

Genome-wide inbreeding and coancestry patterns in dairy cattle



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Introduction

Genome-wide estimates of F & f more accurate:

Actual percentage

Detect distant relationships

Can be calculated for particular regions of the genome

Introduction

Selection:

Low genetic diversity (high F & f)

Fitness:

High genetic diversity (low F & f)

Different **degrees of diversity** on genomic regions could be detected

Objective

To evaluate the variation of inbreeding and coancestry based on SNP markers information at the **chromosomal level** and at **specific chromosome regions** in the Spanish Holstein population

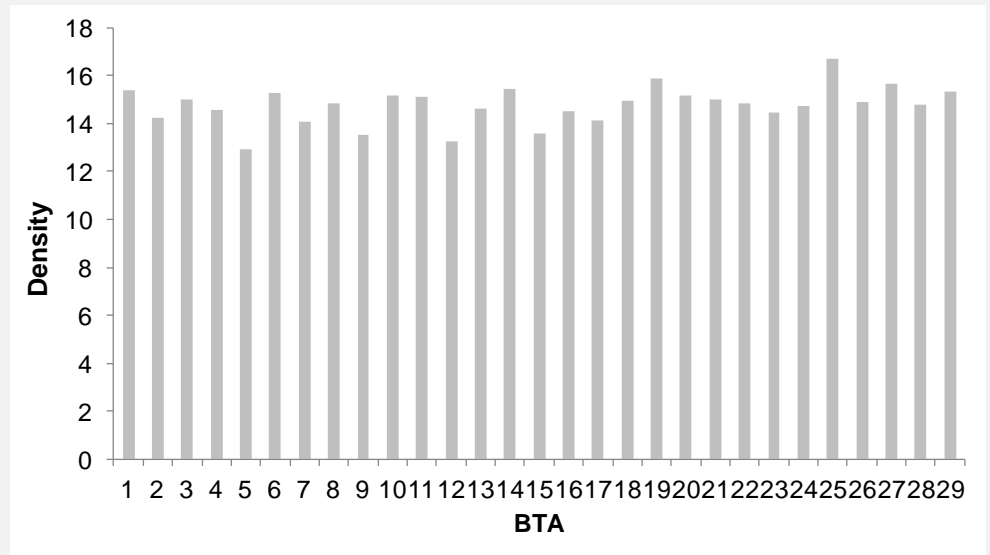
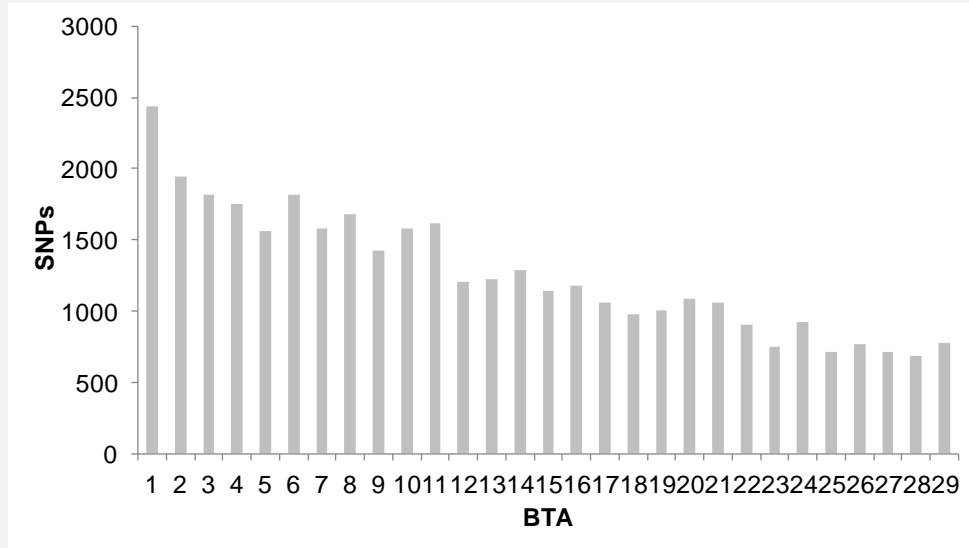
Materials & Methods

Genomic data:

- **36,693 autosomal SNPs**
(Illumina Bovine SNP 50 BeadChip)
- **10,569 genotyped individuals**



