



Use of Wright's fixation index (F_{st}) to detect potential selective sweeps in Nelore Cattle

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INTRODUCTION:



NELORE CATTLE



Hump cattle or Zebu cattle
Originally from India

Main breed in Brazil

Imported and established: \approx 1874 to 1962



INTRODUCTION: SELECTION PROGRAM OF HUMP CATTLE BREEDS



Selection experiment initiated in 1978:

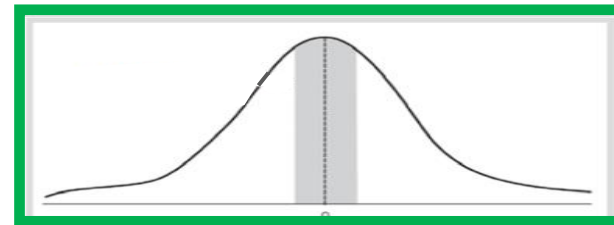
Background: To reduce the high slaughter ages (it was ~ 45 months).

Objective: To prove the benefits of selection in zebu beef cattle.

How: In 1980, the existing herd was split into **three** selection lines. Selected based on **yearling body weight** phenotypes.

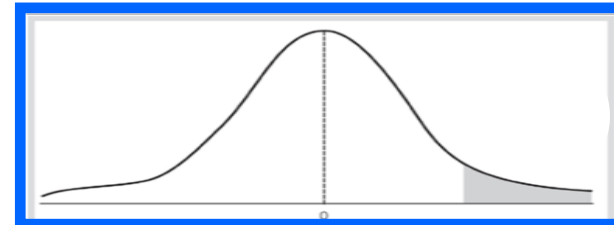
NeC
Nelore **C**ontrol
60 heifers

Closed line
Stabilizing selection



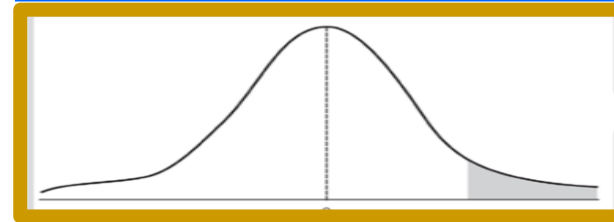
NeS
Nelore **S**election
120 heifers

Closed line
Positive selection



NeT
Nelore **T**raditional
170 cows

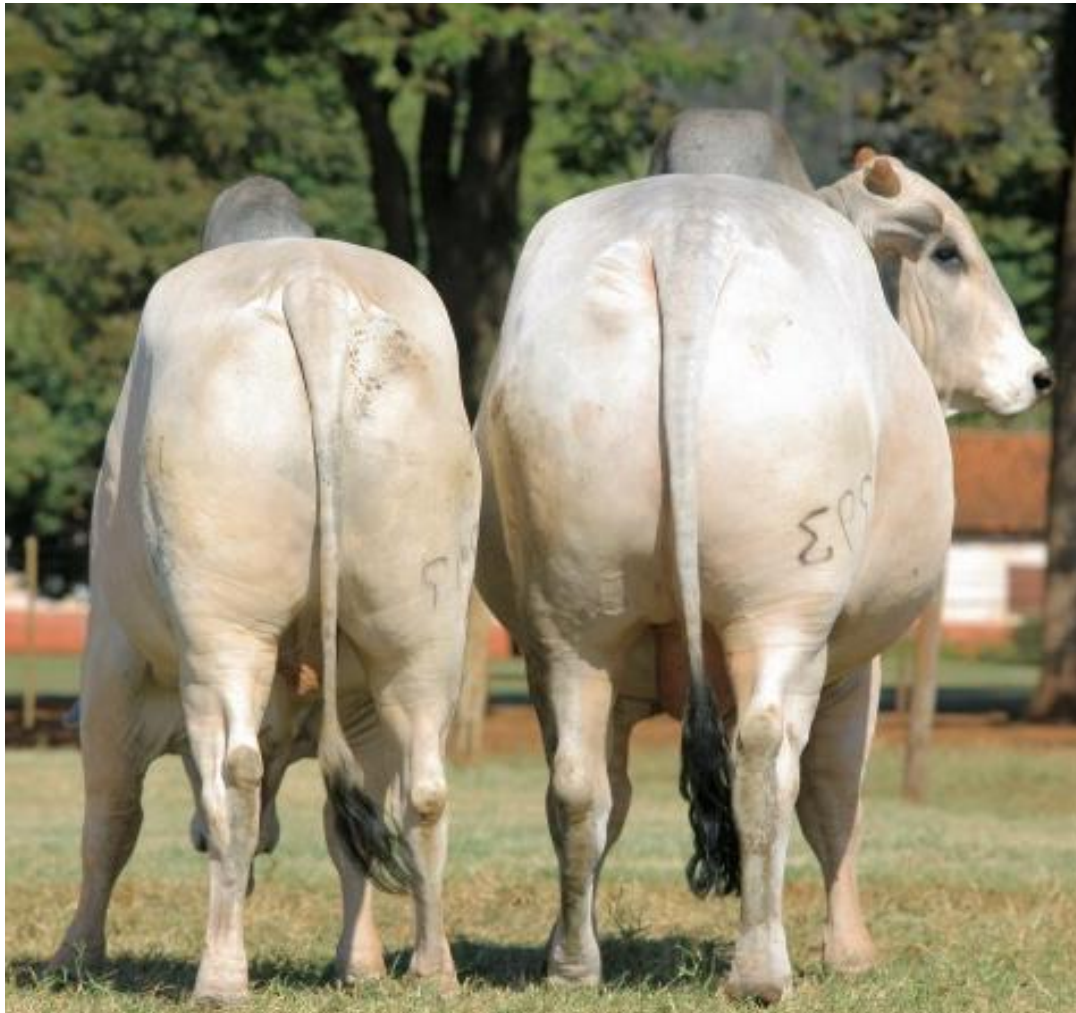
Not a closed line
Positive selection



INTRODUCTION: SELECTION PROGRAM OF HUMP CATTLE BREEDS



NeC



NeC

NeS

NeT

OBJECTIVE



To detect genomic regions with **high** level of **differentiation** due to the **selection for growth** between the **three lines** of **Nelore Cattle**.

METHODS: PIPELINE PRACTICES



803 Animals born between 2004-2012 (gen. 7 to 10)

- **Genotyping**

Illumina BovineHD (777K)

