

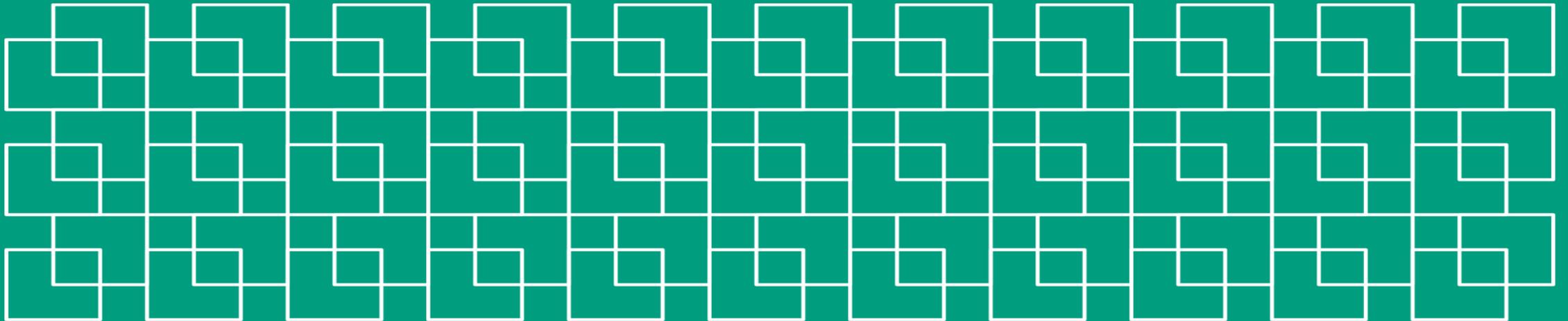
# *Screening for selection signatures in Norwegian Red*

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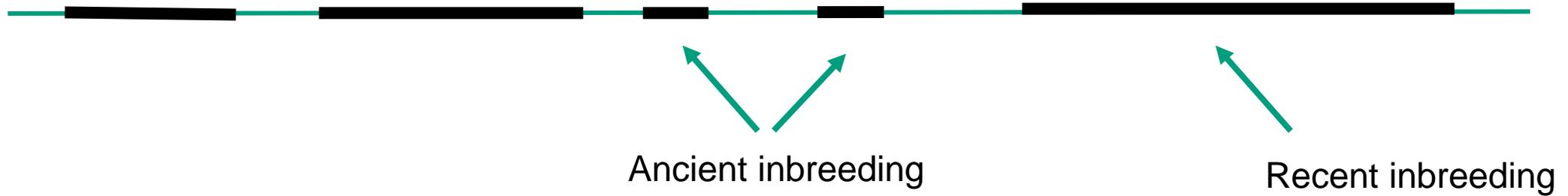
# Motivation

- Genomic inbreeding using runs of homozygosity (ROH):
  - Rate of inbreeding ( $\Delta F$ )
  - Effective population size ( $N_e$ )



# Runs of homozygosity (ROH)

Chromosome

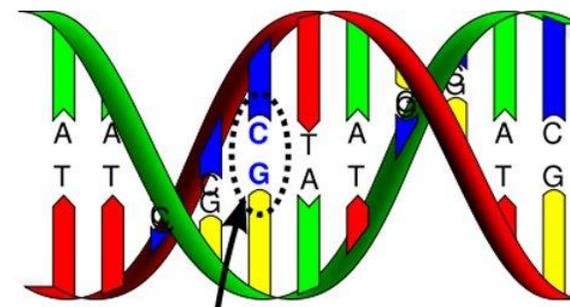
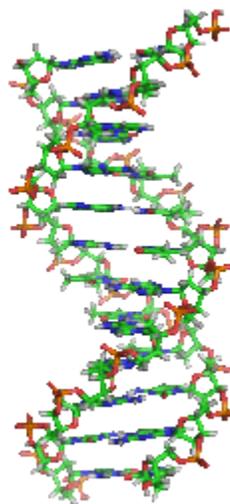


$$F_{ROH} = \frac{\sum L_{ROH}}{\sum L_{AUTO}}$$

# What if.....

We could narrow this down?

