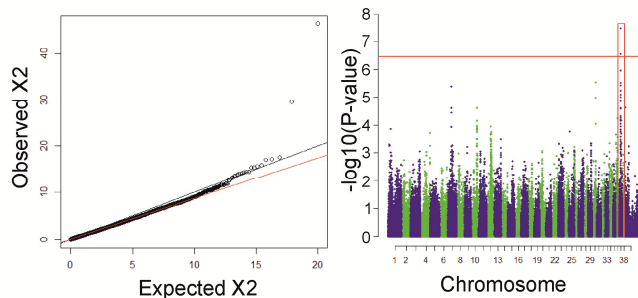
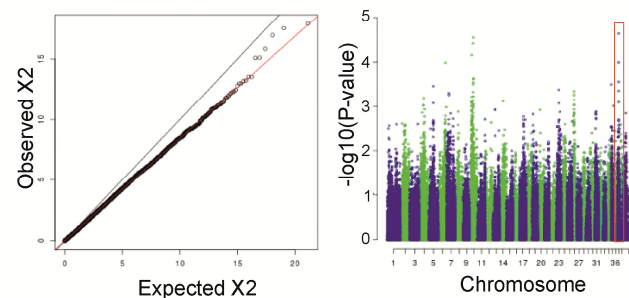


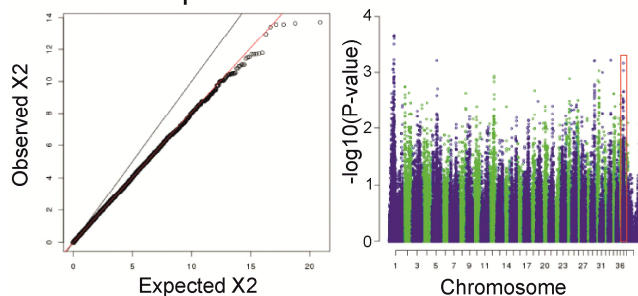
A. Belgian Shepherds



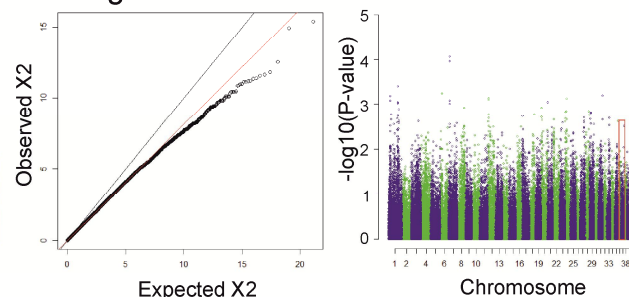
B. Schipperkes



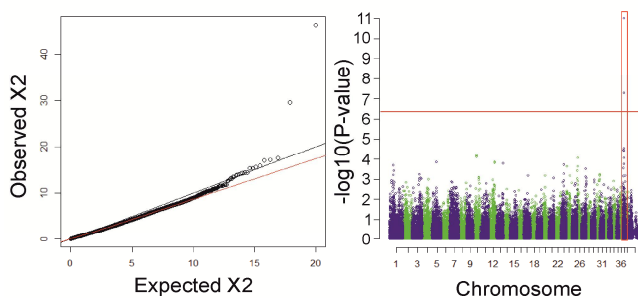
C. Finnish Spitzes



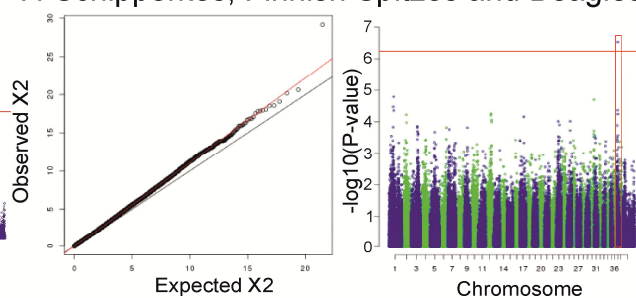
D. Beagles



E. All four breeds combined



F. Schipperkes, Finnish Spitzes and Beagles



Additional Figure 2. Results of the genome-wide association study (GWAS). Quantile-quantile and association plots of the GWAS in four dog breeds individually (A-D), and combined cohorts (E-F). The red line on the Manhattan plots for Belgian Shepherds (A), Schipperkes, Finnish Spitzes and Beagles (E) and all four breeds (F) represents the p-value level of genome-wide significance. The GWAS in Schipperkes, Finnish Spitzes or Beagles alone did not reach genome-wide significance. CFA37 is highlighted with a red outline in the Manhattan plots.