

# Supplementary Material

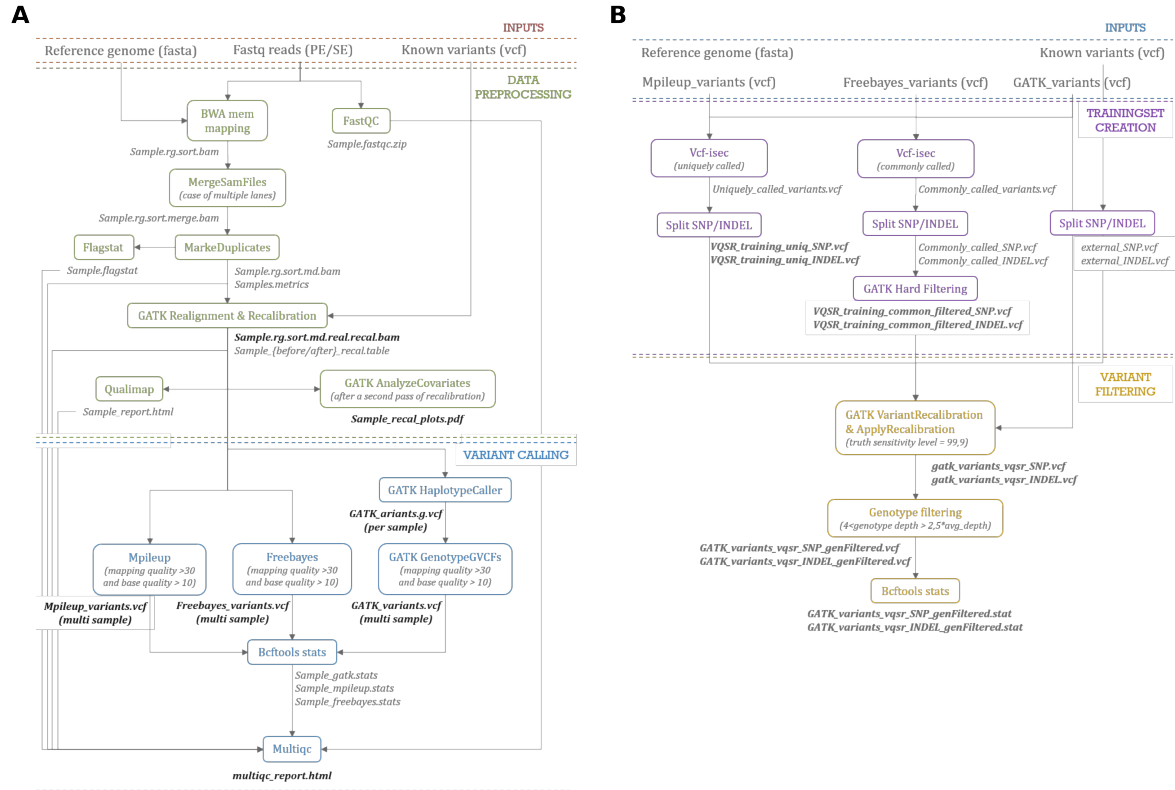


Figure S1: **Alignment and variant calling pipeline.** **A.** In the alignment step samples are treated independently and analyzed using the three callers. They are finally merged into 3 files, one per caller. **B.** In the variant calling step, GATK variants (SNPs/InDels) are filtered using information on good quality and poor quality training sets. A final filter on genotypes coverage is applied. The final output of the alignment and calling pipeline is shown in bold

