

Supplementary Figure S1: IVs used in the MR analysis.

N: the number of SNPs; EA: effective allele; OA: other alleles; SE: standard error

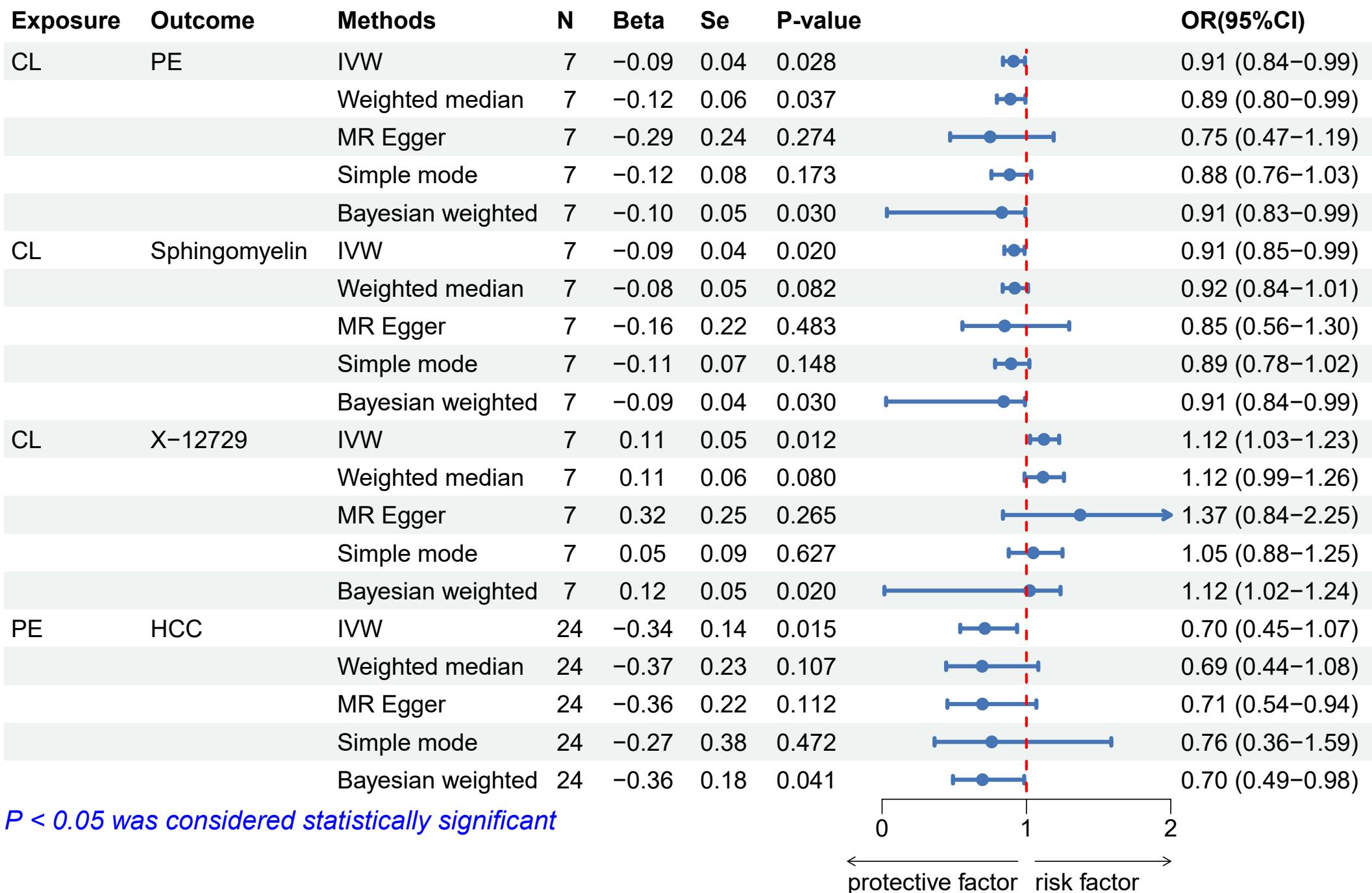
Exposure	Outcome	Methods	N	Beta	Se	P-value	OR(95%CI)
HCC	CL	IVW	30	0.03	0.05	0.54	1.03 (0.94–1.12)
		Weighted median	30	<0.01	0.03	0.90	1.00 (0.94–1.05)
		MR Egger	30	-0.01	0.02	0.66	0.99 (0.95–1.03)
		Simple mode	30	0.05	0.05	0.34	1.05 (0.95–1.16)
PE	CL	IVW	12	-0.2	0.47	0.68	0.82 (0.33–2.06)
		Weighted median	12	-0.02	0.14	0.91	0.98 (0.74–1.30)
		MR Egger	12	0.04	0.11	0.71	1.04 (0.84–1.29)
		Simple mode	12	-0.07	0.24	0.78	0.93 (0.58–1.50)
HCC	PE	IVW	57	-0.01	0.02	0.70	0.99 (0.97–1.02)
		Weighted median	57	<0.01	0.01	0.75	1.00 (0.98–1.02)
		MR Egger	57	-0.01	0.01	0.32	0.99 (0.98–1.01)
		Simple mode	57	0.01	0.02	0.72	1.01 (0.97–1.05)