- **Quality Control required:**

MARKERS

Known Position
Autosomal SNPs
CR > 0.95
Non monomorphic

SAMPLE

CR > 0.90
Replicates
Pairwise with $P(\text{IBD}) > 0.90$

Plink 2009

- **Imputation of missing genotypes**

Beagle 3.3.2

529,172 SNPs and 763 Animals

89

NeC

189

NeS

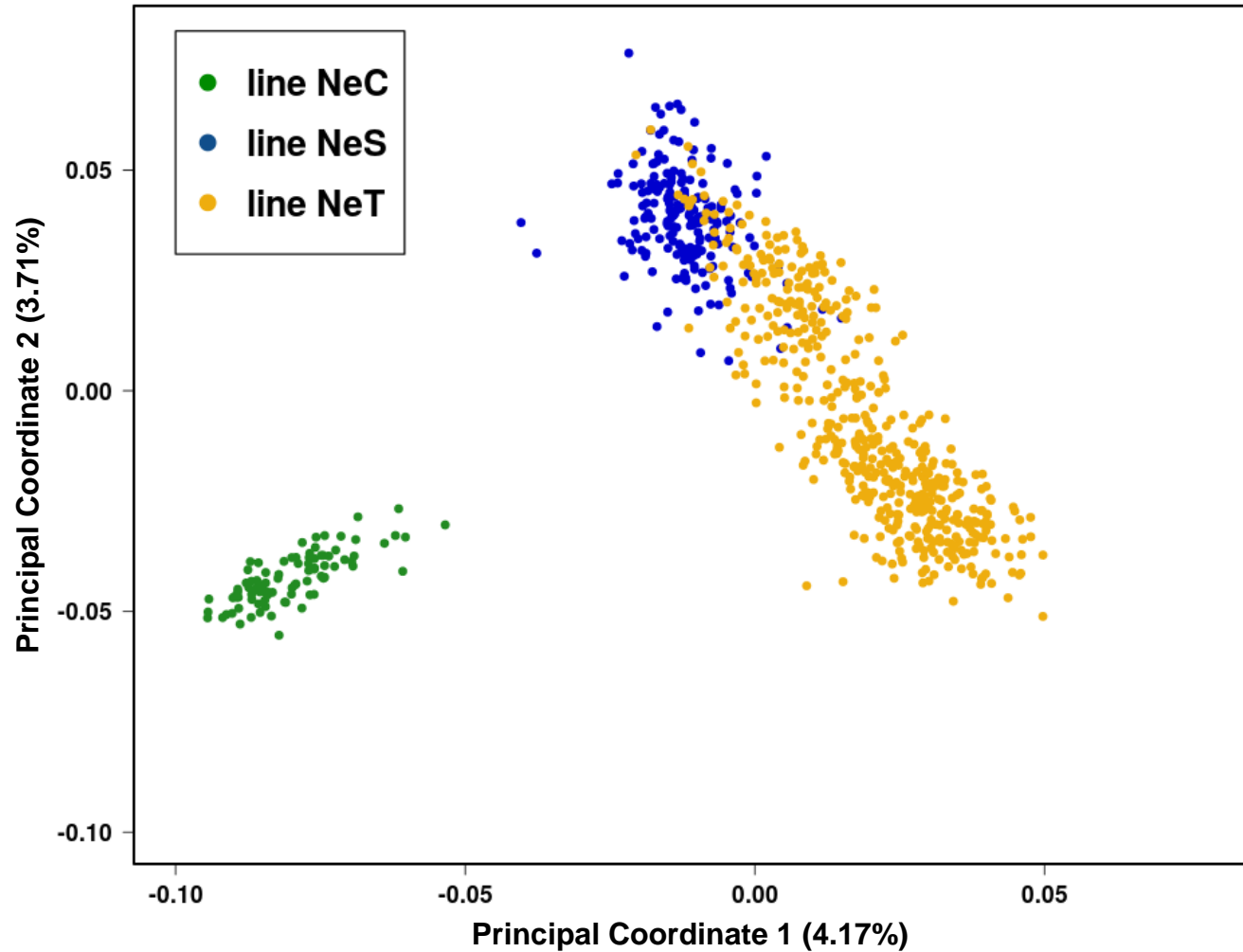
485

NeT

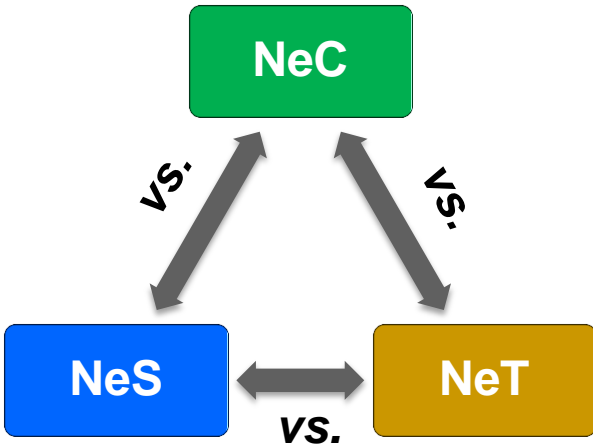
METHODS: POPULATION SUBSTRUCTURE



Multidimensional Scaling Analysis



METHODS: F_{ST} ESTIMATION



$$F_{ST} = \frac{\sum_i n_i (\tilde{p}_i - \bar{p})^2 / \sum n_i}{\bar{p} (1 - \bar{p})} \quad (\text{adapted from: Weir, 1996})$$

where:

