

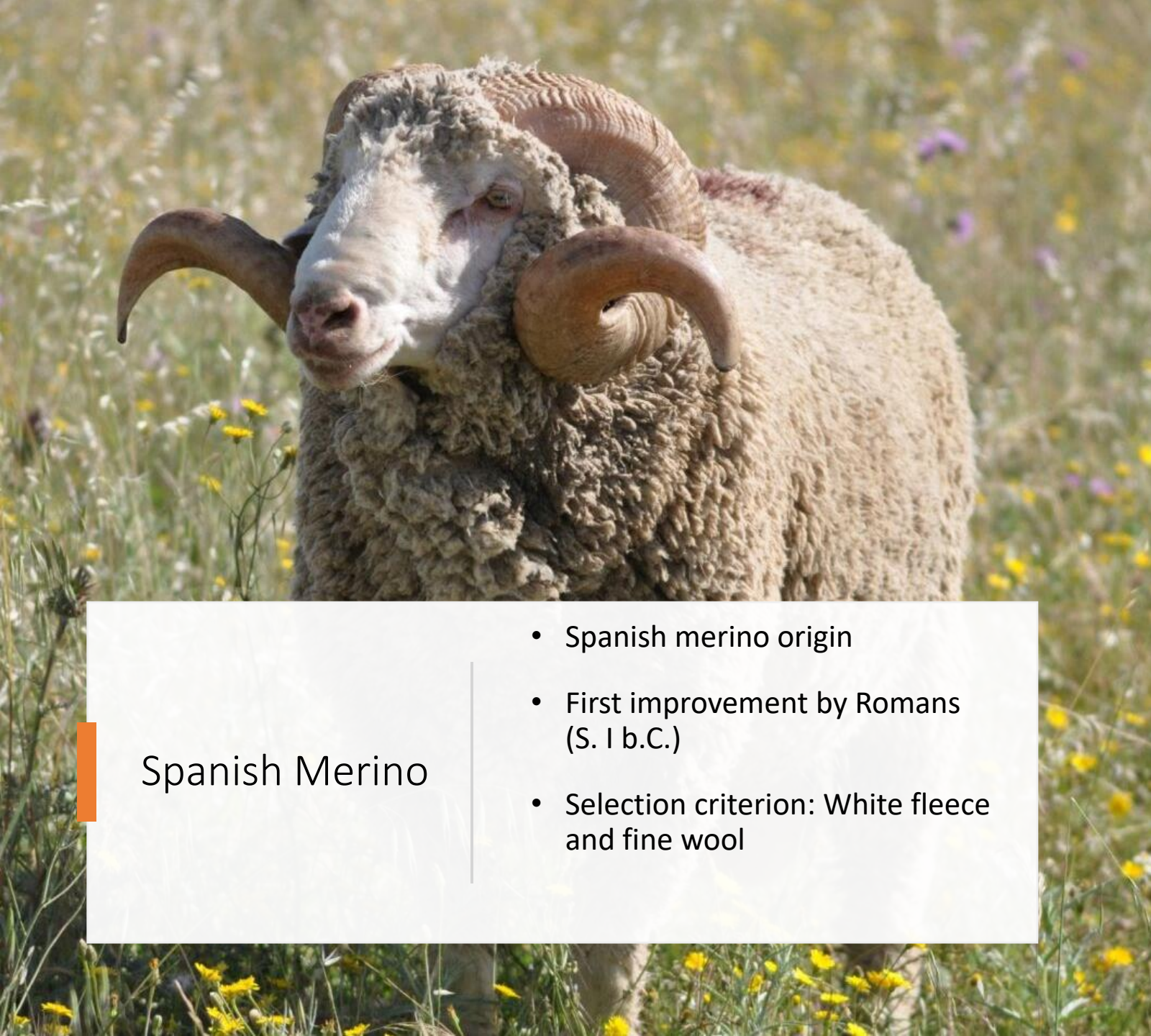
# Valorization of extensive breeding of the Spanish Merino Sheep through the quality wool improvement: Preliminary results of GWAS of fiber diameter from Whole Genome Sequences

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Session 8: Adaptation, resilience and agroecological transition in small ruminants and camelids



## Spanish Merino

- Spanish merino origin
- First improvement by Romans (S. I b.C.)
- Selection criterion: White fleece and fine wool