Materials & Methods



Materials & Methods

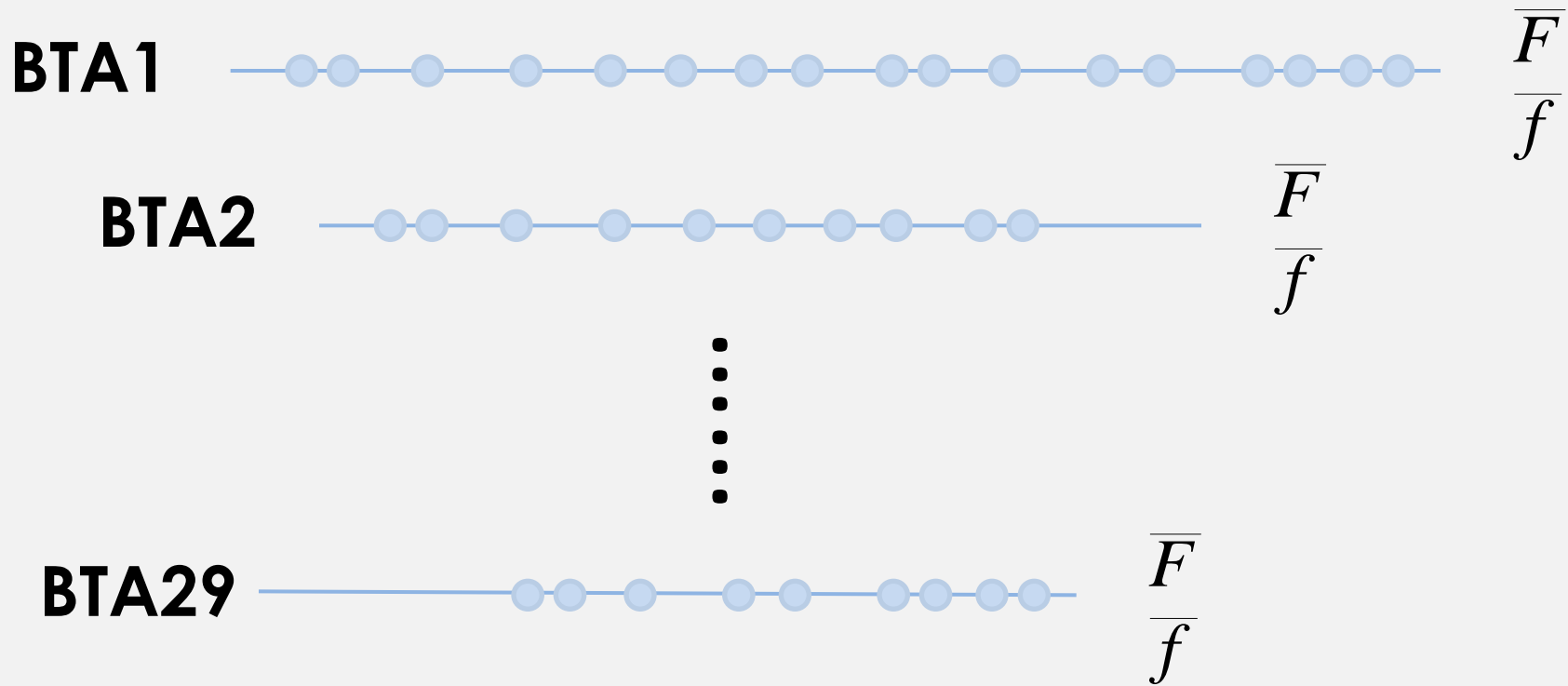
***f* and *F* estimates:**

$$f_{ij} = (1/n_s) \sum_{s=1}^{n_s} \left[\left(\sum_{k=1}^2 \sum_{m=1}^2 I_{s_{k_i m_j}} \right) / 4 \right]$$

$$F_i = 2f_{ii} - 1$$

Materials & Methods

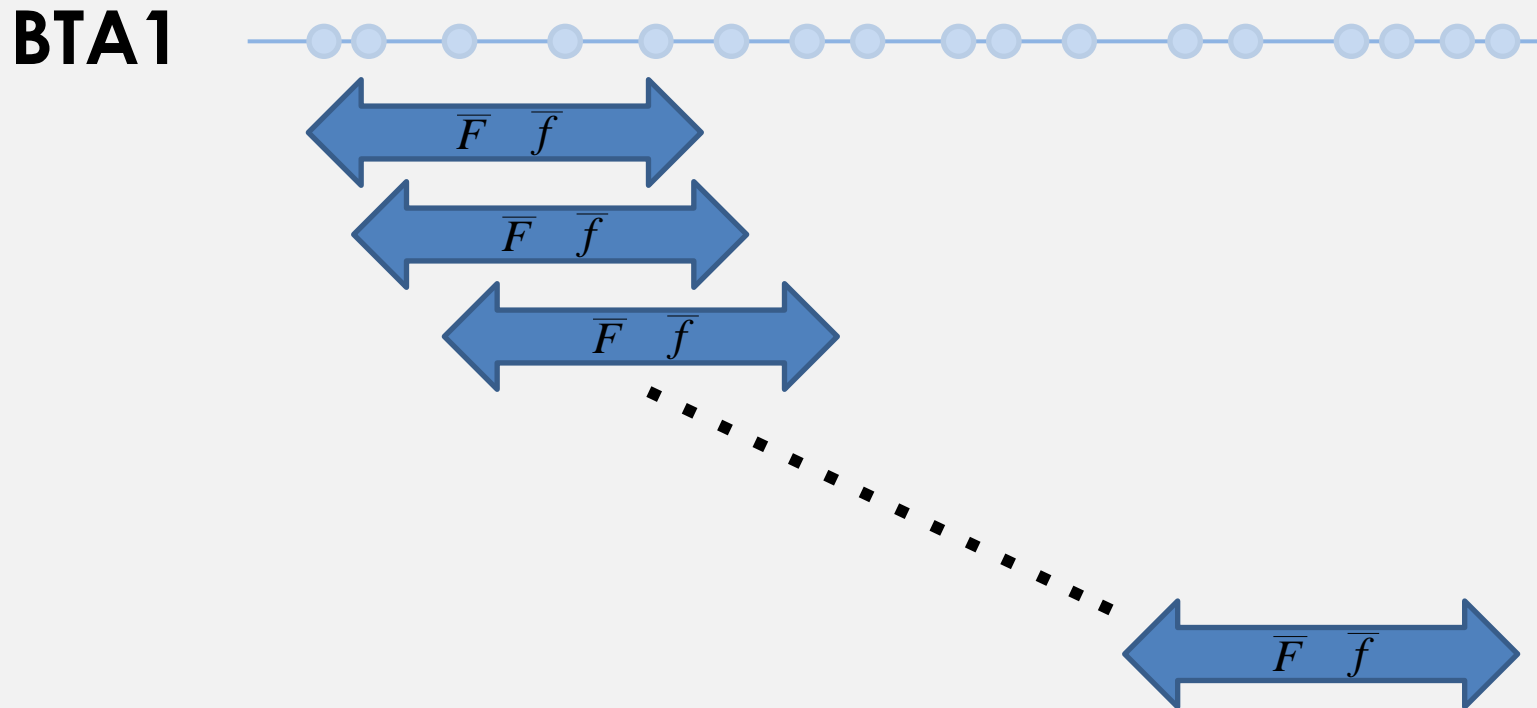
1. Chromosomal estimates (all SNPs for each BTA)