\tilde{p}_i = frequency of given allele in the subpopulation i

\bar{p} = weighted mean of allele frequencies between populations

n_i = size of population i

- Overlapping windows of 100Kb

GTTCATAGCATTATTATTATTATTATTTCAGGACTAGTCATAGCATTATTATTATTA
CAGTATCGTAATAATAATAATAAGTCC TGATCAGTATCGTAATAATAATAAT



75% overlap

95,078 windows
containing 22 ± 5 SNPs on average

METHODS: EMPHIRICAL SIGNIFICANCE THRESHOULD

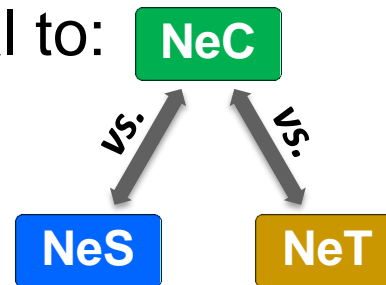


NeS



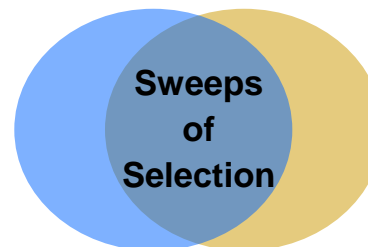
NeT

- kept under the same selection criterion.
Divergences caused by neutral process
- Derived from a common base.
- Time of divergence equal to:

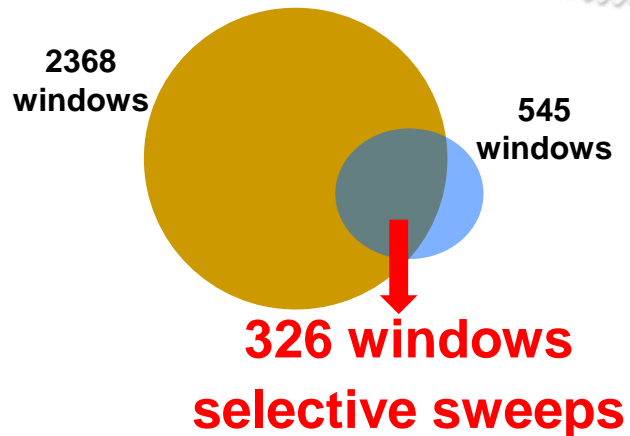
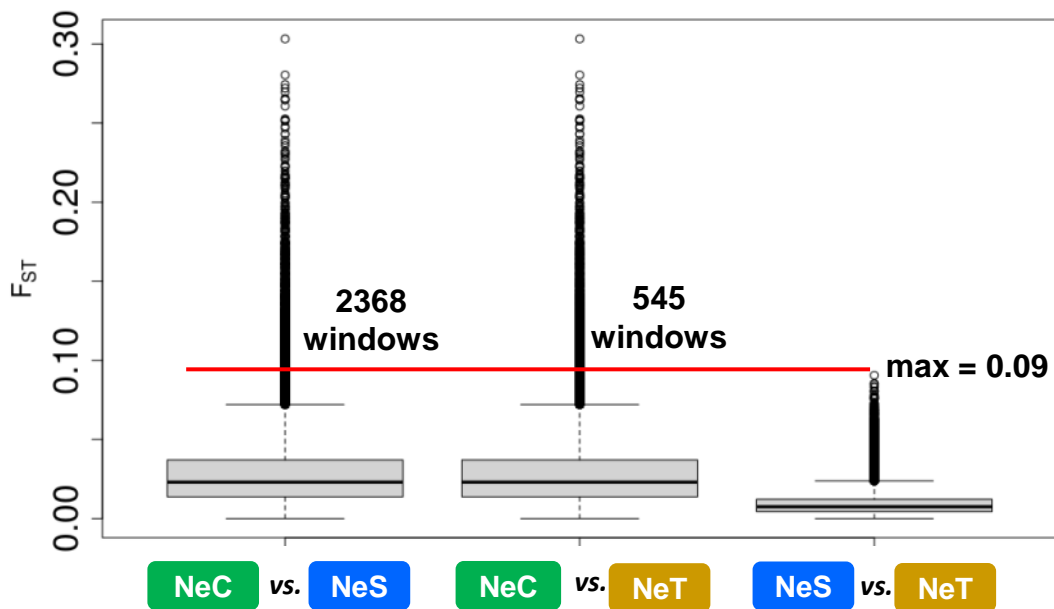


Correspondence with scenarios attempted in simulations to define empirical significance thresholds