1. Segmental level
2. SNP level



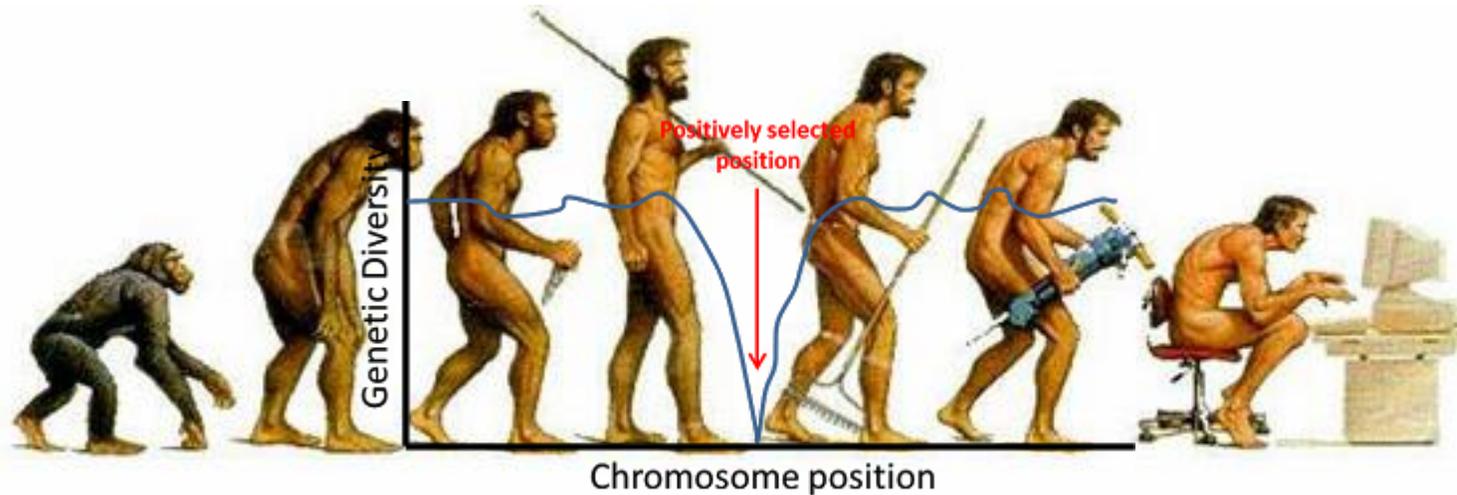


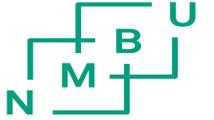
# So what?

- Trace the cause
  - Define individuals that had a great impact on important traits
  - Detect strategic fortunate or unfortunate genetic moves
- Control for inbreeding

# Is it possible?

- Trace selection over time
- Detect selective sweeps
  - Ongoing
  - Historical





# Expectations

- ROH could give us an illustrative pattern on the genome showing:
  - Segments with an excess of homozygosity
  - Segments reaching towards homozygosity at different rates
- ROH could be able to map SNP specific
  - Inbreeding
  - Rate of inbreeding
  - Selection signatures



# Objective

1. Locate segments and markers exposed to inbreeding
2. Map the rate of change over time on a segmental level
3. Search for selection signatures, both historical and ongoing



# Animals and genotyping

- 381 Norwegian Red bulls (1971-2004)
- Illumina HD-panel (708K):
  - Individual call rate > 95 %
  - SNP call rate > 90 %
  - Autosomal SNP only
  - Hardy-Weinberg deviation  $p < 10^{-6}$

