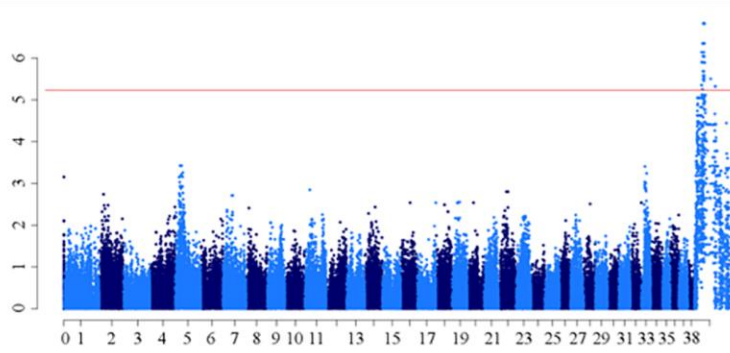
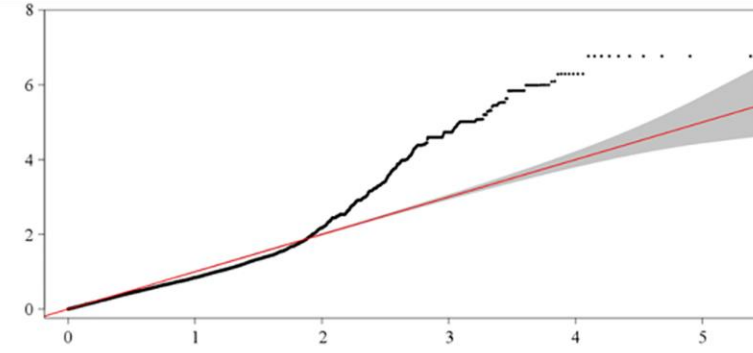
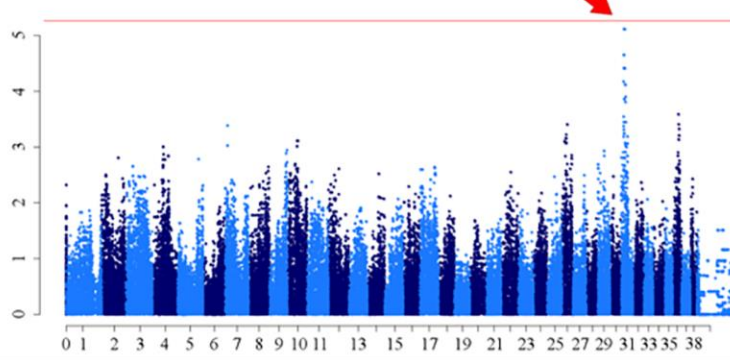
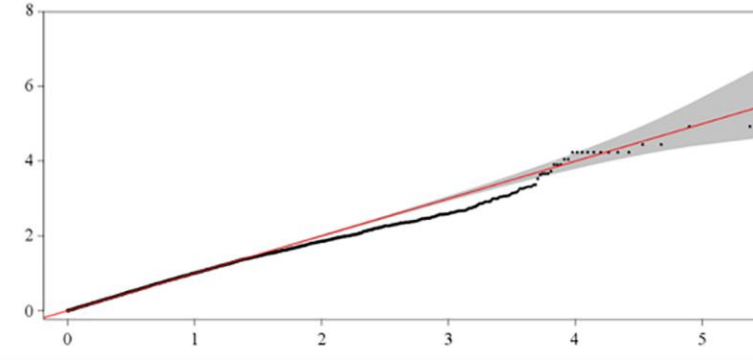
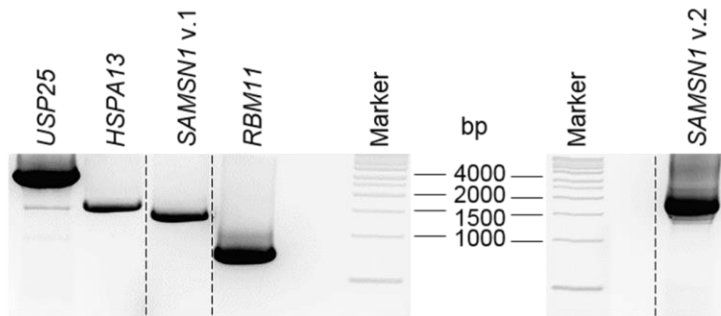
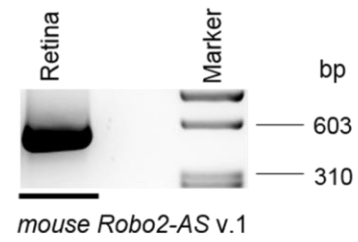


**A****B****C****D****E****F**

**Supplementary Figure S2. Results of genome-wide association study and expression analysis of selected genes.** (A) Manhattan plot showing the negative log of the raw p-values (y-axis) calculated with the mixed-model genotypic association test for XLPR1. On the x-axis, each canine chromosome. Note the peak in canine chromosome X. (B) QQ- plots of the X-chromosome analysis. The plot shows the observed versus expected -log p-values. The diagonal line in the QQ plots indicates the distribution of SNV markers under the null hypothesis. The observed skewing of a marker toward the upper side suggests that it has a stronger association with the pathological condition than one expected by chance. The deviation of observed values from the expected is clearly visible and indicates a consistent difference between cases and controls. The red line shows threshold for genome-wide significance after a Bonferroni correction. (C) Manhattan plot showing the negative log of the raw p-values calculated with the mixed-model genotypic association test for the disease resistance trait (Moderate (N=12) versus Severe (N=15) phenotype). The suggestive peak (indicated with the red arrow under the Bonferroni correction threshold) was used as a starting point for the subsequent phasing of CFA31. (D) QQ-plot of the disease resistance GWAS analysis. We observed no distinct skewing of a marker toward the upper side, suggestive of low power or the incomplete association. (E) Expression of selected genes [*RBM11*, *HSPA13*, *SAMSNI* (v.1 and v.2) and *USP25* transcripts] in 24 wks old normal canine retina. Note: in order to present the data in a streamlined way the irrelevant lanes were spliced out from the 12-wells agarose gel (indicated by dashed lines). (F) Expression of the orthologous *Robo2-AS* v.1 transcript in normal mouse retina (1 month old).