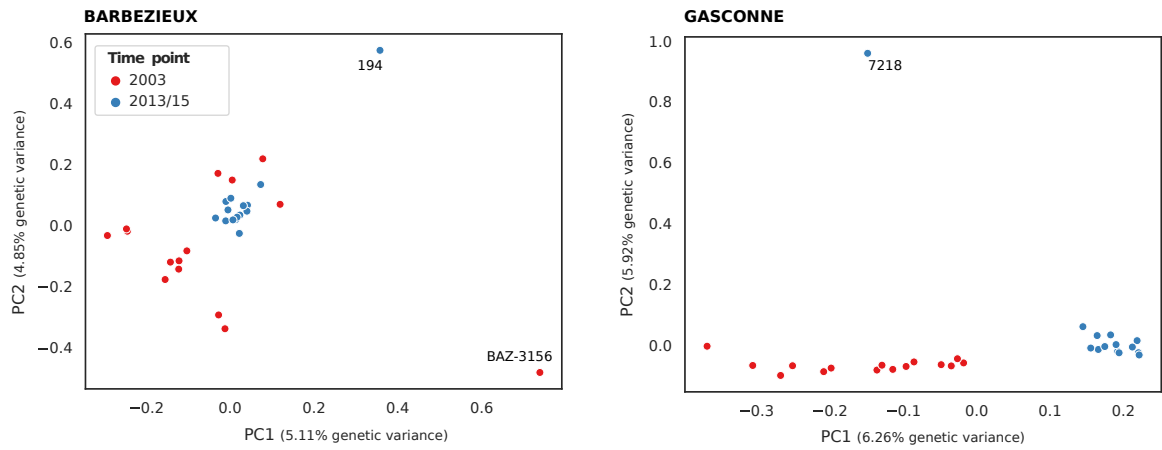


Figure S2: **Breed-specific principal component analysis (PCA)**. The principal component analysis was performed on the two breeds separately after filtering for an LD threshold of 0.5. After LD pruning, a total of 84,930 and 108,403 SNPs were retained for the Barbezieux and Gasconne breed, respectively

