

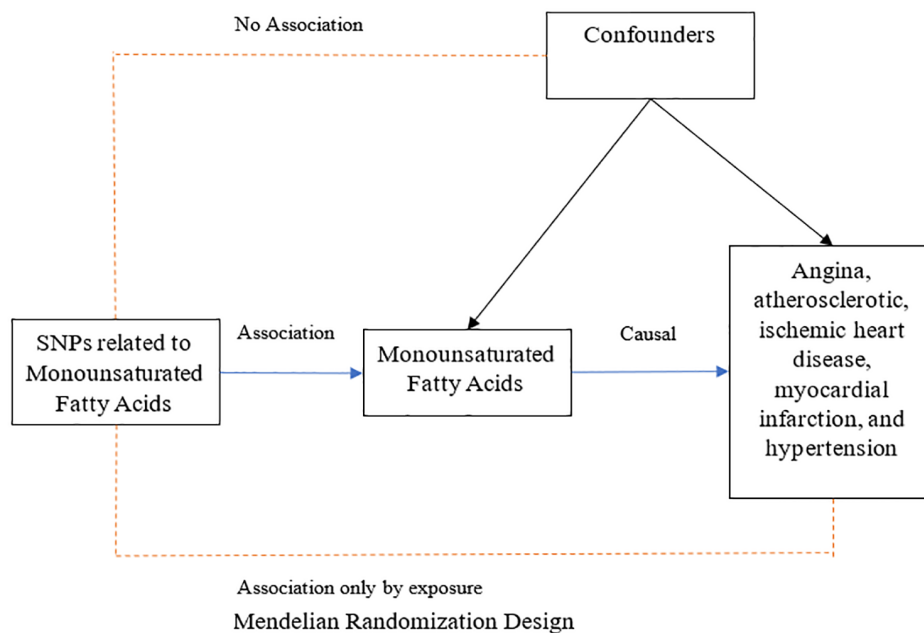


Figure S1: The diagram shows the Mendelian randomization (MR) framework in the current paper. MR utilizes genetic variation as an instrumental variable (IV) to investigate the causal association between exposure and outcome in non-experimental data. For a genetic variant to be a valid instrumental variable, several main assumptions should be satisfied. (i) The IVs (SNPs) are strongly associated with exposure (s) and should be clearly quantifiable. (ii) The SNPs are not linked with any confounder of the exposure-outcome association. (iii) The SNPs do not affect the outcome, except possibly through their association with the exposure(s).

