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Detection of QTL affecting Milk Fatty Acid composition in three French dairy Cattle breeds

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PhénoFinlait

Background

Expectations of consumers evolve:
Improve the nutritional value of bovine milk for human health

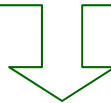


PhenoFinLait: a multispecies consortium gathering research and industry for fine milk composition improvement (bovine, ovine, caprine)



Fine milk composition in Fatty Acids (FA)

Basis for genomic selection



Recording – Estimation of genetic parameters
QTL Detection – Genetic/genomic evaluation

Data

Cattle : 425,000 MIR spectra (milk recording)

88,000 cows - 1,000 herds

Montbeliarde (MO), Normande (NO), Holstein (HO)
about 60 different FA and 20 ratios or sums



Genetic
Parameters

21,947 cows in L1 – 233,395 Test-Day (TD)
101,858 TD with FA profiles

Genetic
Evaluation

56 537 cows in L1, L2, L3 – 269,751 TD with FA profiles
– Repeatability model

Data

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Repeatability model

QTL Detection

2,867 Holstein, 1,924 Montbeliarde, 2,448 Normande in L1-L2
Bovine 50K Beadchip® (500 more LD genotypes to come)
36,913 to 39,683 SNP according to the breed

Traits

- FA expressed in g/100g total fat in milk
- All traits obtained from MIR spectra and prediction equations

Total SAT
C4:0
C6:0
C8:0
C10:0
C12:0
C14:0
C15:0
C16:0
C17:0
C18:0
C20:0

Total UNSAT	
Total MONO	Total POLY
C14:1cis9	C18:2c9c12
C16:1cis9	C18:2cis9t11 (CLA)
C18:1cis9	TotC18:2
C18:1cis11	
C18:1t11t10	
C18:1cis12	
TotC18:1	

omega3
omega6
omega7
Desaturation index
index14
index16
index18

index14

$C14:1cis9 / (C14:0 + C14:1cis9)$

Linkage Disequilibrium and Linkage Analysis

- LDLA Meuwissen et Goddard (2001)

$$\mathbf{y} = \boldsymbol{\mu} + \mathbf{W}\mathbf{v} + \mathbf{Z}\mathbf{u} + \mathbf{e}$$

$\mathbf{y}$ = vector of performances defined as the mean of TD records adjusted for environmental effects

$\mathbf{v}$ = vector of random haplotypes effects

$\mathbf{u}$ = vector of random polygenic effects

$\mathbf{e}$ = vector of random sampling error

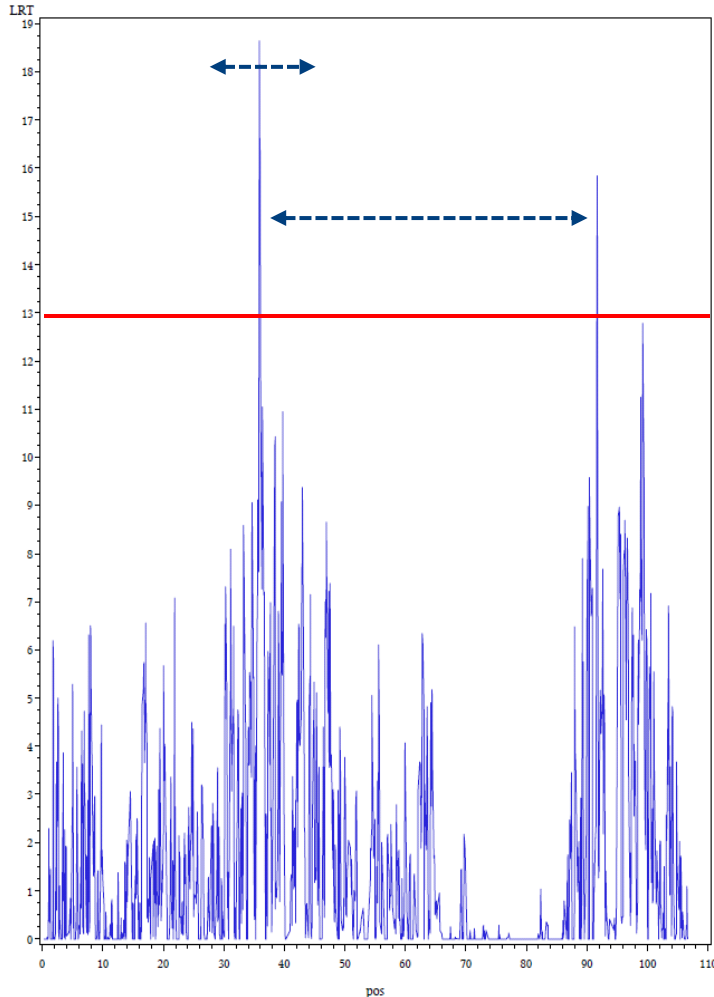
- Genome scan with a sliding haplotype of 6 markers
- **Test statistic : $LRT = 2 [\text{Log}(L1) - \log(L0)]$**

L1 = Likelihood under H1 (model with QTL)

L0 = likelihood under H0 (model with no QTL)