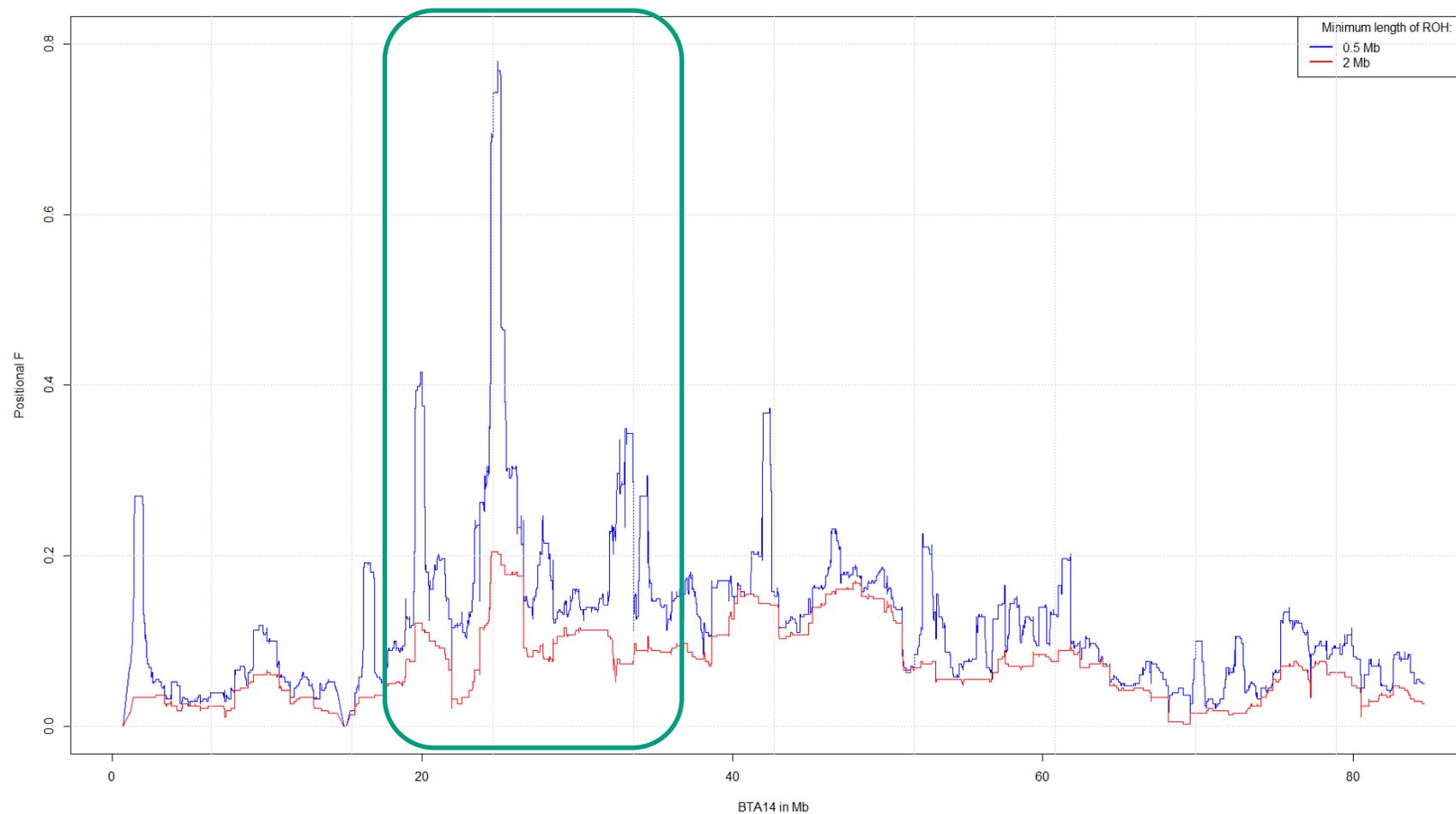


# Positional inbreeding from ROH

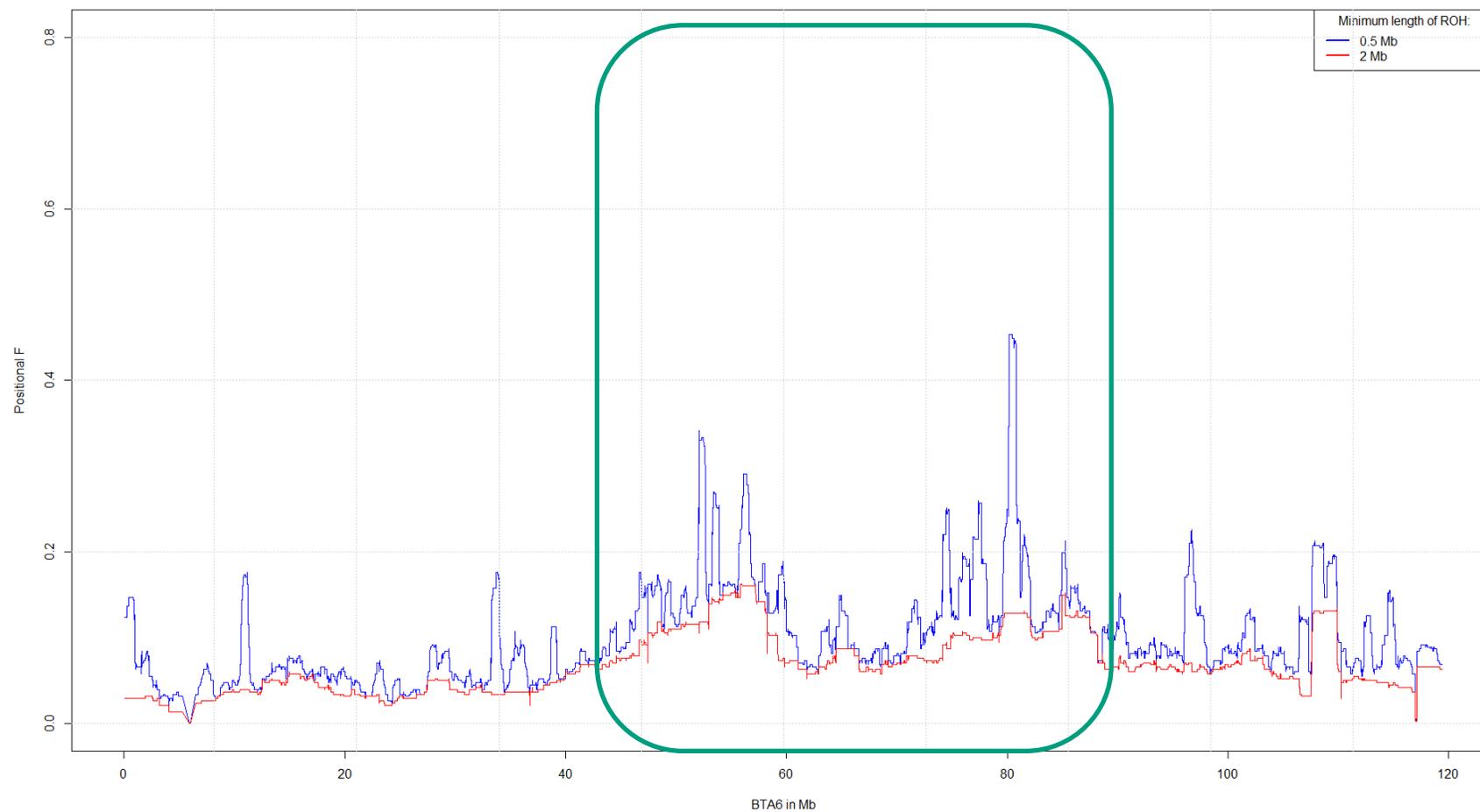
$$F_j = \frac{\sum_{i=1}^N s_{ij}}{N}$$

\* Where  $s_{ij}$  is the status of the locus, whether it is within a ROH or not (1 or 0) and  $N$  is the total number of animals in the dataset

