

EVOLUTION OF ROH'S DISTRIBUTION ALONG THE GENOME OVER A DECADE OF GENOMIC SELECTION IN DAIRY CATTLE



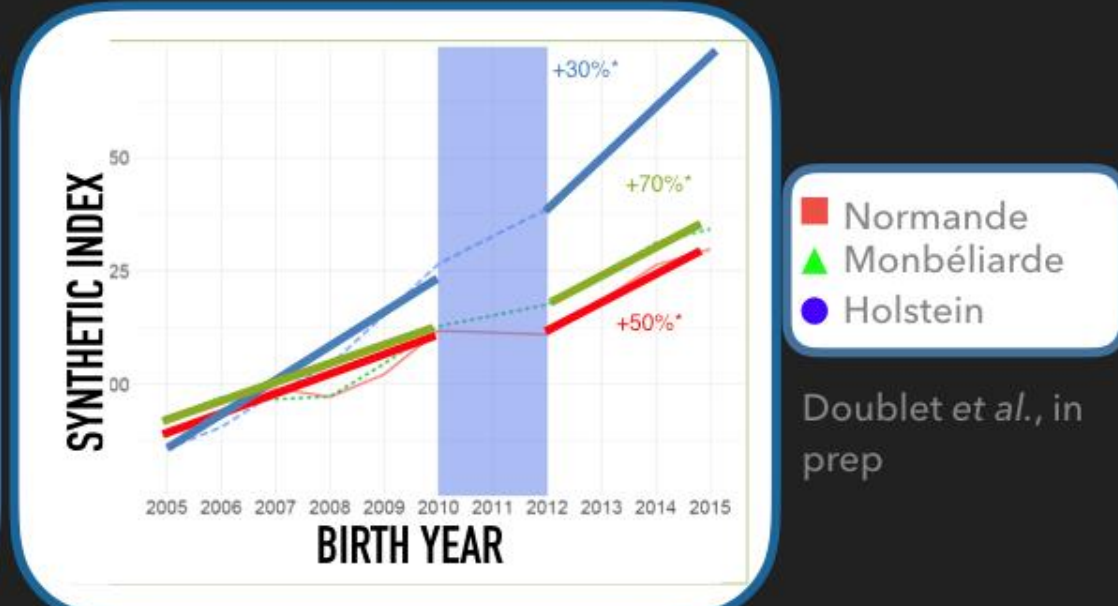
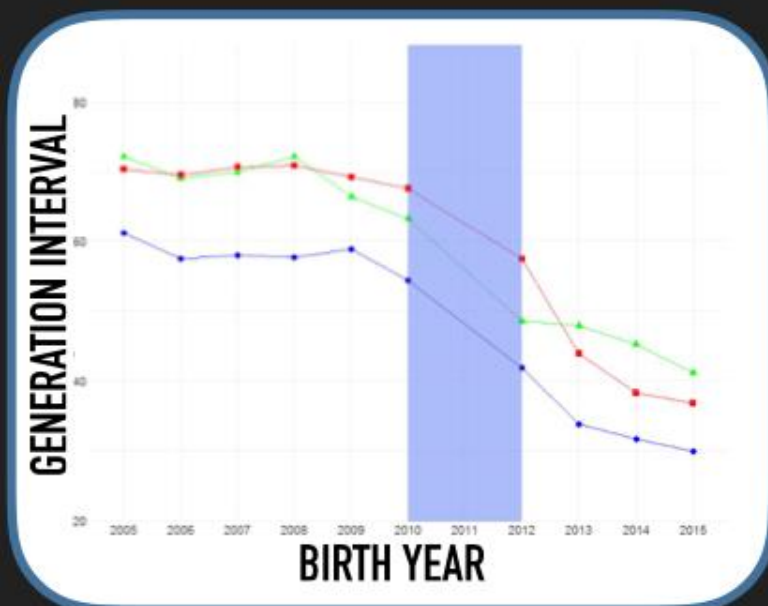
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CHANGES ON EVALUATION METHOD: GENETIC DIVERSITY CONSEQUENCE ?

- ▶ Genomic Selection implemented in 2010 in France for main breeds.
 - ▶ Reduction of the generation interval
 - ▶ Faster decrease of genetic diversity (per year) ?
 - ▶ Reduction of cost for evaluation : More candidates ?
 - ▶ Less intensive use of elite bulls ? Conservation of GD ?