Max. value used as empirical significance threshold



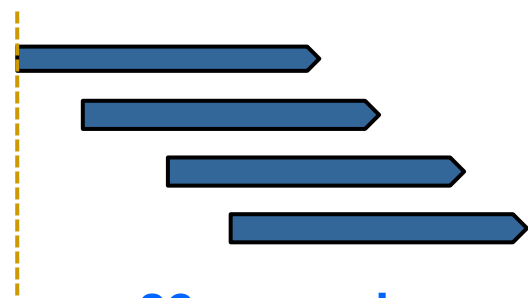
RESULTS: DISTRIBUTION OF F_{ST}



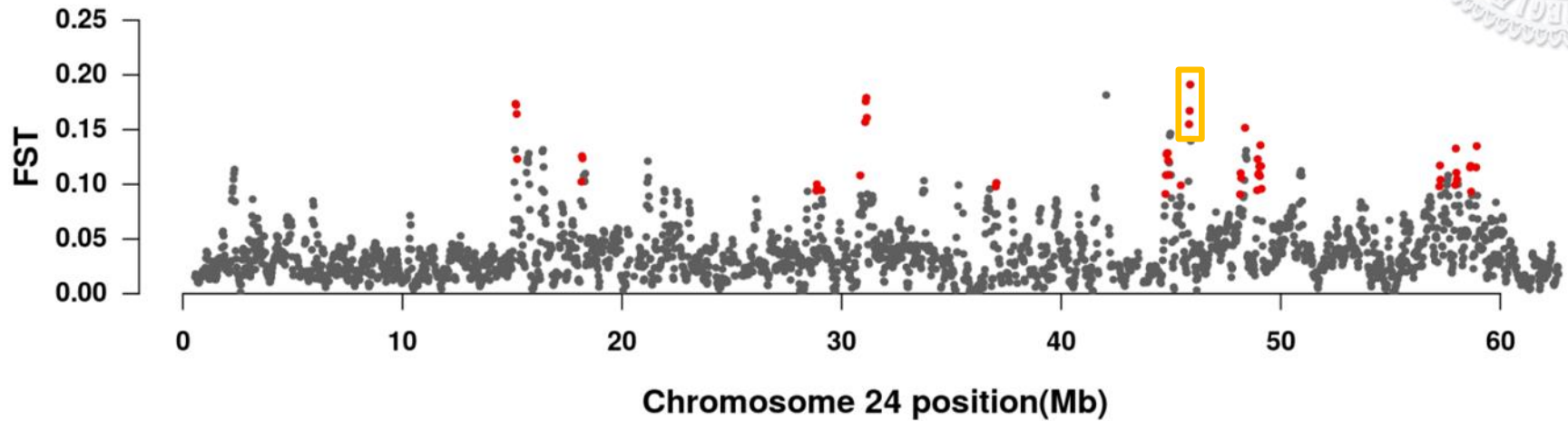
Averages per pairwise

0.029±0.023 0.018±0.015 0.009±0.008

Flori et al. 2012
Senepol herds
geographically isolated
 $\overline{F_{st}} = 0.02$



RESULTS: SWEEPS OF SELECTION



SLC14A1 & SCL14A2

Urea transporters expressed in the rumen.

Ruminants:

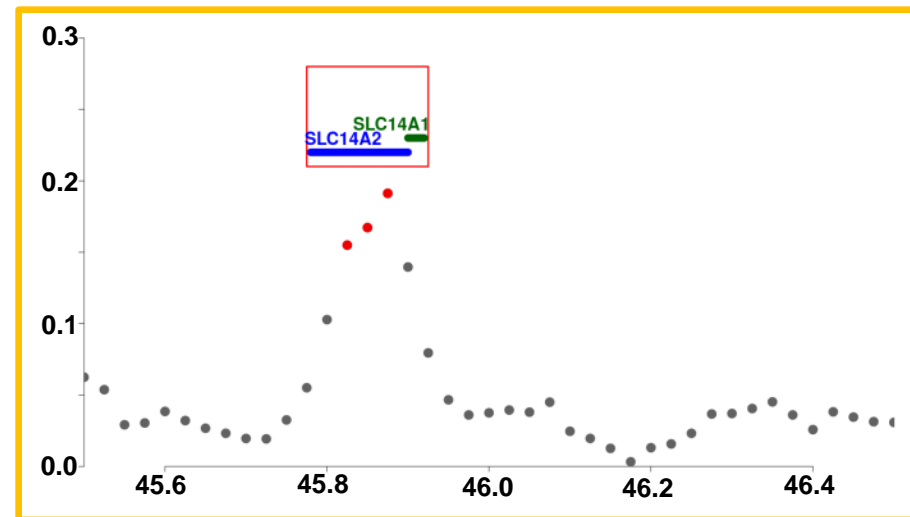
Use urea to microbial protein synthesis.