# $F_j$ BTA 14



# F<sub>j</sub> BTA 6



# Positional rate of change

$$L(\beta_j) = \prod_{i=1}^N \text{Bernoulli}(p_{ij})$$

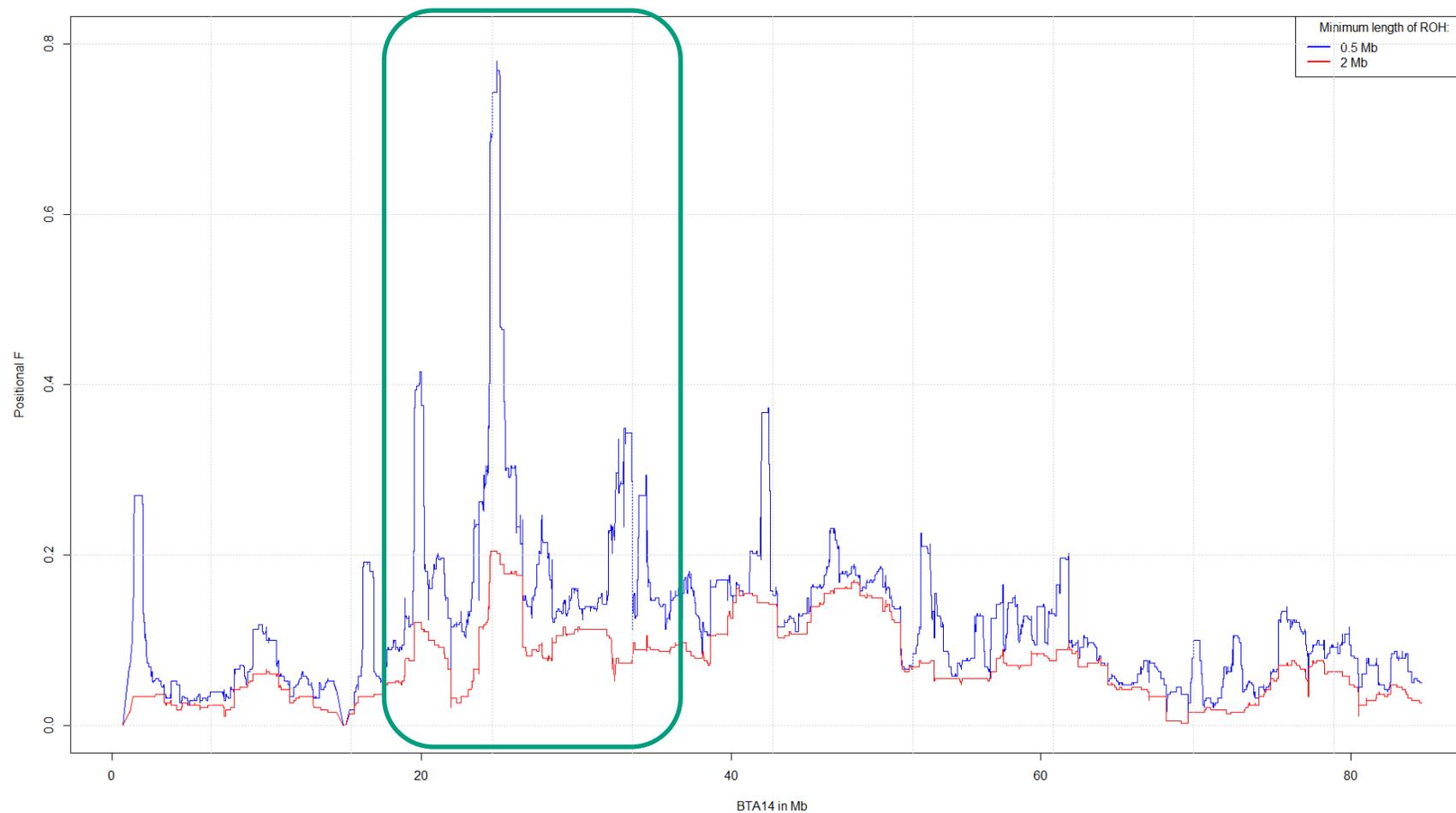
$$p_{ij} = \frac{\exp(\eta_{ij})}{1 + \exp(\eta_{ij})}$$

