



# Whole genome scan to detect QTL for major milk proteins in three French dairy cattle breeds

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PhénoFinlait



# The PhénoFinLait program

## Fine composition of milk

Fatty acids

Proteins

Bovine

Ovine

Caprine

Estimation  
methods

Reference  
databases

Nutritional  
effects

Genetic  
effects

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A French dairy R&D project on fine milk composition

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# Milk protein composition

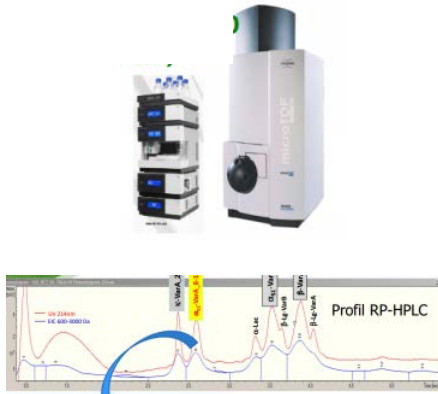
Effects on **techno-functional** milk properties:  
*milk coagulation time, cheese yield, heat stability...*



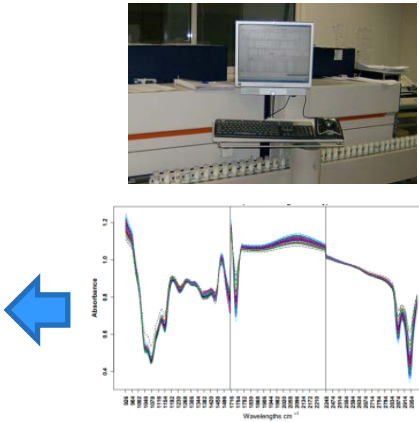
## Milk protein composition

**A reference analysis method**  
*(Liquid Chromatography – Mass Spectrometry)*

**MIR (Mid-Infrared) Spectra**  
routinely collected



Equations of prediction with 450 samples



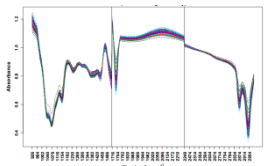
**long and costly**

**Easy to implement with limited additional cost**



# Milk protein composition at a large scale

MIR routinely collected



Equations

$\alpha$ -lactalbumin  
 $\beta$ -lactoglobulin

$\alpha$ s1-casein  
 $\alpha$ s2-casein  
 $\beta$ -casein  
 $\kappa$ -casein

**Whey proteins (WP)**

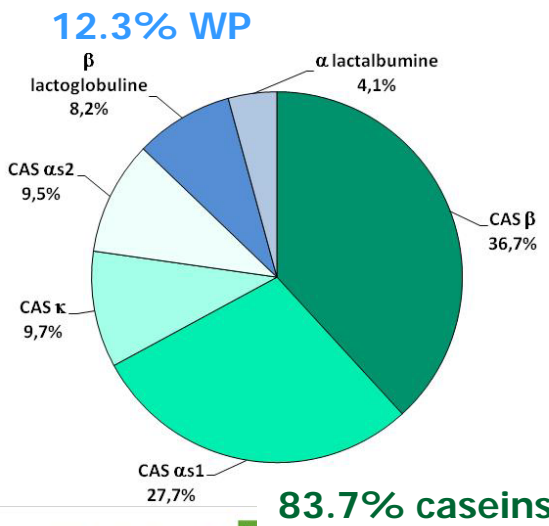
**Caseins**

in g/100g milk  
= % milk

in g/100g protein  
= % protein



**100g proteins**  
ex. in Montbéliarde



	<b>R<sup>2</sup></b>	<b>Relative error</b>
<b>Caseins</b>	80 - 92%	4 - 8%
<b>WP</b>	60 - 70%	12 - 14%

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## Animals: phenotypes

Almost **900,000 test-day records** from **160,253 cows**

**First 3 lactations** with at least **3 test-day records per lactation** retained



Breed	3 first lactations	
	MIR spectra	Cows
<b>Montbéliarde (MO)</b>	344,542	56,676
<b>Normande (NO)</b>	73,347	15,550
<b>Holstein (HO)</b>	89,730	17,983
<b>Total</b>	<b>507,619</b>	<b>90,209</b>