In cattle:

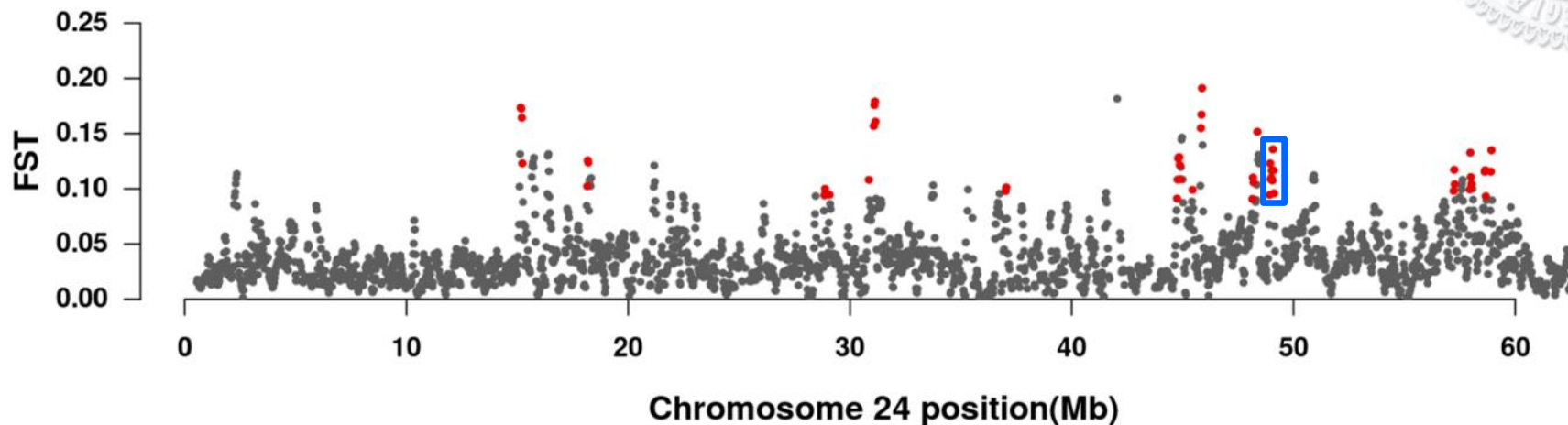
↑ urea transporters at rumen

↑ postabsorptive amino acid use for growth.

Berends et al. 2014



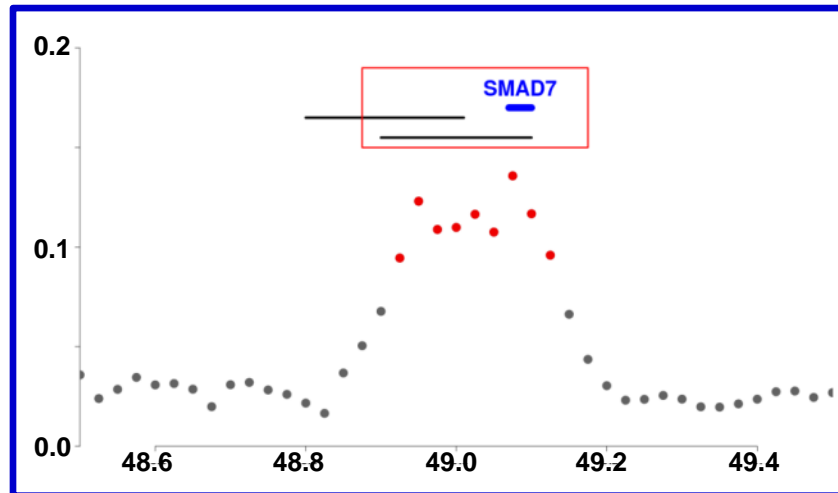
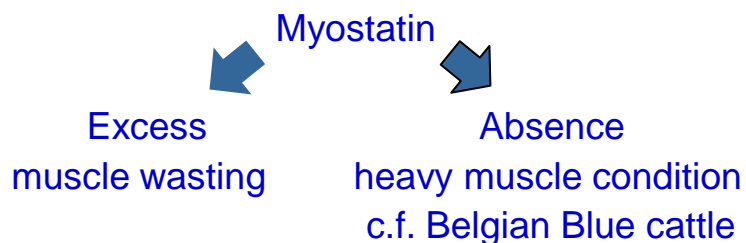
RESULTS: SWEEPS OF SELECTION



SMAD7

Negative regulator of cattle myostatin gene expression.