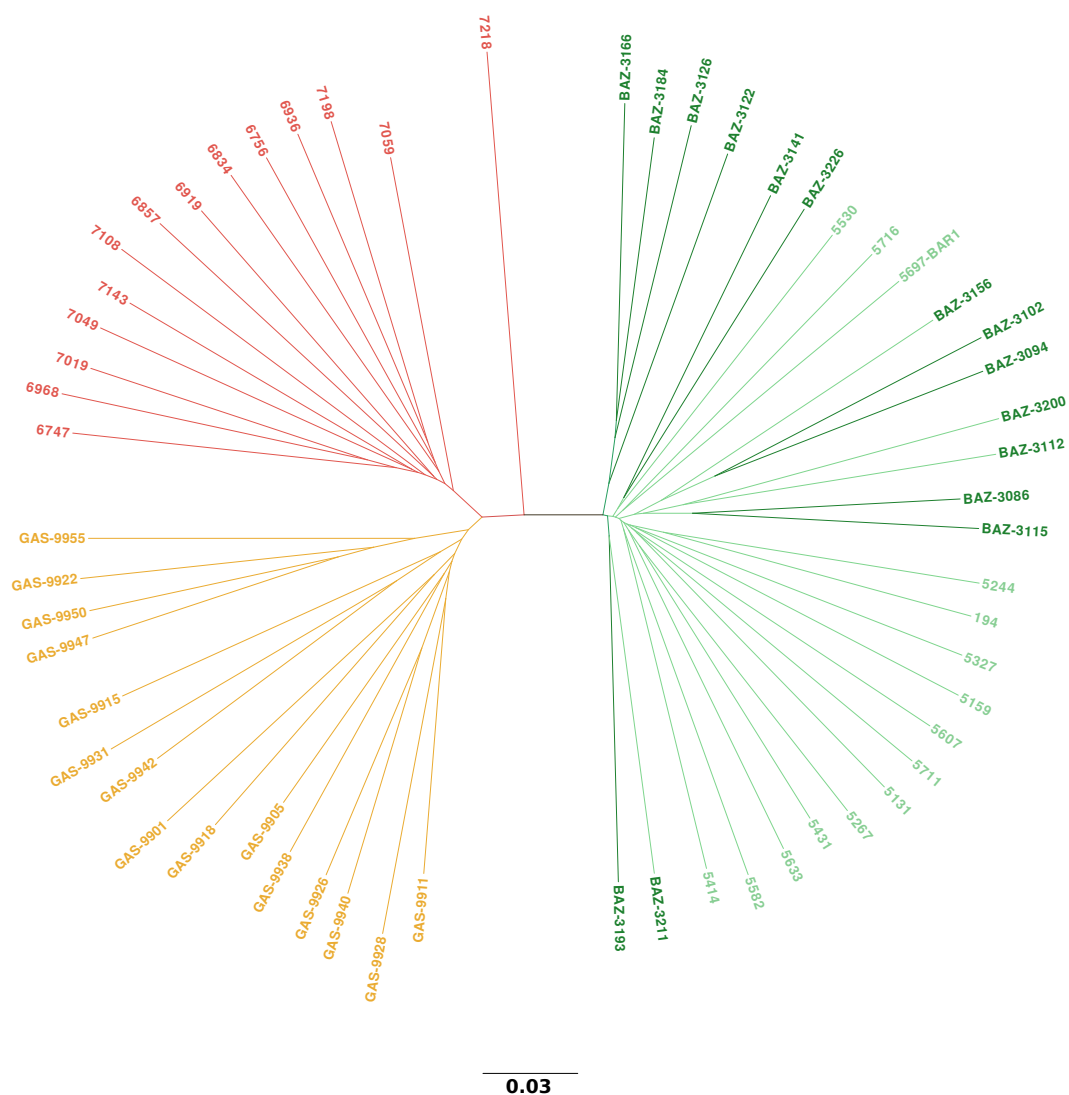


Figure S3: **Neighbour-Joining (NJ) tree.** The NJ tree was constructed from the identity-by-state (IBS) distance relationship matrix estimated on 12,561,354 SNPs after filtering for a missing rate < 10% and a minor allele frequency (MAF) < 0.05. Orange: Gasconne 2003; Red: Gasconne 2013; Dark green: Barbezieux 2003; Light green: Barbezieux 2013

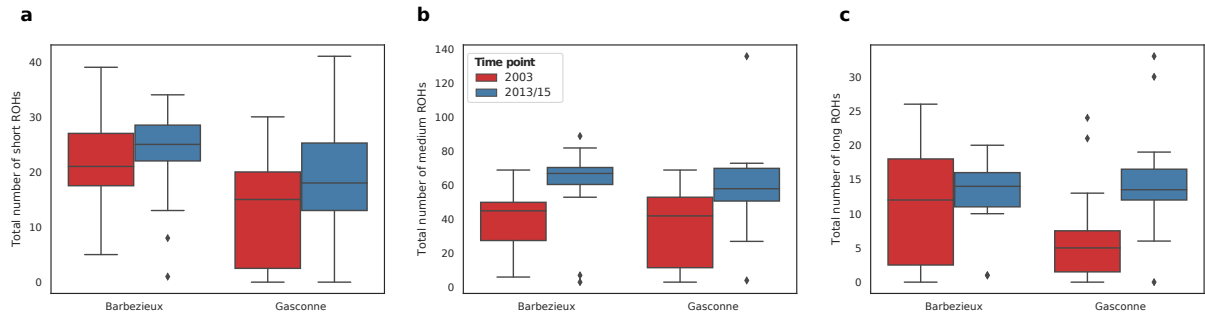


Figure S4: **Number of ROH per individual for different ROH size classes.** The number of ROH in various size classes is indicative of the individual's demographic history. **a.** Short ROHs ( $\leq 100$  kb) indicate ancient inbreeding. **b.** Medium ROHs (0.1-3 Mb) indicate ancient and historic inbreeding. **c.** Long ROHs ( $\geq 3$  Mb) indicate recent inbreeding

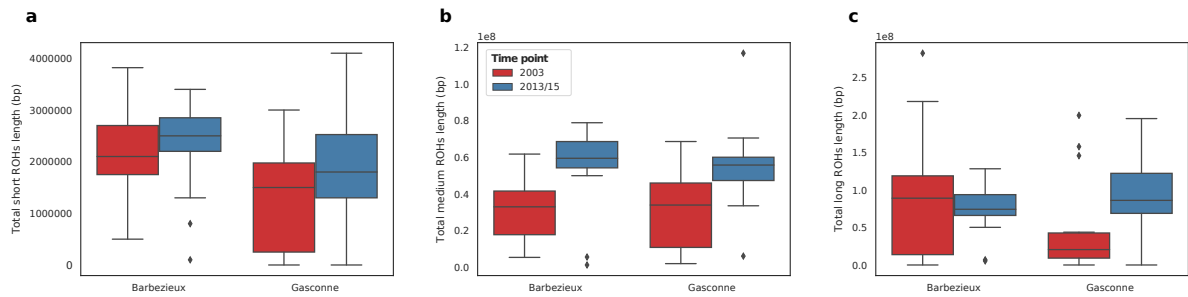


Figure S5: **Summed ROH length per individual for different ROH size classes.** Individuals for each breed are colored based on their time of sampling