## Animals : phenotypes & genotypes

Almost **900,000 test-day records** from **160,253 cows**

**First 3 lactations** with at least **3 test-day records per lactation** retained



Breed	3 first lactations		Cows genotyped 50K BeadChip
	MIR spectra	Cows	
<b>Montbéliarde (MO)</b>	344,542	56,676	2,773
<b>Normande (NO)</b>	73,347	15,550	2,673
<b>Holstein (HO)</b>	89,730	17,983	2,208
<b>Total</b>	<b>507,619</b>	<b>90,209</b>	<b>7,653</b>



## Data analyses

Data pre-corrected for:

**Fixed effects**

**Random effect of the perm. env.**

and then, averaged per cow

$$y = X\beta + Za + Zp + e$$

### Fixed effects

herd\* test-day,  
stage of lactation,  
month \* year of calving,  
analysis laboratory \* spectrometer\* test-month

### Random effects

Genetic effect of the animal (0,  $G s_a^2$ )  
Effect of the permanent environment (0,  $I s_p^2$ )  
Residual effect (0,  $I s_e^2$ )



**LDLA** analyses (linkage + LD analyses - *Meuwissen et Goddard, 2001*) within breed:

SNP effect estimated considering windows of 6 SNP (LD between SNP)

Test statistic = Likelihood Ratio Test (**LRT**)