Rules to define a QTL

C4:0 – BTA 11 - MO



For following plots,

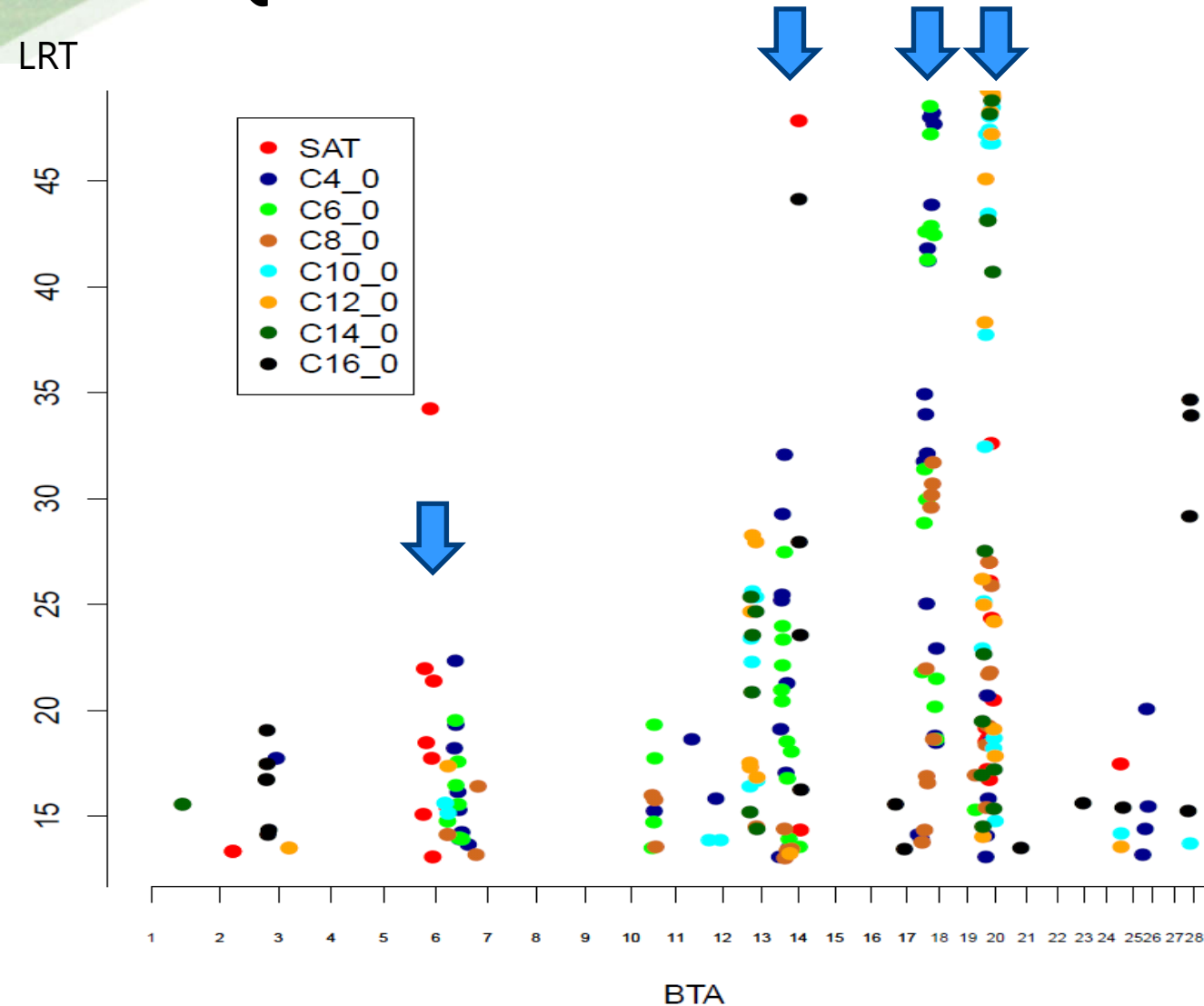
- $LRT > 13$
- Maximum in each 2 Mb interval