*P < 0.05 was considered statistically significant*



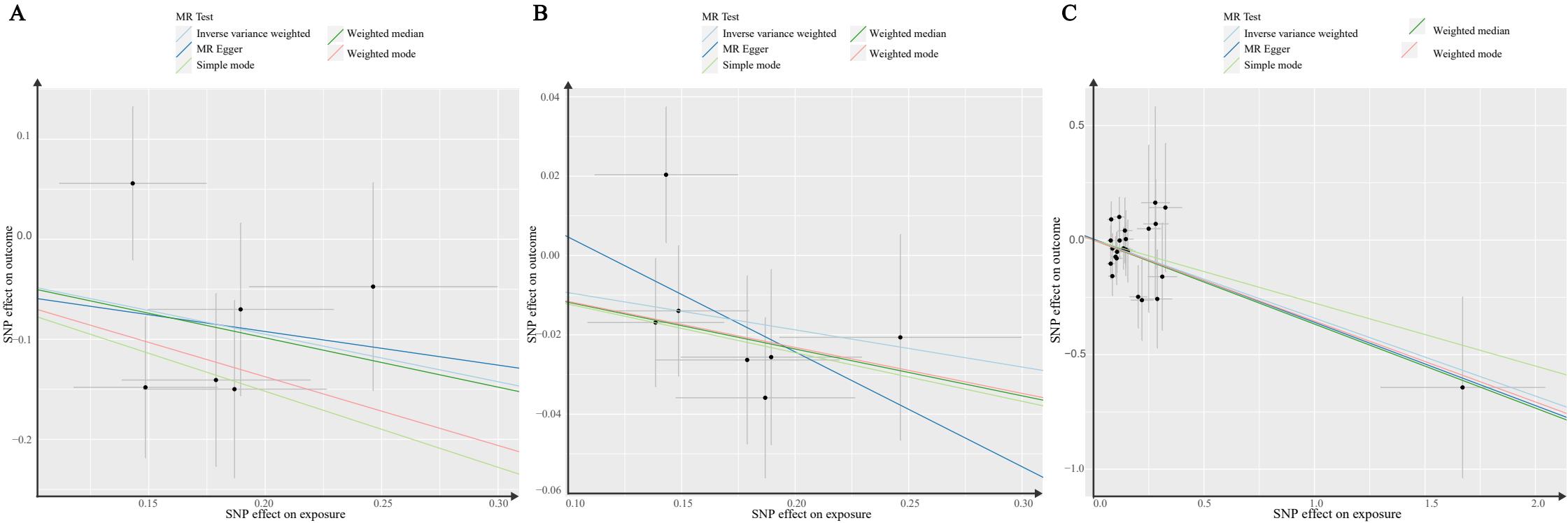
Supplementary Fig. S2: Results of reverse MR analysis.