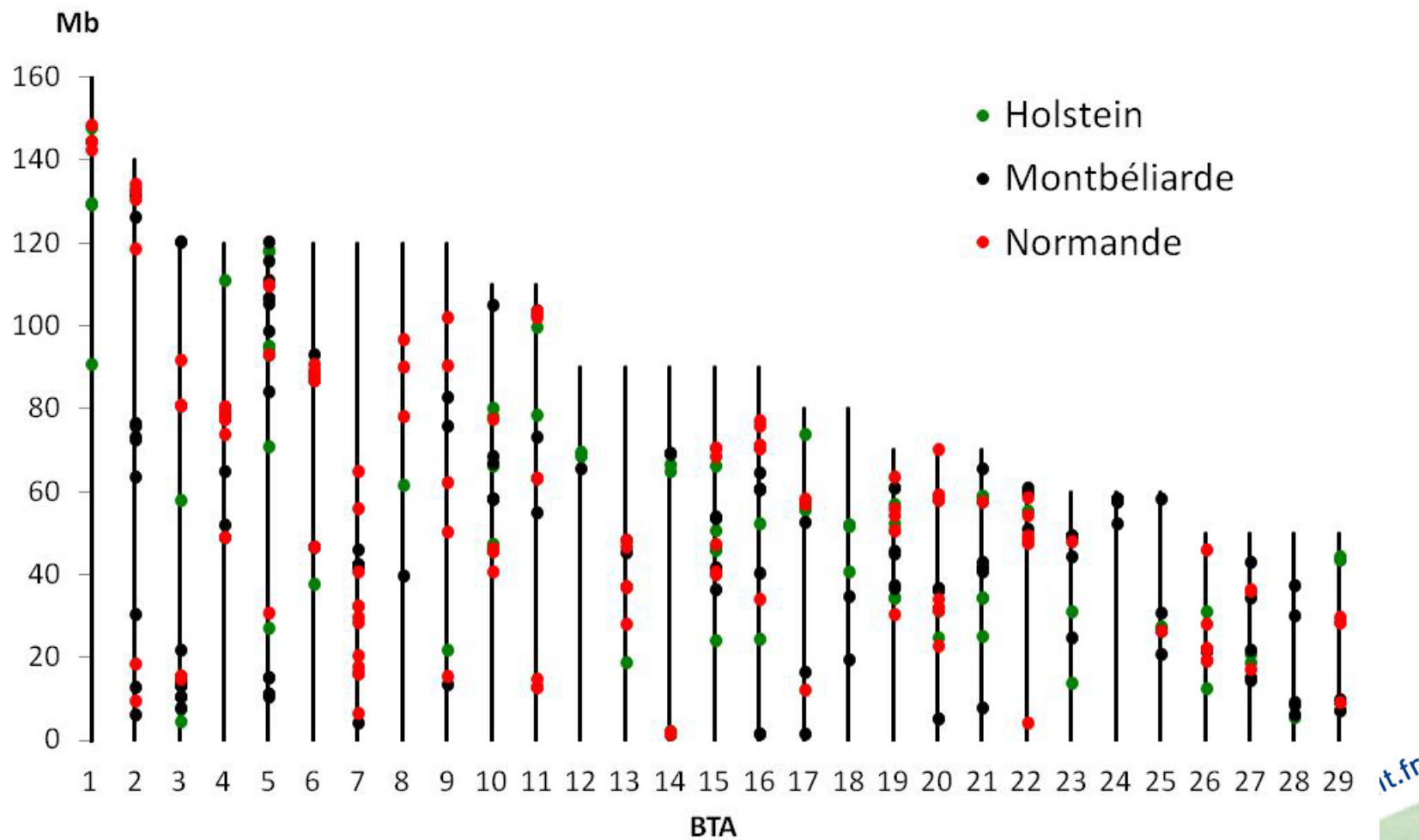


## Results: 2 types of QTL / LRT value

LRT 13	<i>False</i>	<b>Significant</b>	<b>Numerous QTL for all traits</b> <ul style="list-style-type: none"><li>▪ 