For QTL counting,

- Distance between 2 QTL > **10 Mb**

— Short and Medium SAT

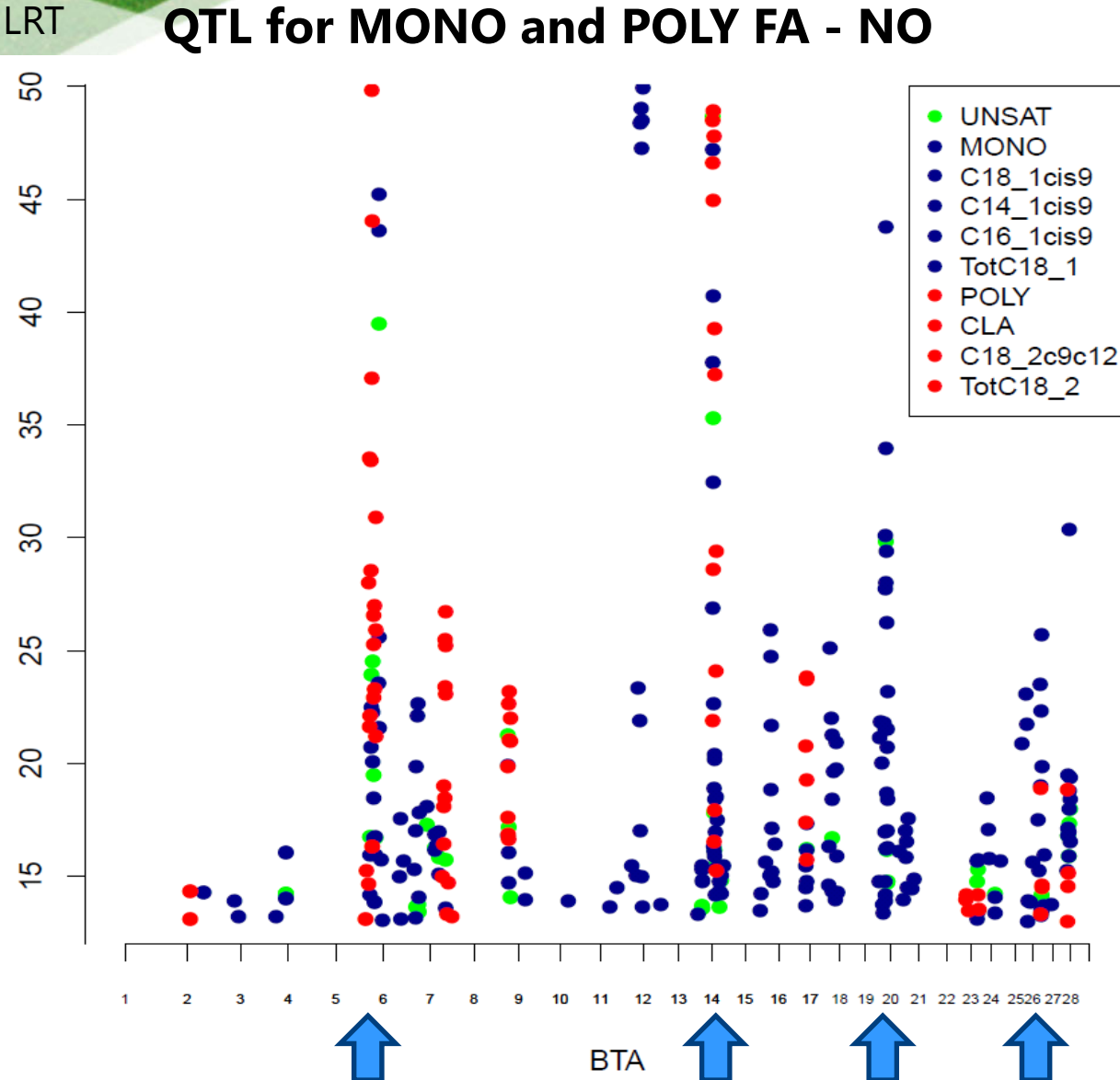
QTL for SAT FA - MO



Nb QTL	Total 3 breeds
C4:0	36
C6:0	29
C8:0	30
C10:0	28
C12:0	20
C14:0	13
C16:0	23

