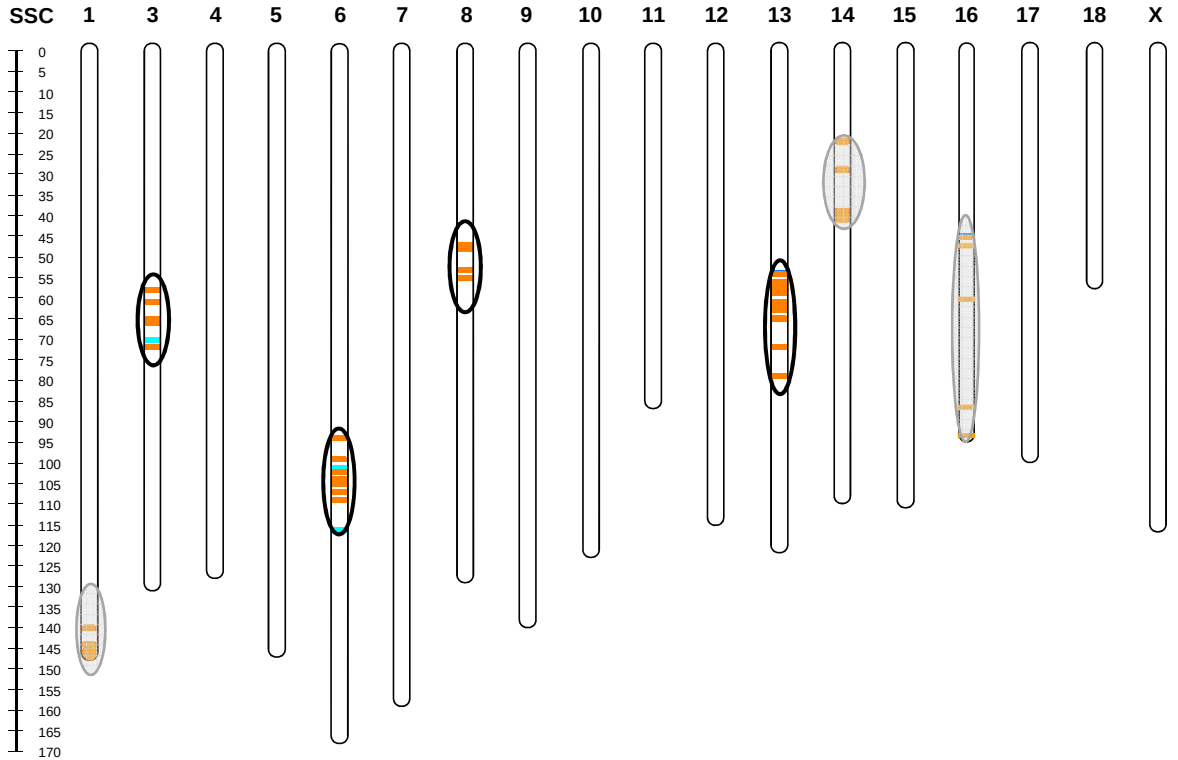


Detection of a QTL on SSC2 ?

Results

Among the 7 tested regions:

- 3 have been excluded
- 4 remained candidate interacting regions



Analysis of a F2 design

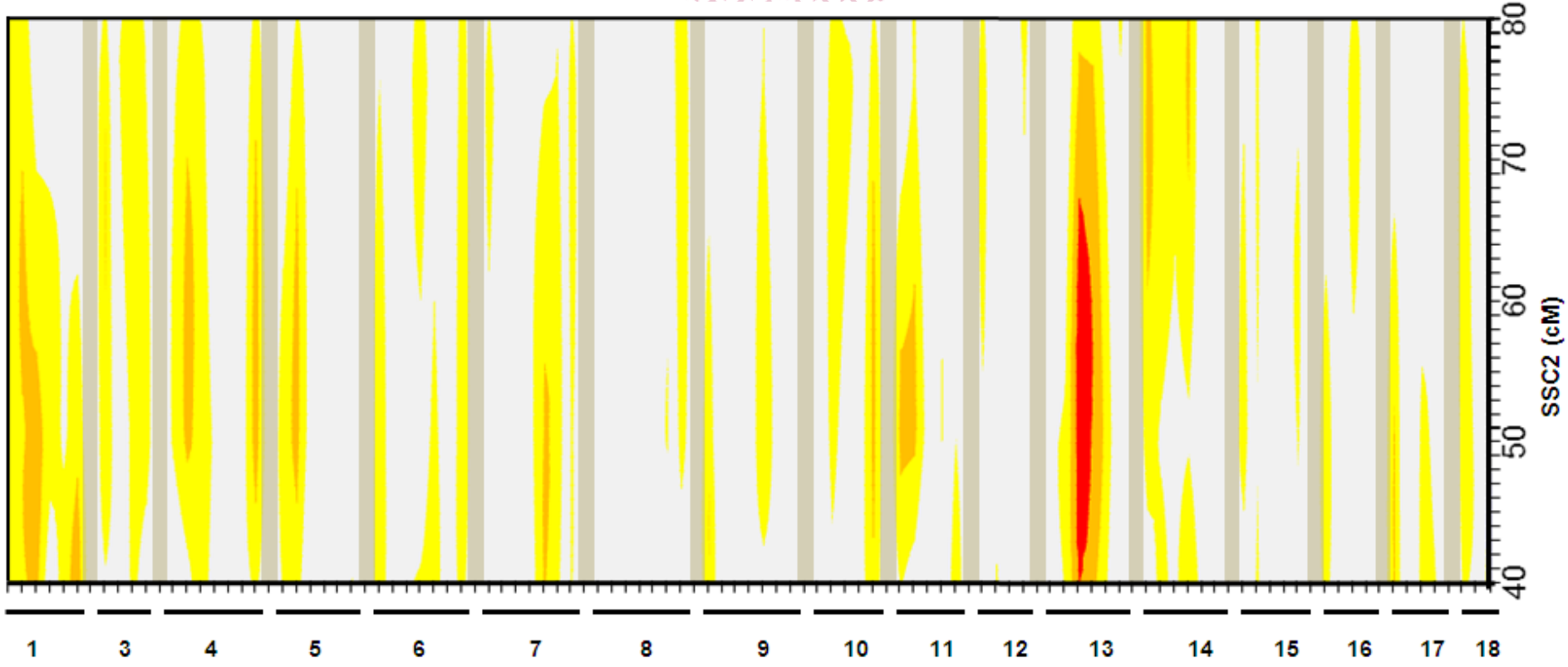
- PORQTL F2 design (Bidanel et al., 2001),
  same breeds
  ancestor of the BC pedigree