172 in MO</li><li>▪ 174 in NO</li><li>▪ 136 in HO</li></ul>
	<i>Positives</i>		
	$\leq 63$ FP		



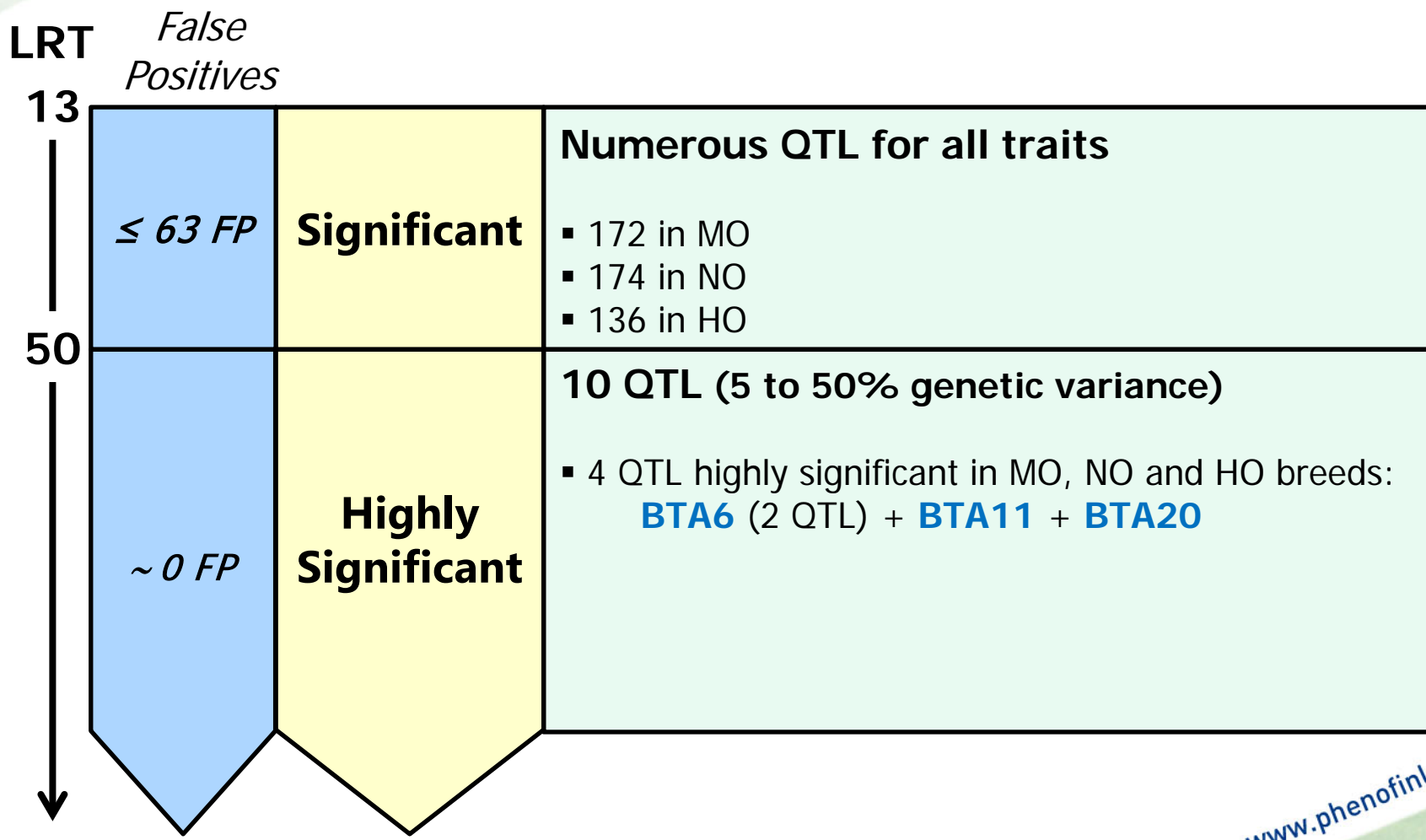
## Results: Significant QTL (LRT $\geq 13$ )