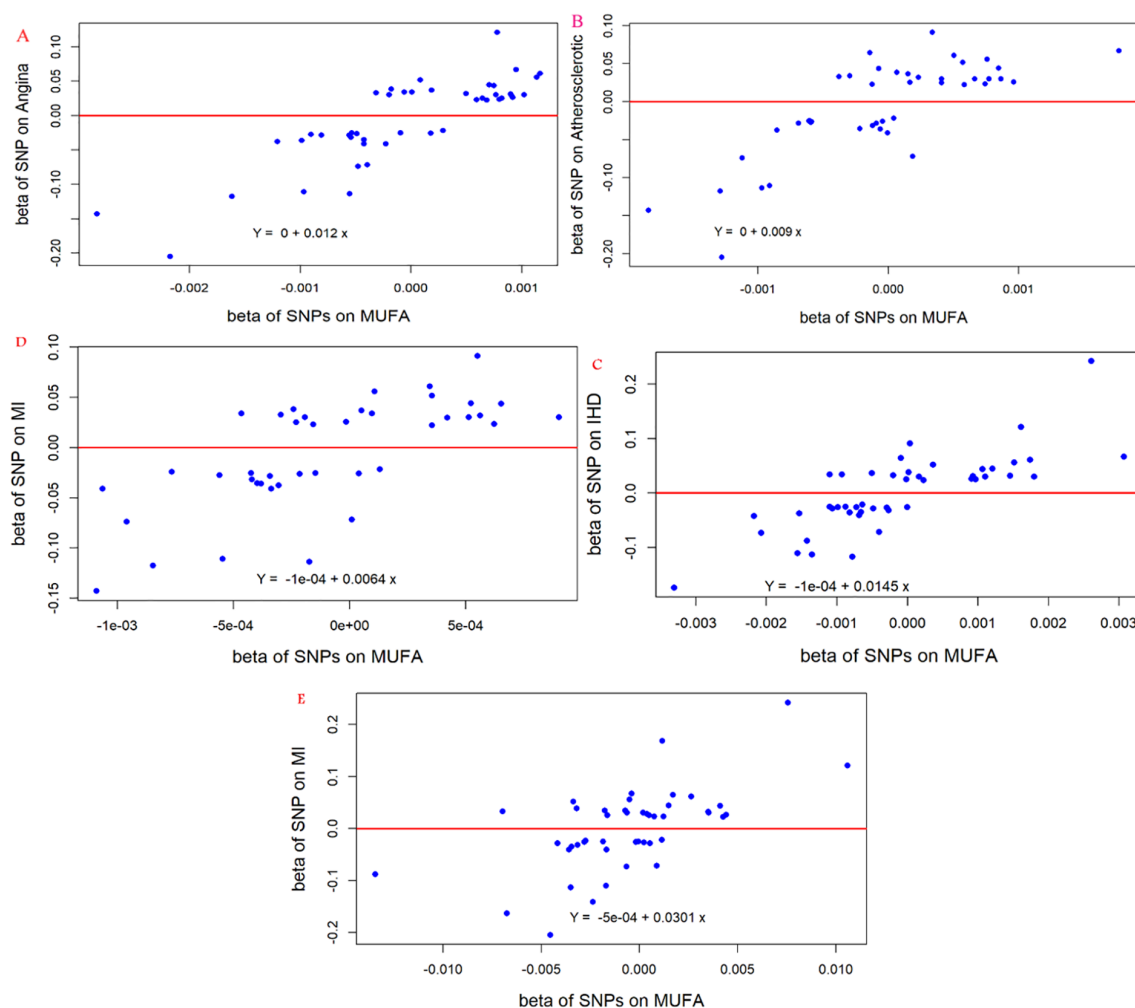


Figure S2: The figure shows the relationship between the undefined causal variables and cardiovascular disease. A: Angina~MUFA; B: Atherosclerotic~MUFA; C: Ischemic heart disease~MUFA; D: Myocardial infarction~MUFA; E: Hypertension~MUFA

FigureS3-1: Angina

MR-Egger with multiplicative random effects

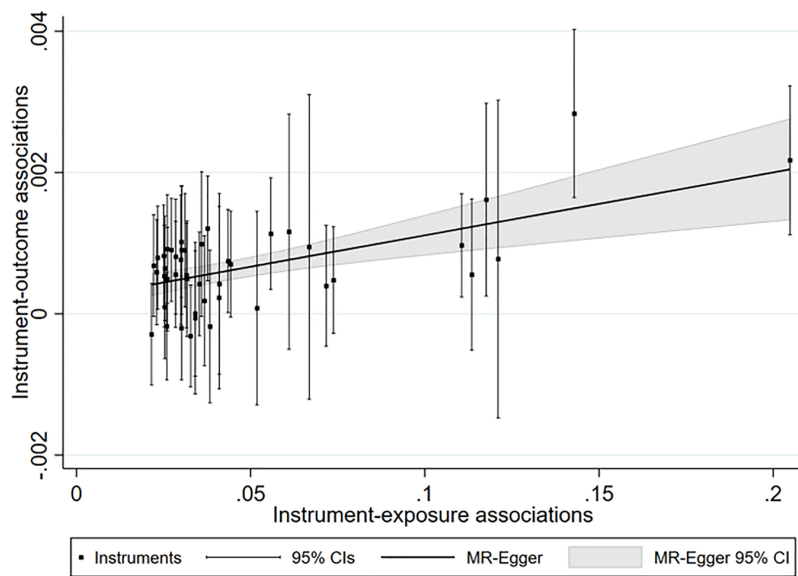
Variable	Coefficient	Standard Error	Z statistic	P value	95% CI
Slope	0.008899	0.0021471	4.14	<0.001	0.005-0.013
Constant	0.000222	0.000112	1.98	0.048	2.4e-06-0.0004

MR-Egger using a t-distribution for inference (P values) and CI limits

Variable	Coefficient	Standard Error	Z statistic	P value	95% CI
Slope	0.008899	0.0021471	4.14	<0.001	0.004-0.013
Constant	0.000222	0.000112	1.98	0.054	-3.9e-06-0.0004

