Supplementary Figures

Gene–Smoking Interaction Analysis for the Identification of Novel Asthma-Associated Genetic Factors

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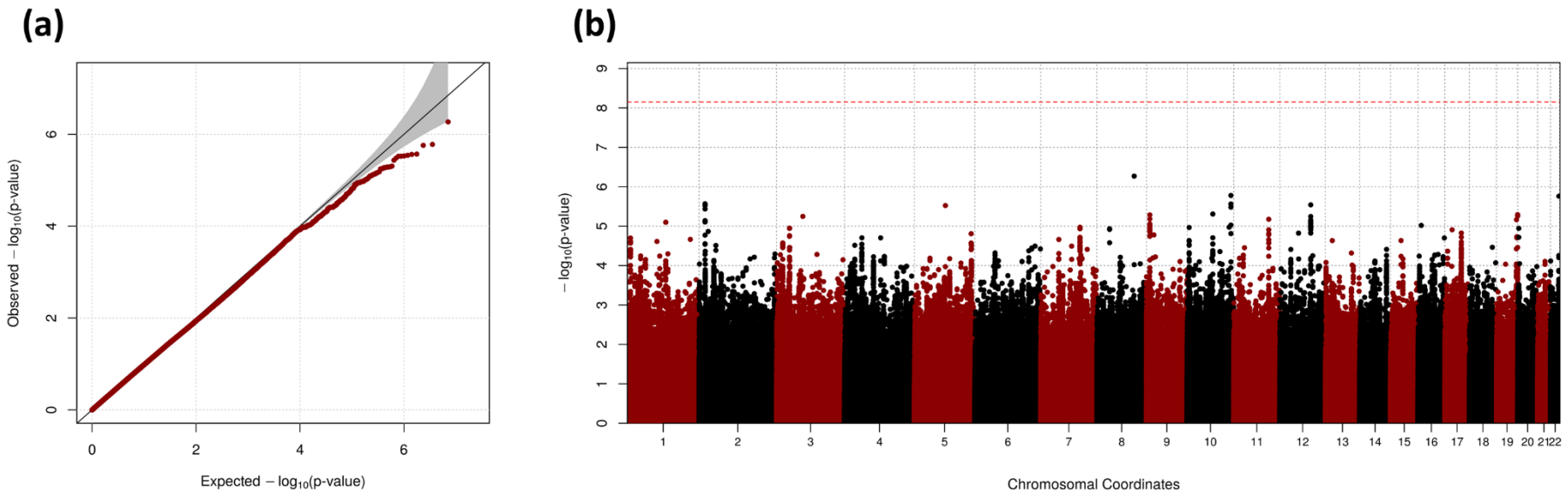

Figure S1. Quantile-quantile (Q-Q) and Manhattan plots for GWAS analysis. (**a**) Q-Q plot showing expected vs. observed $-\log_{10}$(*p*-values). The expected line is shown in black, and 95% confidence interval (CI) bands are shown in gray. (**b**) Manhattan plot of the *p*-values in the gene-environmental interaction analysis for asthma disease. The horizontal red line denotes the threshold for 0.05 genome-wide significance level by a Bonferroni correction of 7.08×10^{-9}.

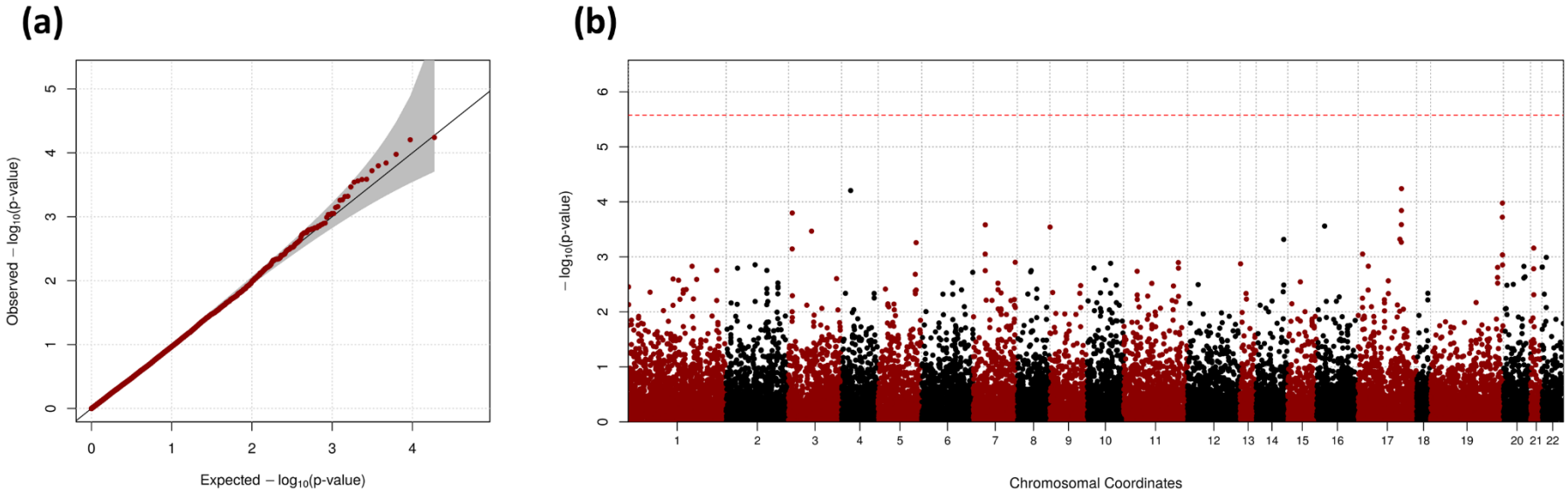

Figure S2. Quantile-quantile (Q-Q) and Manhattan plots for gene analysis. (**a**) Q-Q plot showing expected vs. observed –$\log_{10}$(*p*-values). The expected line is shown in black, and 95% confidence interval (CI) bands are shown in gray. (**b**) Manhattan plot of the *p*-values in the gene-environmental interaction analysis for asthma disease. The horizontal red line denotes the threshold for 0.05 genome-wide significance level by a Bonferroni correction of 2.66×10^{-6}.