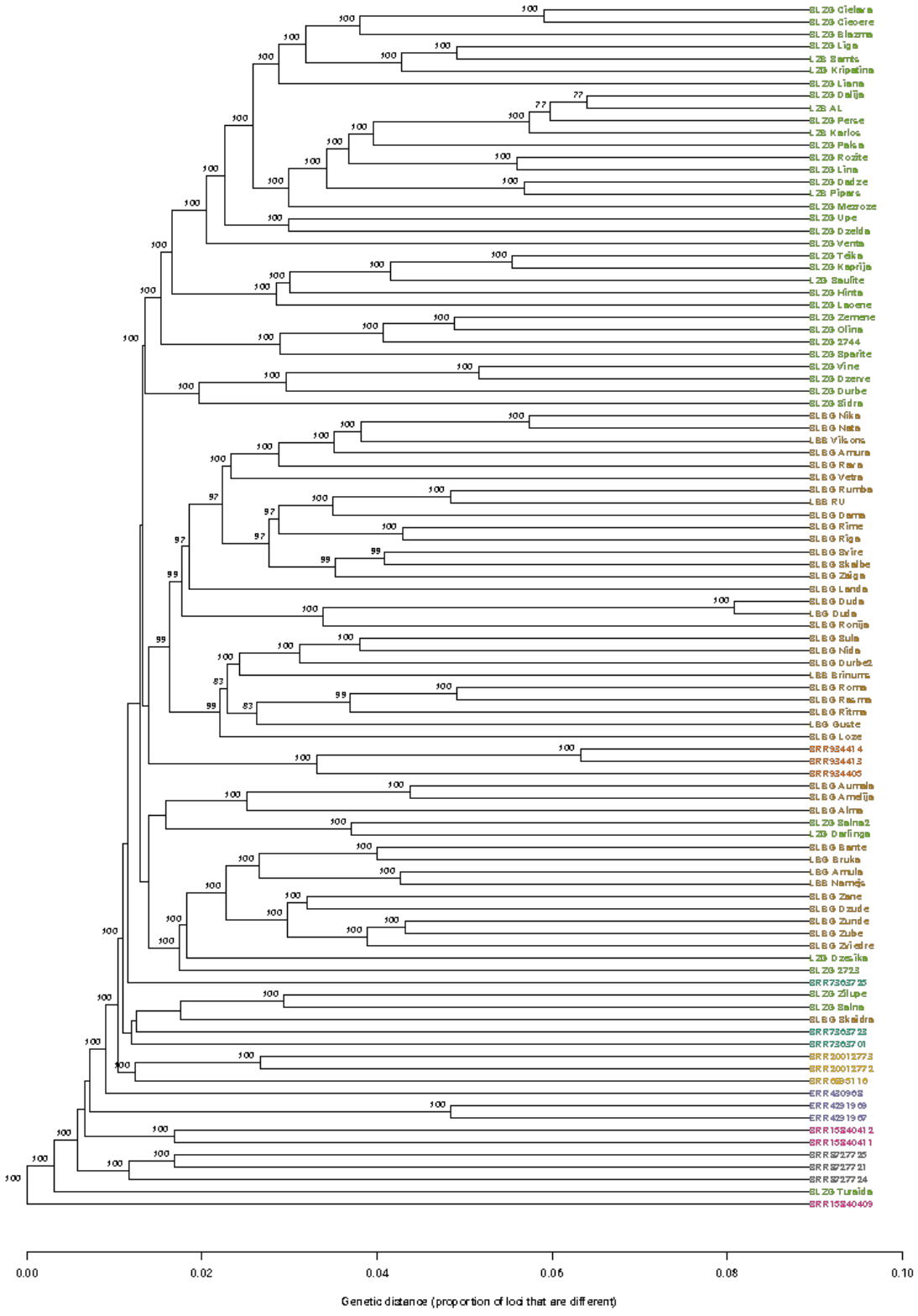

Supplementary Figure S11. Genetic distance tree based on the UPGMA algorithm representing the genetic relatedness of all the samples analysed in the present study. The tree was reconstructed using 100 bootstrap replicates to assess branch support. Tips are coloured according to the breed.