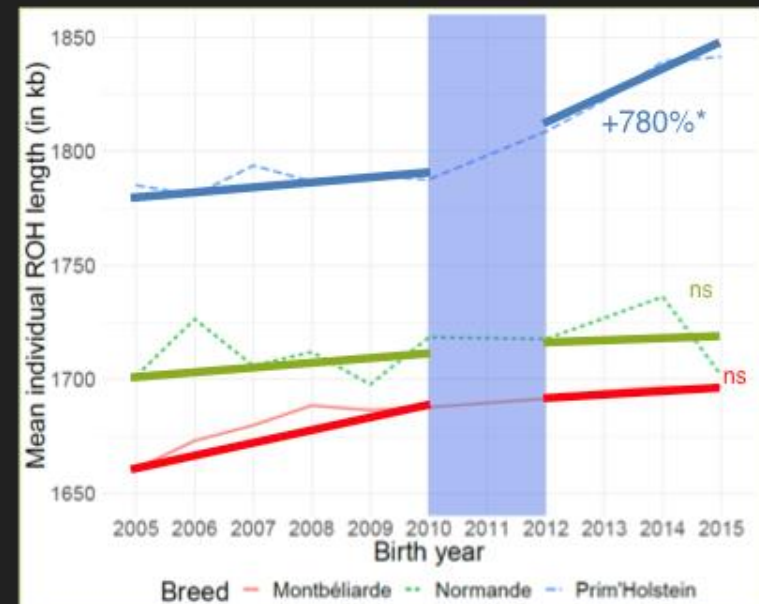
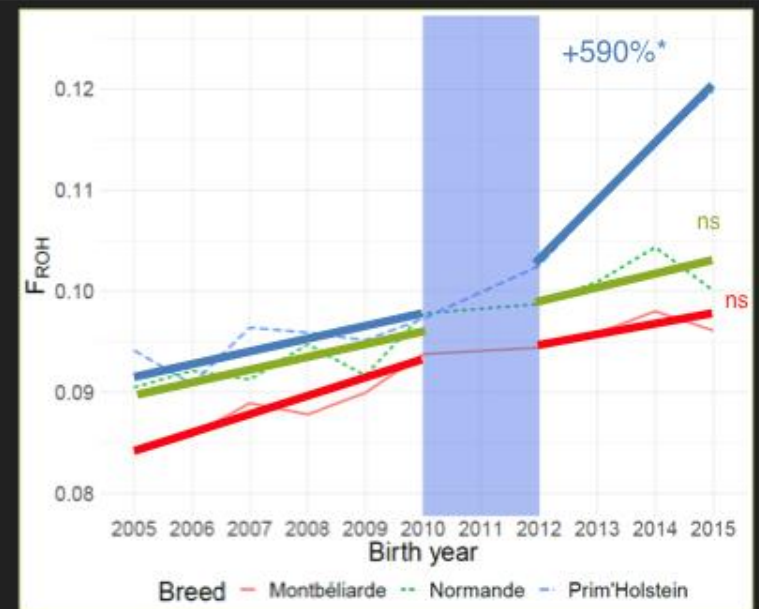
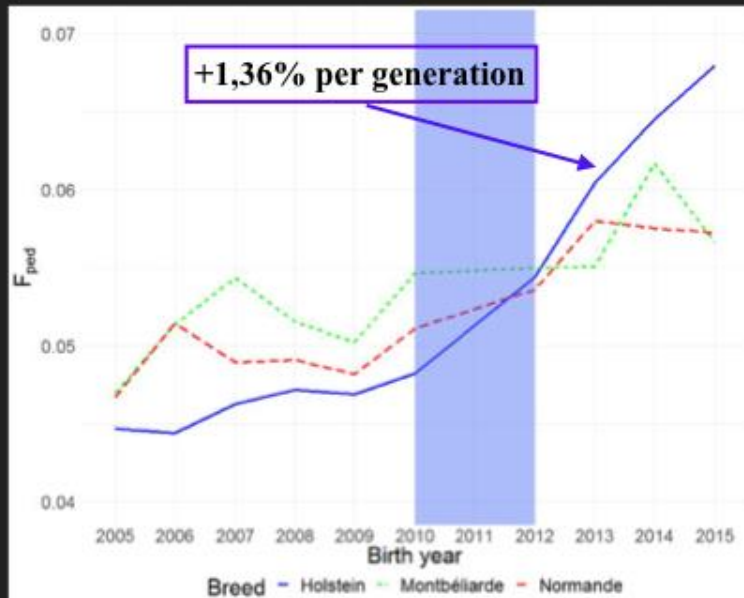
Doublet *et al.*, in prep

GENOMIC SELECTION & DIVERSITY

FIRST OBSERVATIONS AT THE INDIVIDUAL LEVEL

(DOUBLET ET AL., IN PREP)

- ▶ Large increase in mean inbreeding mainly in Holstein
- ▶ Revealed by both pedigrees and molecular data (ROH)
- ▶ Due to recent inbreeding



WHAT ABOUT GENOME LEVEL ?

- ▶ What can we learn from ROH ?
 - ▶ Are inbred regions of the genomes the same for all individuals ?
 - ▶ Is the genome homogeneous in terms of inbreeding ?
 - ▶ What can we learn about population history ?



