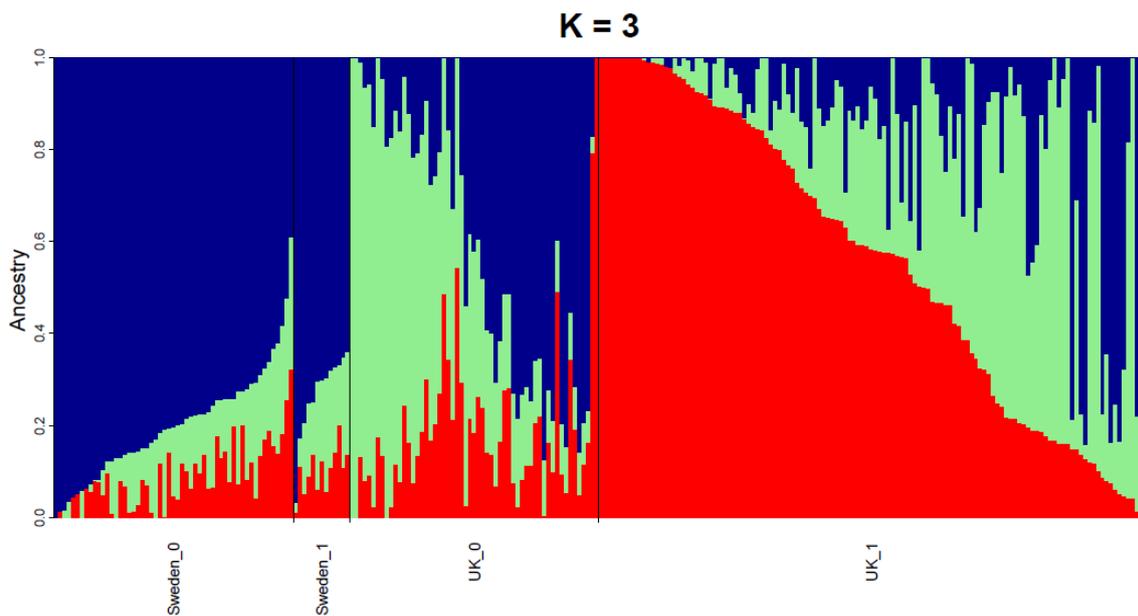


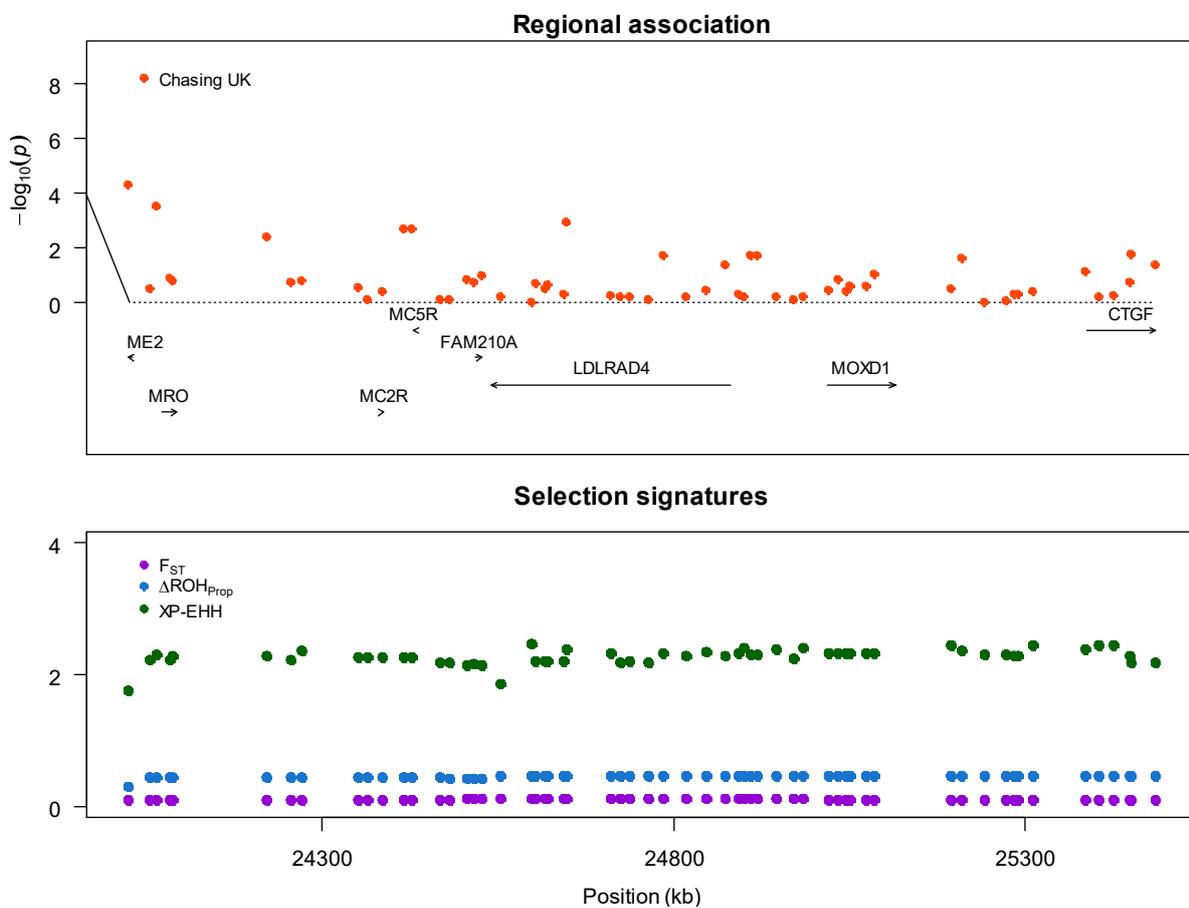
## Appendices

**Figure A1** Ancestry proportions of GSDs based on genotypes of SNPs from putatively selected regions assuming three underlying ancestries ( $K = 3$  clusters) as revealed by ADMIXTURE. Each cluster is represented by a