— UNSAT FA

QTL for MONO and POLY FA - NO



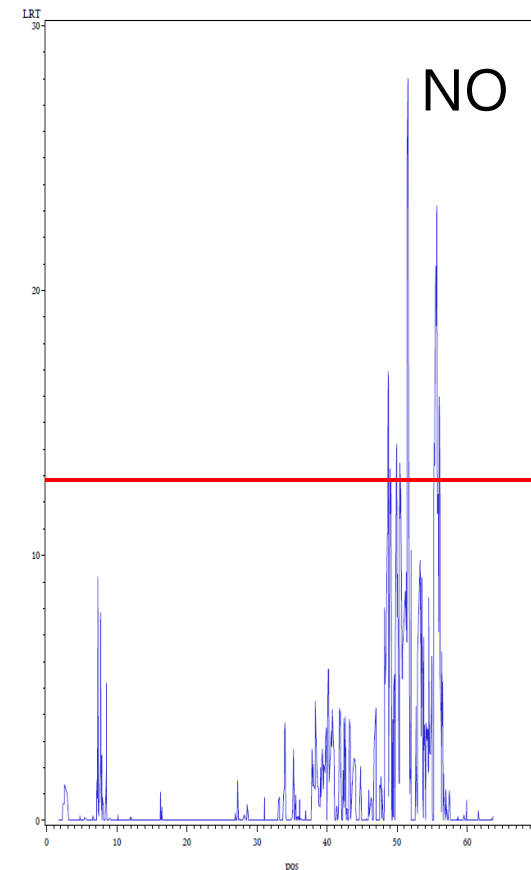
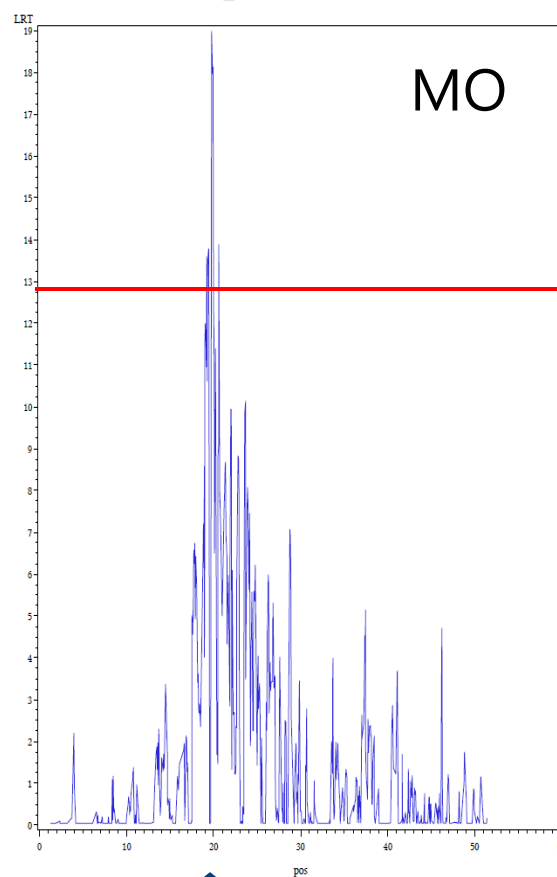
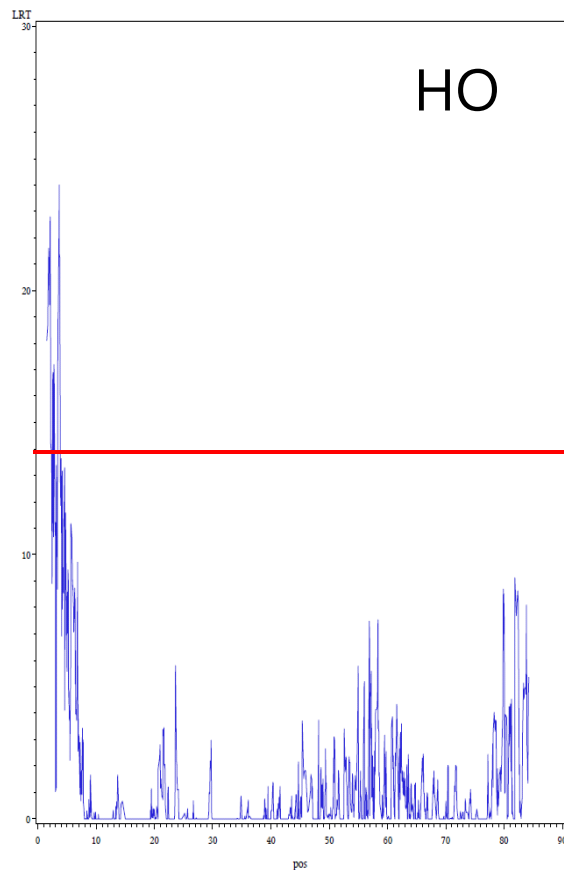
Nb QTL	Total 3 breeds
omega3	24
omega6	19
C14:1cis9	28
C16:1cis9	29
C18:1cis9	28
CLA	17
Tot_C18:1	24
C18:2cis9cis12	12

