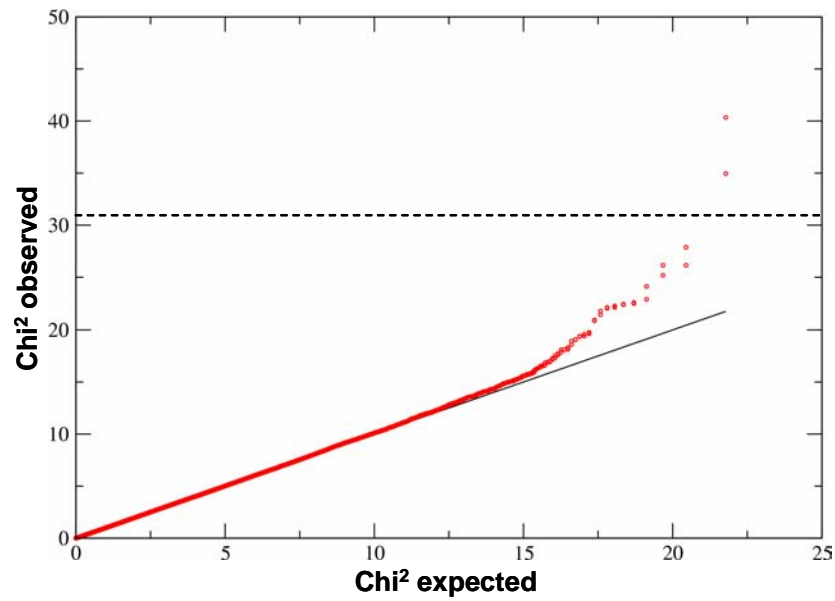
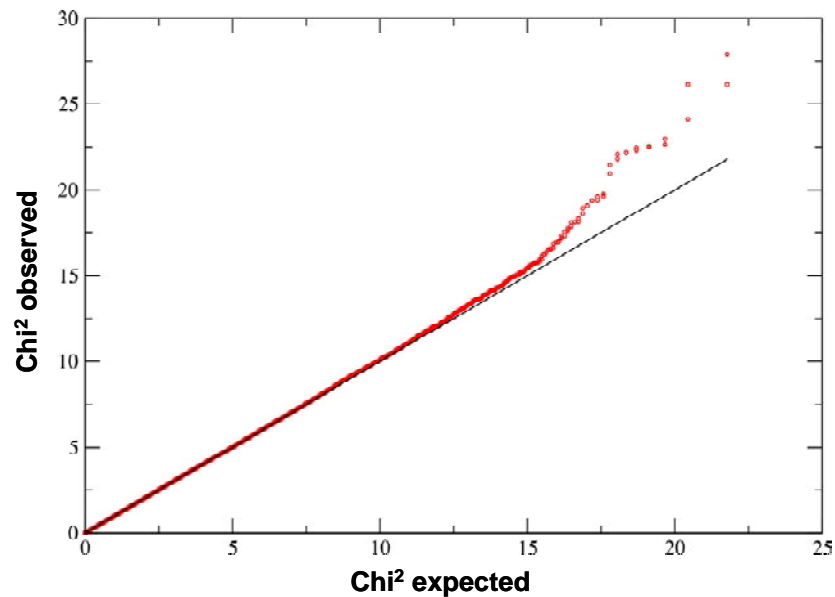


a)



b)



**Supplementary Figure 1. A Q-Q plot of the genome-wide association results.**

a) A Q-Q plot of the 653,025 adjusted Chi<sup>2</sup>-statistics (red circles) from the analysis of single SNPs and two marker haplotypes. The equiangular line (black line) is included in the plot for reference purpose. The dashed horizontal line indicates the threshold for genome-wide significance assuming a Bonferroni correction for the 653,025 SNP's / haplotypes and three phenotypes tested. b) A Q-Q plot of the 652,739 adjusted Chi<sup>2</sup>-statistics (red circles) from the analysis of single SNPs and two marker haplotypes, excluding SNPs in the *TCF7L2* gene. The equiangular line (black line) is included in the plot for reference purpose.