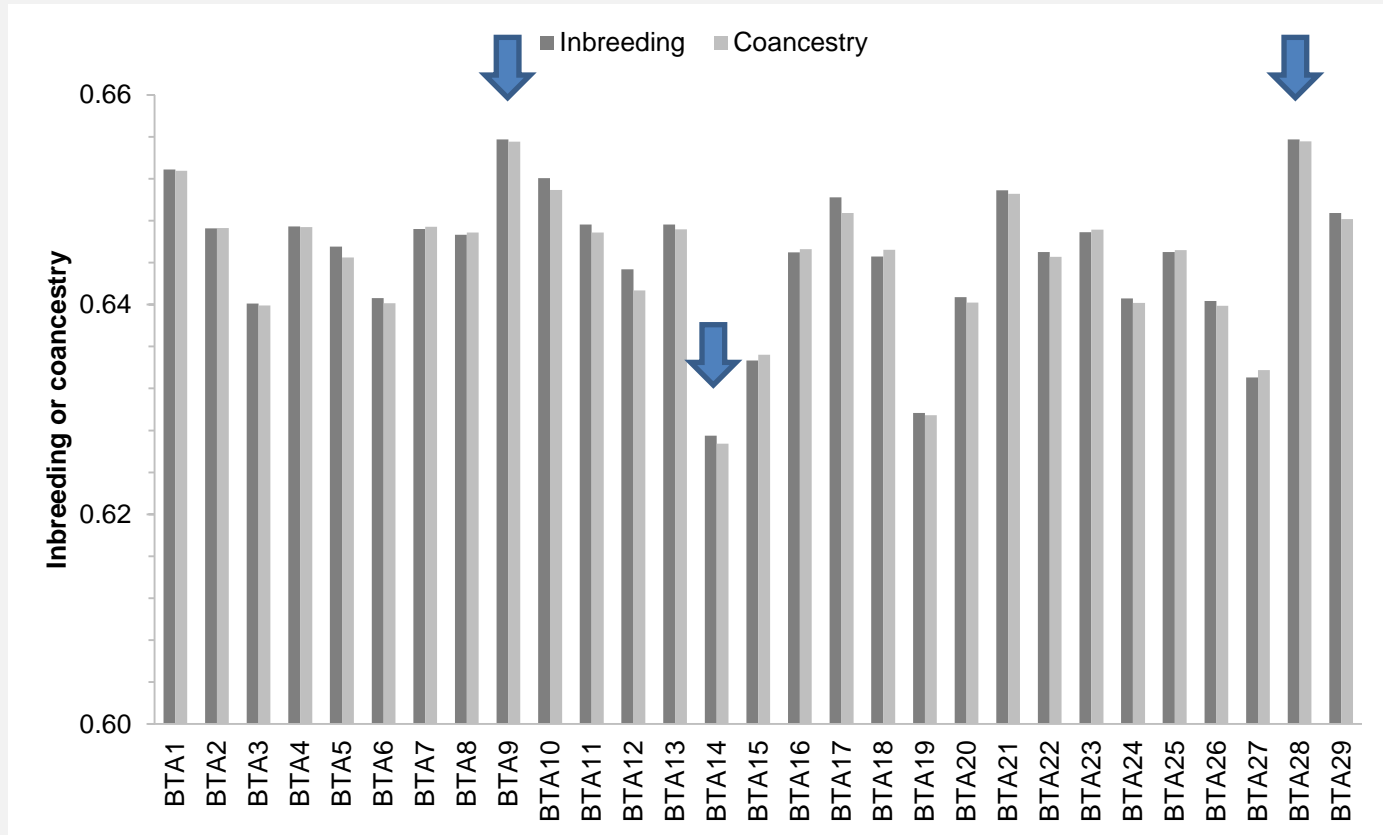
Materials & Methods

2. Intra-chromosomal estimates:

