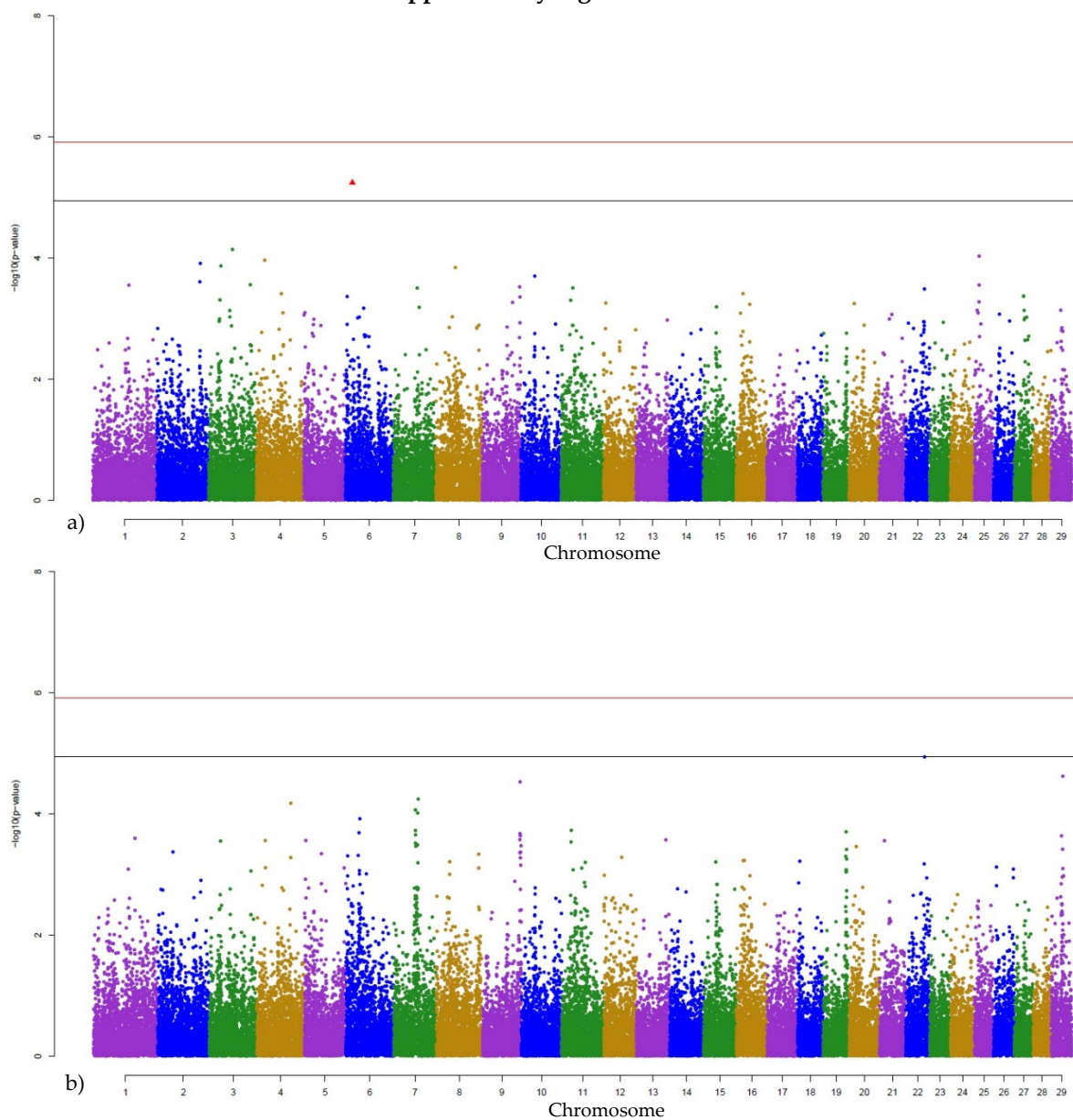
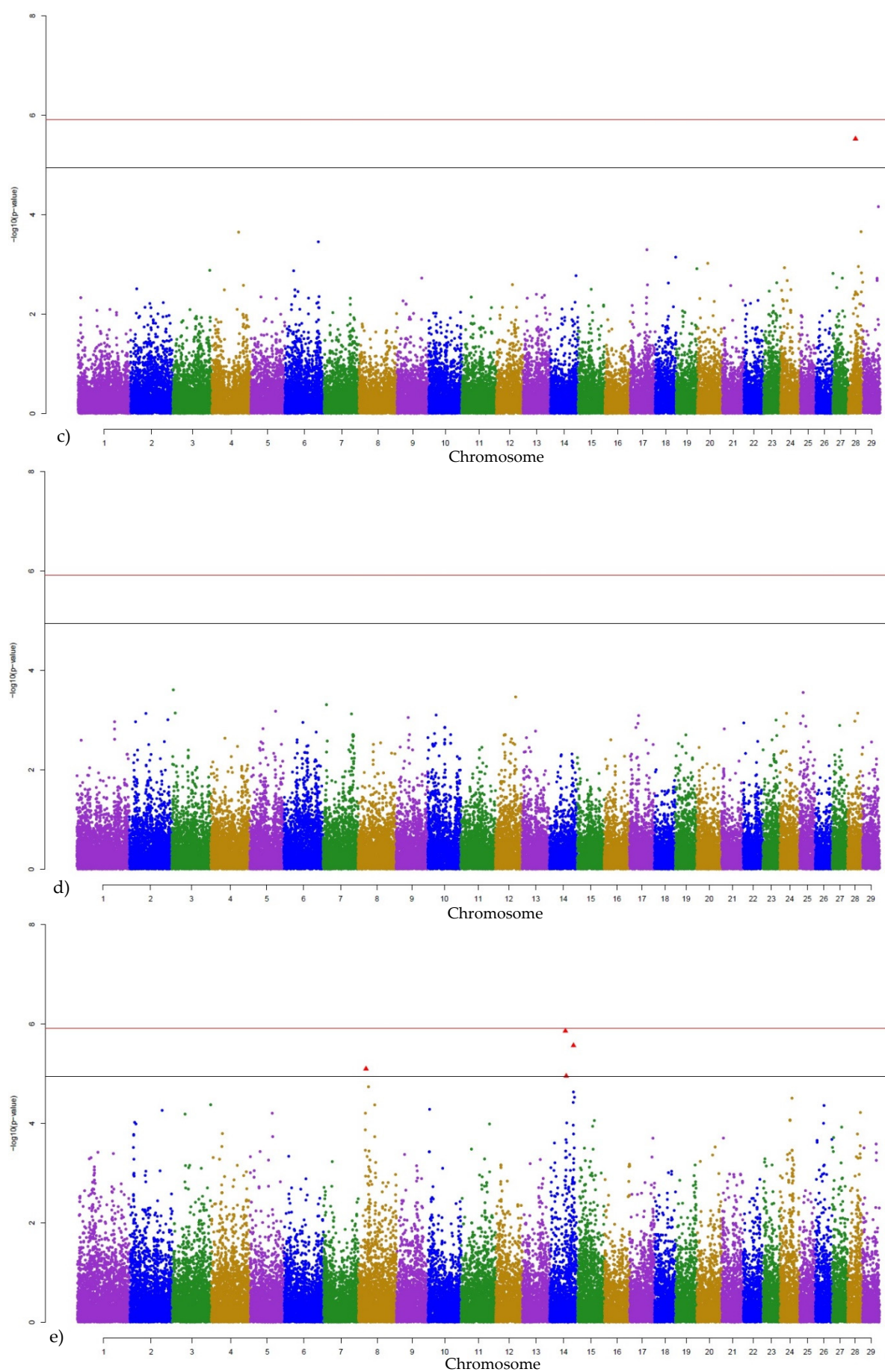
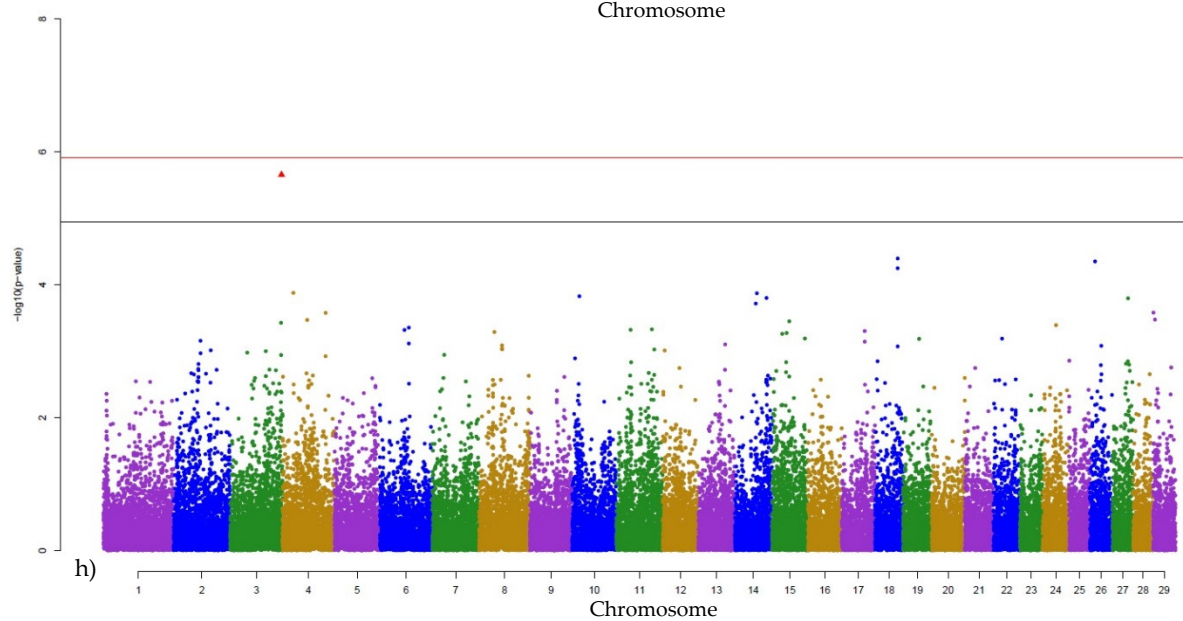
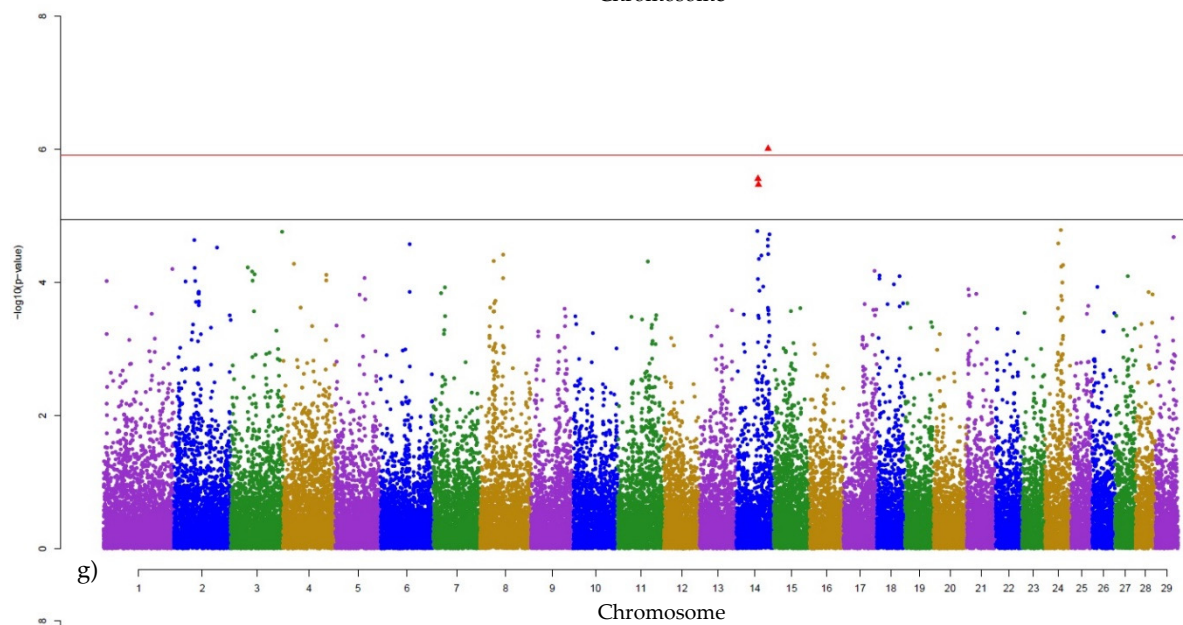
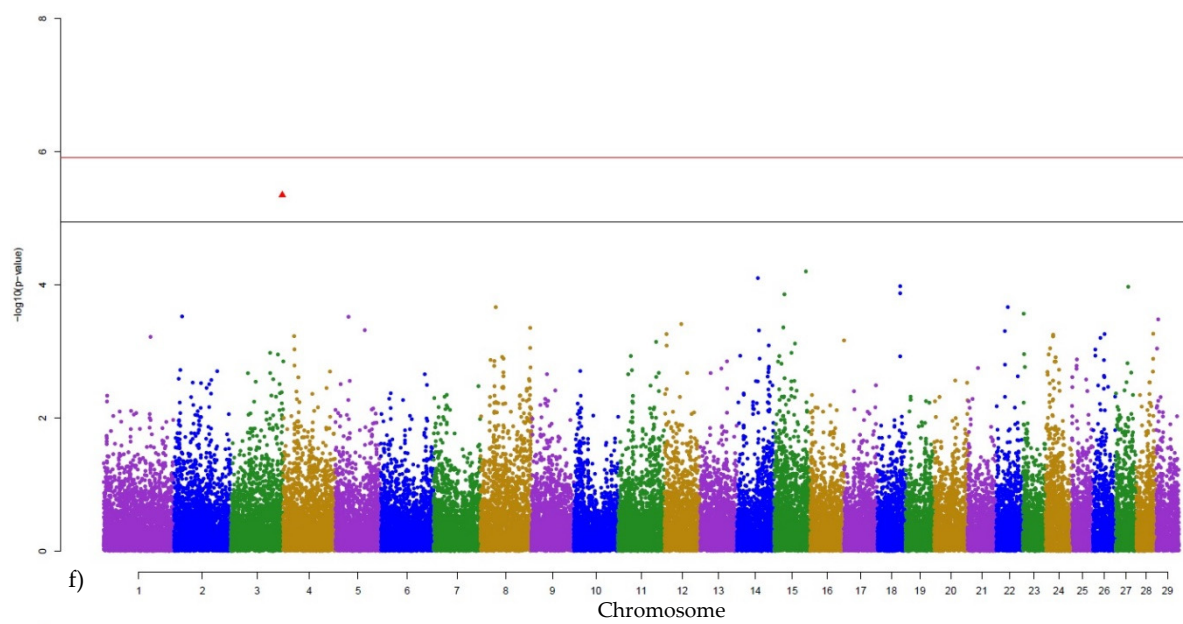