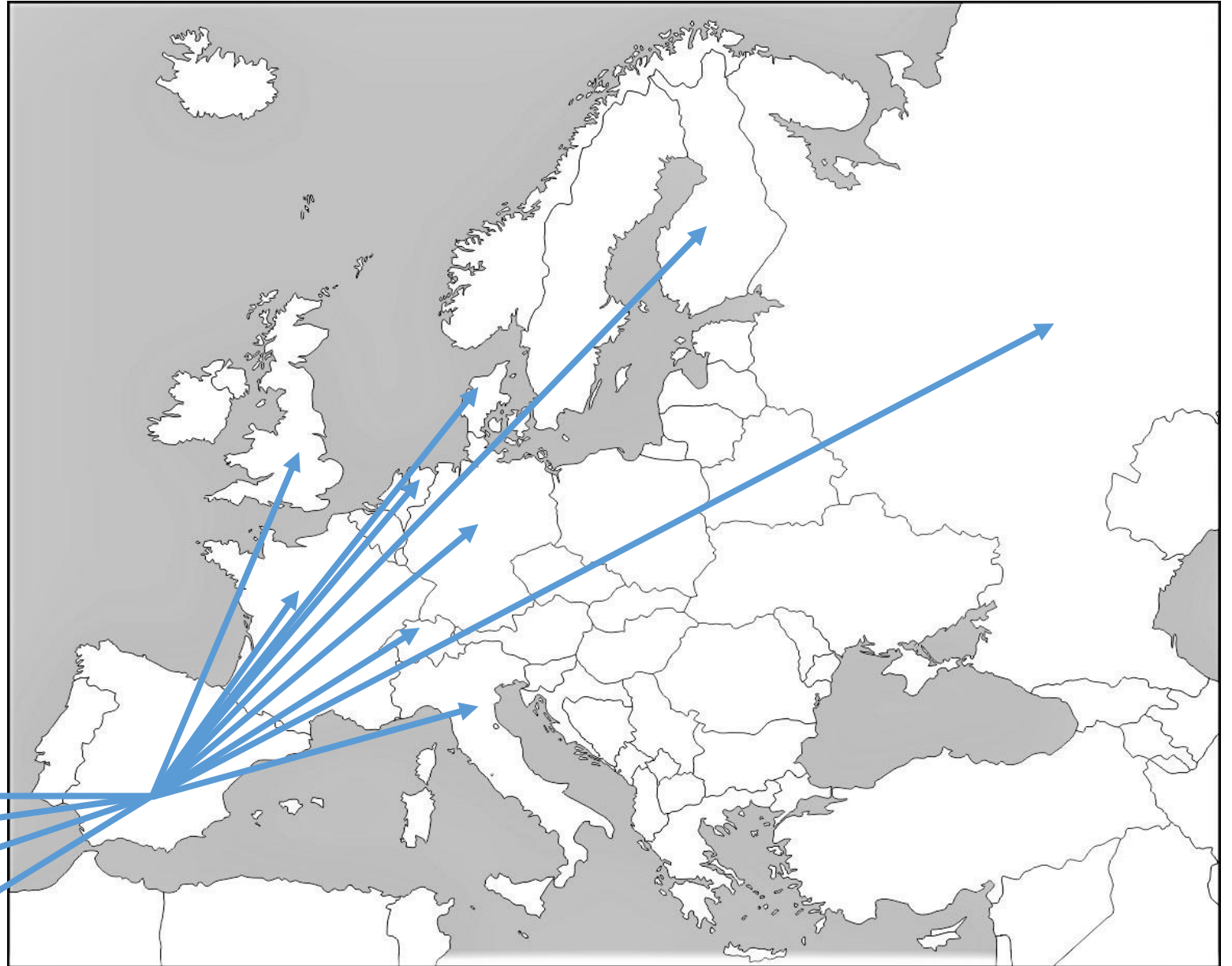


# Spanish Merino



Shield of the Honored Council of the Mesta

- Sweden (1715)
- Russia (1720)
- France (1725)
- Germany (1765)
- Austria (1775)
- Netherlands (1786)
- England (1792)
- Italy (1793)
- USA (1793)
- Argentina (1794)
- Uruguay (1794)
- Denmark (1797)
- Australia (1802)



- USA (1793)
- Argentina (1794)
- Uruguay (1794)
- Australia (1802)