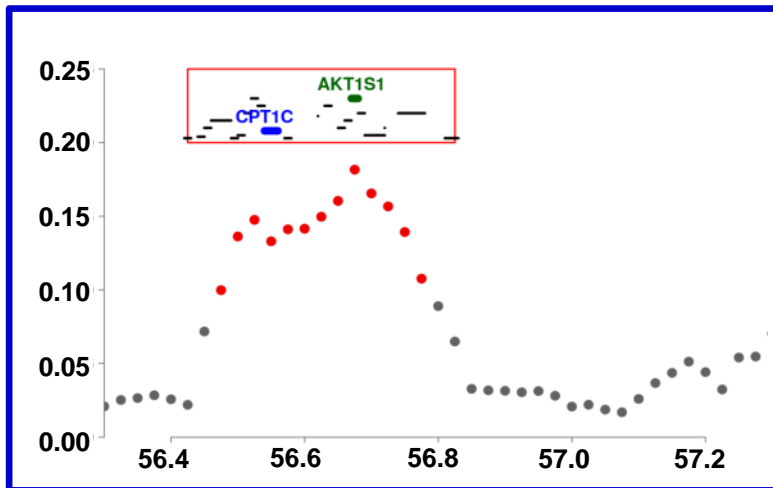
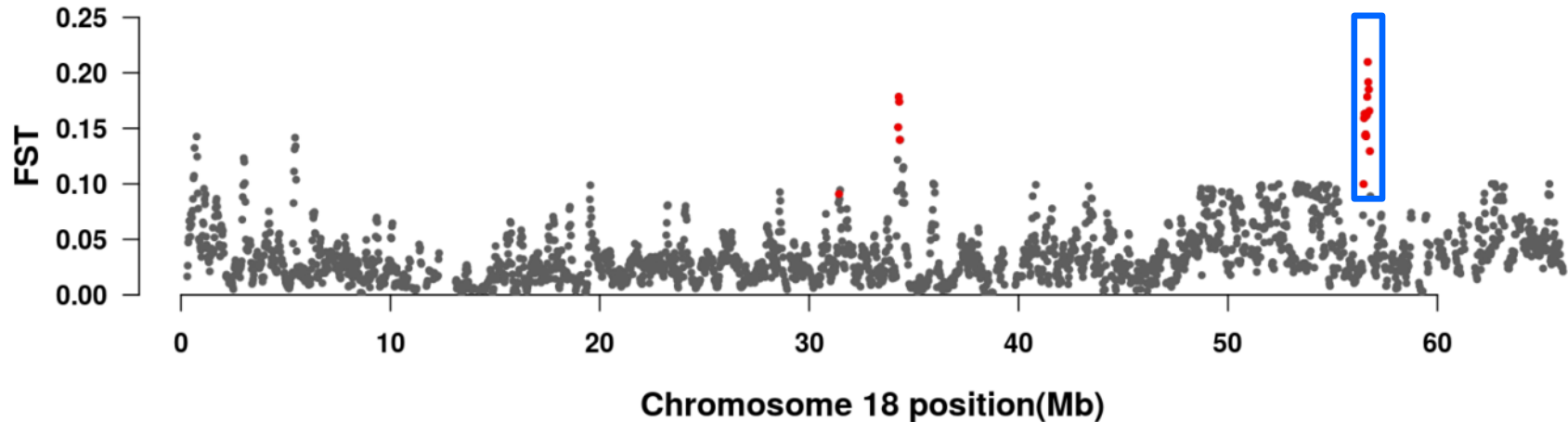
Forbes et al. 2004



RESULTS: SWEEPS OF SELECTION



Largest selective sweep → Chromosome 18



CPT1C

Ghrelin and leptin signaling pathways.