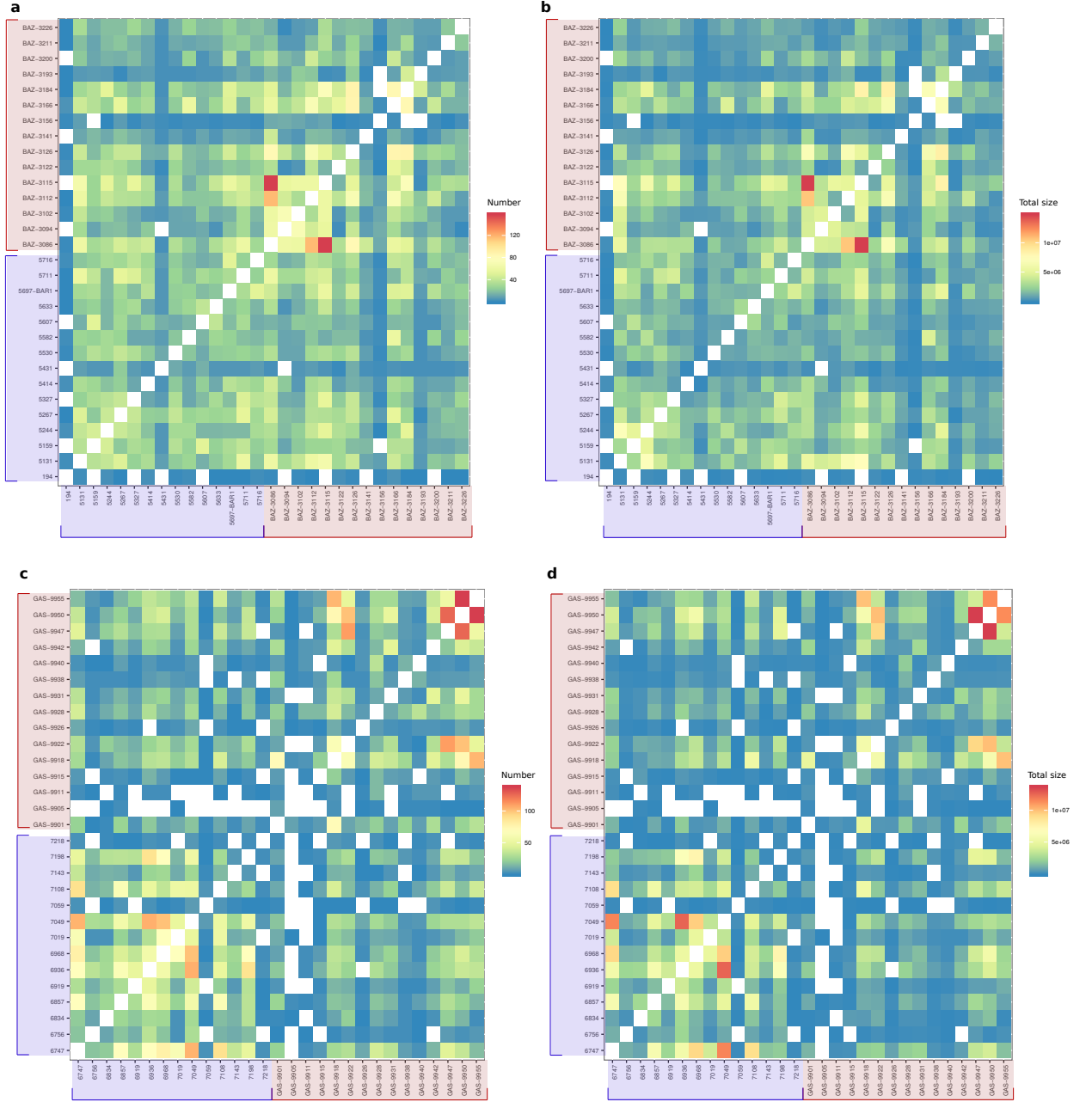


Figure S6: **Number of identity-by-descent (IBD) segments and their total size.** **a.-c.** Pairwise number of IBD segments between individuals in the Barbezieux and Gasconne, respectively. **b.-d.** Total size of pairwise IBD segments in the two populations, respectively. Individuals sampled in 2003 are highlighted in red, whereas those sampled in 2013/15 are in blue

