

Genome wide SNP-data for the assessment of genetic diversity in Swiss sheep breeds



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Objective

In the context of the global sheep hapmap project 7 indigenous Swiss sheep breeds were subject to a **detailed analysis of genetic diversity and selection signatures** in Swiss sheep breeds.

For each breed 24 individuals were genotyped for the Illumina OvineSNP50 BeadChip. After filtering 47'975 SNPs remained for final analysis. The analysis was conducted using plink (Purcell 2010), admixture (Alexander et al. 2012) and distruct (Rosenberg 2007).



Conclusions

- The genomic relationships between VBS and VRS are not surprising, as the two breeds are geographically limited to the same region.
- For SMS - an endangered breed - the known influence of SWA could be confirmed with the genomic data.
- ERS seems to be a conglomerate of different genetic sources.
- The selection signature for VBS/VRS in the region of the KIT-gene is explained with differences in the fraction of white coat color. However, analysis of selection signatures based on larger data sets is recommended.

Results

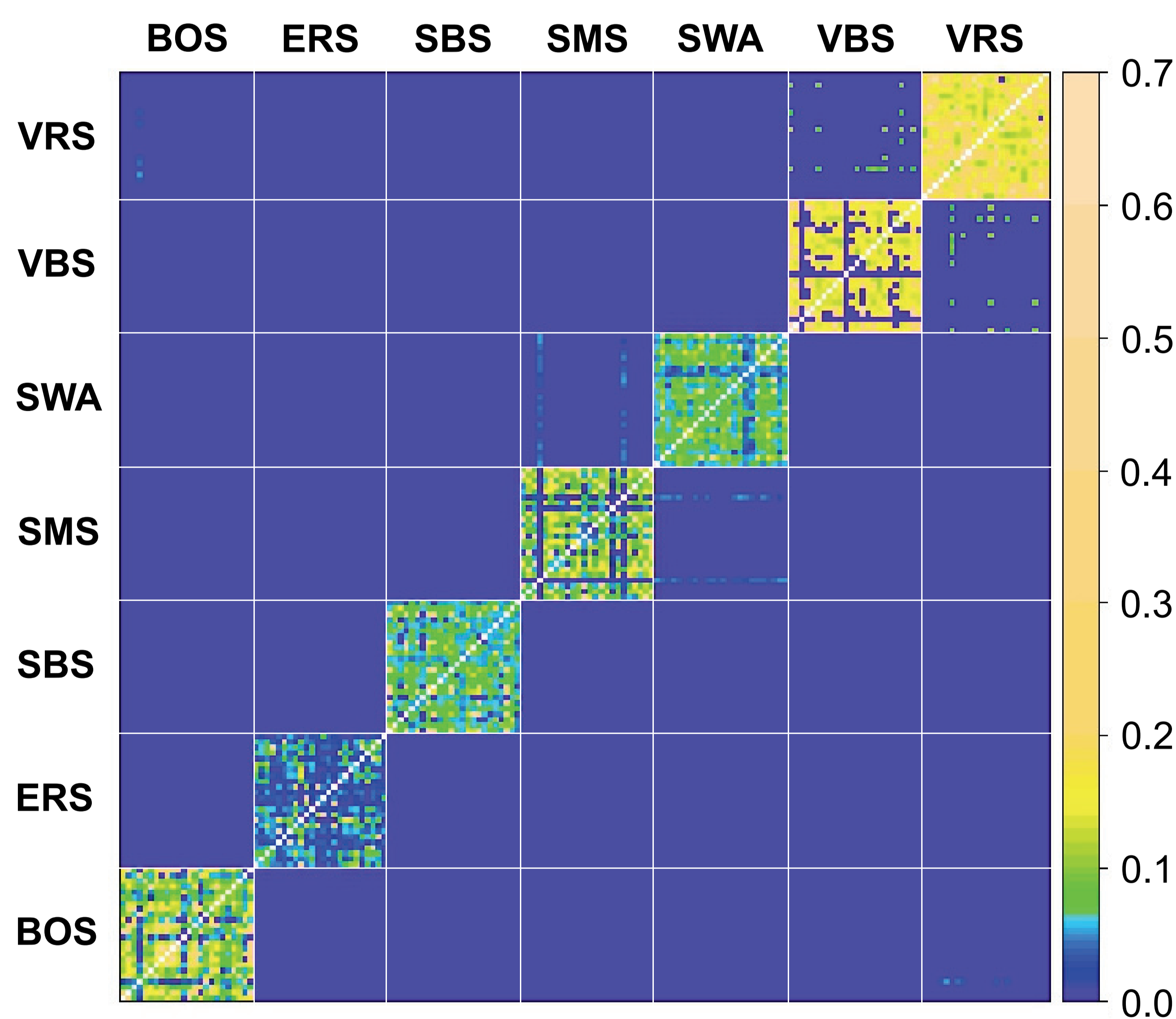


Figure 1: Genomic relationships within and between breeds

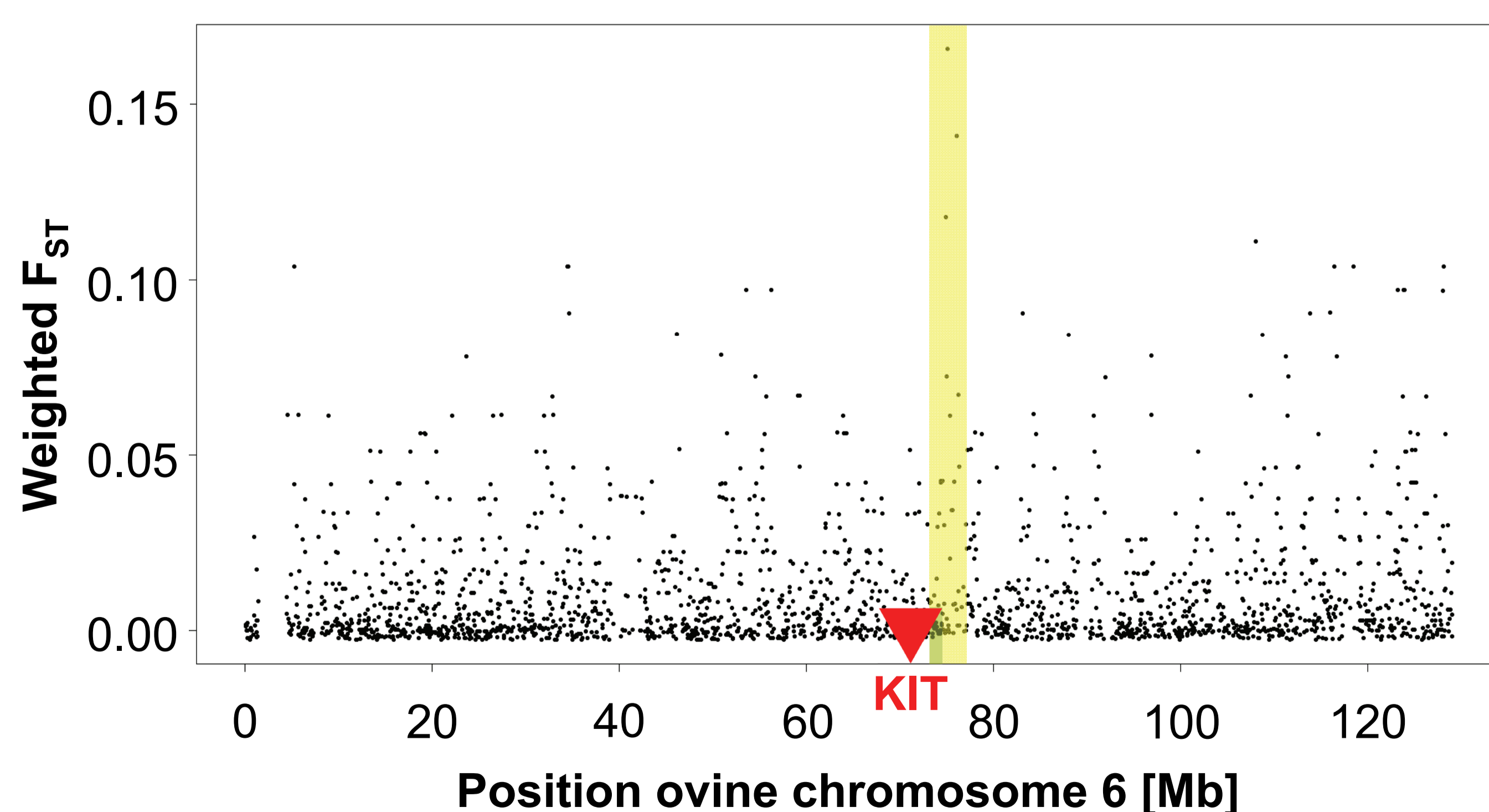


Figure 3: Weighted F_{ST} -values for VBS / VRS on chromosome 6

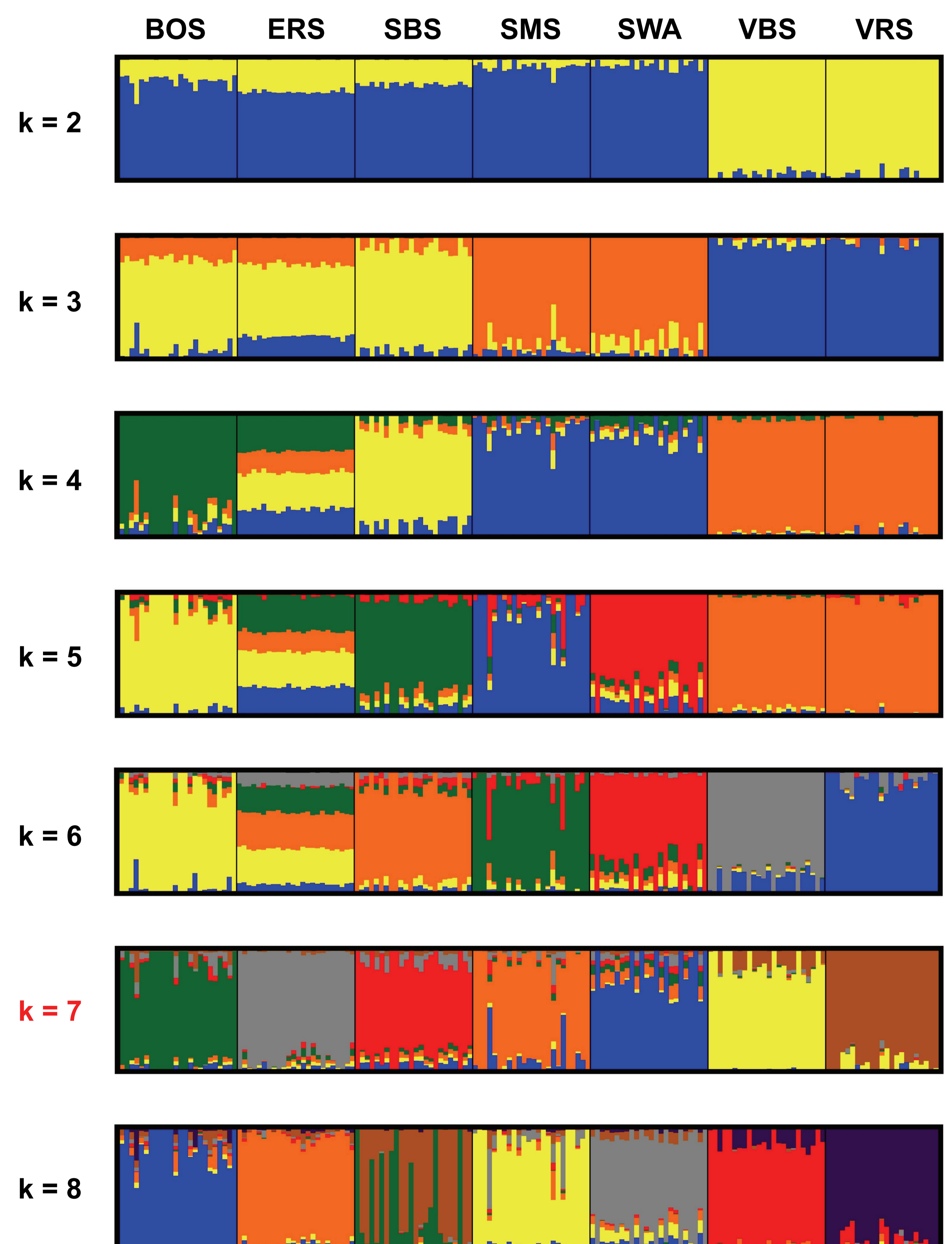
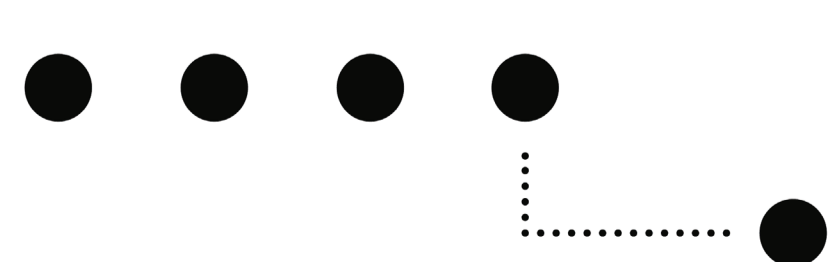
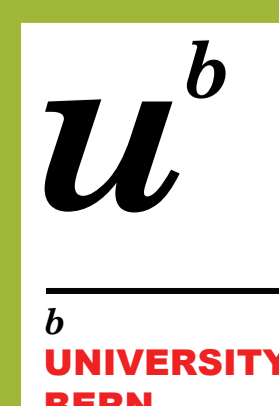


Figure 2: Results cluster-analysis for $k = 2 - 8$, (based on the cross-validation error, the best fit was $k = 7$)



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