

Genomic study of milk performance in fat-tailed and thin-tailed Mediterranean dairy sheep

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OBJECTIVE

To compare the genetic profiles of lactation milk yield (LMY) and milk fat (FC), protein (PC), and lactose content (LC) between **fat-tailed Chios** and **thin-tailed Frizarta** sheep by deriving genomic heritability estimates and identifying associated single nucleotide polymorphisms (SNPs) and candidate genes

METHODS

- 317 Chios and 346 Frizarta ewes
- 4 farms (2 farms/breed)
- Individual records of daily milk yield, FC, PC, and LC → collected monthly for 2 years
- LMY and weighted means of FC, PC, and LC → used for further analyses
- Genotypes (Illumina OvineSNP50)
- Variance components of studied traits (ASReml v4.2)
- Genome-Wide Association Studies (GEMMA v0.98.1)
- Bonferroni correction for multiple comparisons → determination of genome-wide and suggestive significance thresholds

RESULTS

- Polygenic inheritance pattern
 - No common SNPs/genes between breeds
- Chios** → $h^2=0.42-0.70$
- 1 genome-wide and 11 suggestive significant SNPs
 - 28 candidate genes (some of which involved in climate adaptation, fat-tail development and relevant traits)
- Frizarta** → $h^2=0.34-0.62$
- 7 suggestive SNPs
 - 15 candidate genes

DISCUSSION – CONCLUSIONS

Results suggest a distinct genetic control of milk performance in the two breeds, possibly related to the diverse evolutionary trajectories of fat-tailed and thin-tailed sheep.