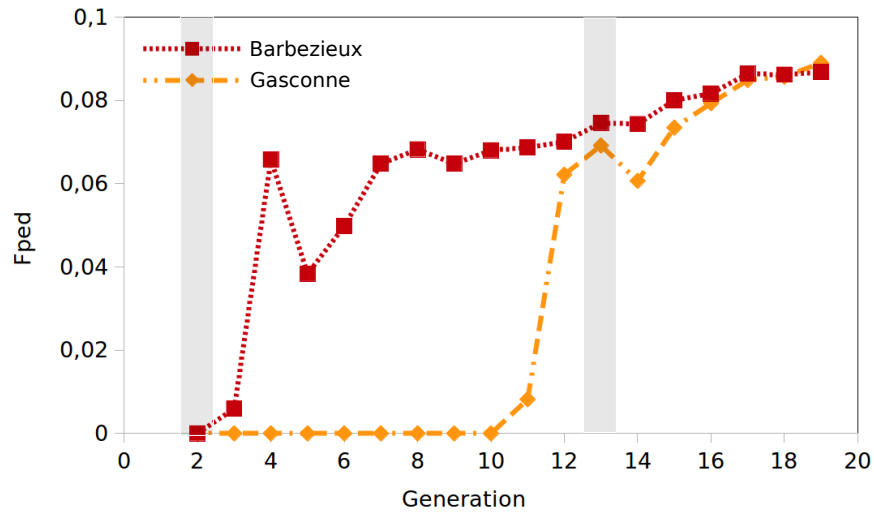


Figure S7: **Trend in pedigree-based inbreeding coefficient ( $F_{PED}$ )**. Generation 3 (year 2003) and 13 (year 2013) are highlighted in grey

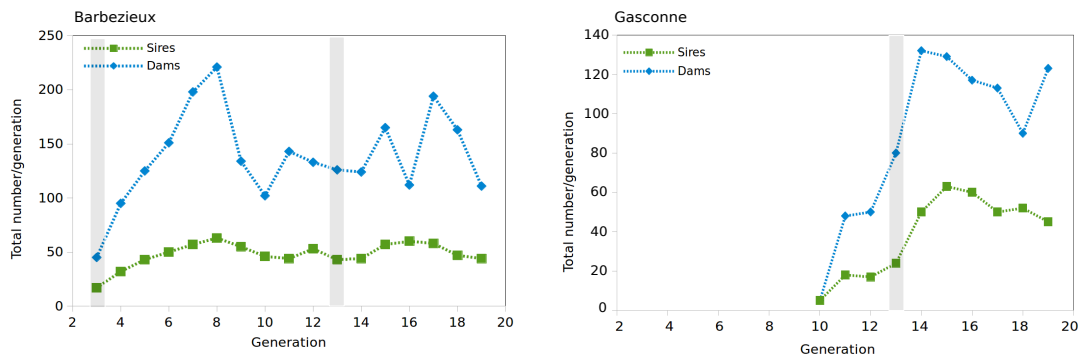


Figure S8: **Trend in population size** . Generation 3 (year 2003) and 13 (year 2013) are highlighted in grey

