

Supplementary Materials

Genetic predisposition to diabetes mellitus causally increases acute pancreatitis risk

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Supplementary Table 1. 73 pleiotropic SNPs jointly associated with AP and T2D identified by PLACO analysis.

Supplementary Table 2. 12 independent genomic risk loci identified through pleiotropic analysis between AP and T2D.

Supplementary Table 3. Top 10 hub genes in the protein-protein interaction network ranked by the MCC algorithm.

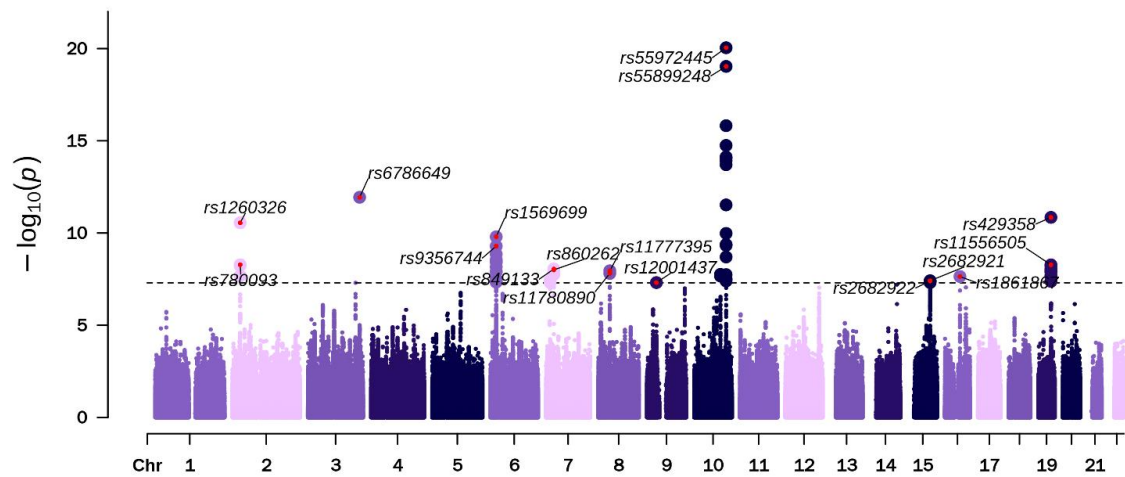
Supplementary Table 4. Information of SNPs associated with T2D.

Supplementary Table 5. Information of SNPs associated with AP.

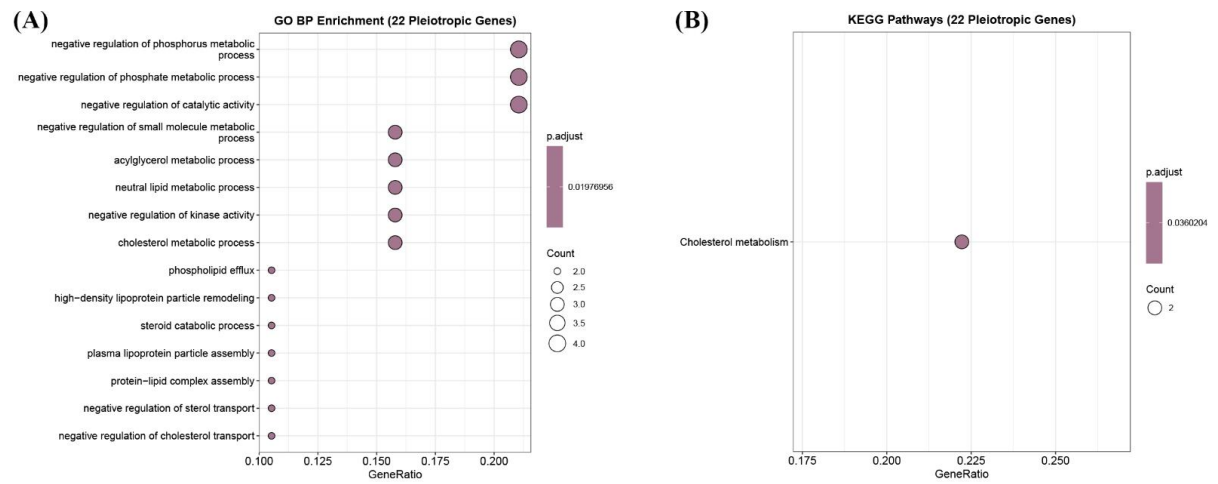
Supplementary Figure 1. Manhattan plot for PLACO results.

