

BJORL-D-25-00246

Material Supplementary

Table S1 List of the Identification (ID) for each of the 1400 plasma metabolites.

Table S2 Causal associations between proteins and chronic rhinosinusitis identified by deCODE pQTL-based Mendelian randomization.

Table S3 Causal associations between proteins and chronic rhinosinusitis identified by UKB-PPP pQTL-based Mendelian randomization.

Table S4 Mendelian randomization analysis of causal effects between UKB-PPP pQTL-derived proteins and deCODE pQTL-derived proteins in chronic rhinosinusitis.

Table S5 Mediation statistics for all tested axes: protein-protein and protein-metabolite pathways in chronic rhinosinusitis.

Table S6 Mendelian randomization analysis of CRS-associated metabolites and their relationship with IL23R protein.

Table S7 Detailed information of Single Nucleotide Polymorphisms (SNPs) serving as instrumental variables in Mendelian Randomization (MR) analyses for the LAT-IL23R-amino acid metabolic axis.

Table S8 Mendelian randomization, sensitivity analysis, and MR-PRESSO results of the LAT-IL23R amino acid axis.

Table S9 Summary of dataset characteristics and purposes in this study.

Figure S1

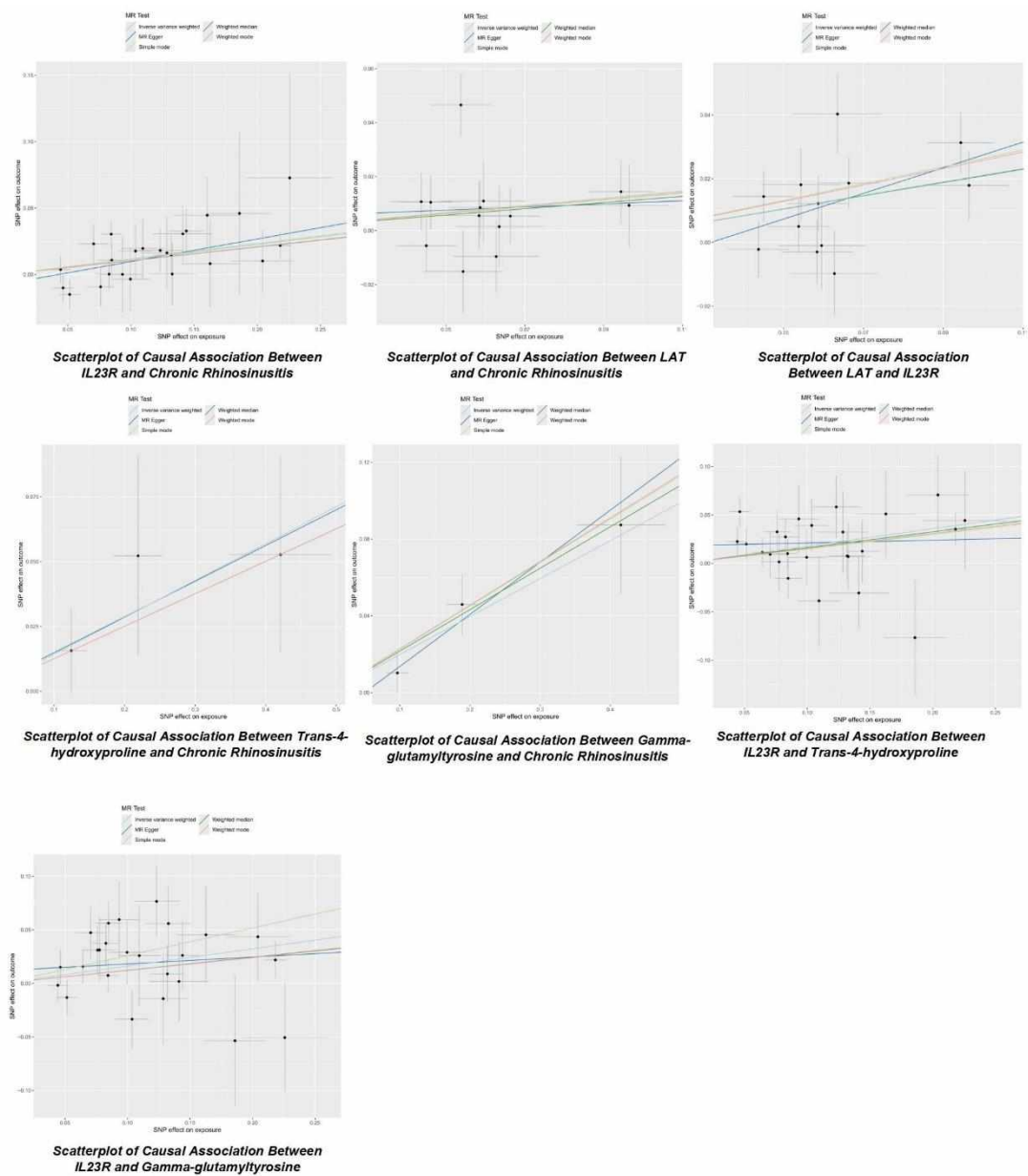


Figure S2

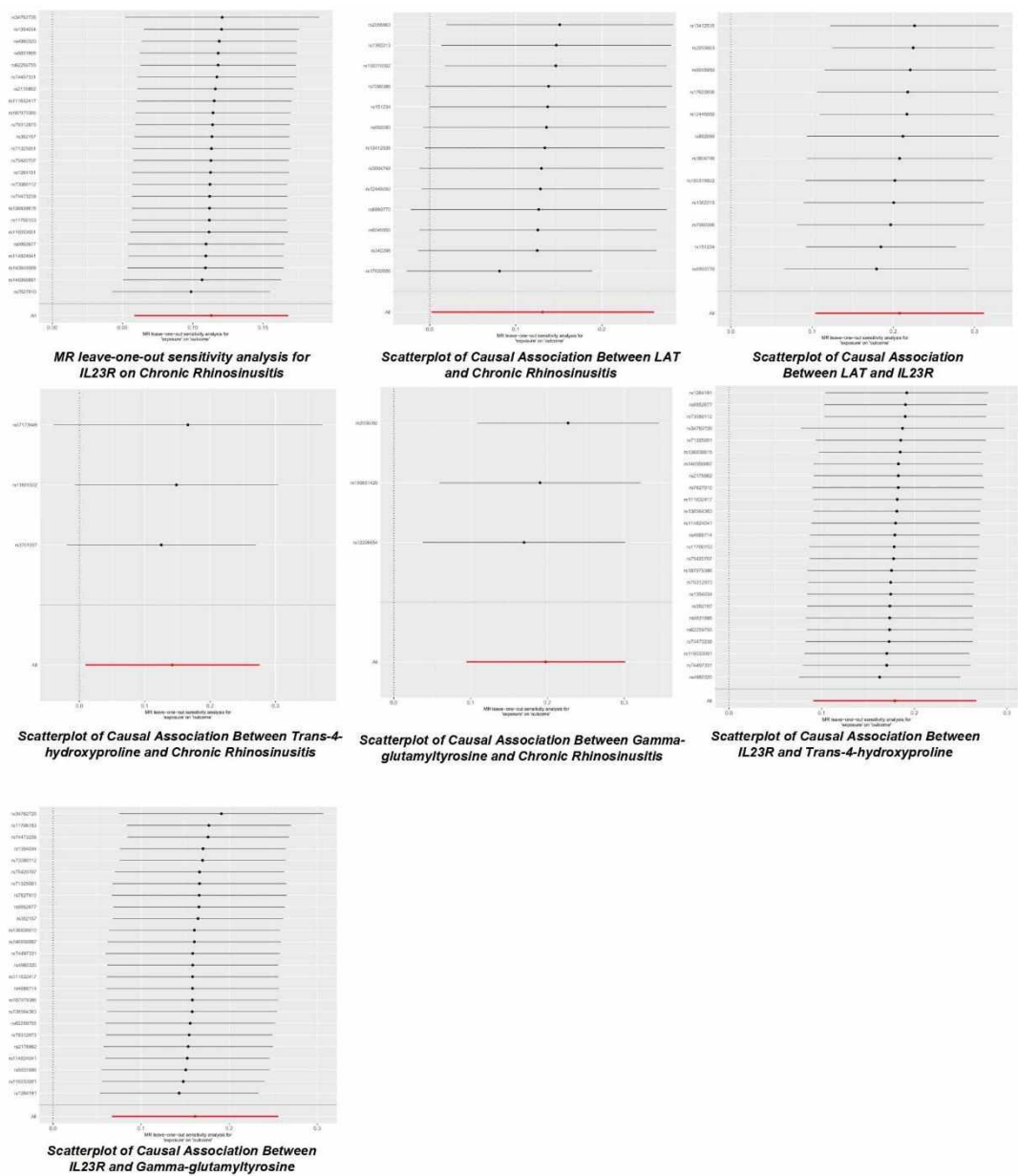


Figure S3