# Spanish Wool Market

- Crisis of the 1960s
- Selection criterion
- Wool to meat
- Current census. Merino type and Pure Merino
- Current wool market
- Carbon footprint









# GENUINE MERINO



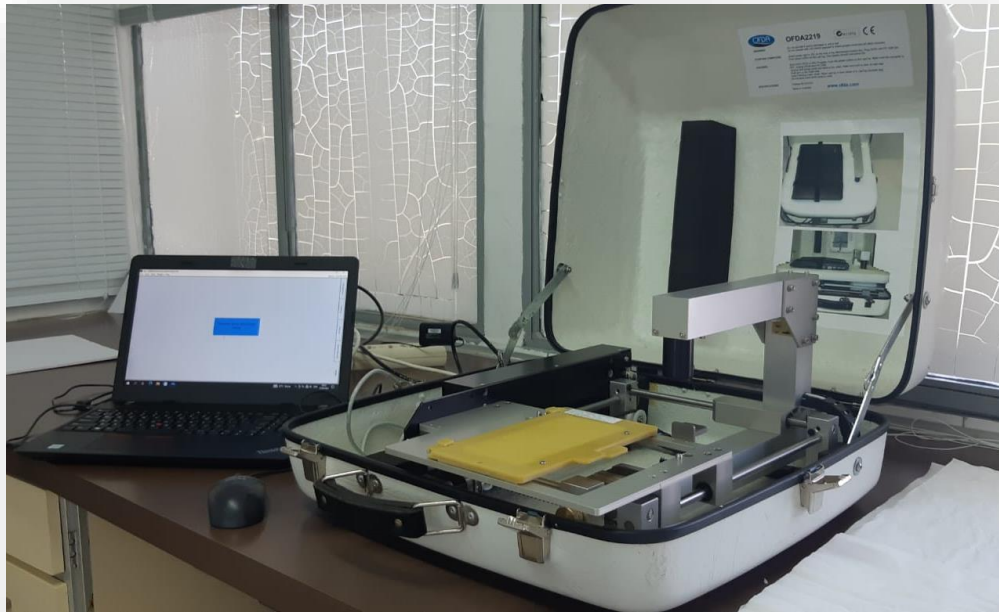
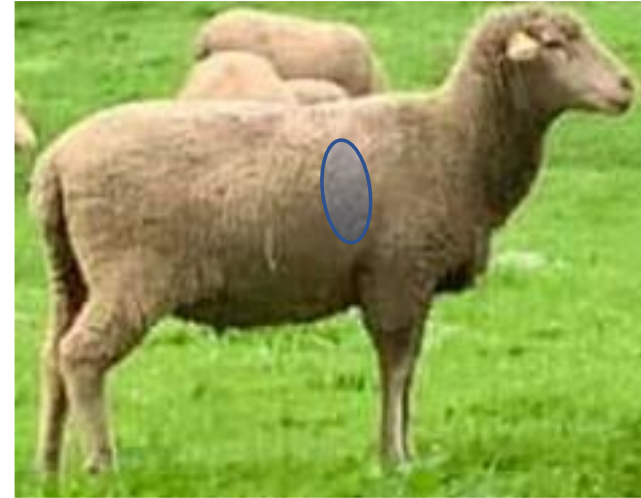
ASOCIACIÓN NACIONAL  
CRIADORES GANADO MERINO



# OFDA 2000

(Optical Fibre Diameter Analysis)

- **Fiber Diameter (FD)**
- **Standard Deviation (SD)**
- **Coefficient of Variation (CV%)**
- **Comfort Factor (CF%)**
- **Staple Length (SL)**
- ....





# Wool parameters

Table 1. Descriptive statistical of the wool parameters related to Fiber Diameter (FD) and Staple Length analysed (SD), obtained from the Spanish Merino population analysed.