colour and the length of the specific coloured segment indicates the dog's proportion of membership in that cluster. The labels indicate the origin of the dog (Sweden or UK) and the coat colour (1 = saddle tan, 0 = sable, black or others).

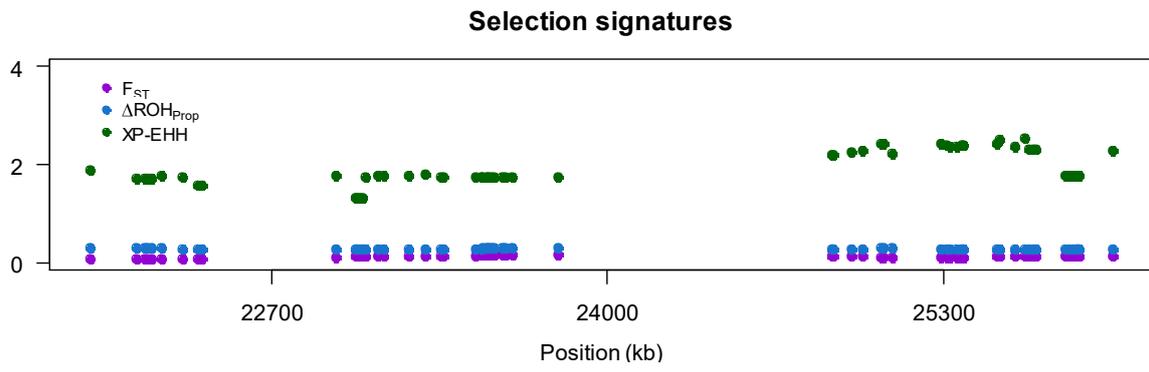
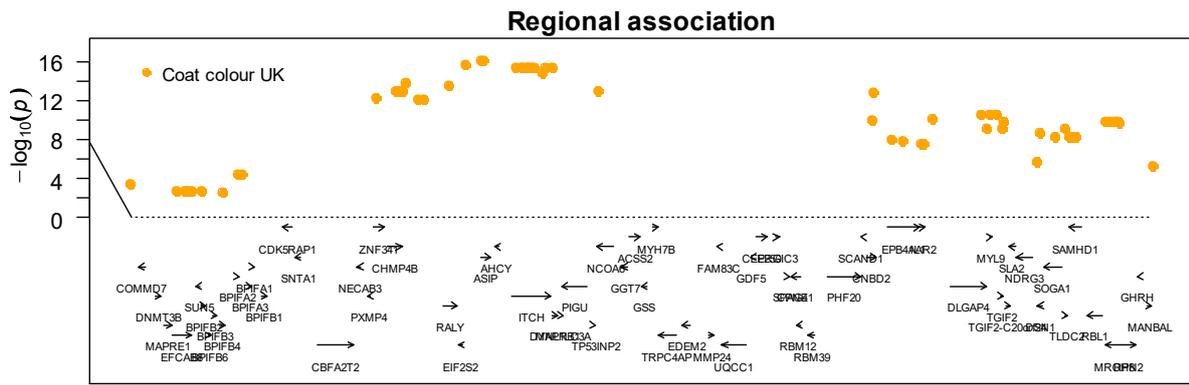