N: the number of SNPs; SE: standard error; IVW: Inverse Variance Weighted

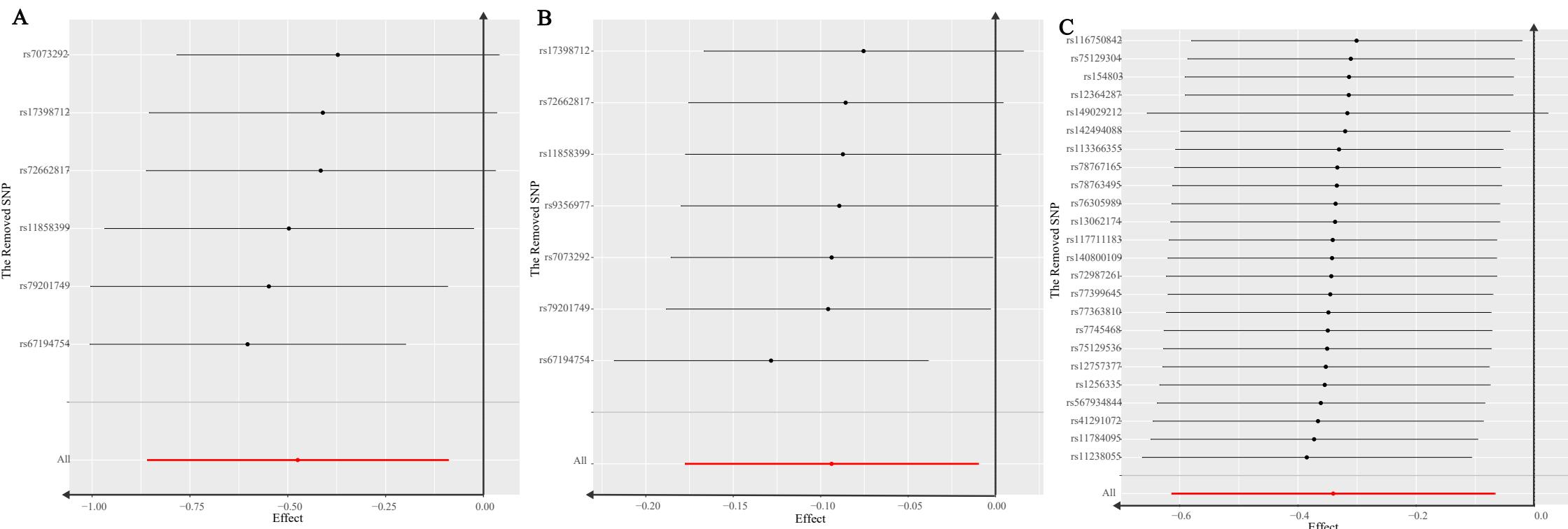


Supplementary Fig. S3: Main results of the MR analysis.

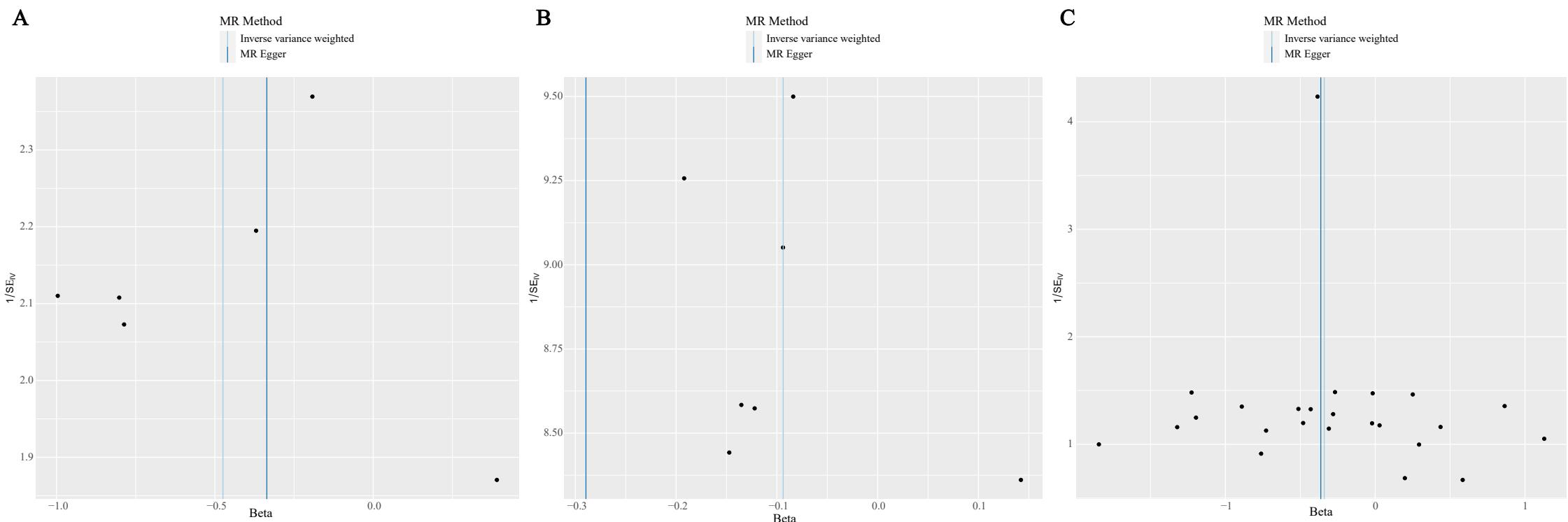
N: the number of SNPs; SE: standard error; IVW: Inverse Variance Weighted



Supplementary Figure S4: Scatter plots. The y-axis represents the causal effect of IVs on the outcome, while the x-axis represents the effect on the exposure. The slope illustrates the effect of exposure on the outcome. (A) illustrates the trends of effects between CL and HCC. (B) illustrates the trends of effects between CL and PE. (C) illustrates the trends of effects between PE and HCC.

