

Figure 1: Distribution of p-values for regression models with maximum temperature in April. Each horizontal line shows a possible threshold, either using Bonferroni correction or False Discovery Rate [9]. The labels indicate how many models are significant at this level, the number of associated SNPs are in parenthesis.

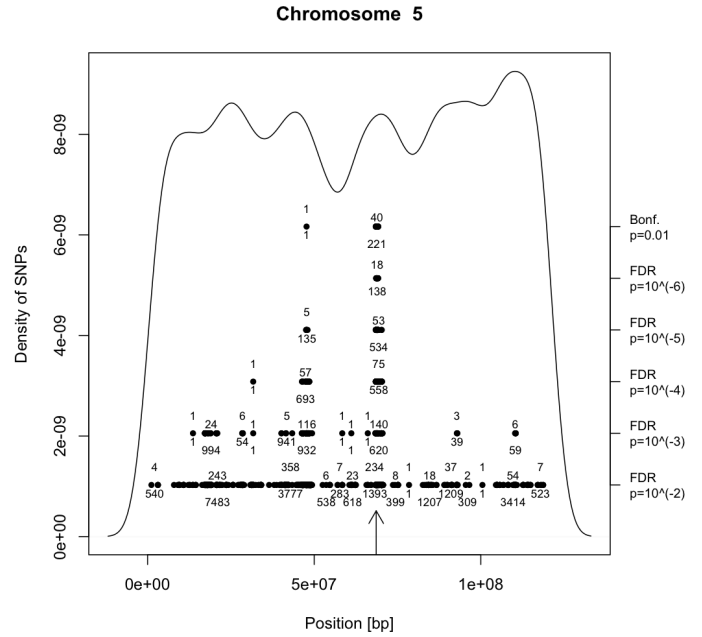


Figure 2: Solid line shows the overall SNPs density on chromosome 5. Horizontal plots represents the SNPs that were detected for different thresholds. These SNPs were grouped when they were closer than $2 \cdot 10^6$ bp. Each cluster is summarized by the number of SNPs it spans (below) and among these, the number of SNPs under selection (above). The vertical spacing between plots is arbitrary. The arrow points out the SNP BovineHD0500019261.

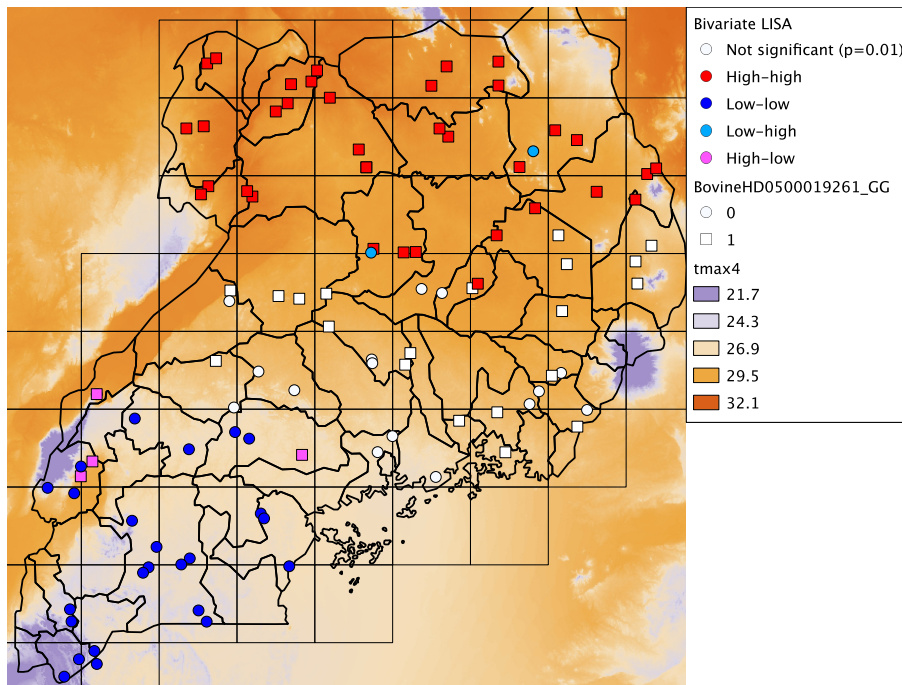


Figure 3: Bivariate local Moran's I between BovineHD0500019261_GG and the mean temperature in April (background layer) for the 102 Ugandan cattle. This indicator measures the spatial correlation between the state of the marker and the temperature averaged over the 20 nearest sampling points. Dots shape indicate where the marker is present (square) or absent (circle) and their color shows the type of association (red=high-high, dark blue= low-low, pink=high-low and light blue=low-high, white=non-significant ($p=0.01$, 10'000 permutations)). The sampling phase was planned following a regular grid to ensure an even spatial representation.