$$\eta_{ij} = [\eta_{1j} \dots \eta_{Nj}]'$$

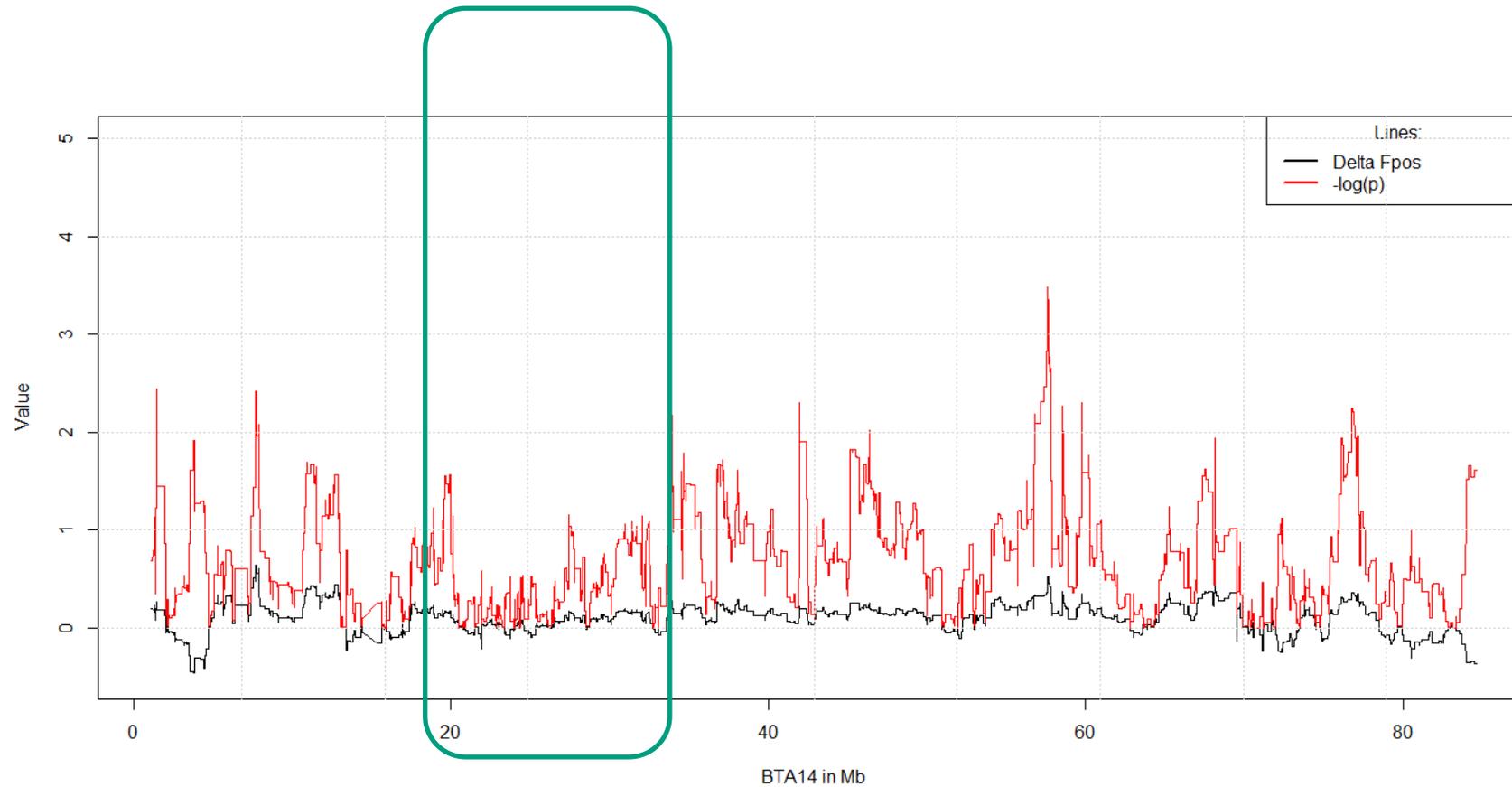
$$\log \text{it}(p_{ij}) = \eta_{ij} = \mu_j + \beta_j t_i$$

\* Where  $\mu$  is the intercept and  $\beta$  is slope of the regression, while  $t$  is CGE of individual  $i$