Known regions

BTA 14 - C8:0

BTA 26 - C14:1cis9

BTA 19 - Tot C18:1



DGAT1



SCD1



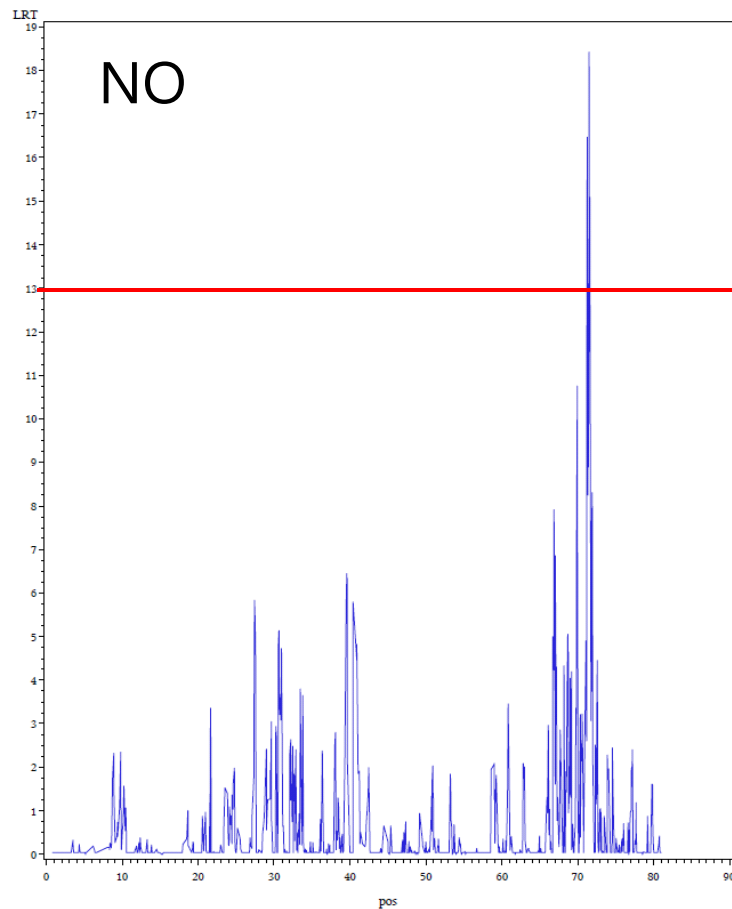
FASN

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— Focus on some regions

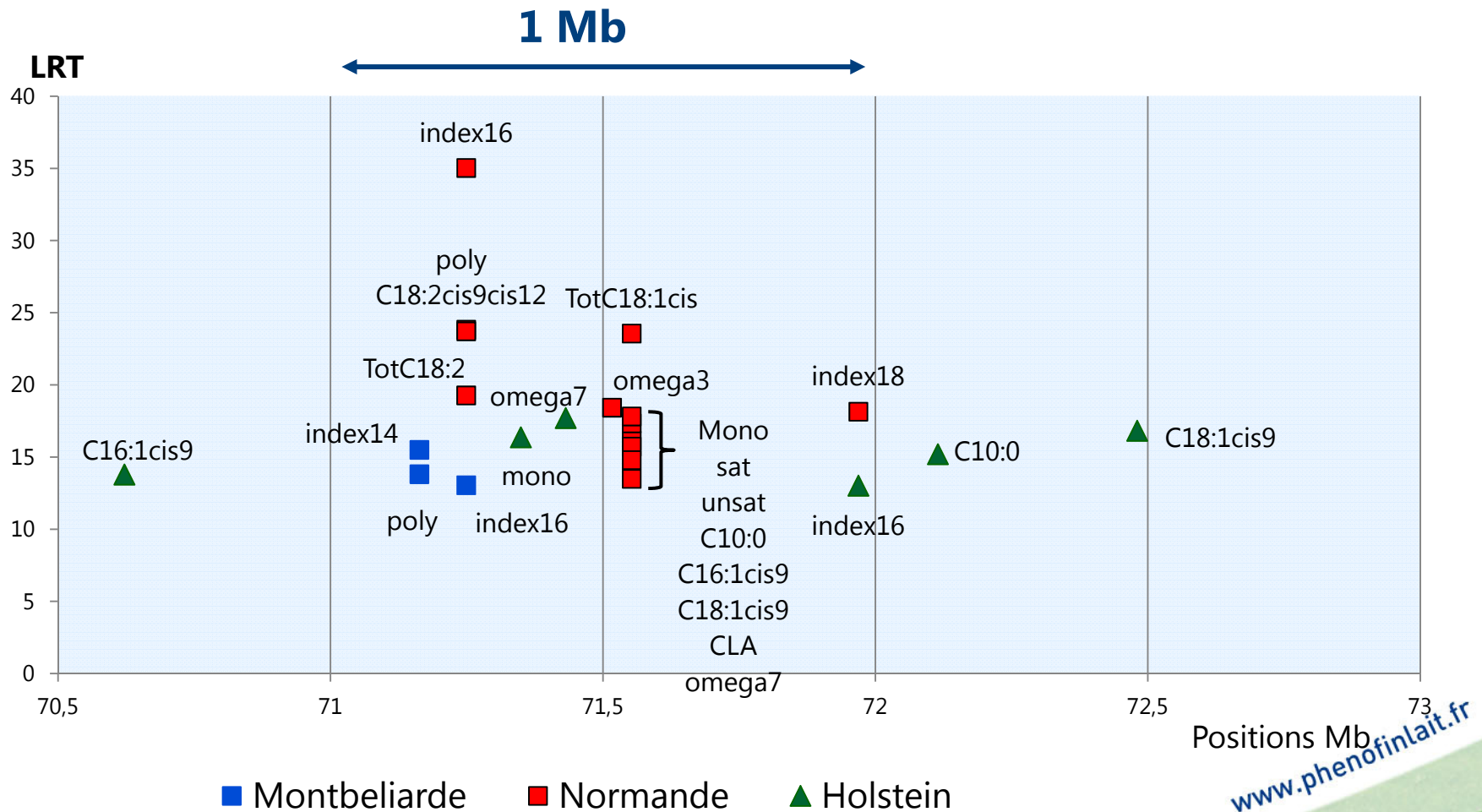
BTA 16 – Omega3



Fine localisation

BTA 16

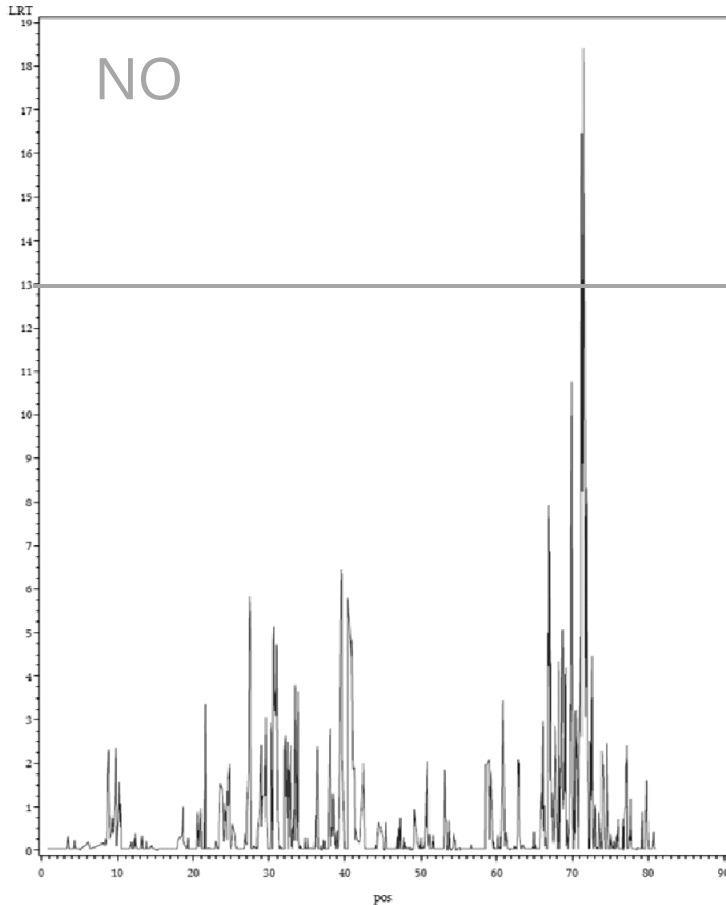
QTL for 17 traits detected in the 70.6 – 72.5 region



