

Genetic diversity of three local chicken breeds using high-density SNP-data

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Introduction

Appenzell Barthuhn (AB), Appenzell Spitzhauben (AS) and Schweizerhuhn (SH) are the three local Swiss chicken breeds.

Goal: analysis of genetic diversity and estimation of genomic inbreeding coefficients for these three breeds using high-density SNP-genotypes



Appenzell Barthuhn



Appenzell Spitzhauben



Schweizerhuhn

Results

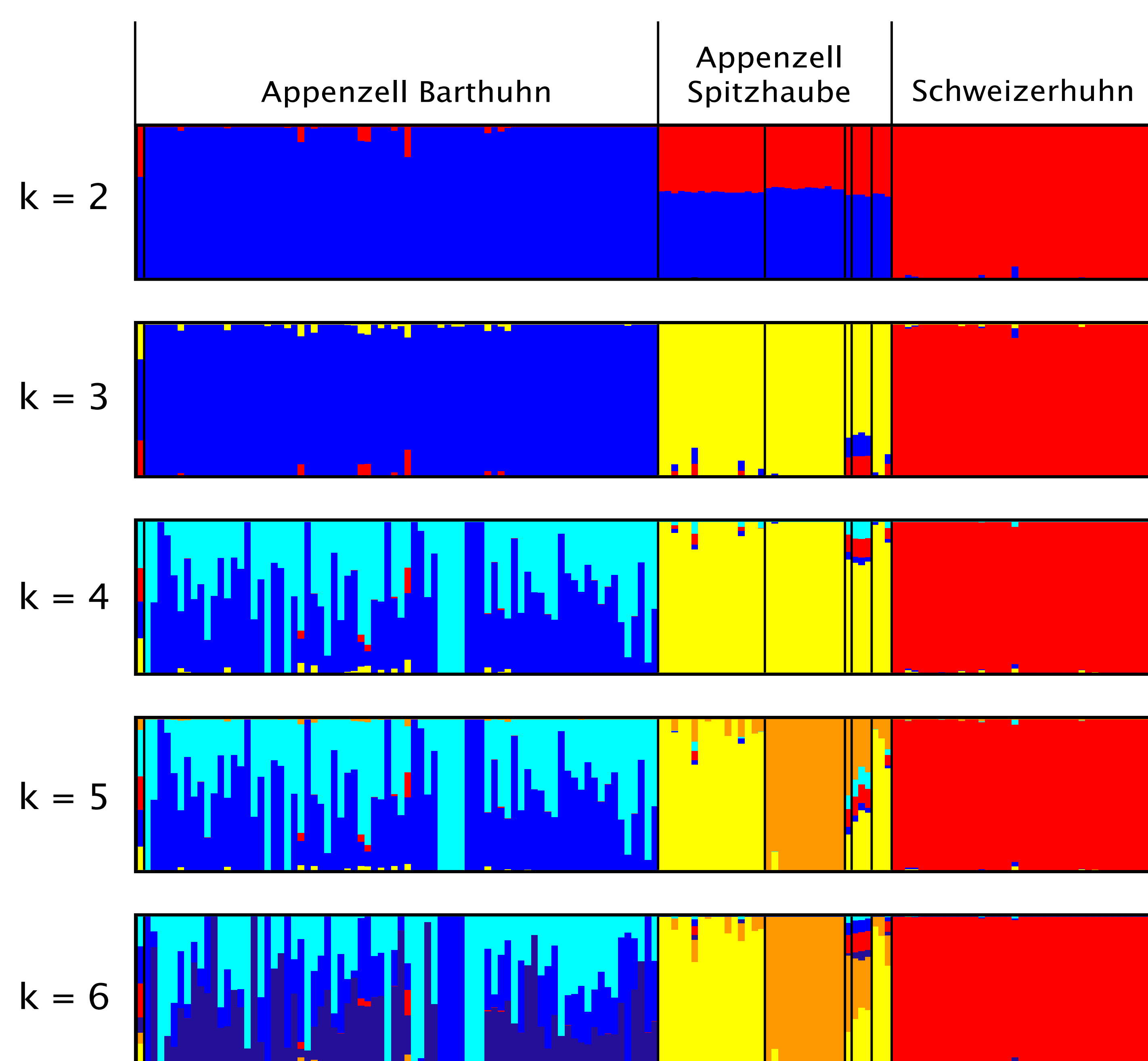


Figure 1: Estimated population structure of the three local chicken breeds, separated by breed and feather colour