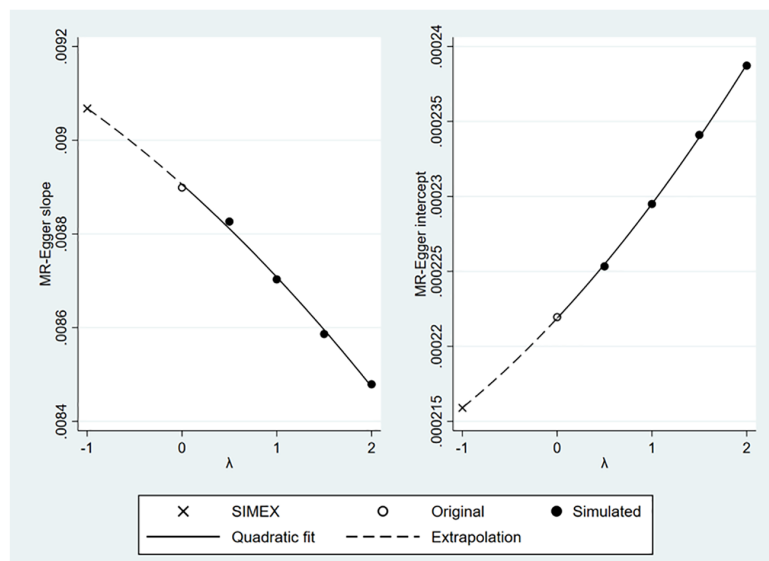
MR-Egger using the radial formulation

Variable	Coefficient	Standard Error	Z statistic	P value	95% CI
Slope	0.00887	0.0023691	3.74	<0.001	0.004-0.013
Constant	0.4964624	0.2862974	1.73	0.083	-0.065-1.057



SIMEX suppressing bootstrapped SEs

Variable	Coefficient	Standard Error	Z statistic	P value	95% CI
Slope	0.0090679	0.002545	3.56	<0.001	0.004-0.014
Constant	0.0002159	0.0001188	1.82	0.069	-1.6e-5-0.0004



FigureS3-2: Atherosclerotic

MR-Egger with multiplicative random effects

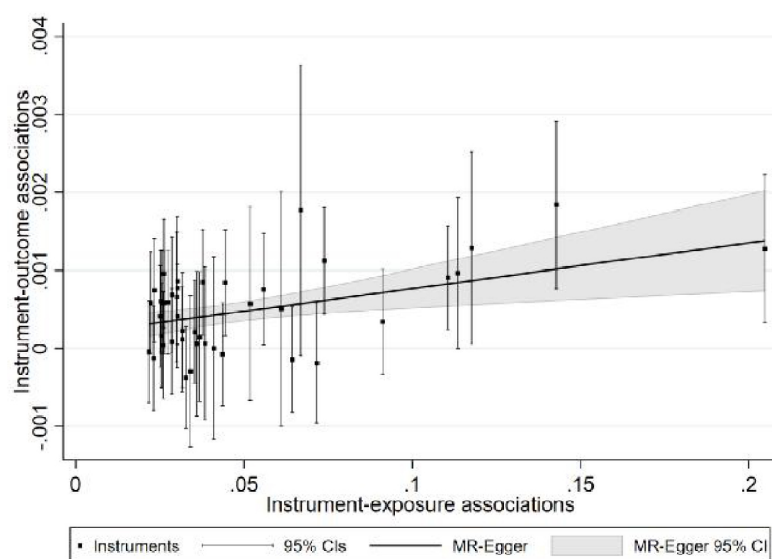
Variable	Coefficient	Standard Error	Z statistic	P value	95% CI
Slope	0.0058388	0.0019517	2.99	0.003	0.002-0.010
Constant	0.0001836	0.0001063	1.73	0.084	-0.00002-0.0003

MR-Egger using a t-distribution for inference (P values) and CI limits

Variable	Coefficient	Standard Error	Z statistic	P value	95% CI
Slope	0.0058388	0.0019517	2.99	0.003	0.002-0.010
Constant	0.0001836	0.0001063	1.73	0.092	-0.0003-0.0004

MR-Egger using the radial formulation

Variable	Coefficient	Standard Error	Z statistic	P value	95% CI
Slope	0.005364	0.0020875	2.57	0.010	0.001-0.009
Constant	0.5459538	0.2979891	1.83	0.067	-0.038-1.13



SIMEX suppressing bootstrapped SEs

Variable	Coefficient	Standard Error	Z statistic	P value	95% CI
Slope	0.005998	0.0023349	2.57	0.010	0.001-0.010
Constant	0.0001766	0.0001179	1.50	0.134	-0.00005-0.0004