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## Results: 2 types of QTL / LRT value



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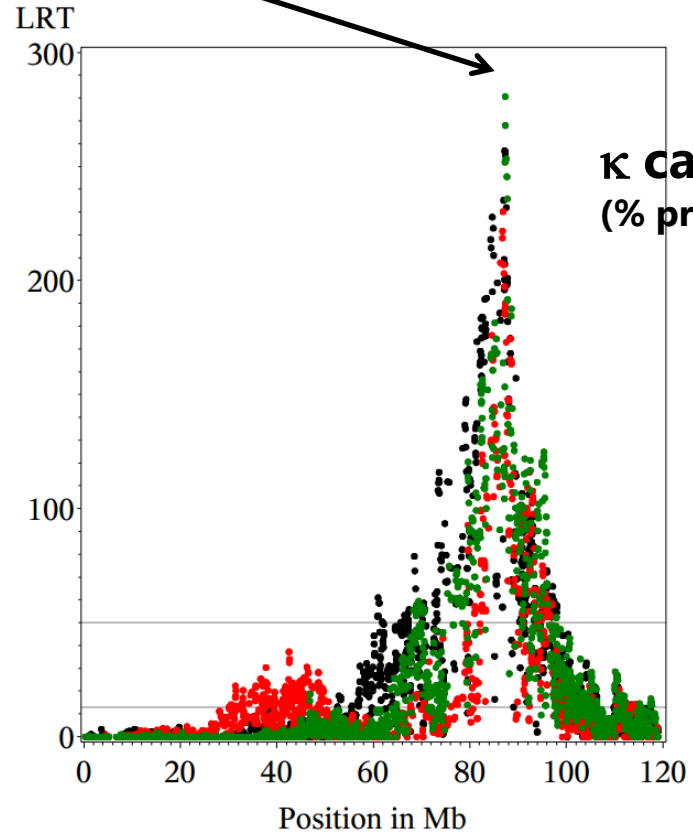
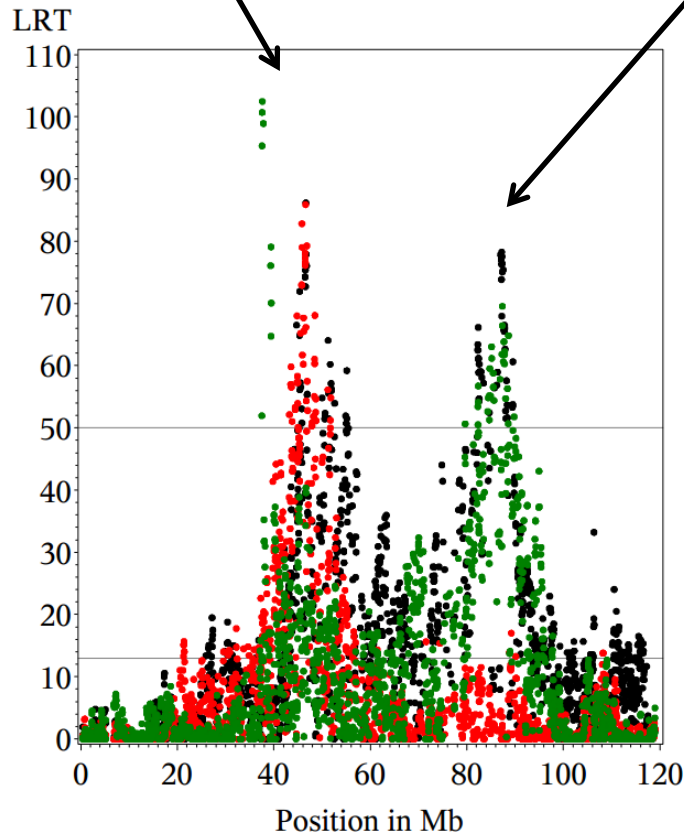
## BTA6 – 2 QTL for caseins