Ramirez et al. 2013

In cattle:

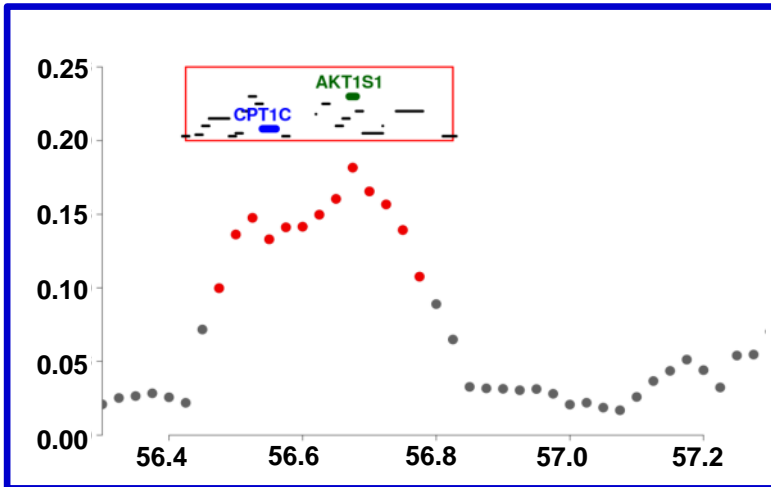
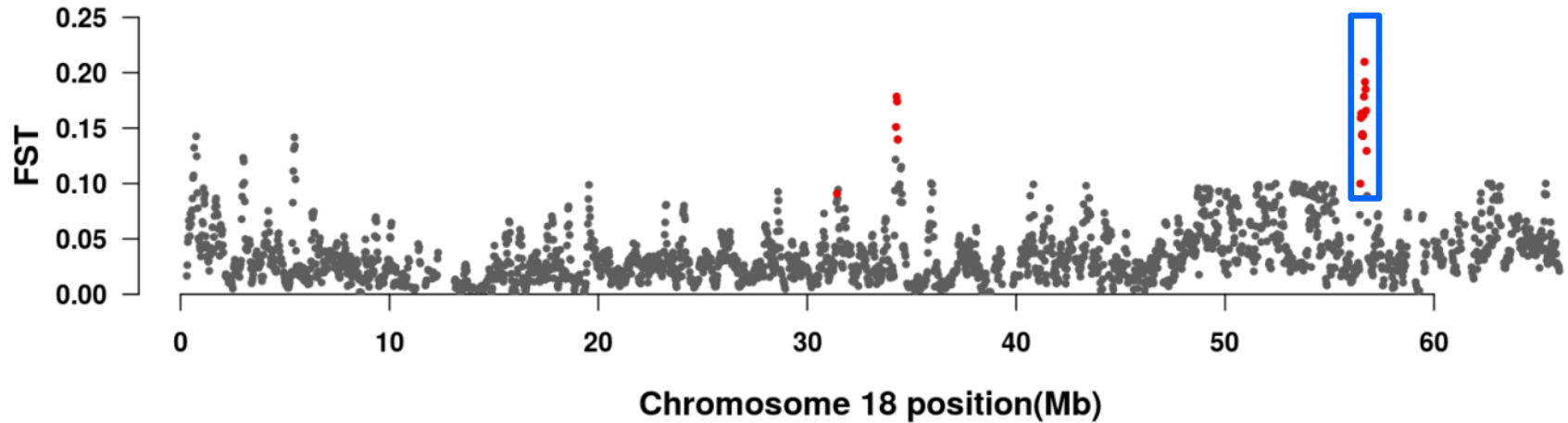
Overexpressed gene in longissimus dorsi muscle during finishing phase.

Moisá et al. 2013

RESULTS: SWEEPS OF SELECTION



Largest selective sweep → Chromosome 18



AKT1S1:

Mediator of IGF-1 effects on cell growth
Wang et al. 2012

Regulator of insulin sensitivity in skeletal muscle.

Wiza et al. 2014

CONCLUSIONS:



Ten generations of selection have created selective sweeps in low intensity.



Nevertheless, regions containing plausible genes to be under selection, due to their already known metabolic functions, were targeted as putative selective sweeps.

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Thank you for your attention !!!!!

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