**Figure A2** Fine-mapping of target regions under divergent selection between German Shepherd dog populations. Particularly compelling regions that showed evidence of divergent selection in all three selection signature test statistics (SNP windows-based  $F_{ST}$ ,  $\Delta ROH_{Prop}$ , and XP-EHH) are located on Chr 1, 24 and 32. The plots illustrate the FDR-adjusted P-values from association analyses for phenotypic traits (behaviour, coat colour, coat length) (above, “Regional association”) and the selection signature test statistics (below, “Selection signatures”) for all SNPs in these regions. The plots were created using a modified R code from that of Saxena et al. 2007<sup>91</sup>.

Chromosome 1 (24.0 to 25.5Mb)

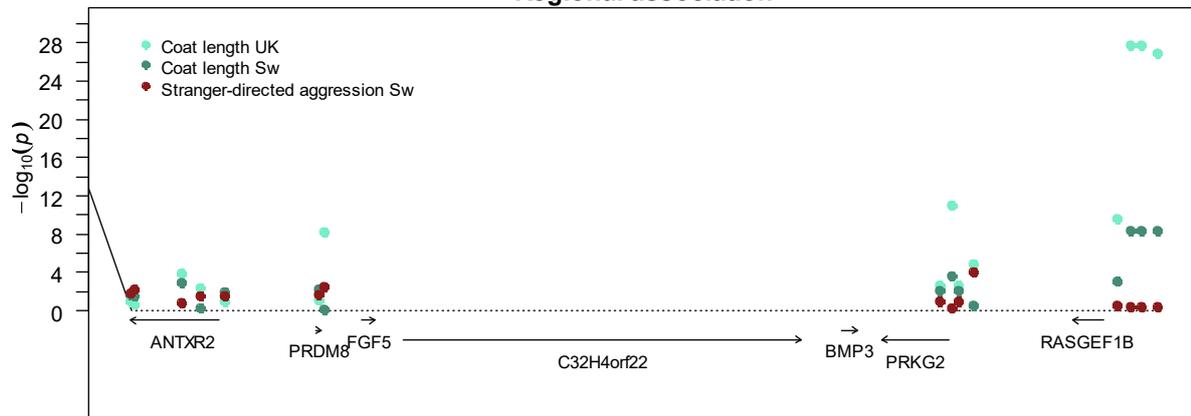


Chromosome 24 (22.0 to 26.0Mb)



# Chromosome 32 (53.5 to 56.7Mb)

## Regional association



## Selection signatures