- Interaction analyses :

  SSC2 QTL region

  ~ 100 microsatellites covering all the autosomes

Confirmation in a F2 design

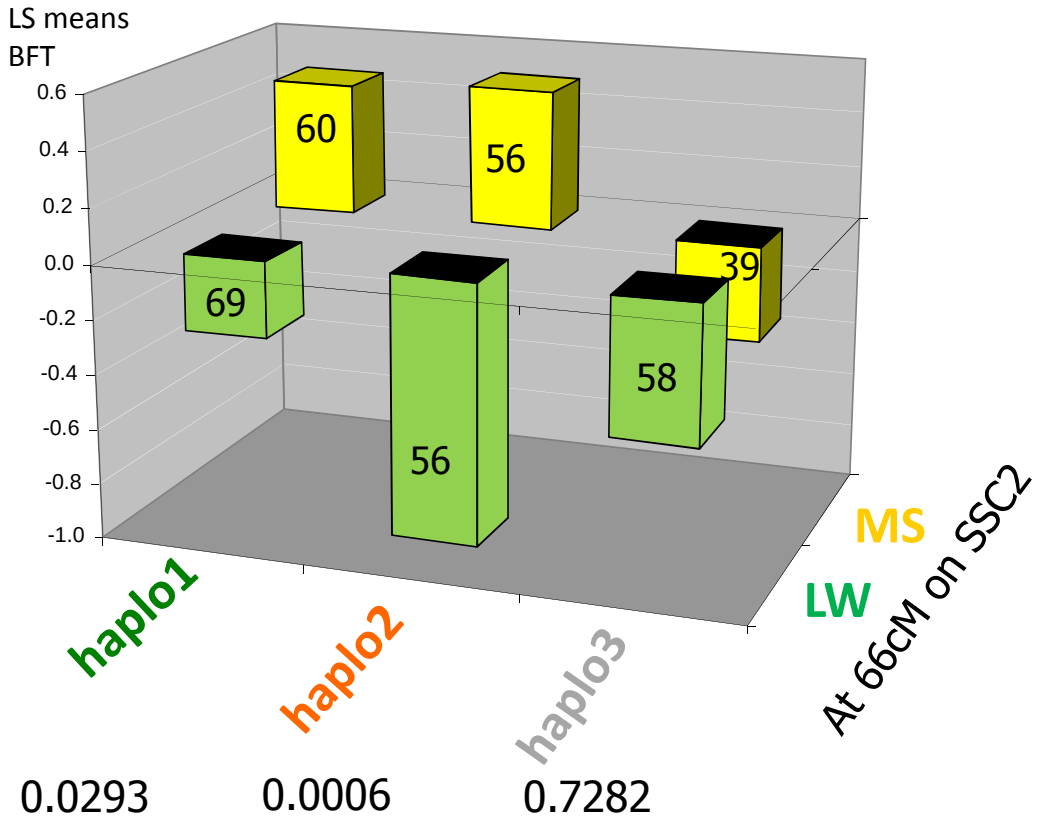


Confirmation of SSC13

Interaction SSC2 – SSC13

Analysis of the SSC13 region in the BC pedigree:

Sire A	haplo1	/ haplo3
Sire B	haplo1	/ haplo3
Sire C	haplo1	/ haplo2
Sire D	haplo2	/ haplo2



Conclusion

- QTL underlying fatness traits on SSC2: 37 – 67 cM
- Interactions with at least SSC13
- Interactions with SSC3, SSC6, SSC8 to be confirmed / invalidated

Thank you for your attention

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