BIOLOGICAL MATERIAL

- ▶ 3 Breeds
- ▶ 50k SNP array
- ▶ All males that have been used
- ▶ 2005-2015 period
- ▶ ROH computed using Plink 1.9 (Chang et al, 2015)

Montbéliard

1472 individuals
(\approx 132 per year)



Normande

1117 individuals
(\approx 101 per year)



Holstein

5430 individuals
(\approx 493 per year)



SUMMARY STATISTICS

- ▶ Sharing of ROH within the population (PPROH)
- ▶ Mean length of the ROH (in kb)

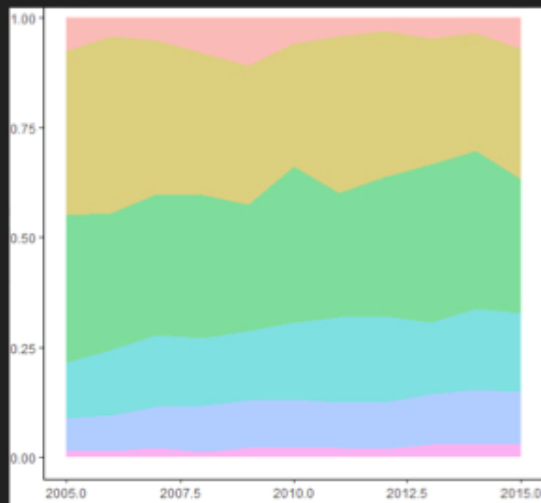
	SNP1	SNP2	SNP3	SNP4	SNP5
<i>Individual 1</i>	ROH1			ROH2	
<i>Individual 2</i>			ROH3		
<i>Individual 3</i>			ROH4		
<i>Individual 4</i>		ROH5			
<i>PPROH_{snp}</i>	25%	50%	75%	100%	0%

- ▶ One measure of ROH frequency and mean length for each SNP

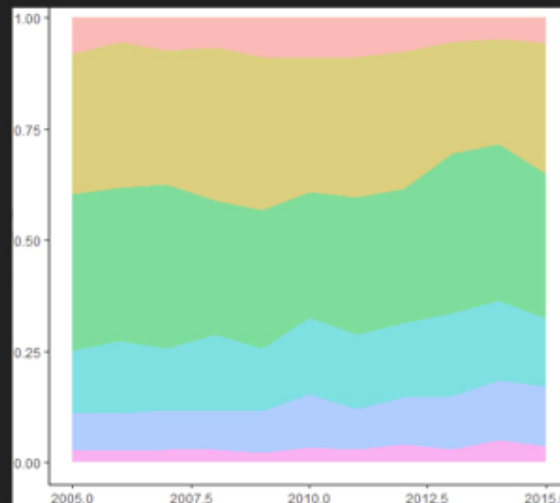
TIME DYNAMICS OF ROH WITHIN POPULATION

- ▶ Holstein: Increase of largely shared ROH
 - ▶ **Increase of global relatedness among individuals**
- ▶ Almost stable in other breeds
 - ▶ **Comparable with pedigree results: Good alternative**

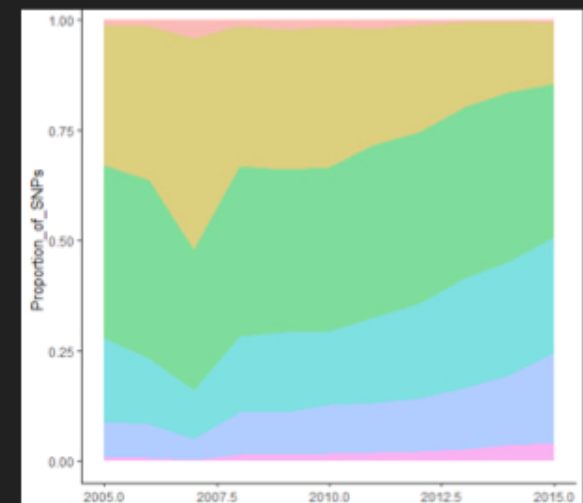
Cluster	PPROH _{SNP} (%)
1	0 to 5
2	5 to 10
3	10 to 15
4	15 to 20
5	20 to 30
6	≥30