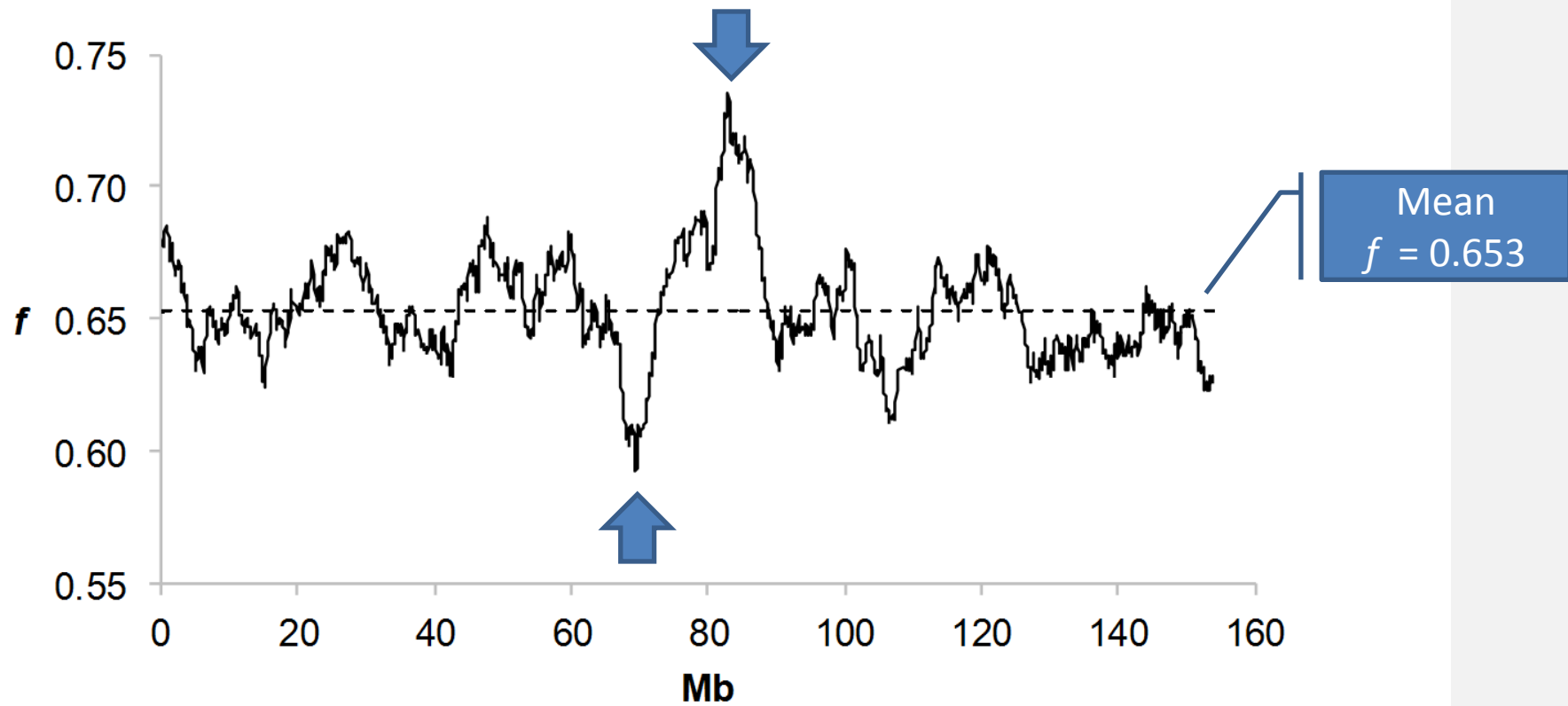
Approximately 5 Mb – Window: 1 SNP to the right