1 QTL at 46 Mb

1 QTL at 87 Mb



Casein genes



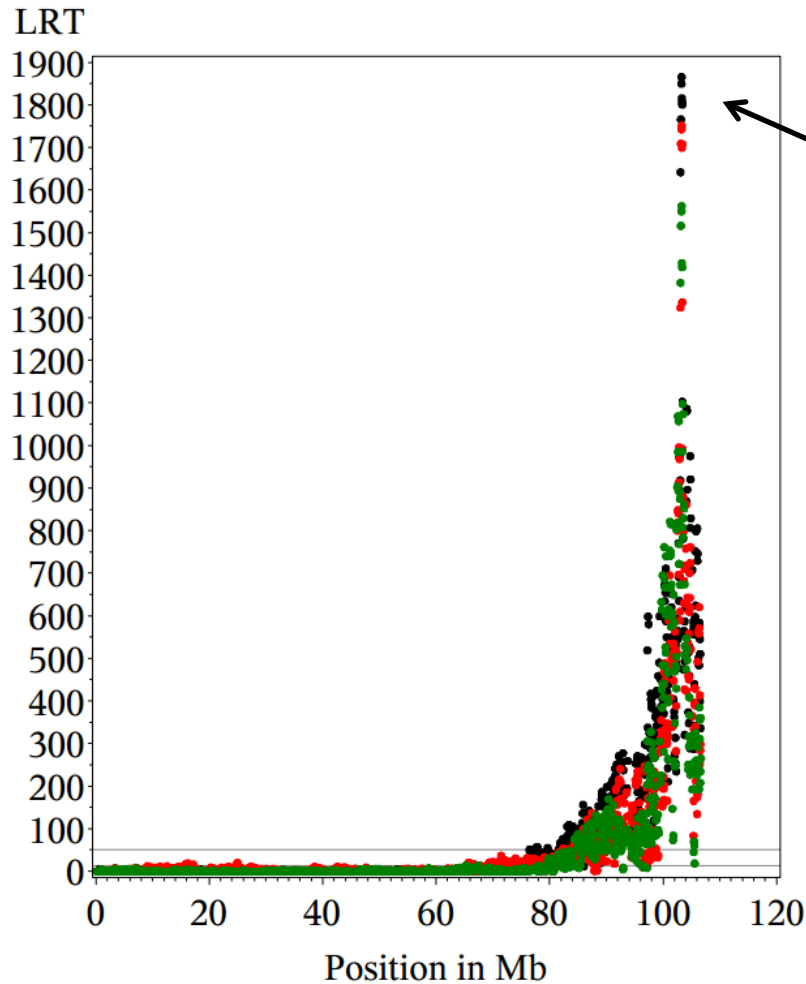
- MO 
- NO 
- HO 

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## BTA11 – 1 QTL for $\beta$ lactoglobulin



**1 QTL at about 103 Mb**

With a **huge**  
LRT max = 1900 !!!