Montbéliarde



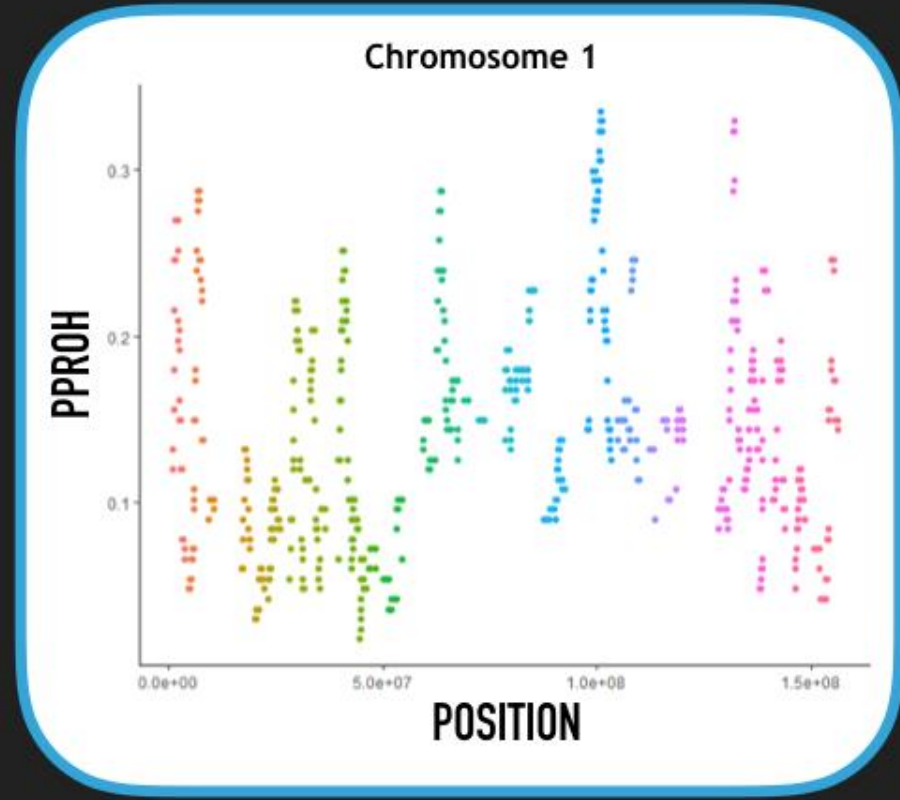
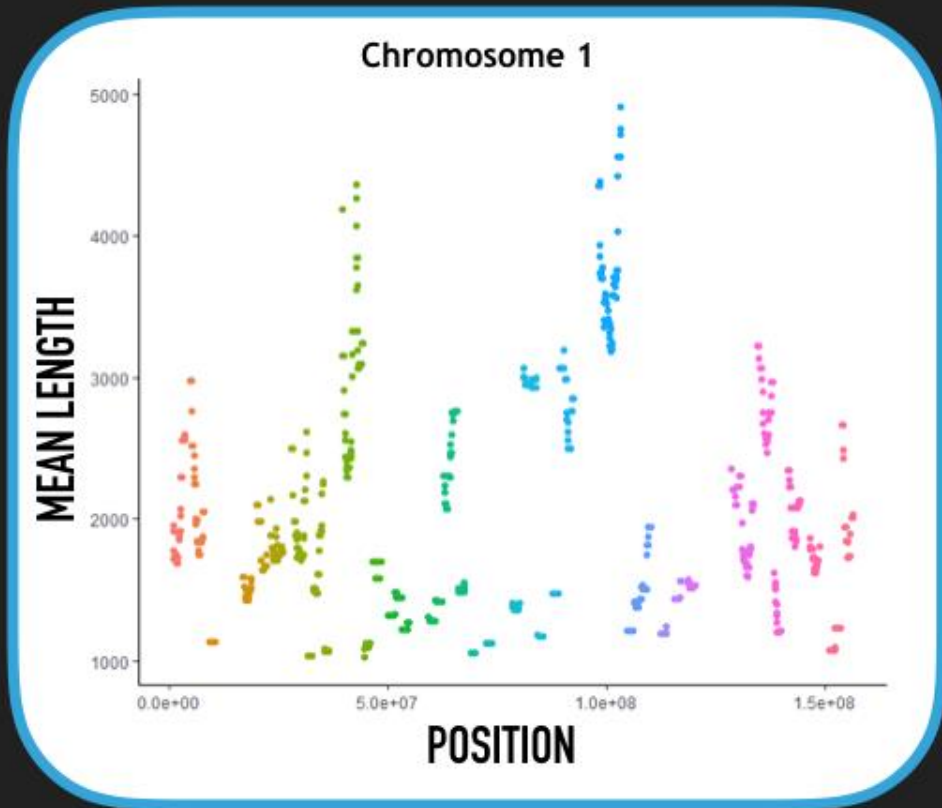
Normande



Holstein

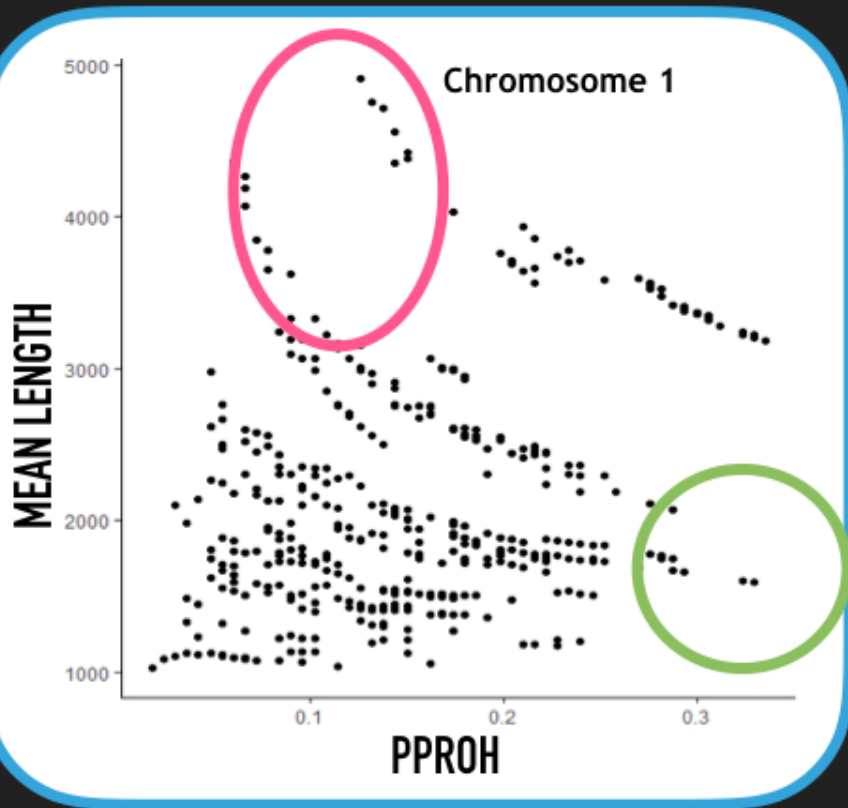
RESULTS: ROH ALONG THE GENOME

HOMOGENEITY ALONG THE GENOME ?