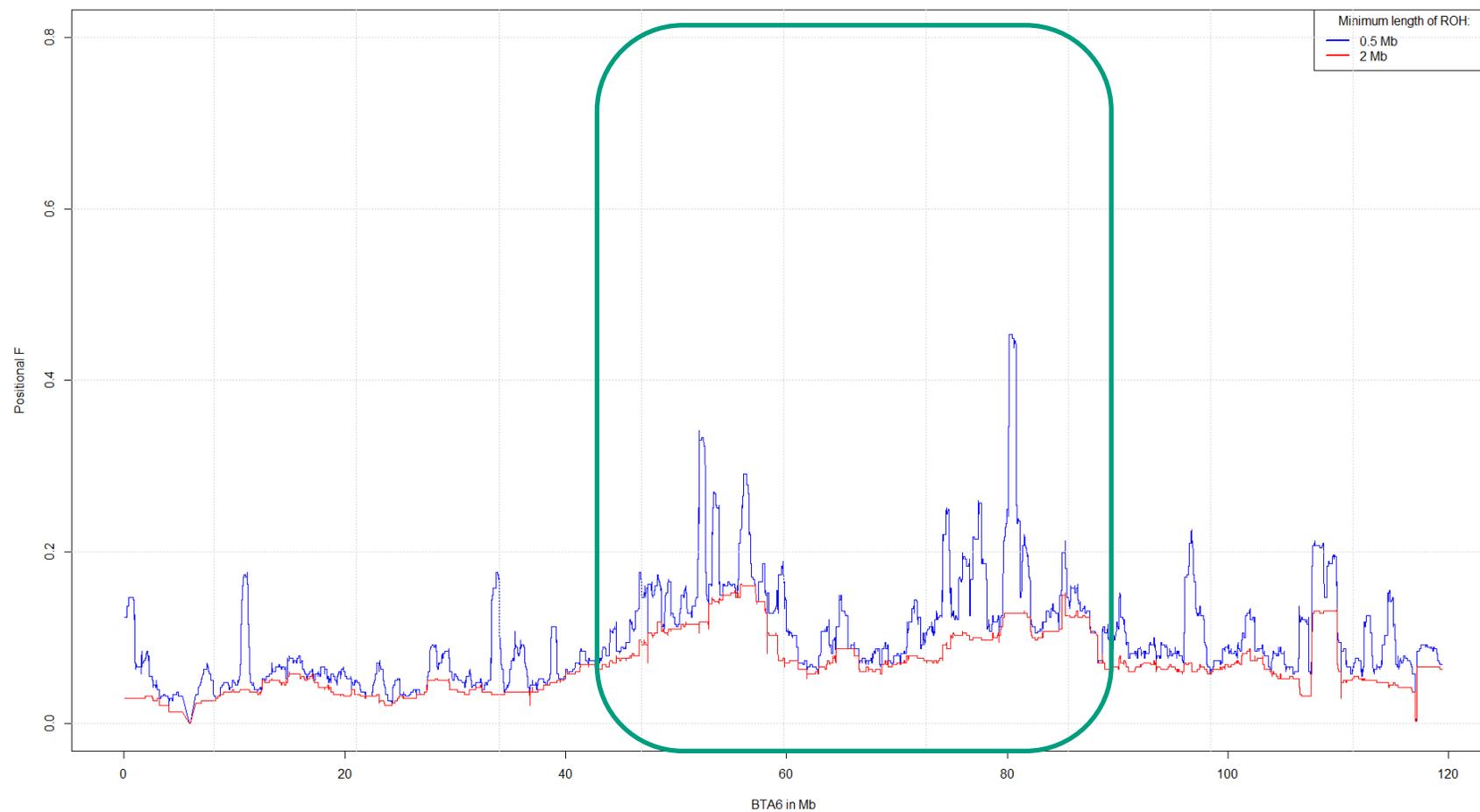
# $F_j$ BTA 14



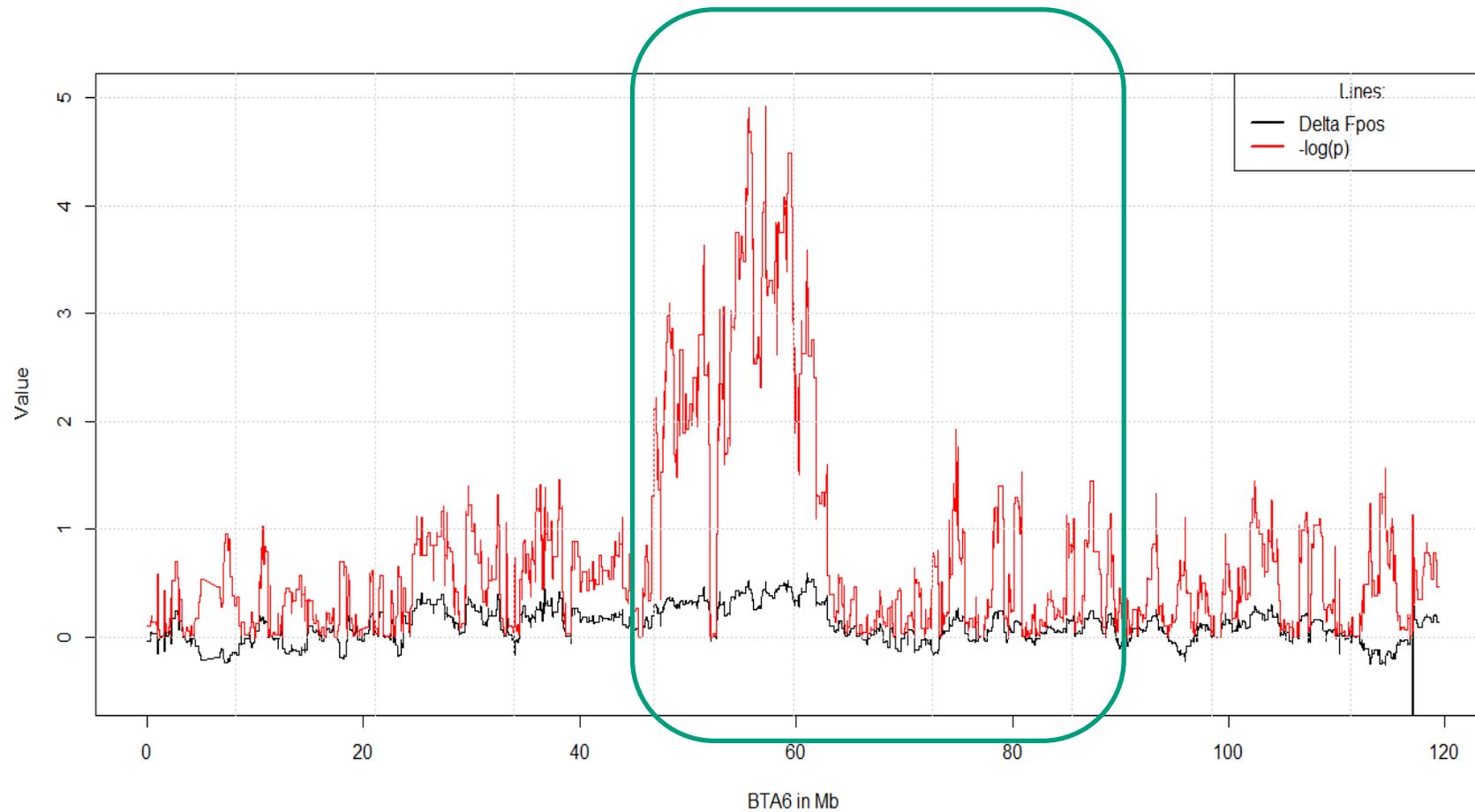
# The slope of change at BTA 14



# F<sub>j</sub> BTA 6



# The slope of change BTA 6





# Take home messages

- ROH located segments and markers exposed to inbreeding
- ROH mapped the rate of change over time both over segments and markers
- ROH did also make it possible to search for selection signatures
  - Ongoing
  - Historical