Supplementary Figure 2. Functional enrichment analysis of candidate pleiotropic genes.

Supplementary Figure 3. Scatter plot of MR analyses.

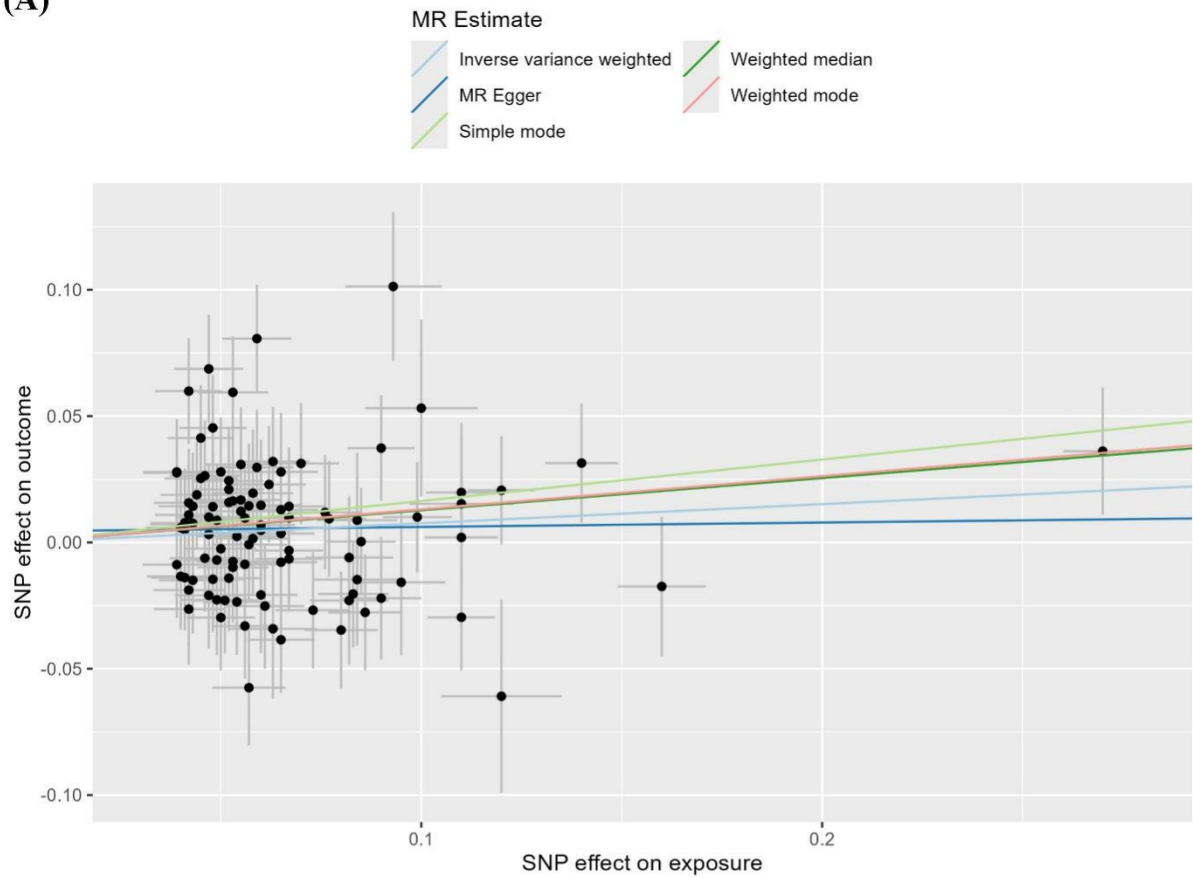


Supplementary Figure 1. Manhattan plot for PLACO results. The Manhattan plot depicts chromosomes (x-axis) against observed $-\log_{10} P_{\text{PLACO}}$ values (y-axis). The black dotted line represents the threshold of $P_{\text{PLACO}} = 5 \times 10^{-8}$, and the dots above indicate significant pleiotropic variants ($P_{\text{PLACO}} < 5 \times 10^{-8}$).