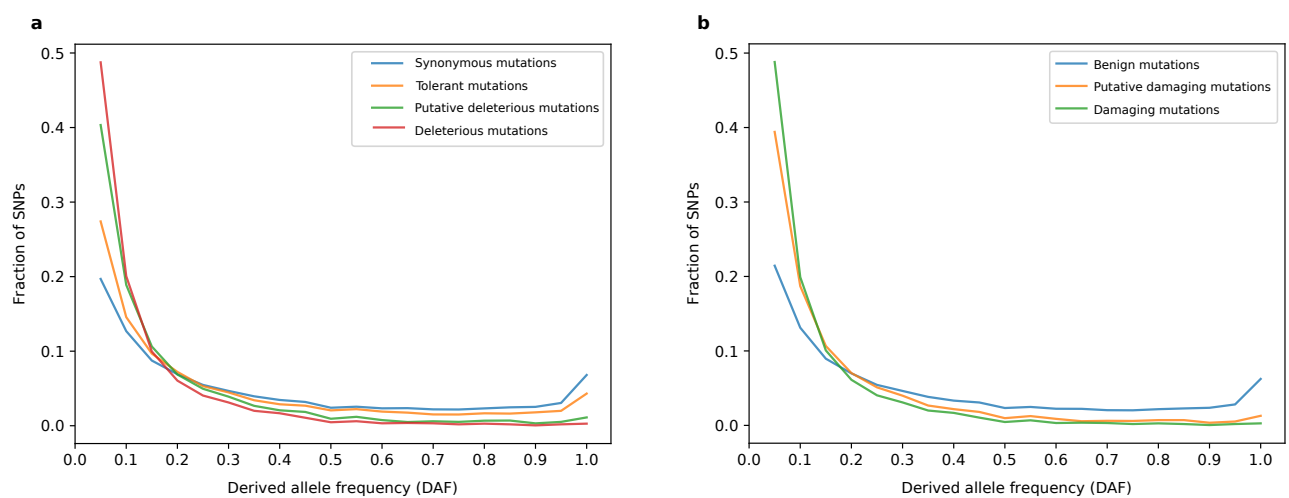


Figure S9: **Derived allele frequency distribution.** **a.** Derived allele frequency distribution of protein-coding variants, classified into synonymous, nonsynonymous tolerated (SIFT > 0.05), nonsynonymous putative deleterious (SIFT ≤ 0.05), and nonsynonymous deleterious (SIFT ≤ 0.05; GERP > 1.0). **b.** Derived allele frequency distribution of protein-coding variants classified into benign (i.e. synonymous, tolerated), putative damaging, and truly damaging

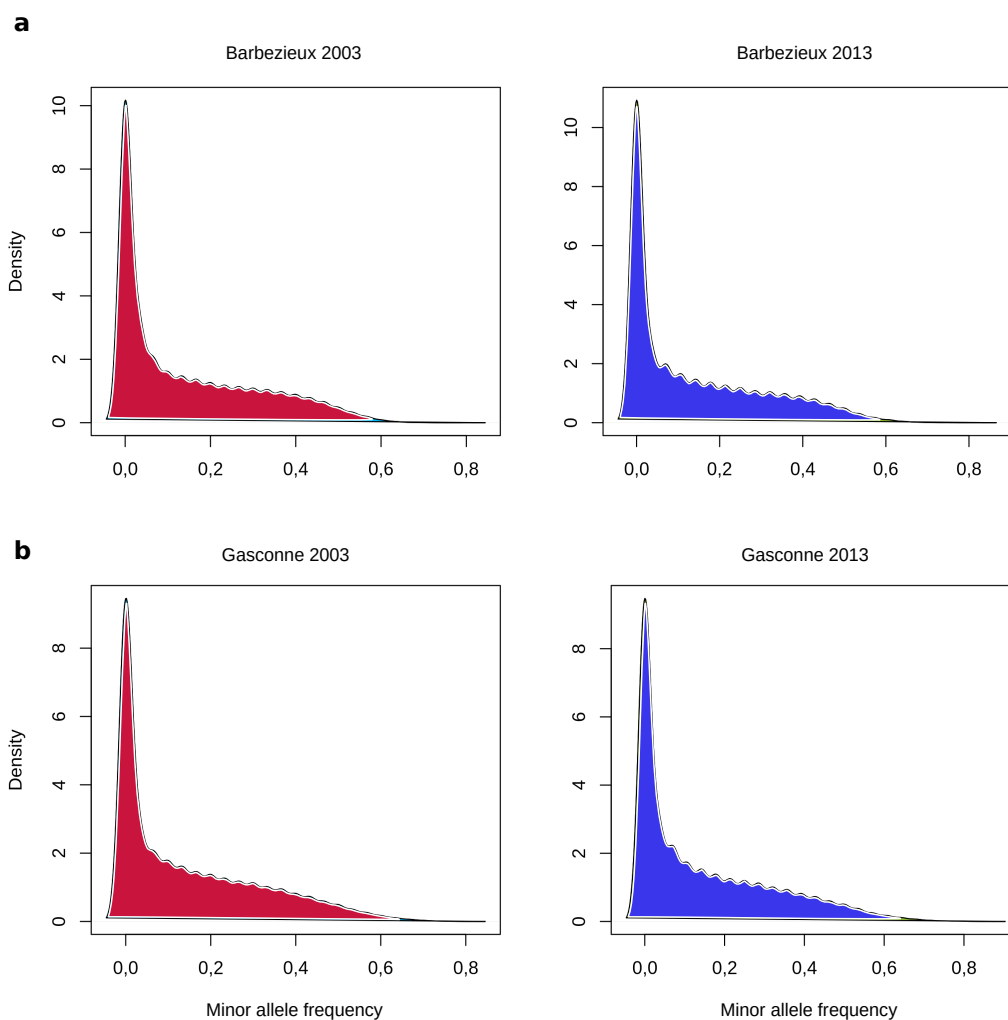


Figure S10: **Temporal changes in allele frequency.** **a.** Allele frequency distribution of the Barbezieux breed in 2003 (left) and 2013 (right). **b.** Allele frequency distribution of the Gasconne breed in 2003 (right) and 2013 (left)