

## QTL enrichment analysis of candidate regions identified in Croatian Holstein cattle

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### Abstract

Holstein cattle, as the most widespread dairy breed, have undergone intensive artificial selection, leading to reduced genetic diversity and the need for genetic monitoring in local populations. Understanding the genetic basis of economically important traits requires identifying genomic regions under selection and assessing their functional impact. This study focused on QTL enrichment analysis within candidate regions under selection in Croatian Holsteins. A total of 417 cows were genotyped using the Illumina BovineSNP50 BeadChip, with 26,887 autosomal SNPs retained after quality control. Using four complementary selection detection methods (eROHi, iHS, nSL, and HRiD), nine candidate regions were identified across different chromosomes, with 1,592 mapped QTLs. Among these, 68.22% were linked to milk production traits, with significant enrichment confirmed through functional analysis. The strongest selection signal was an eROHi region on chromosome 6, while HRiD regions on chromosomes 4, 21, and 23 were associated with QTLs related to health, exterior, production, meat, and carcass traits. These findings highlight the dominant selection pressure for milk production while revealing its impact on other economically relevant traits, contributing to a better understanding of the genetic architecture and breeding dynamics of Croatian Holsteins.

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