Table 1: Average F_{ROH} for the AB, AS and the SH breed

	AB	AS	SH
Average F_{ROH}	0.238 ± 0.074	0.397 ± 0.109	0.181 ± 0.06

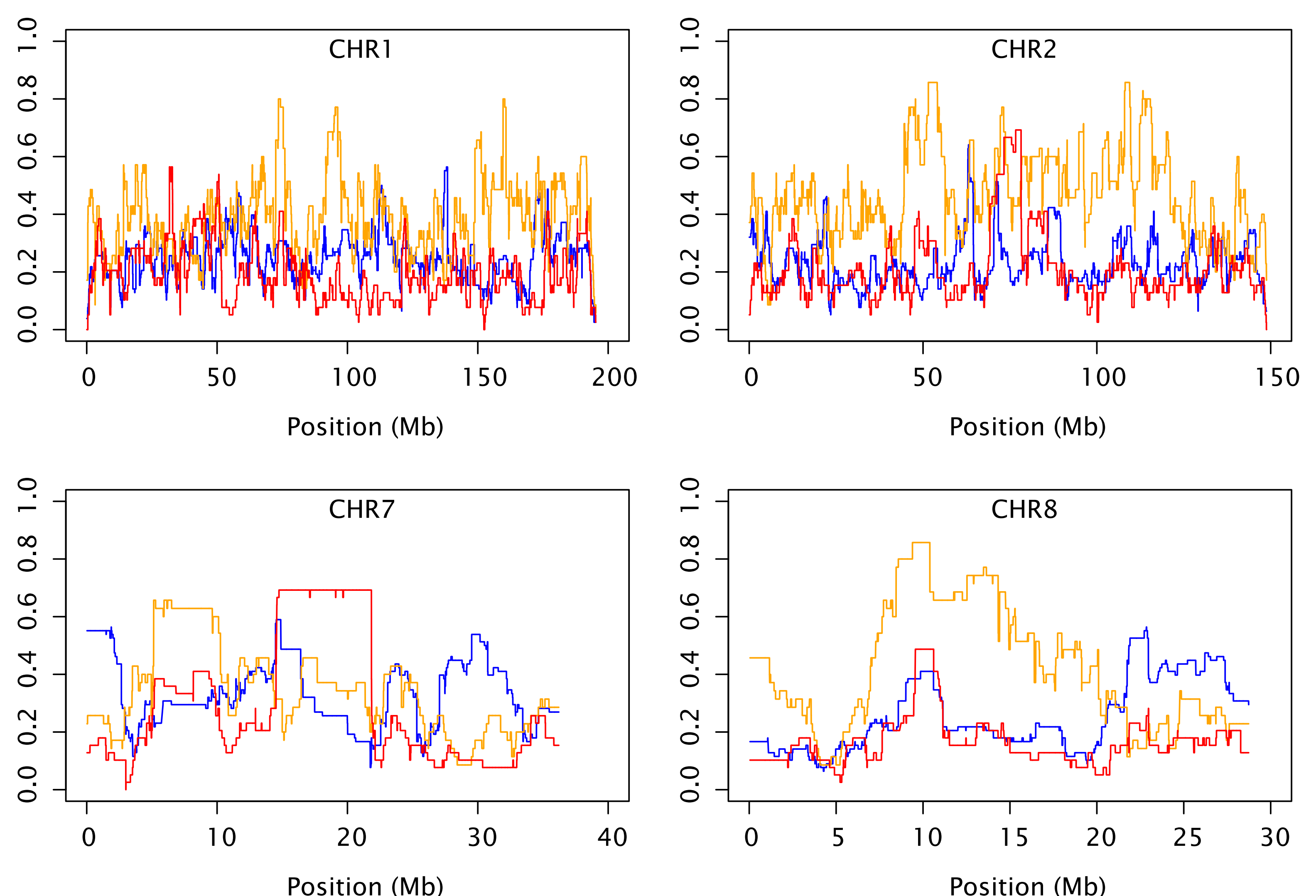


Figure 2: Proportion of individuals of the three breeds (AB: blue line; AS: orange line; SH: red line) having a SNP in a ROH for Chromosome 1, 2, 7 and 8.

Conclusions

- Cluster analysis supports the assumption that admixture with additional breeds is frequent in AB
- Breeding on different plumage colours resulted in sub-structures in the AS breed
- Genomic inbreeding coefficients at remarkable level were found for all three breeds; being highest in AS followed by AB and SH
- The majority of SH-individuals has the region between 14.6-21.8 Mb on CHR7 in a ROH. Structural changes in this region are described in the context of the rose comb phenotype

Material and Methods

After quality control genotypes of 152 chicken and 309'428 SNPs were available. ADMIXTURE was applied for structure analysis. Runs of homozygosity were derived with PLINK and used for the estimation of genomic inbreeding coefficients (F_{ROH}).

Acknowledgements

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