Results



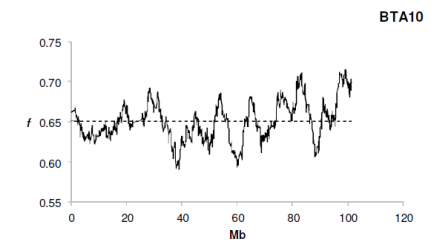
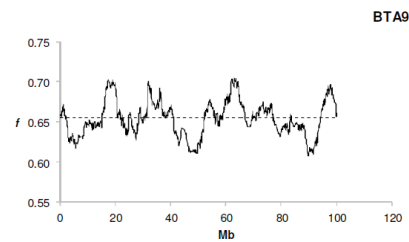
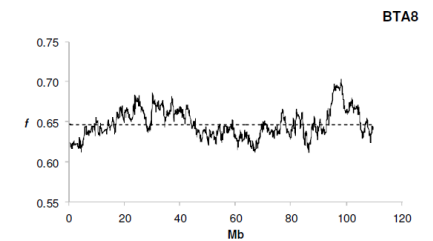
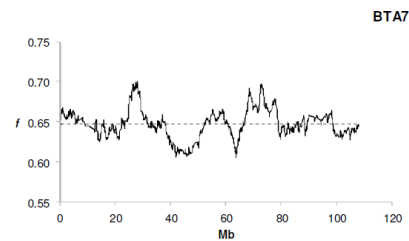
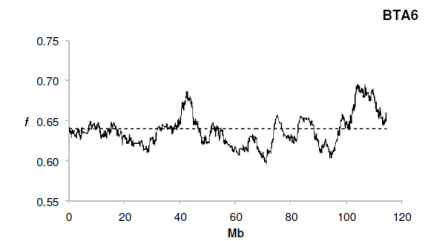
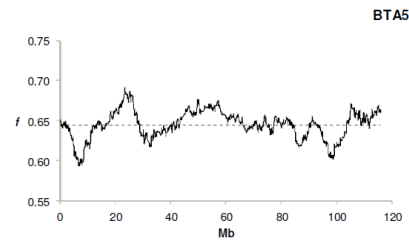
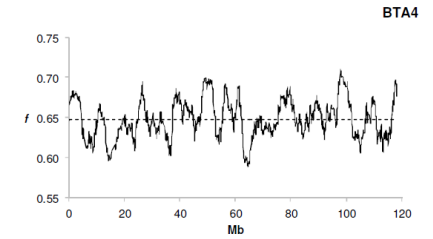
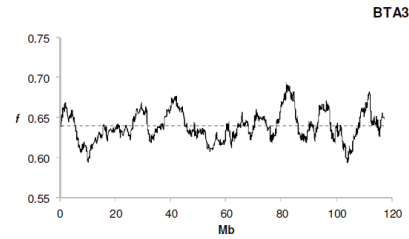
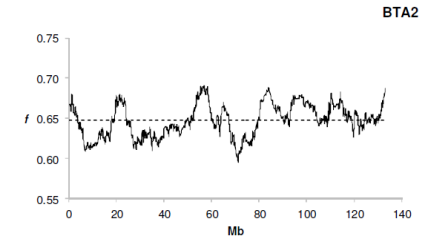
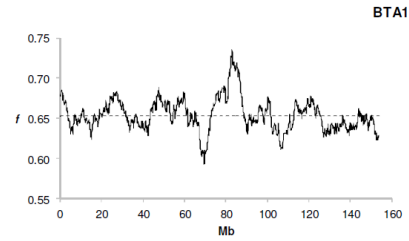
Results



Patterns of coancestry in BTA1

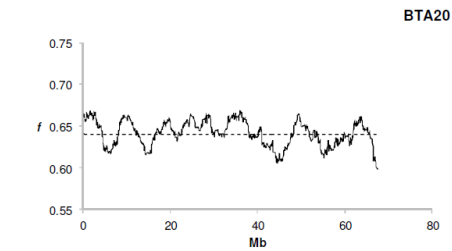
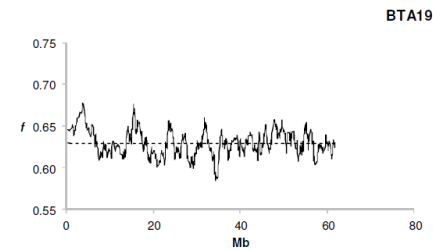
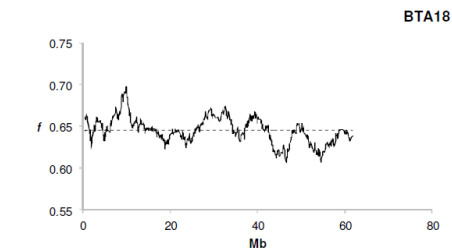
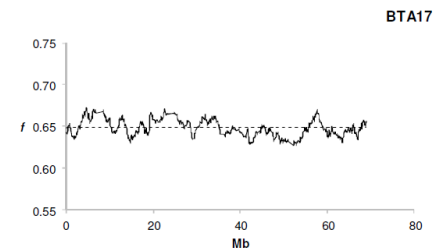
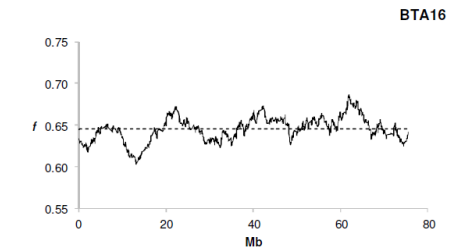
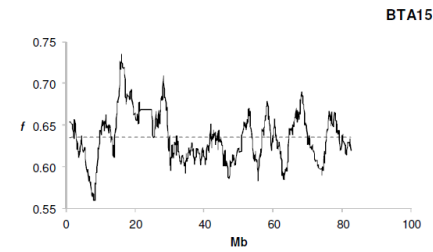
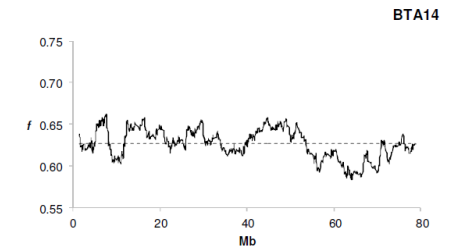
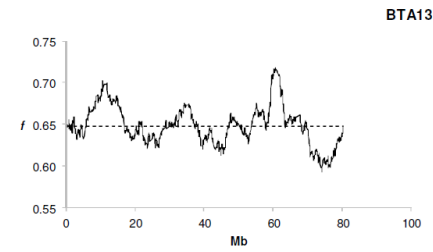
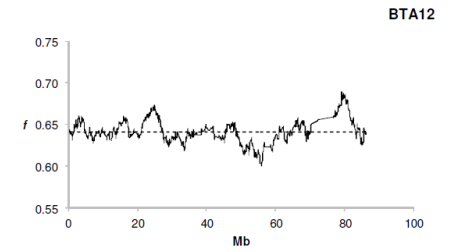
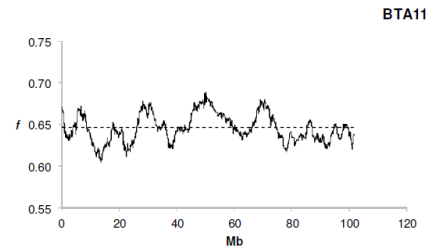
Results