- ▶ Heterogeneity in terms of size along the genome
- ▶ Sharing of ROH also differs along the genome

LINKS BETWEEN SIZE AND FREQUENCY IN THE POPULATION



Long ROH:

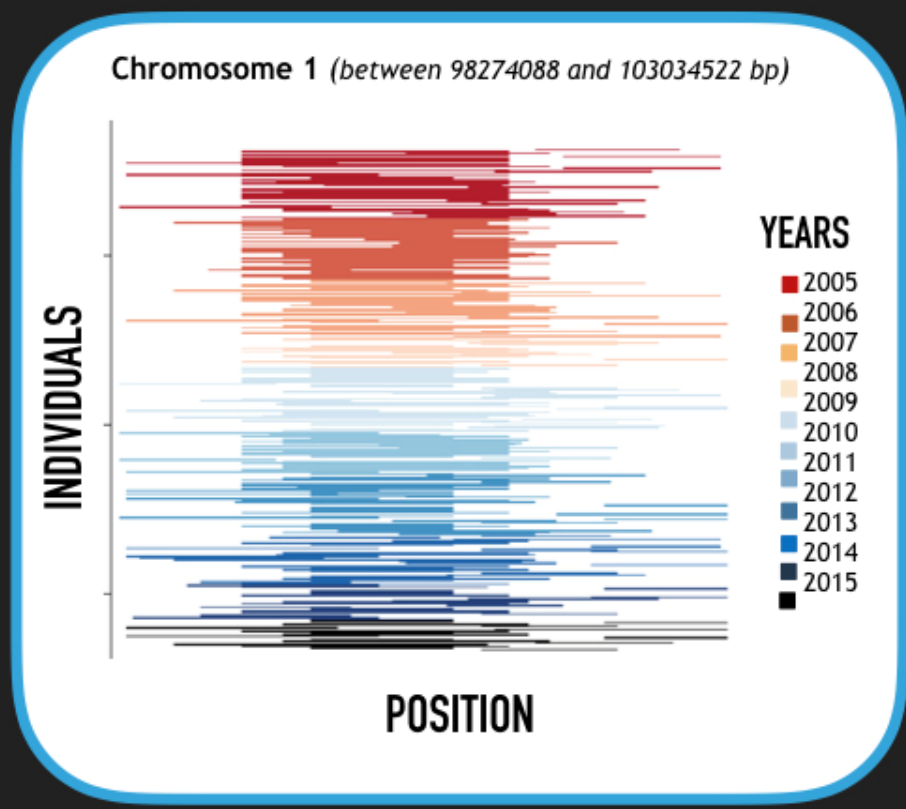
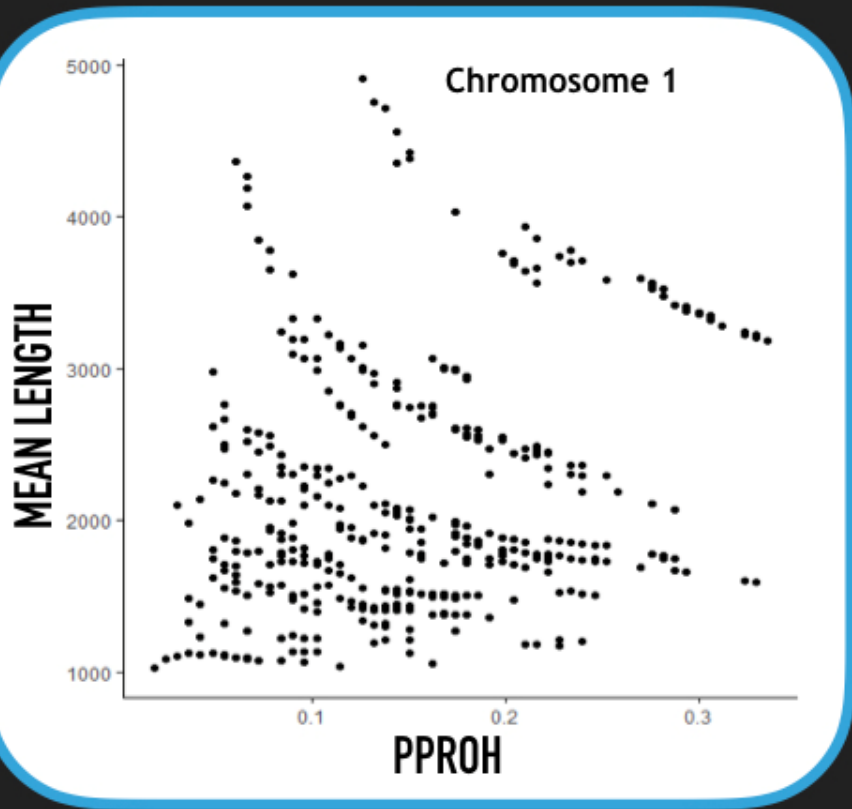
- ▶ Recent IDB segment
- ▶ Less frequent in the population