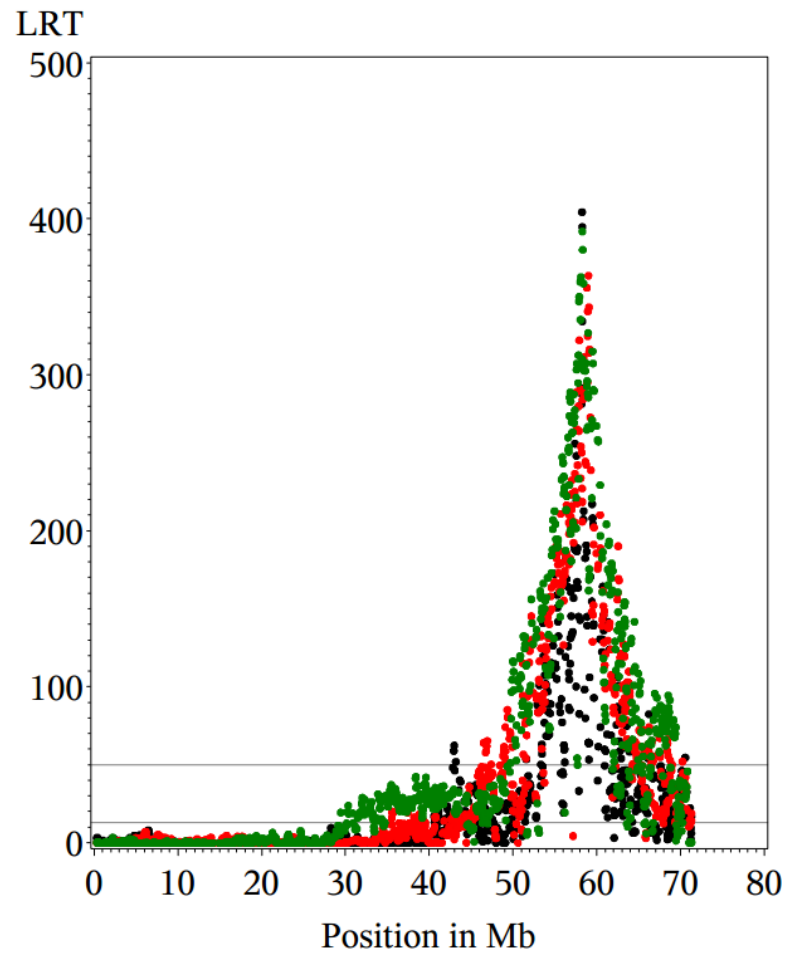
→  $\beta$  lactoglobulin gene  
Where mutation acting on  $\beta$   
lactoglobulin content

- MO
- NO
- HO





# BTA20 – 1 QTL for $\alpha$ lactalbumin



**1 QTL at about 58 Mb**

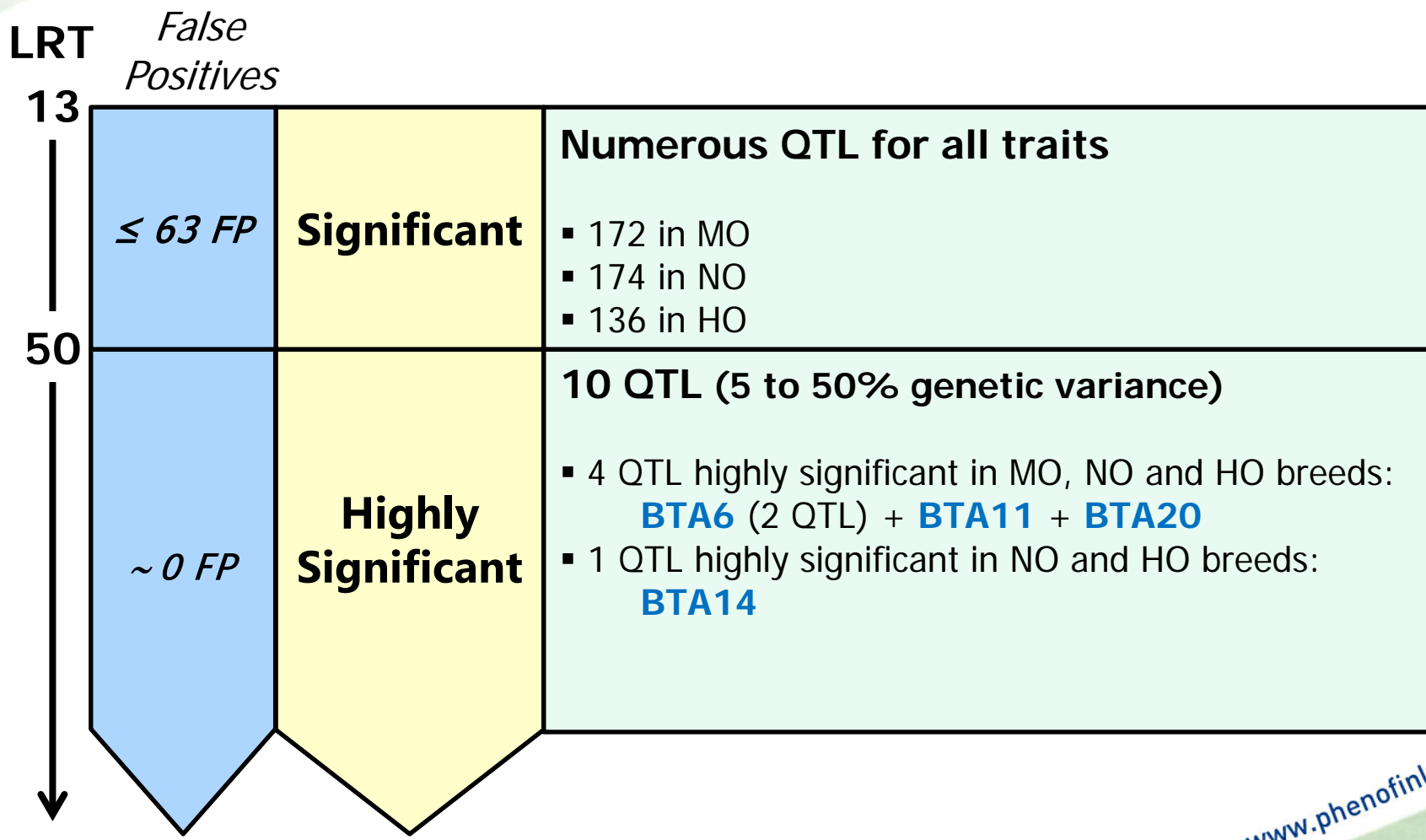
→ Candidate gene ?