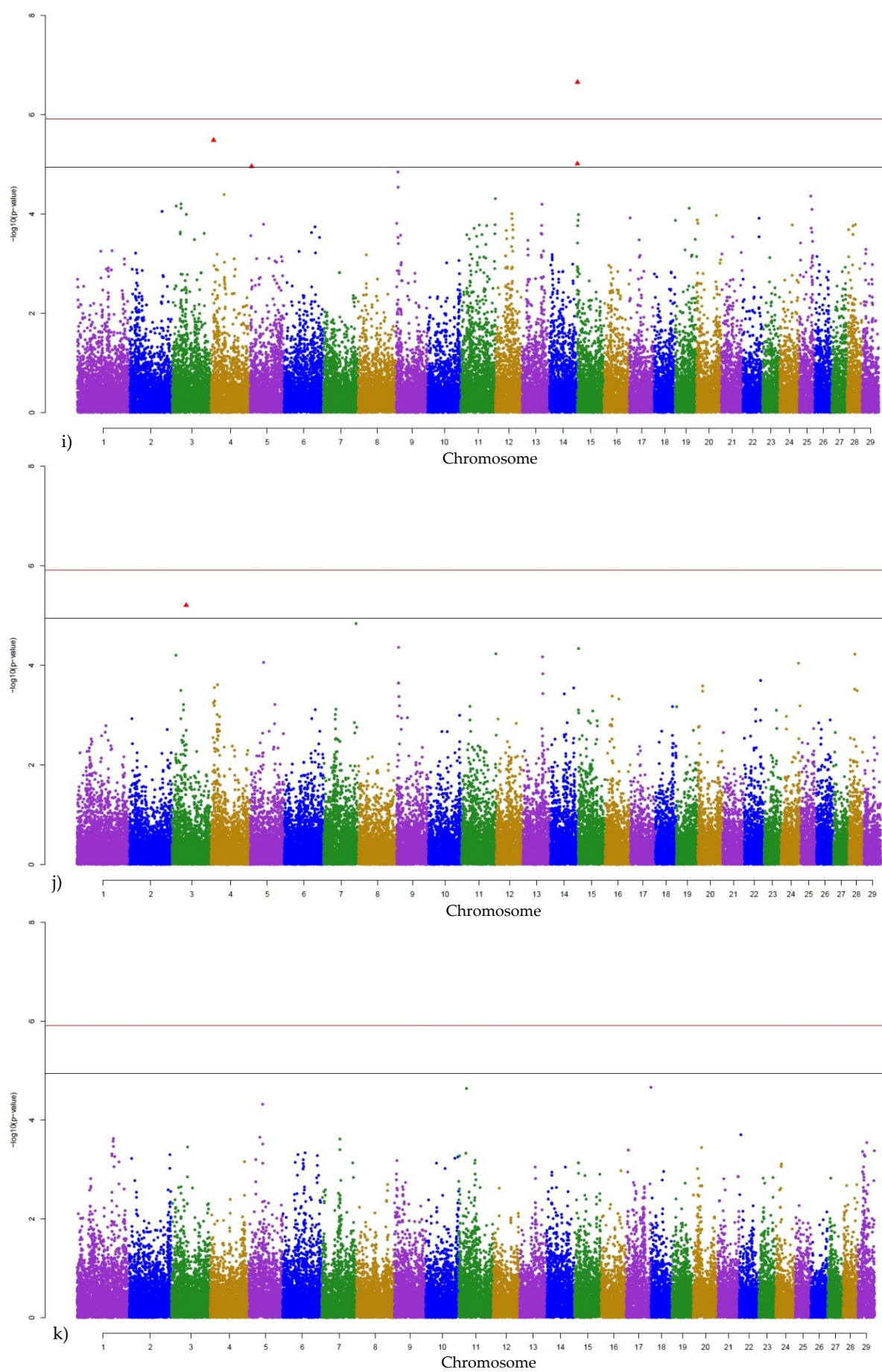


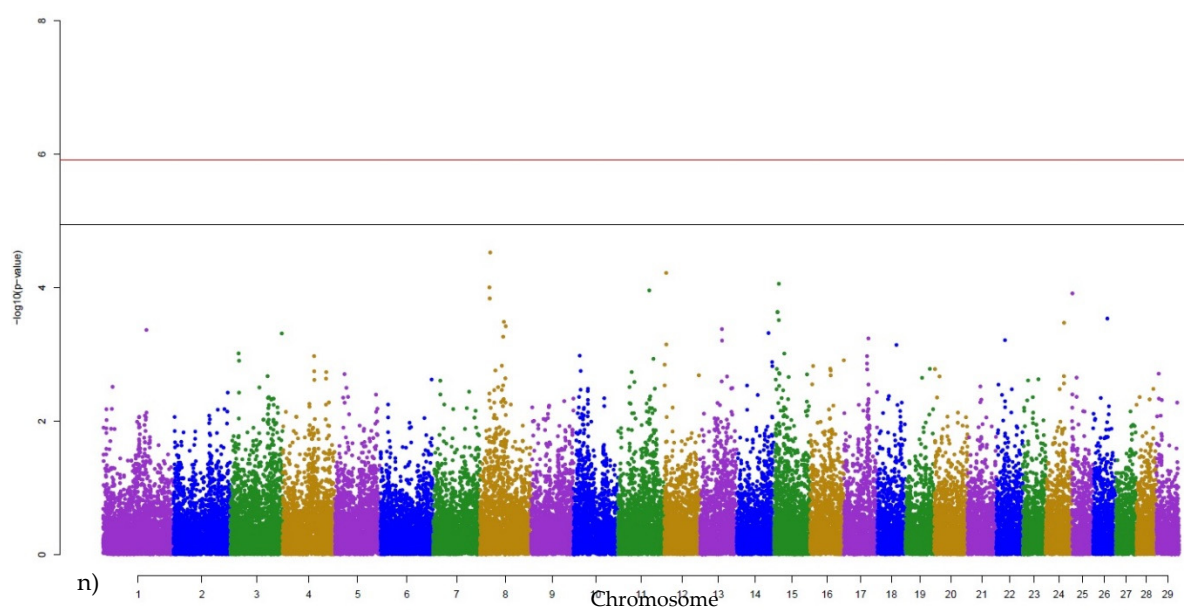
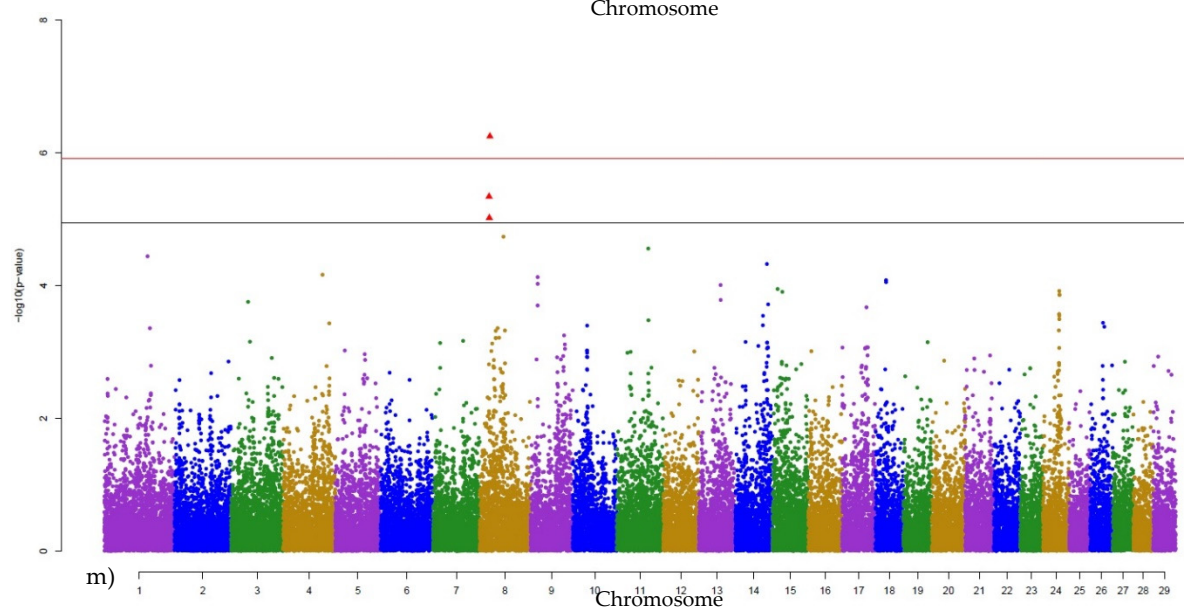
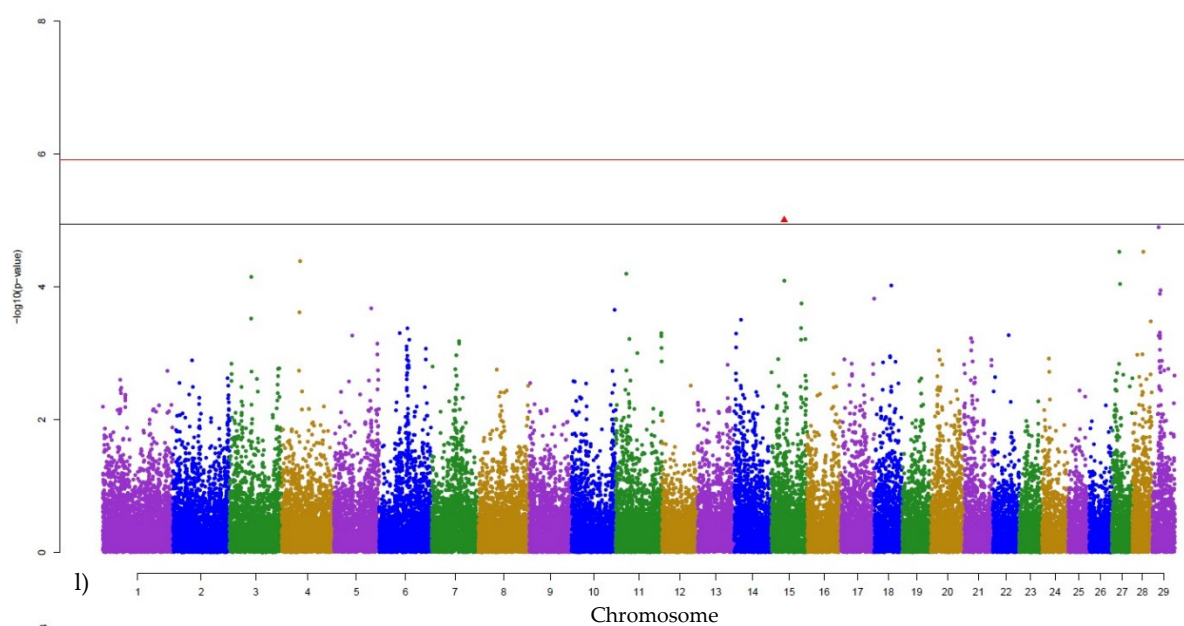
Supplementary Figure 1:











Supplementary Figure 1. Manhattan plot displaying the GWAS results (p-values) of the main SNP effects for a) segmented neutrophils, c) banded neutrophils, e) MINOR pathogens (*Coagulase-negative staphylococci* and *Corynebacterium sp.*), g) cultural negative, i) *Aerobic bacilli*, k) *Aesculin hydrolyzing streptococci* and m) *Coagulase-negative staphylococci*. Manhattan plot displaying the GWAS results (p-values) of interaction of the SNP effects and the effects of cows in the housing systems for b) segmented neutrophils, d) banded neutrophils, f) MINOR pathogens (*Coagulase-negative staphylococci* and *Corynebacterium sp.*), h) cultural negative, j) *Aerobic bacilli*, l) *Aesculin hydrolyzing streptococci* and n) *Coagulase-negative staphylococci*. Bonferroni-corrected genome-wide significance (red line) and less conservative threshold (grey line) ($P_{sugg} = 0.05/4479 = 1.12 \times 10^{-5}$) are shown. Red triangles highlight the significant SNP.