BTA1 – BTA10



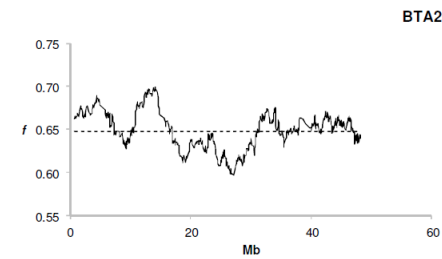
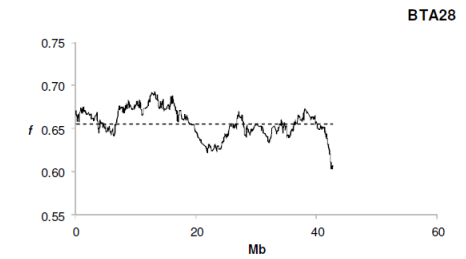
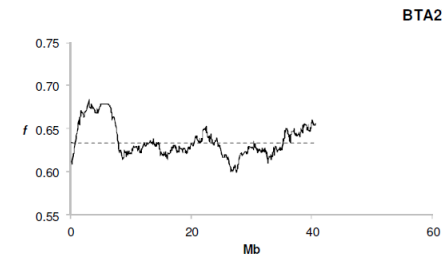
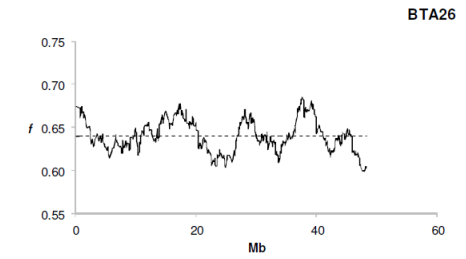
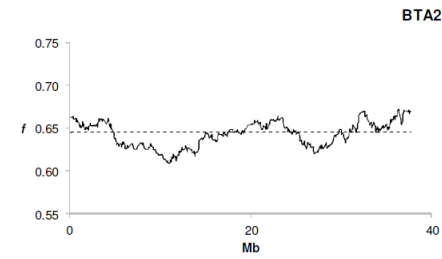
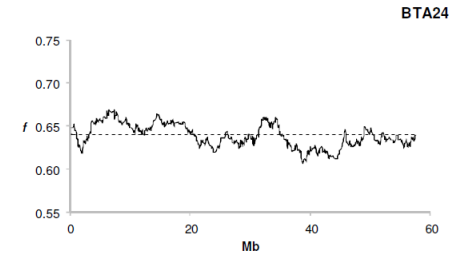
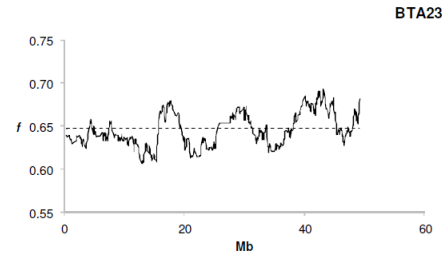
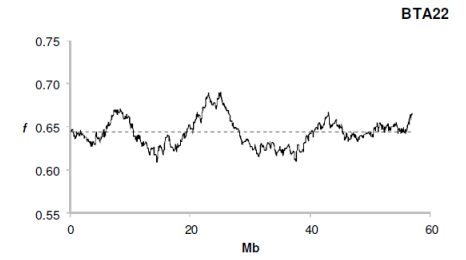
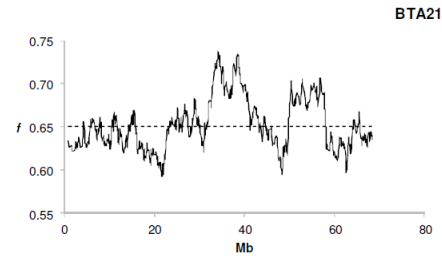
Results