Short ROH:

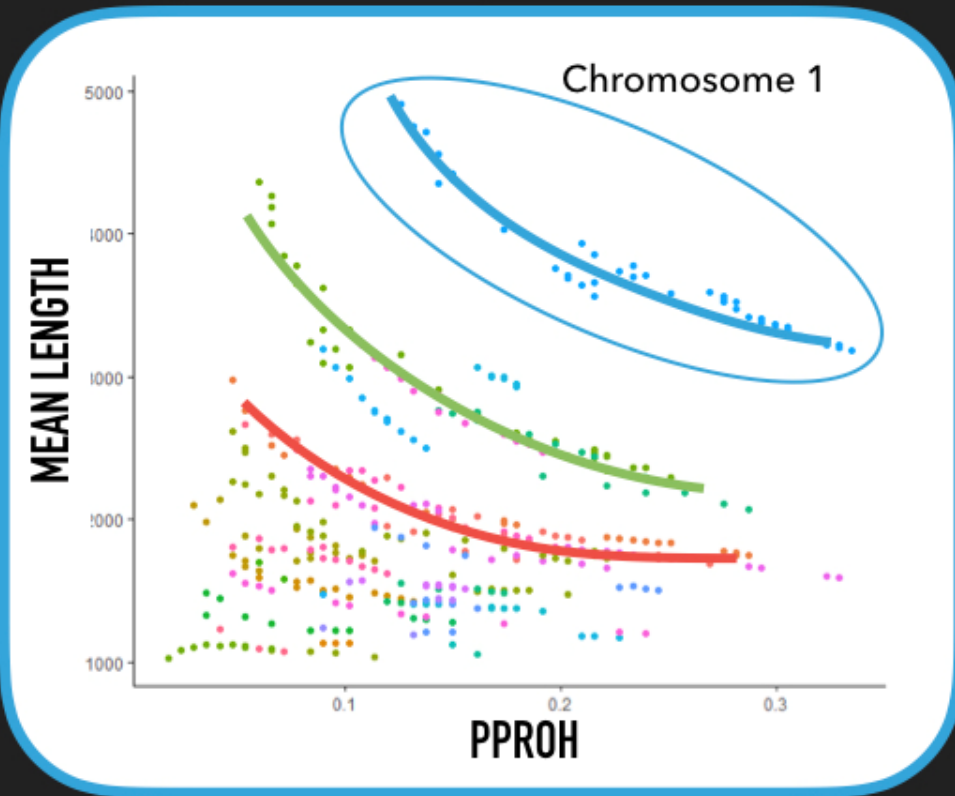
- ▶ Old IDB segment
- ▶ More frequent in the population

