

Genome-wide identification of selection signatures across altitudinal gradients in dairy sheep breeds

Supplementary material 1

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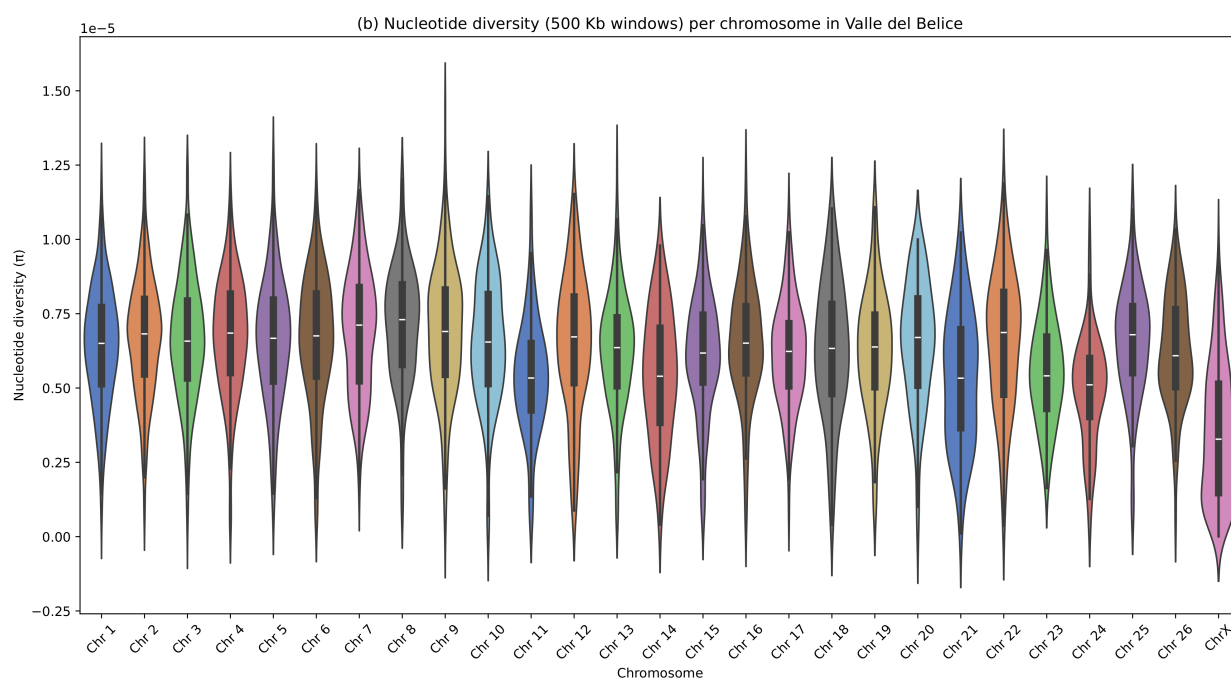
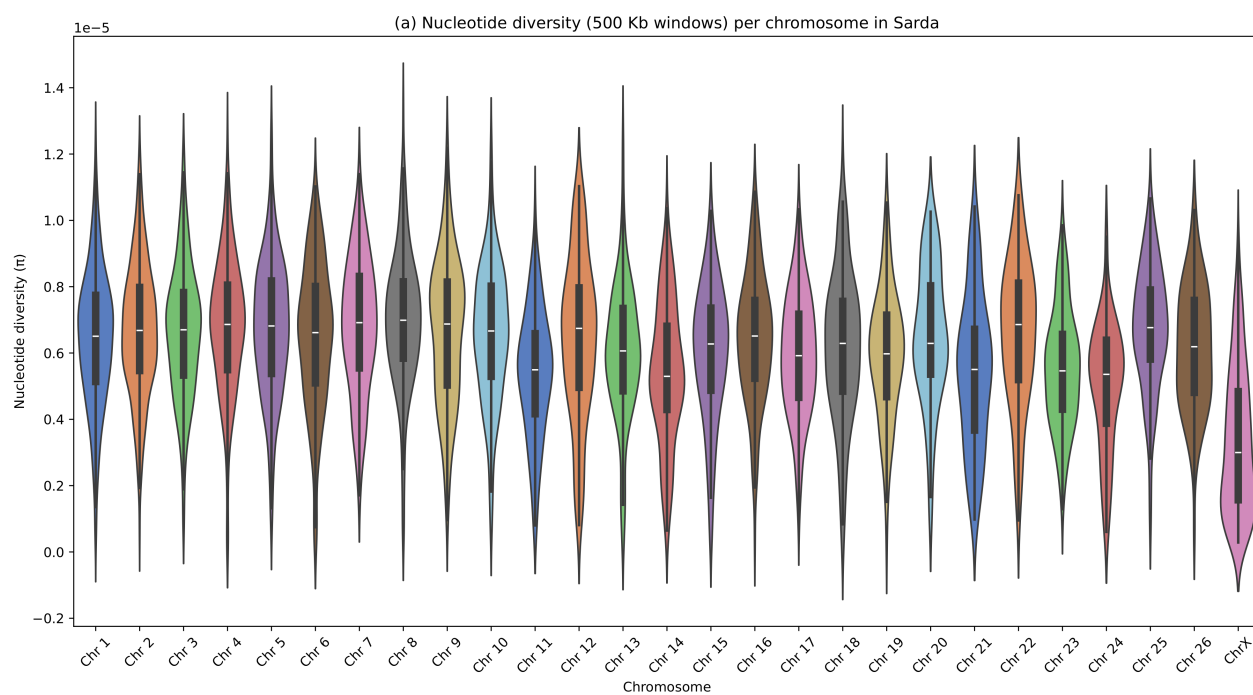