BTA11 – BTA20



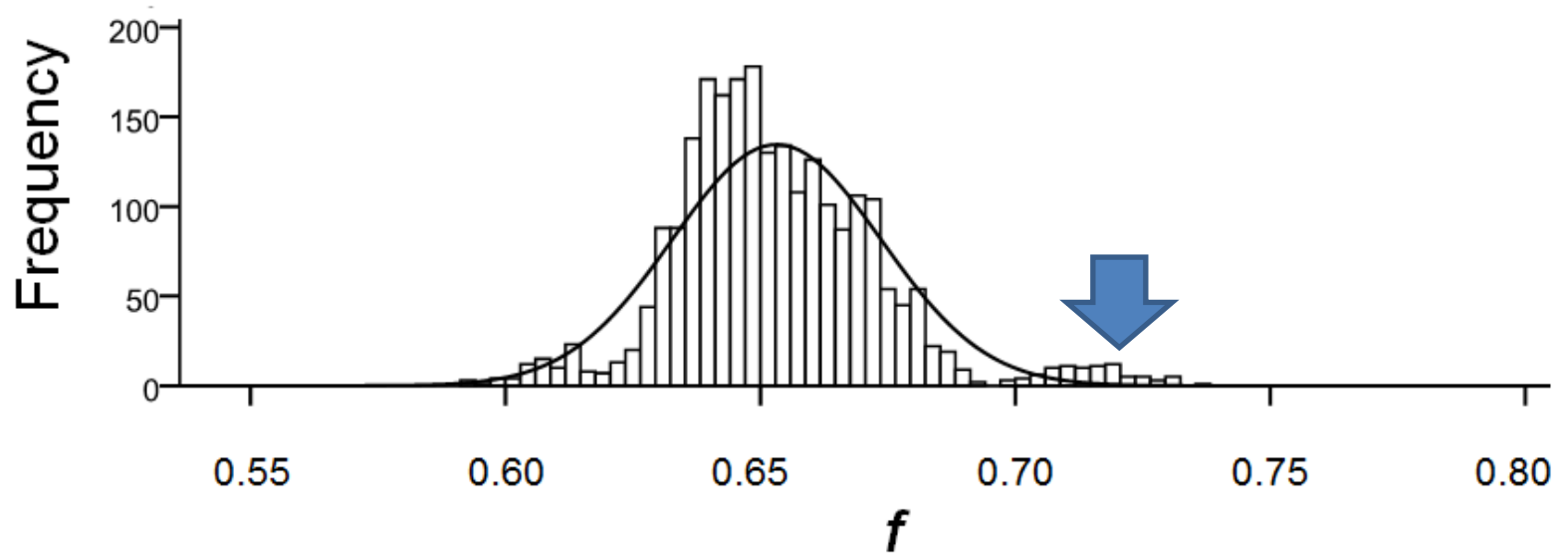
Results

BTA21 – BTA29



Results

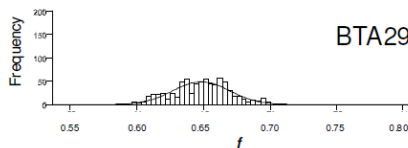
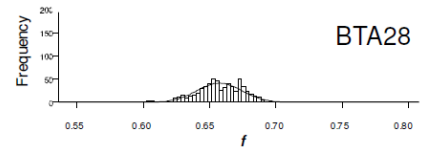
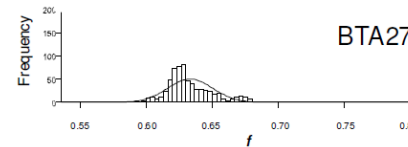
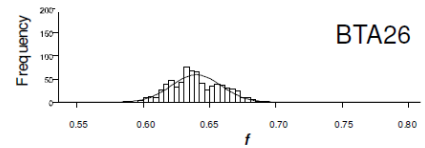
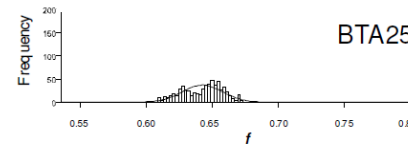
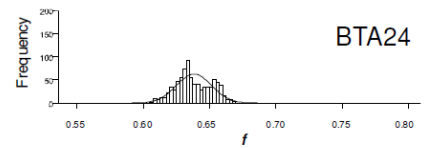
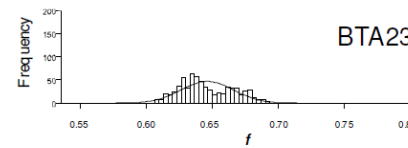
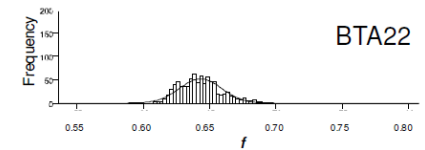
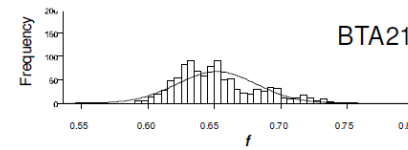
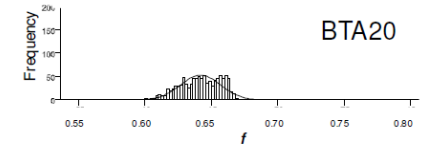
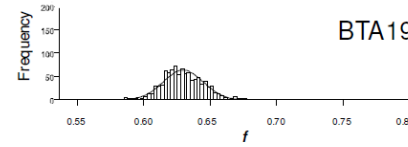
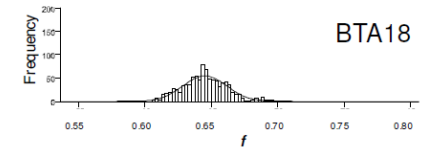
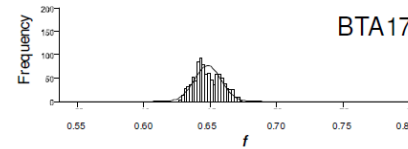
Frequency distribution of f patterns in BTA1