- ▶ **Global negative relationship among length & frequency of ROH**

LINKS BETWEEN SIZE AND FREQUENCY IN THE POPULATION



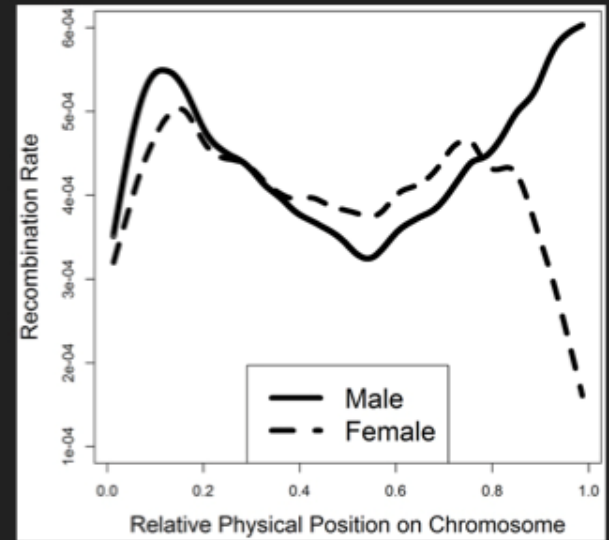
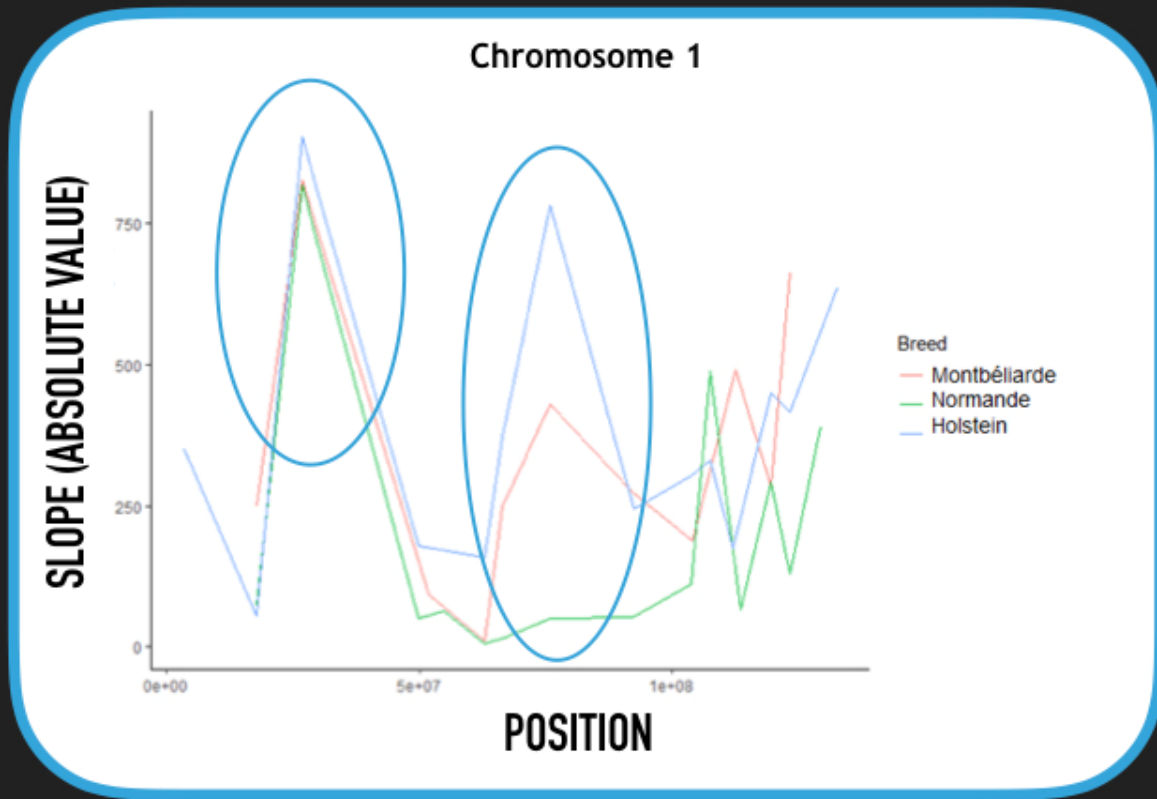
LINKS BETWEEN SIZE AND FREQUENCY IN THE POPULATION



- ▶ Exponential relationship
- ▶ Year + Group effects
- ▶ $R^2 \simeq 0.65$
- ▶ Slope variable according genomic regions
- ▶ No relationship under a certain length (1700kb)

▶ **Variable recombination rates ?**

RECOMBINATION RATES

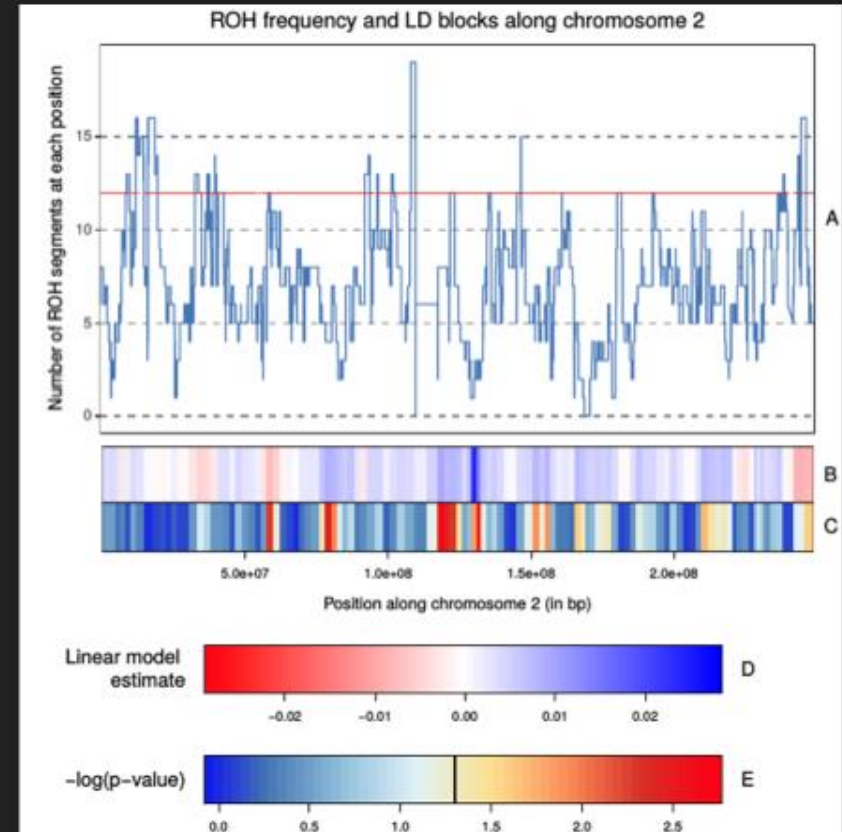


Ma et al., 2015

- ▶ Males recombination rates estimated with ROH fit previous estimates
- ▶ Heterogeneity among breeds

TAKE HOME MESSAGE

- ▶ Holstein breed
 - ▶ Increase of the number and length of ROH
 - ▶ Increase of kinship revealed by ROH sharing
- ▶ Variable observed inbreeding along genome