— Focus on some regions

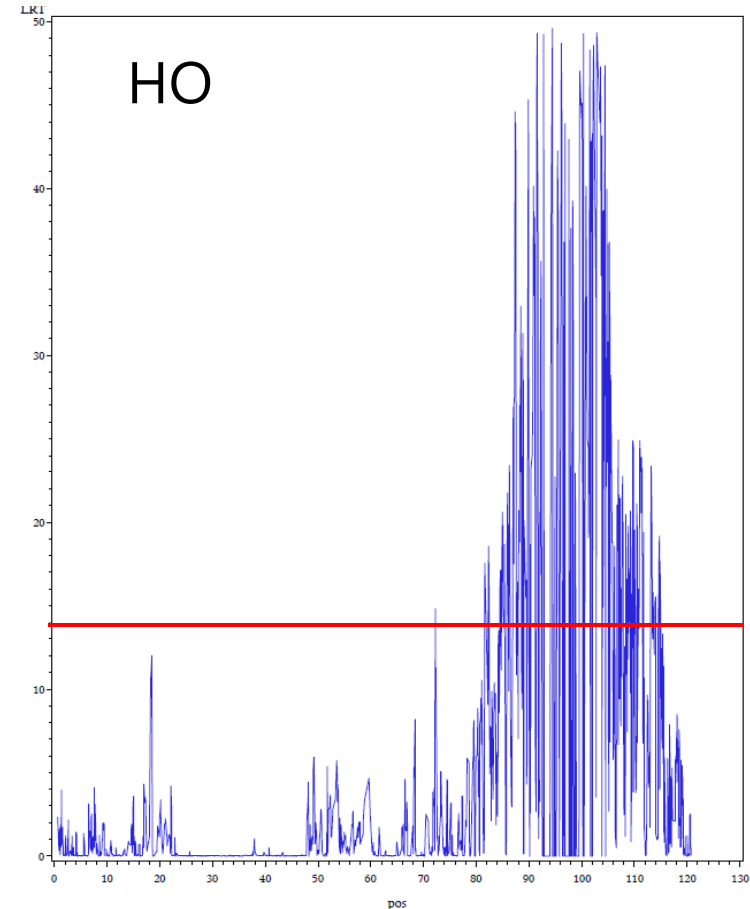


BTA 16 – Omega3



Fine localisation

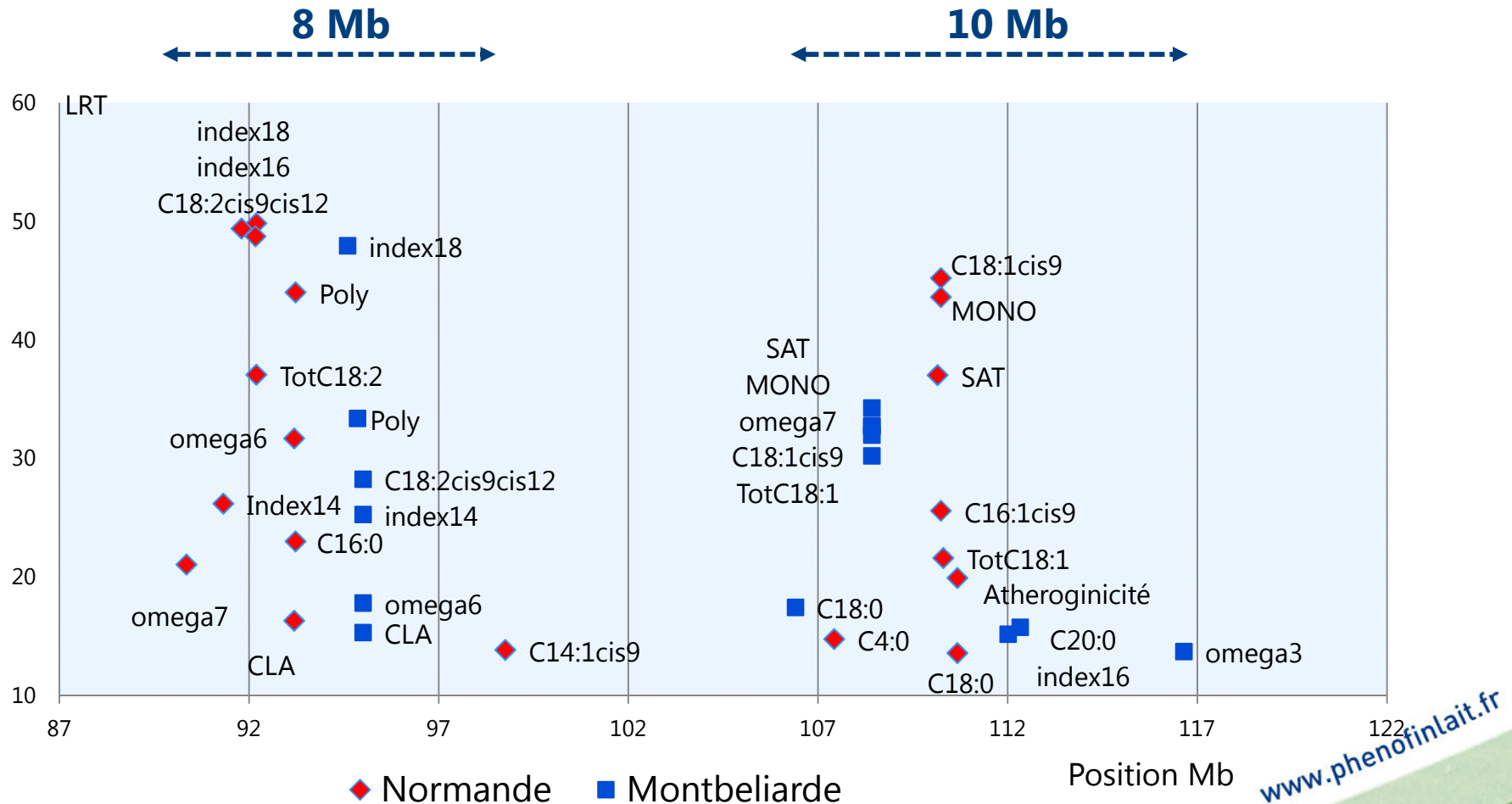