Results

BTA17 – BTA29

**Kolmogorov-
Smirnov: all normal
distributions**

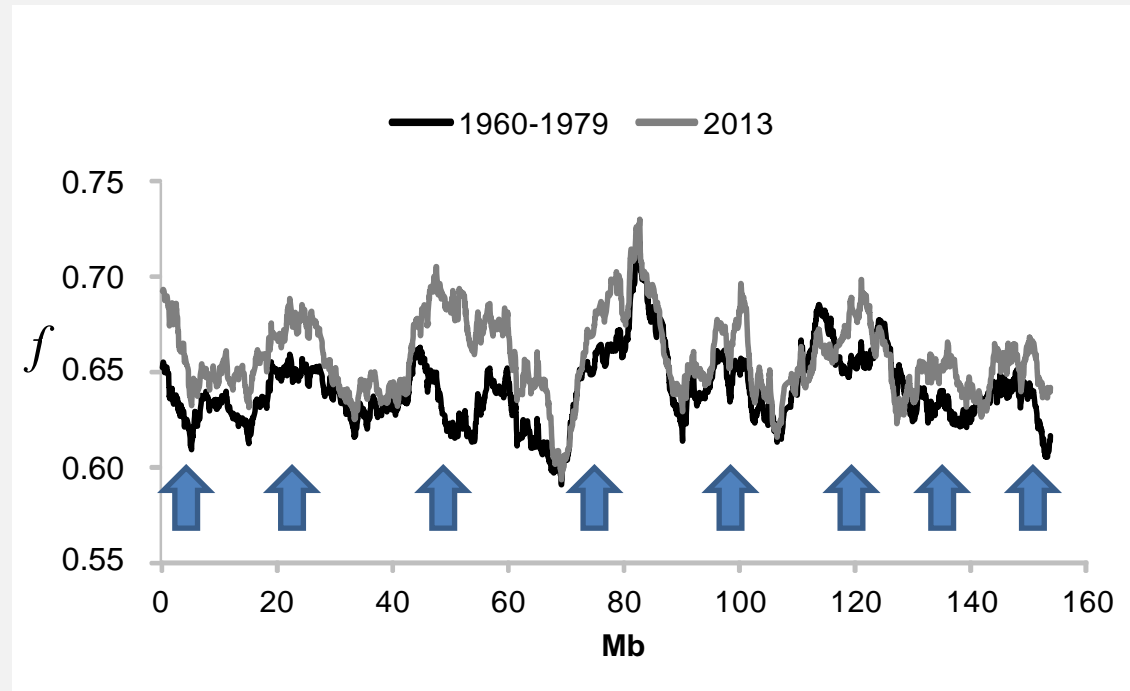


Take home message

- Differences in inbreeding and coancestry between **chromosome regions** provide a more **detailed picture of the genetic diversity**
- The **management of populations** could be improved with the inclusion of this **chromosomal and intra-chromosomal information** about inbreeding and coancestry
- The differences of coancestry patterns could highlight the **effect of artificial selection** in those genomic regions

Thanks for your attention

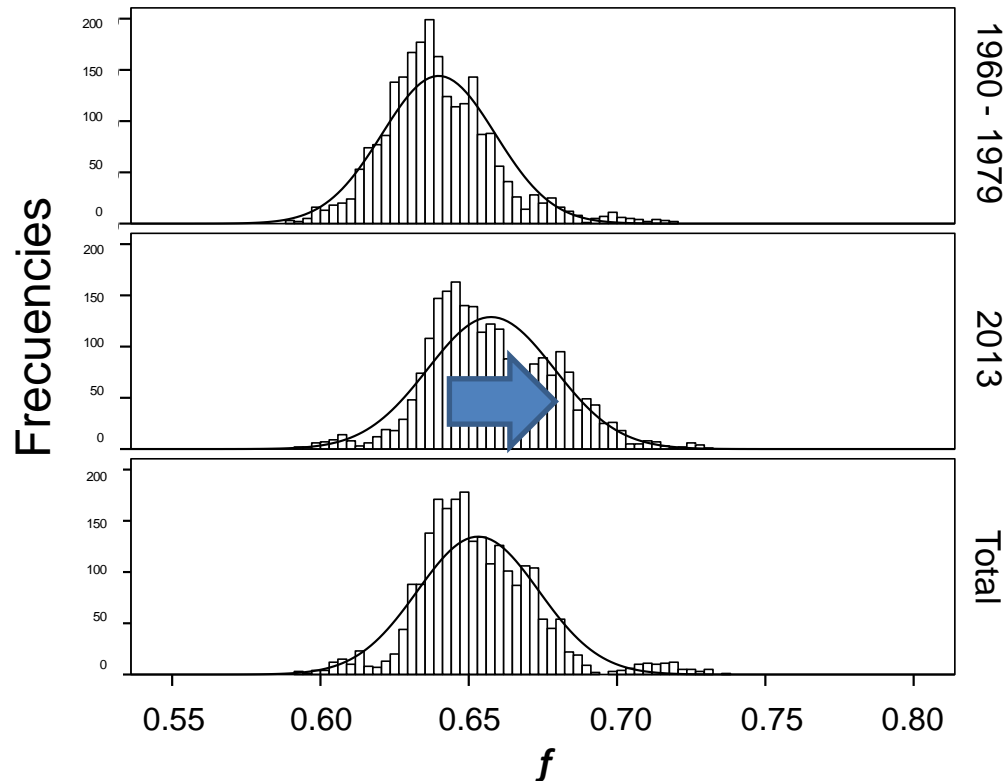
Results



Selection

Patterns of f on BTA1 in 100 animals born between 1960 – 1979 and 100 animals born in 2013

Results



Frequency distribution of f patterns on BTA1