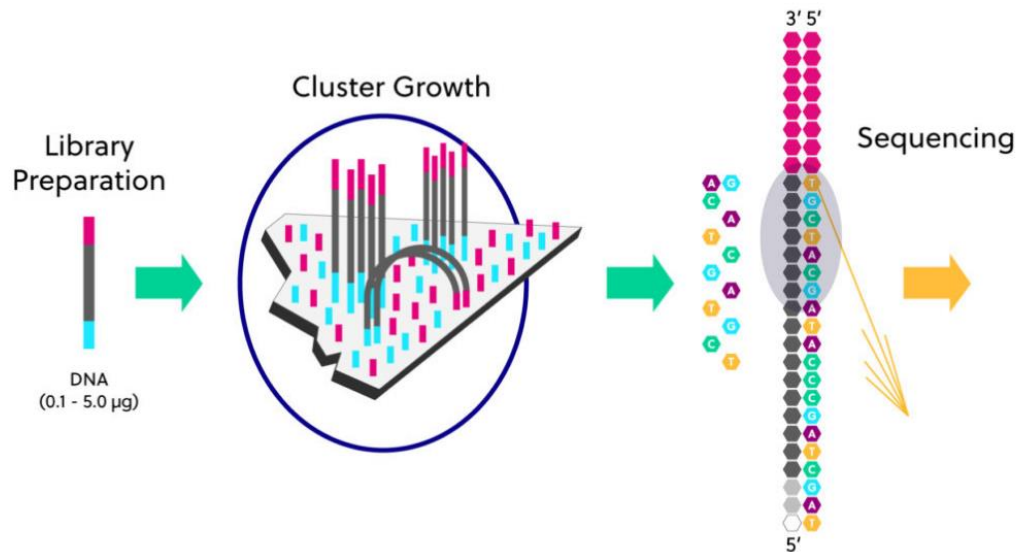
Sample	Min	Max	Mean
Fiber Diameter ( $\mu$ )	15.2	28.5	22.2
Standard Deviation FD ( $\mu$ )	2.3	6.6	3.8
Coefficient of Variation FD (%)	12	29	17.48
Comfort Factor (%)	70.8	100	95.7
Staple Length (mm)	15	85	42