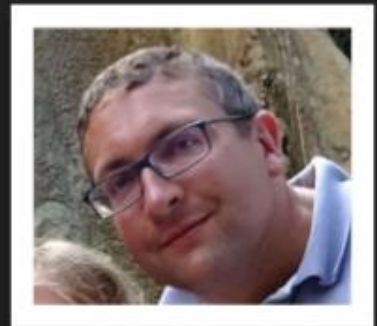


Consider ROH for computing genetic relatedness Doublet *et al.*, in prep

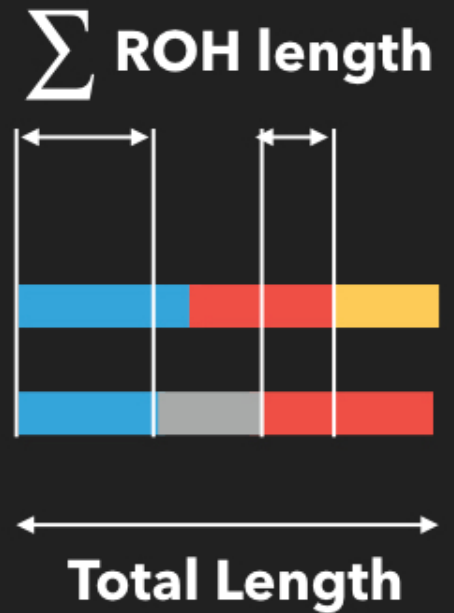
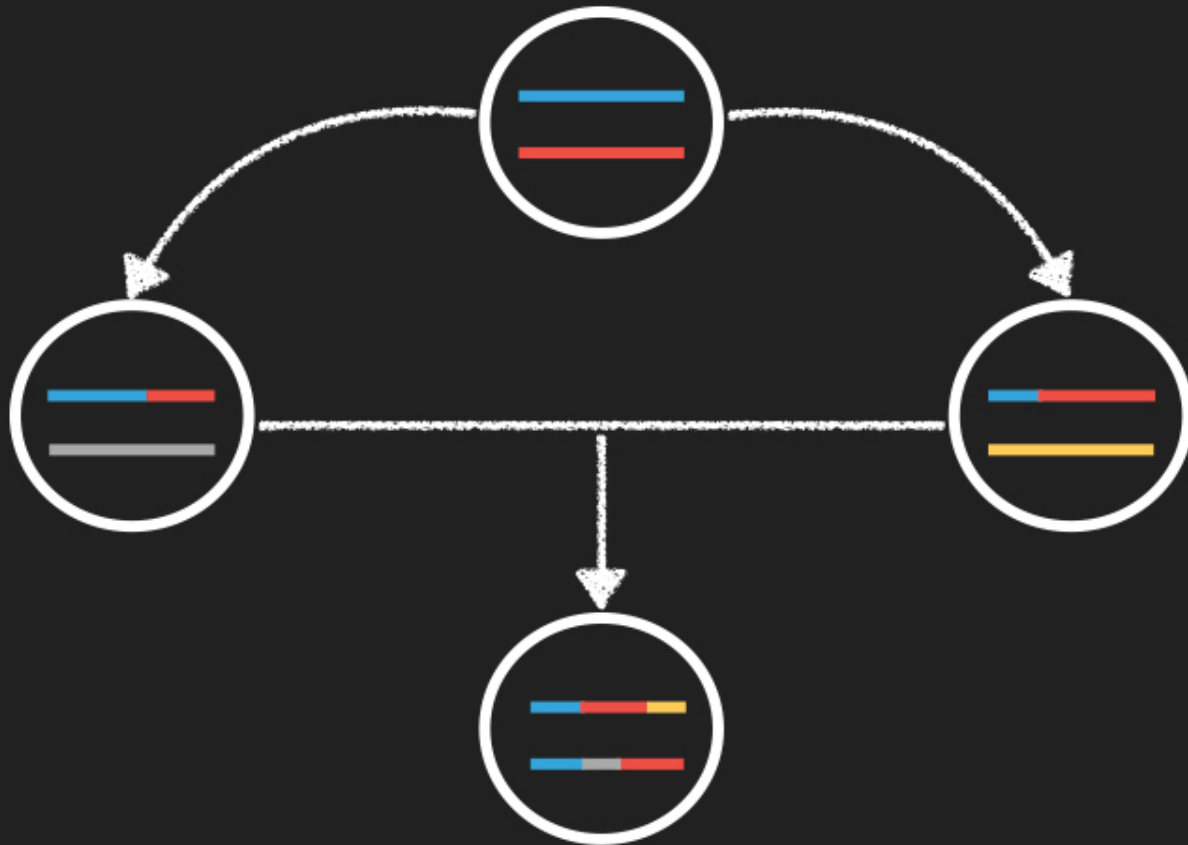
Consider genome position for ROH estimation

Link between ROH length and inbreeding not so simple

THANK YOU



ROH: RATIONALE



$$F = \frac{\sum ROHlength}{Totallength}$$

ROH length = $f(\text{Age Common Ancestor})$

EVOLUTION OF ROH OVER TIME