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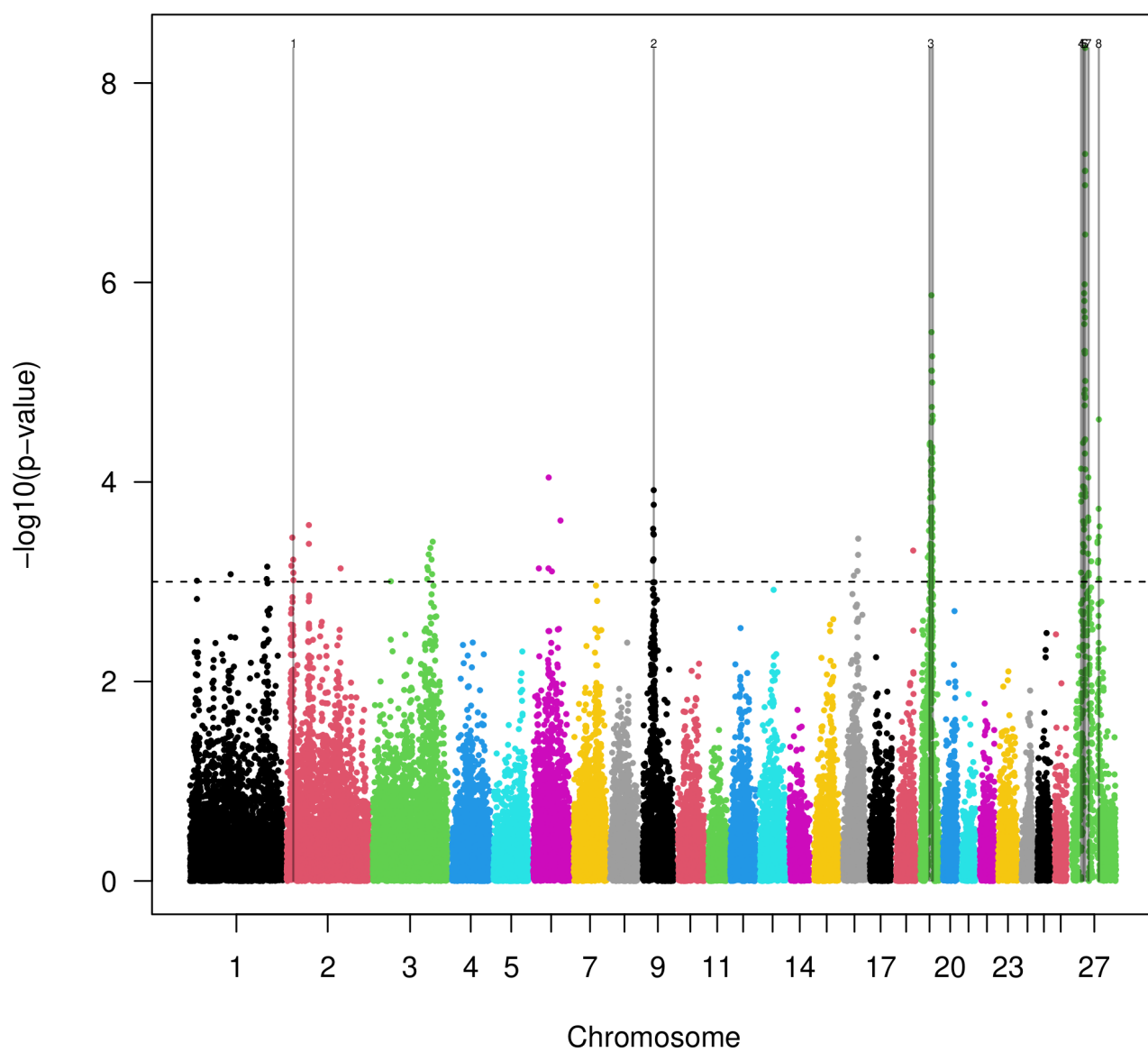
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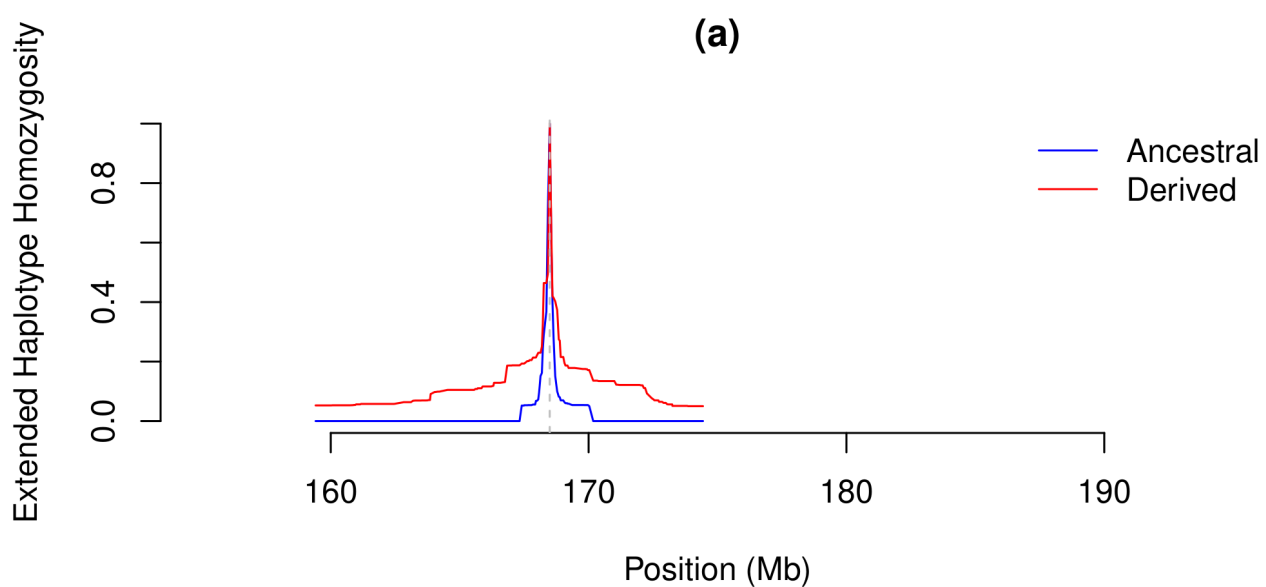
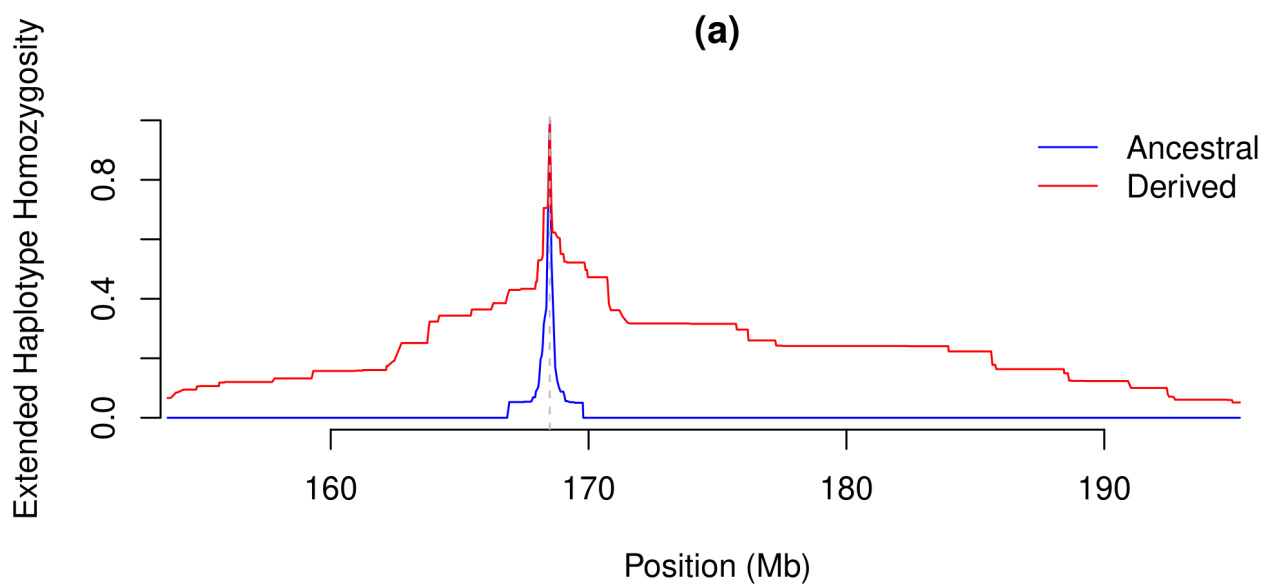
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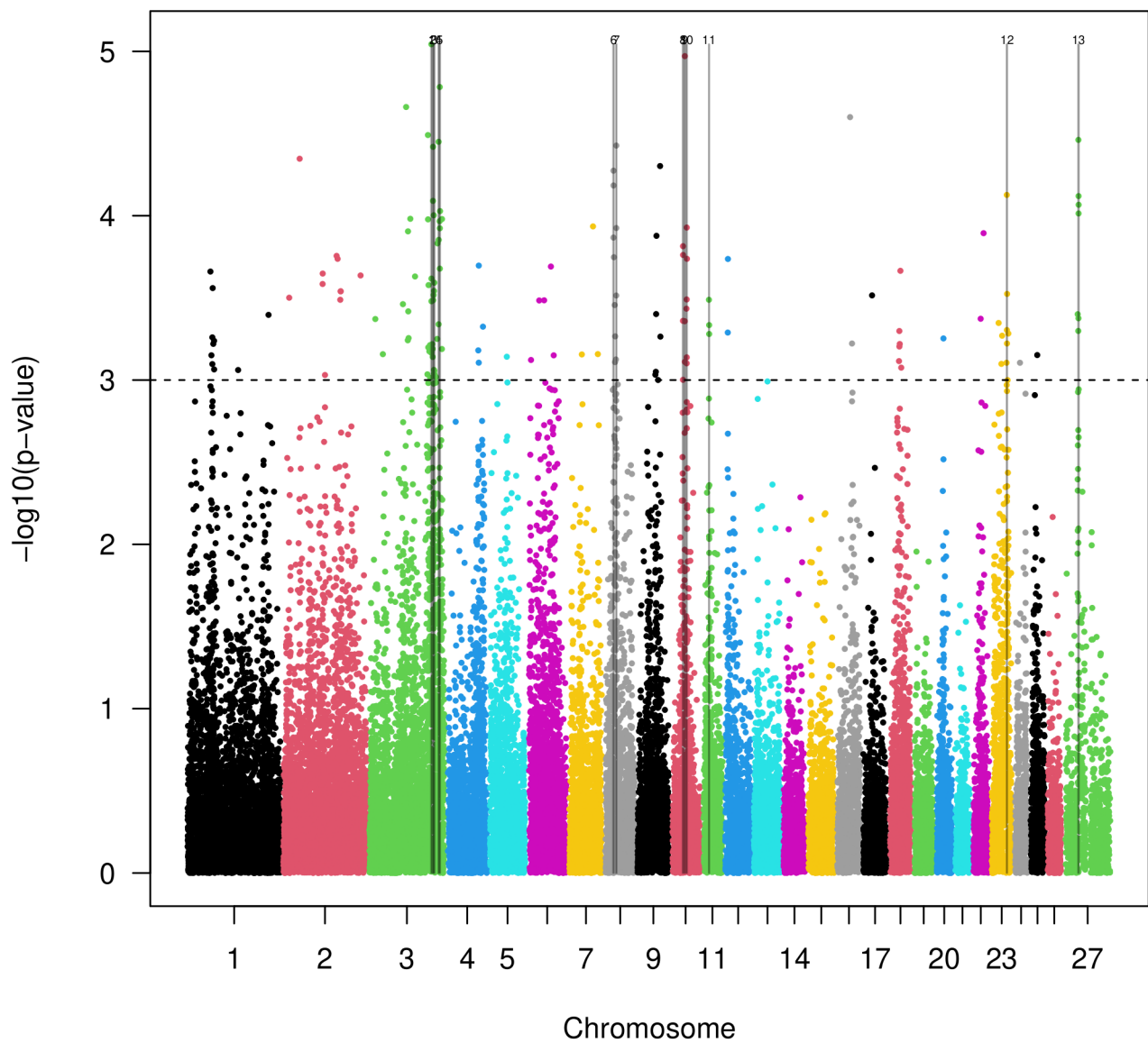
Supplementary Figure S1. Average nucleotide diversity per chromosome, estimated in non-overlapping 500 Kb windows, in Sarda and Valle del Belice.



Supplementary Figure S2. Manhattan plot of the iHS test results for the Sarda breed obtained via joint analysis of the three ecotypes (SAR_C, SAR_M and SAR_P). The horizontal dashed lines mark the significance threshold applied to detect the outlier SNPs ($-\log(p\text{ values}) = 3$).



Supplementary Figure S3. Extended haplotype homozygosity decay plot around rs401844951, located within the *ANKS1B* gene, in (a) Mountain ecotype of Sarda (b) Plain ecotype of Sarda.



Supplementary Figure S4. Manhattan plot of the iHS test results for the Valle del Belice breed obtained via joint analysis of the three ecotypes (SAR_C, SAR_M and SAR_P). The horizontal dashed lines mark the significance threshold applied to detect the outlier SNPs ($-\log(p \text{ values}) = 3$).