BTA 5 – MONO



Imprecise localisation

BTA 5: MO and NO

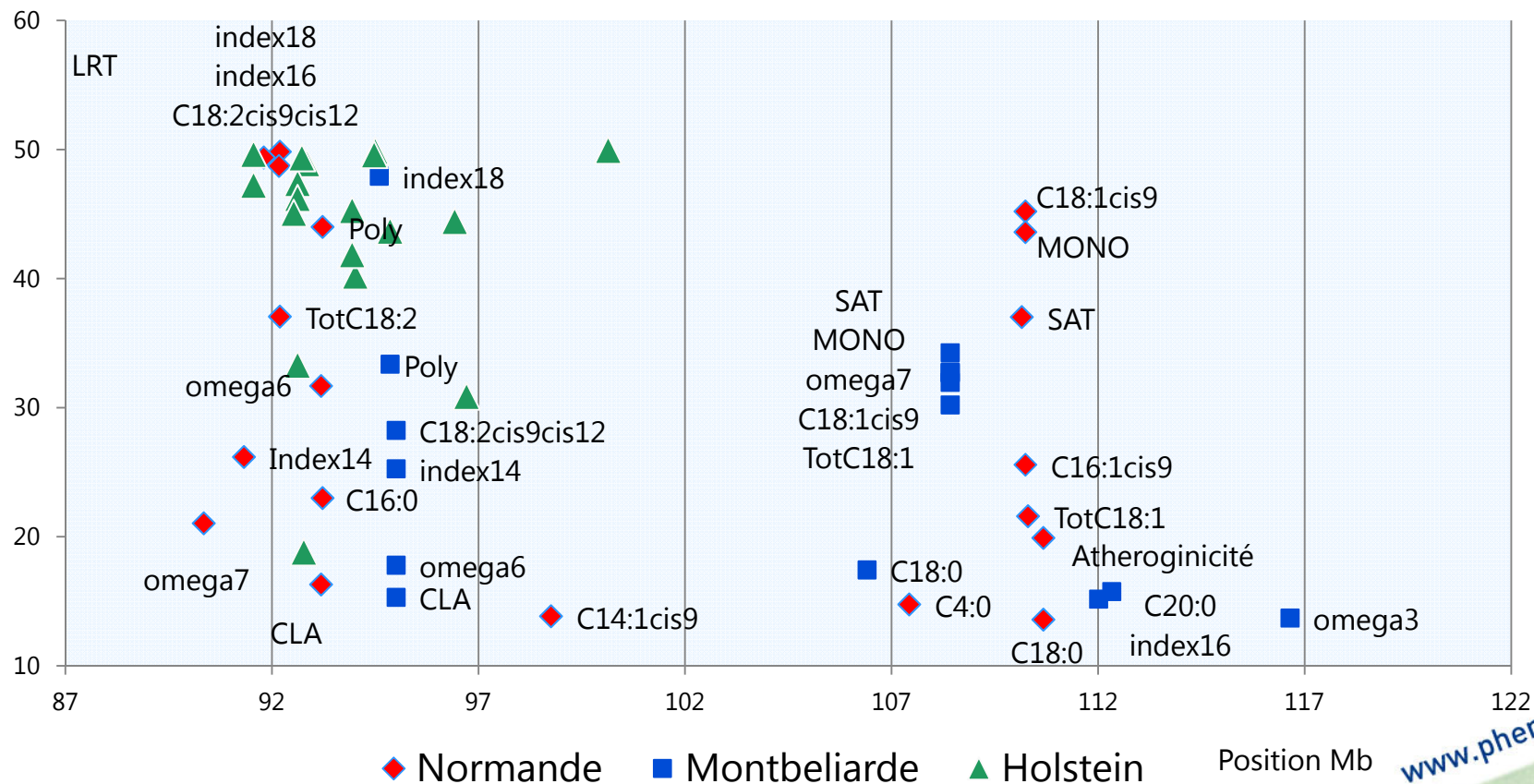
QTL for 23 traits detected - Probably 2 regions