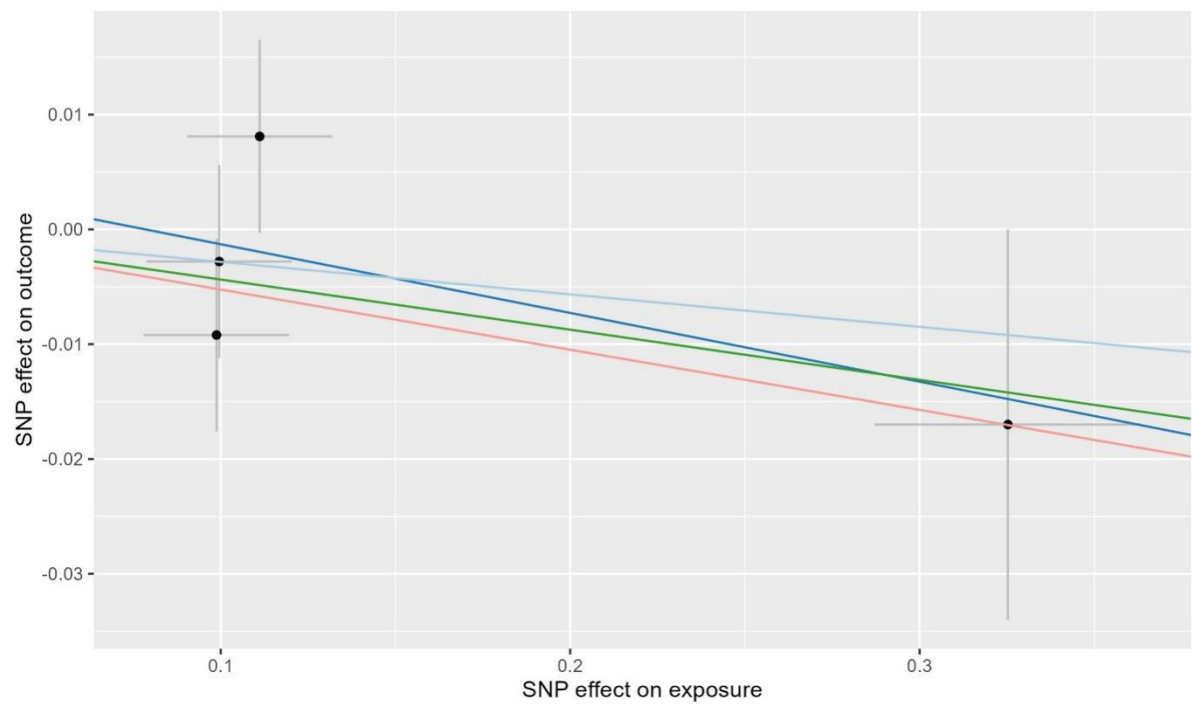


Supplementary Figure 2. Functional enrichment analysis of candidate pleiotropic genes. (A) Gene Ontology (GO) biological process (BP) enrichment. (B) Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment. The size of the dots represents the number of genes, and the color gradient indicates the adjusted P -value (P_{adj}).

(A)



(B)



Supplementary Figure 3. Scatter plot of MR analyses. (A) Effect of genetically predicted T2D on AP. (B) Effect of genetically predicted AP on T2D.