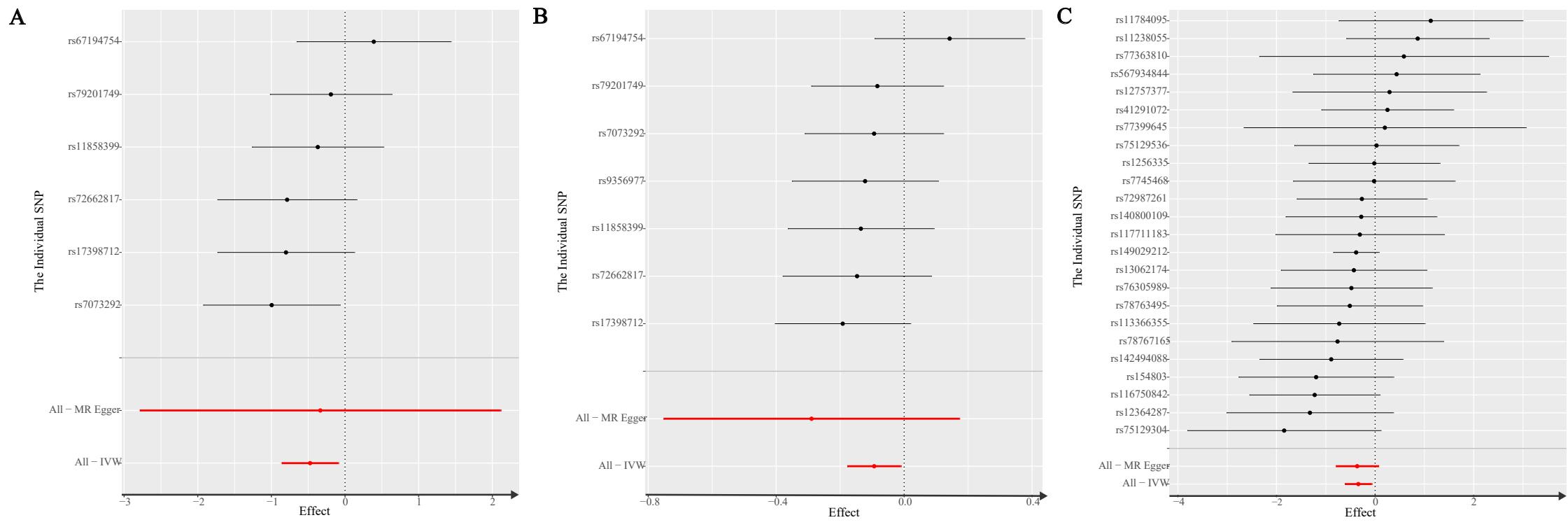


Supplementary Figure S5: Leave-one-out analysis. The y-axis represents the removed SNPs, and the x-axis represents the effect of the remaining SNPs on the outcome. (A) illustrates the stability of SNPs between CL and HCC. (B) illustrates the stability of SNPs between CL and PE. (C) illustrates the stability of SNPs between PE and HCC.



Supplementary Figure S6: Funnel plots. Symmetry indicates the absence of heterogeneity in IVs.

(A) illustrates the heterogeneity of SNPs between CL and HCC. (B) illustrates the heterogeneity of SNPs between CL and PE. (C) illustrates the heterogeneity of SNPs between PE and HCC.



Supplementary Figure S7: Forest plots. The y-axis represents individual SNPs, while the x-axis represents the effect of each SNP on exposure.  
 (A) illustrates the association between each SNP and the outcome between CL and HCC. (B) illustrates the association between each SNP and the outcome between CL and PE. (C) illustrates the association between each SNP and the outcome between PE and HCC.

Table S1 The results of sensitivity analysis.

Exposure	Outcome	Cochran's Q			Egger regression		MR-PRESSO P-value
		Q	Q_df	Q_pval	Intercept	P-value	
CL	HCC	5	5	0.389	-0.02	0.916	0.550
CL	PE	5	6	0.529	0.03	0.437	0.455
PE	HCC	16	23	0.874	0.87	0.893	0.878

Cochran's Q test was utilized to examine heterogeneity. Egger regression and MR-PRESSO were used to identified horizontal pleiotropic

CL: *C. leptum*; PE: phosphoethanolamine; HCC: hepatocellular carcinoma;