— BTA 5: MO, NO and HO

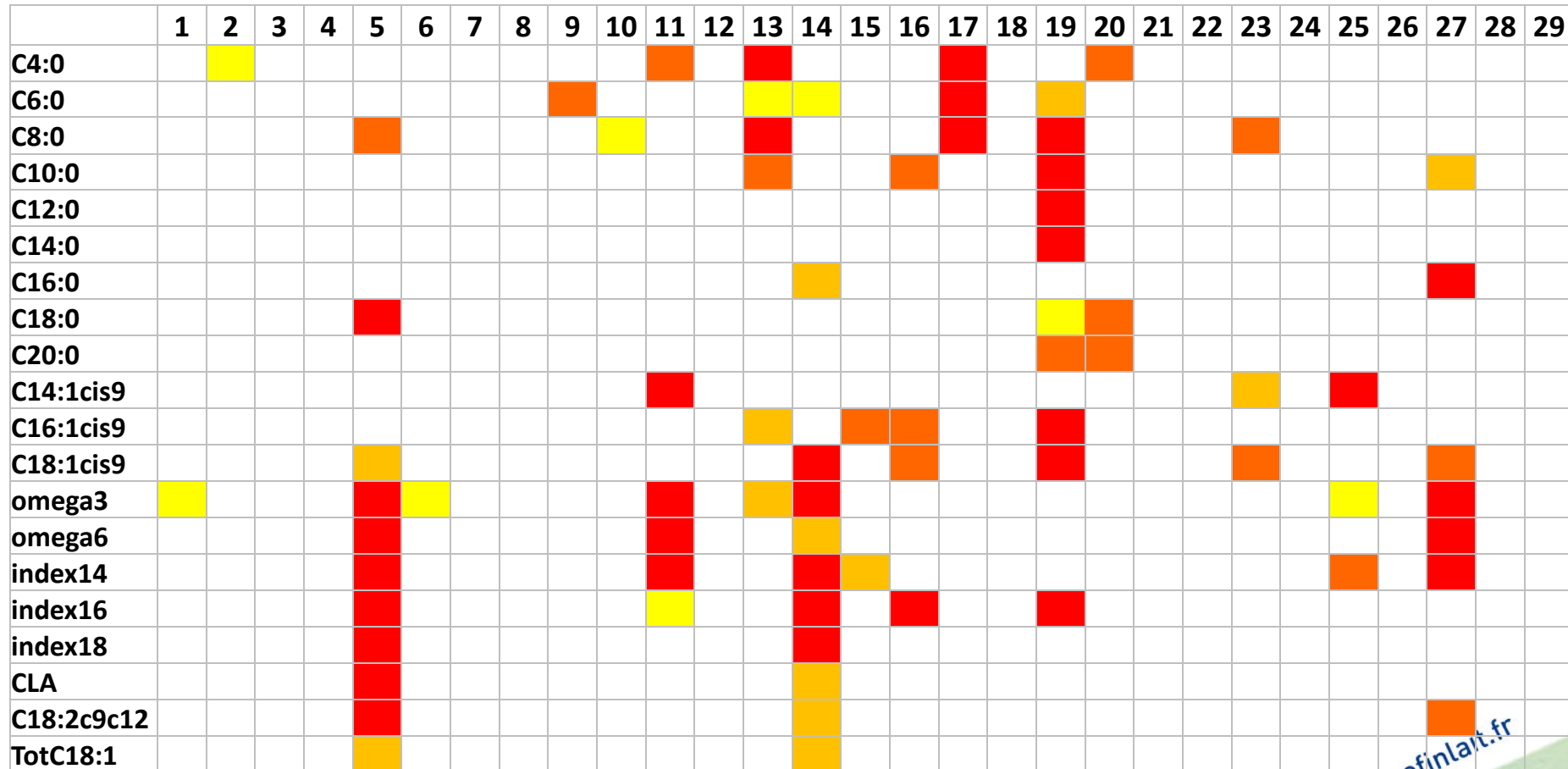
The first region is shared across the three breeds

8 Mb



Summary of QTLs shared accross breeds

QTLs are assumed to be shared if the distance between peaks < 2 Mb



HO-MO-NO

HO-NO

HO-MO

MO-NO

Conclusion and perspectives

- With restrictive LRT threshold of 13, around 20-30 significant QTL detected in average per traits.
- Regions known: BTA14, BTA26, BTA19.
- New regions shared for some traits: BTA 5, 11, 13, 16, 20.
- Regions shared between different FA, and/or between breeds.
- **Next step:** improve localisation with multi-QTL analysis

Acknowledgments:

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Thank you for your attention



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