Figure 1: LMY

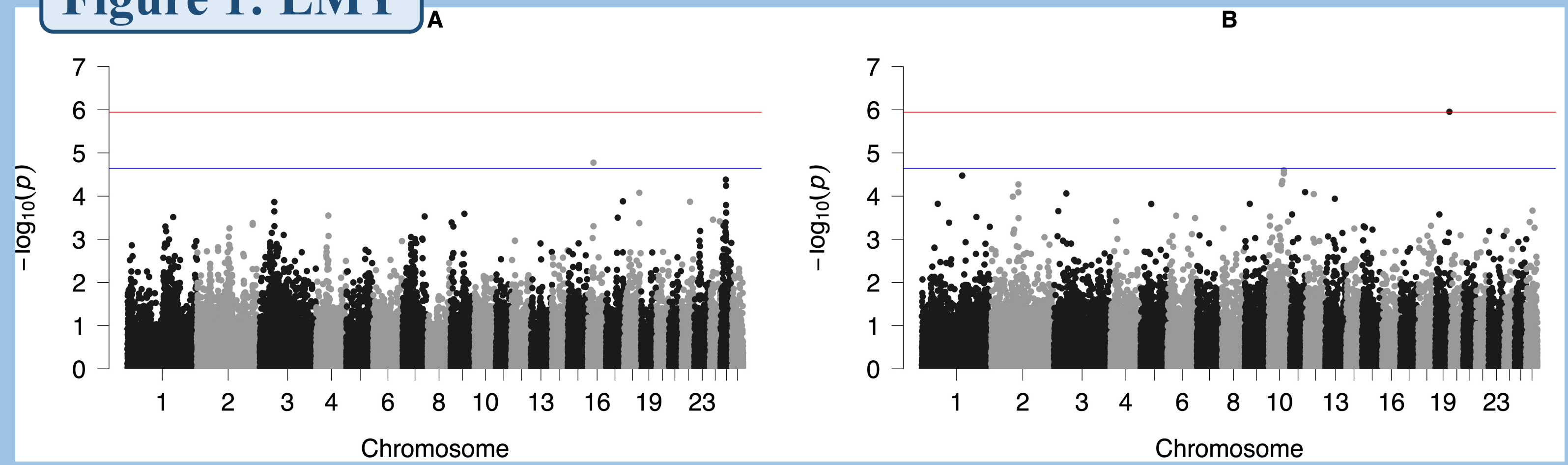


Figure 2: FC

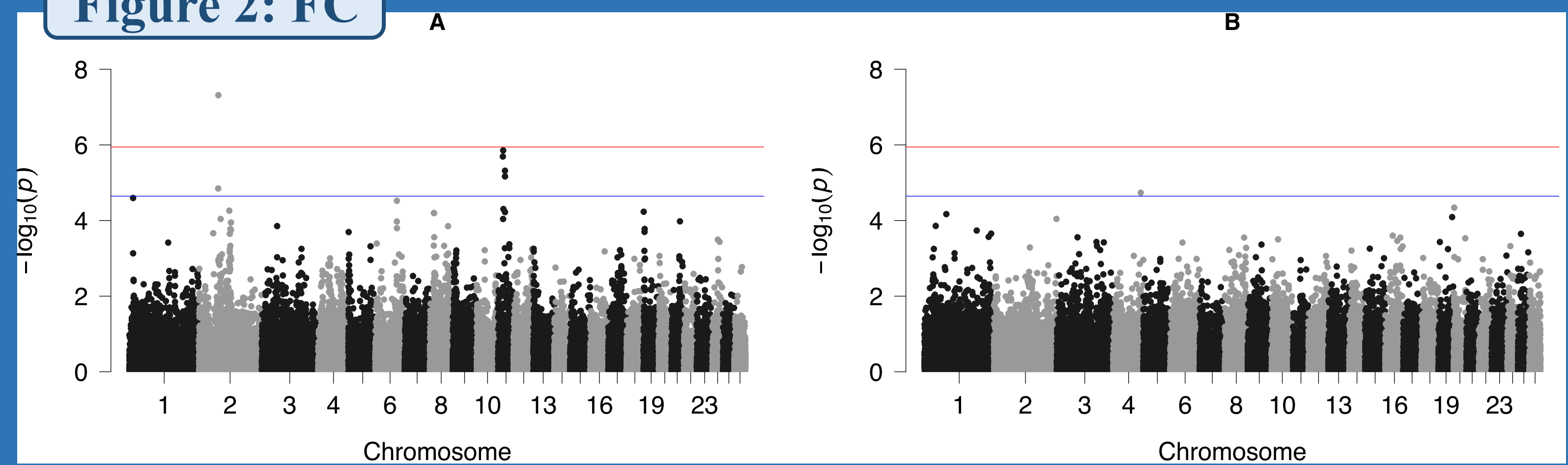


Figure 3: PC

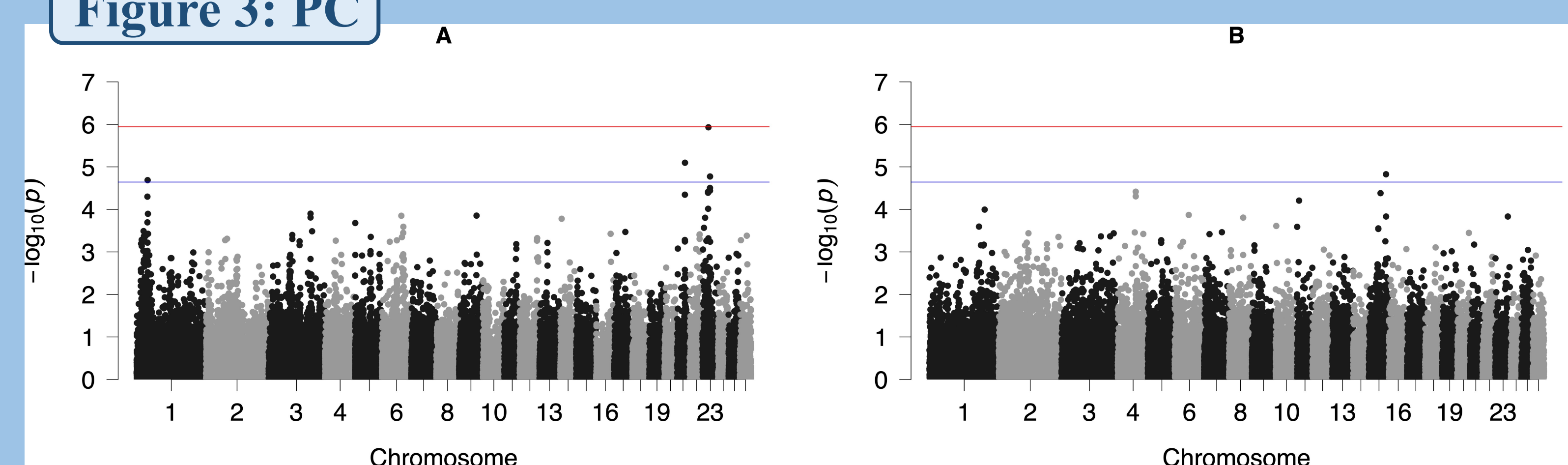
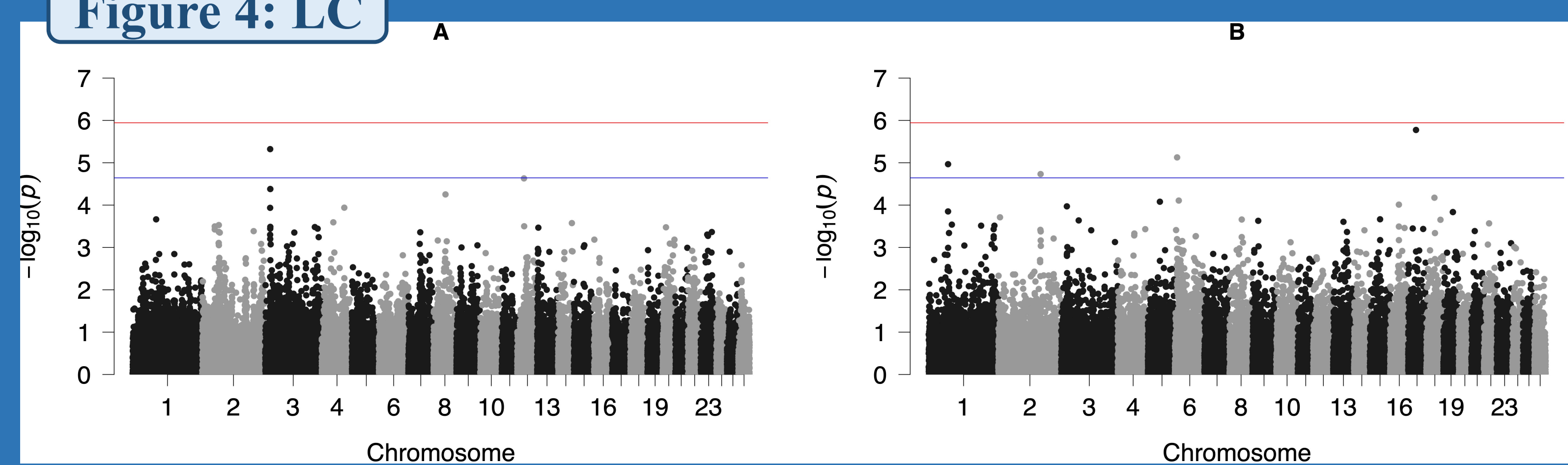


Figure 4: LC



Manhattan plots illustrating SNP associations with LMY (Figure 1), FC (Figure 2), PC (Figure 3) and LC (Figure 4) of Chios (A) and Frizarta (B) sheep. Red and blue lines mark the genome-wide and suggestive significance thresholds, respectively.

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