- MO
- NO
- HO



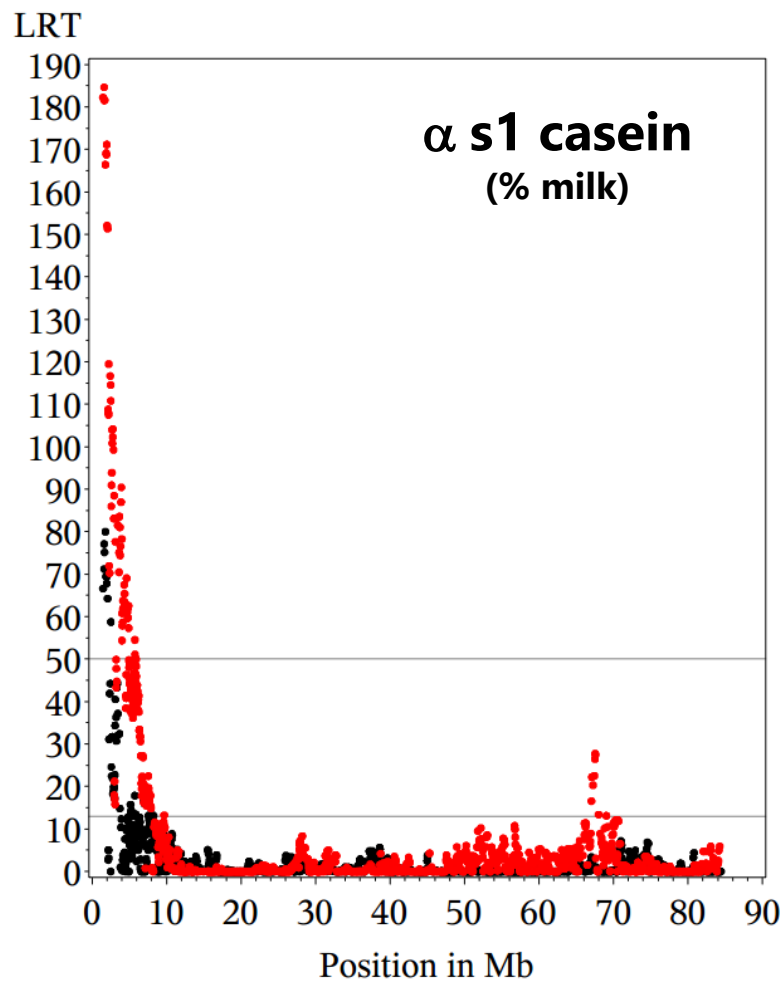


## Results: 2 types of QTL / LRT value





## BTA14 – 1 QTL for several traits



1 QTL at about 1.8 Mb

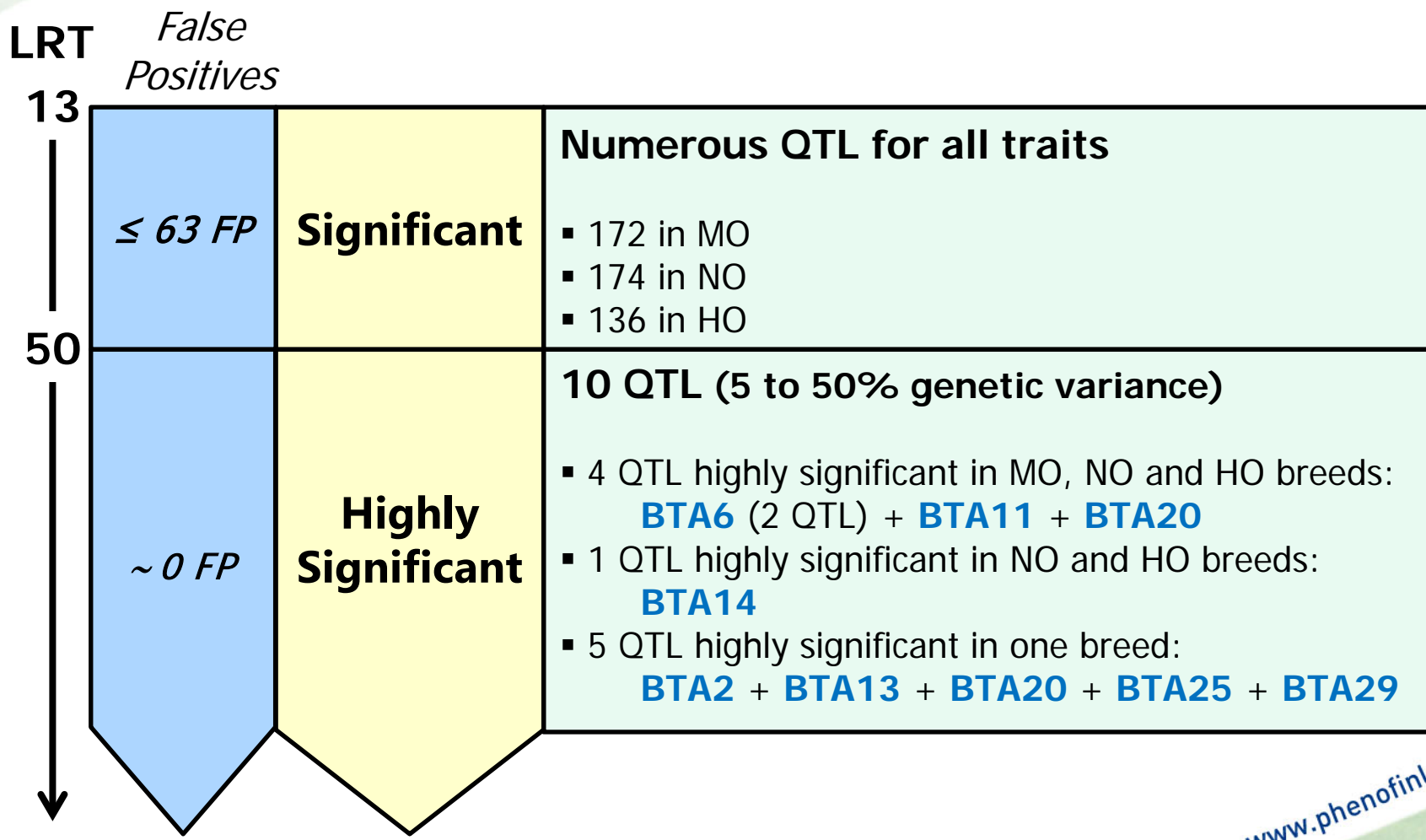
→ DGAT1 mutation







## Results: 2 types of QTL / LRT value



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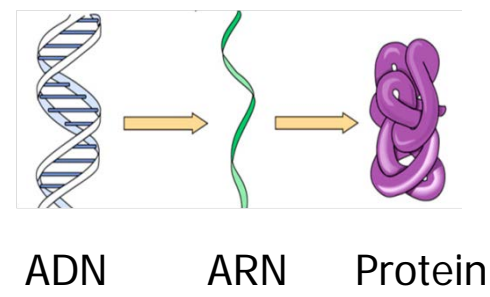




# Conclusions

With protein composition predicted from MIR spectra, a very **large number of QTL** in the 3 breeds, some with **large effects**

Protein composition estimated by MIR spectra + genotyping of cows can be used for **genomic selection**



Identification of new **mutations** using **sequences** and status of bulls for the QTL

PhénoFinLait population = first **reference population** for genomic selection



# PARTNERS



# FUNDINGS



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