# WHOLE GENOME SEQUENCING:

41,308,360 DNA variants

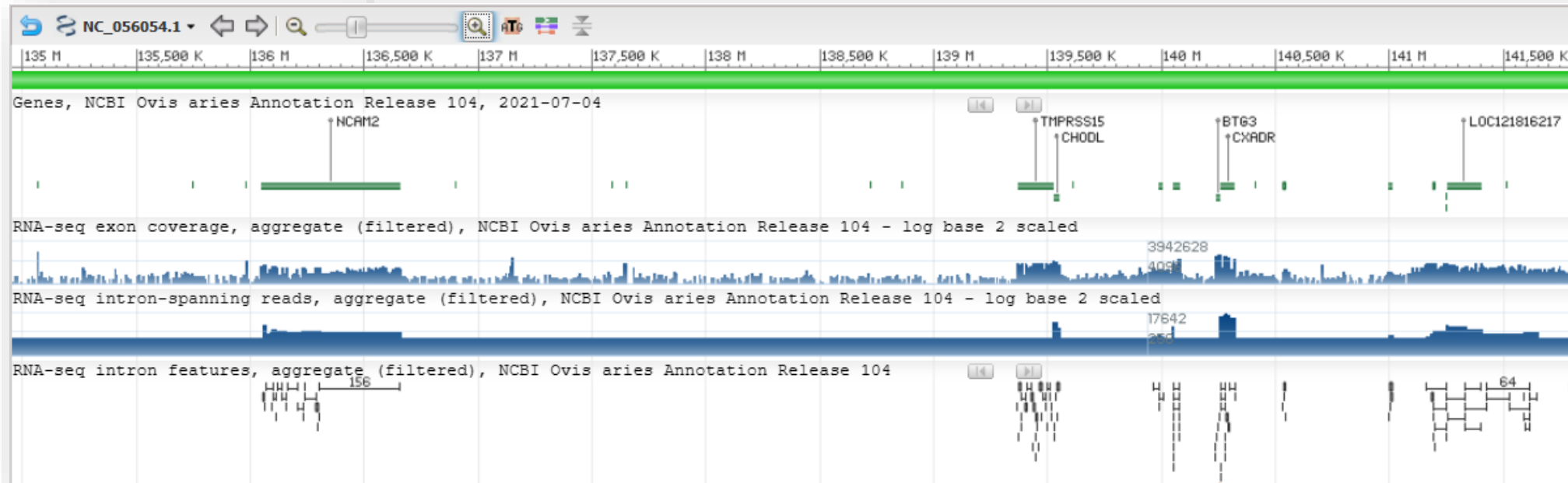
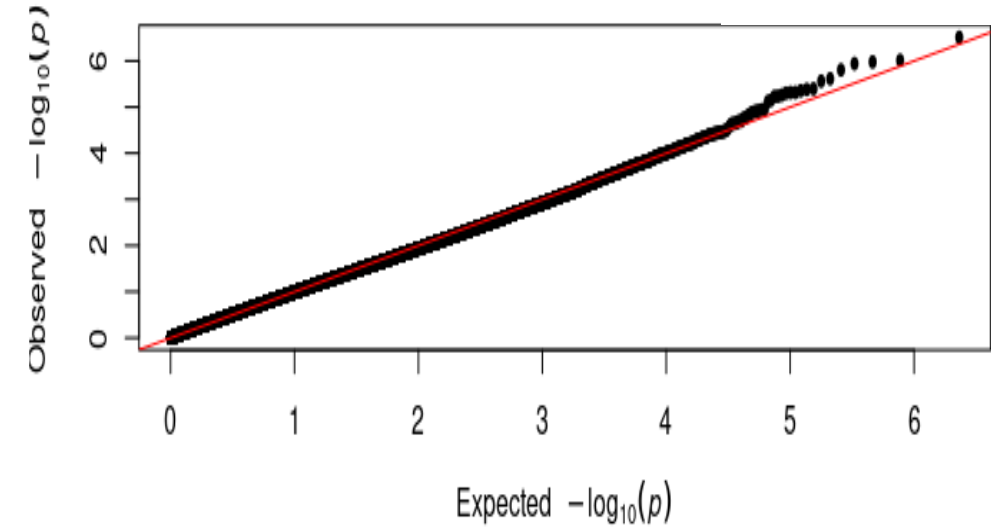
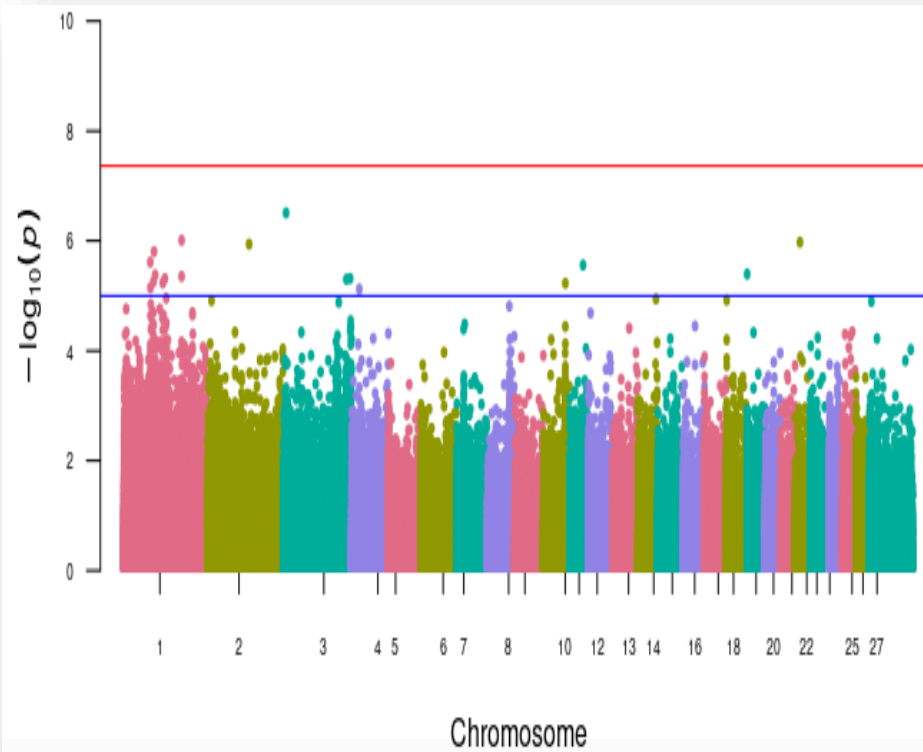
- Group selection
- Blood extraction
- DNA purification
- Library preparation
- Sequencing
- Data processing



```
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[M::mem_pestat] (25, 50, 75) percentile: (43, 100, 180)
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[M::mem_pestat] mean and std.dev: (109.00, 91.93)
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```

# GWAS

- 17 regions
- 1 Mb window
- 39 genes







Thank you