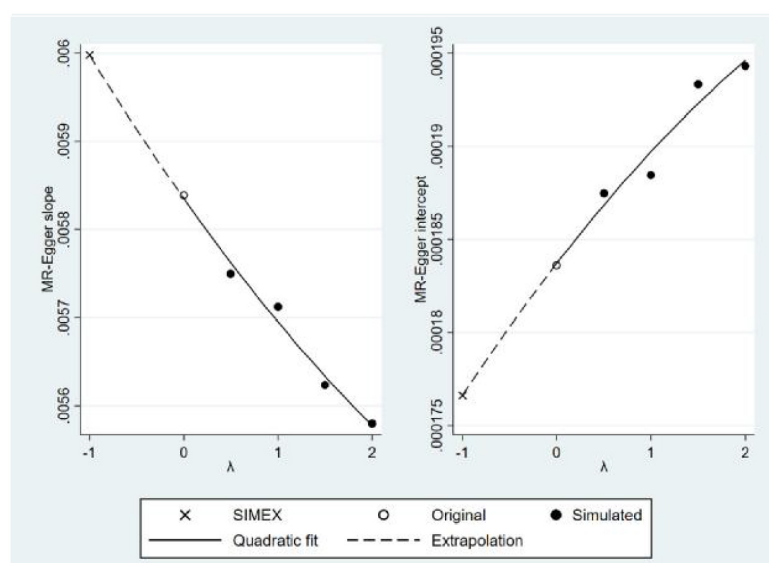


Figure S3-3: Ischemic Heart Disease

MR-Egger with multiplicative random effects

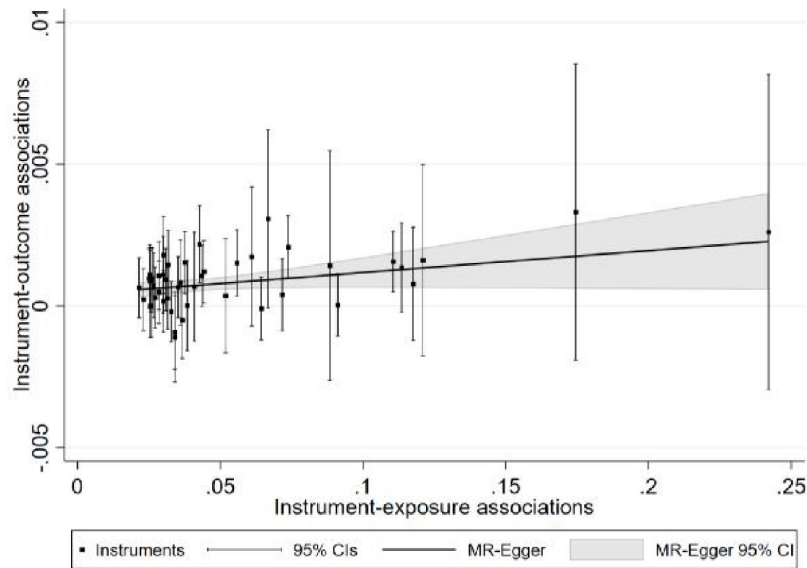
Variable	Coefficient	Standard Error	Z statistic	P value	95% CI
Slope	0.0077169	0.0041847	1.84	0.065	-0.0005-0.015
Constant	0.0004043	0.0002039	1.98	0.047	4.62e-06-0.0008

MR-Egger using a t-distribution for inference (P values) and CI limits

Variable	Coefficient	Standard Error	Z statistic	P value	95% CI
Slope	0.0077169	0.0041847	1.84	0.072	-0.0007-0.016
Constant	0.0004043	0.0002039	1.98	0.054	-6.68e-06-0.0008

MR-Egger using the radial formulation

Variable	Coefficient	Standard Error	Z statistic	P value	95% CI
Slope	0.0069123	0.0046324	1.49	0.136	-0.002-0.016
Constant	0.6753341	0.3495485	1.93	0.053	-0.009-1.36



SIMEX suppressing bootstrapped SEs

Variable	Coefficient	Standard Error	Z statistic	P value	95% CI
Slope	0.0077299	0.0023024	3.36	0.001	0.003-0.12
Constant	0.0004039	0.0001092	3.70	<0.001	0.0002-0.0006

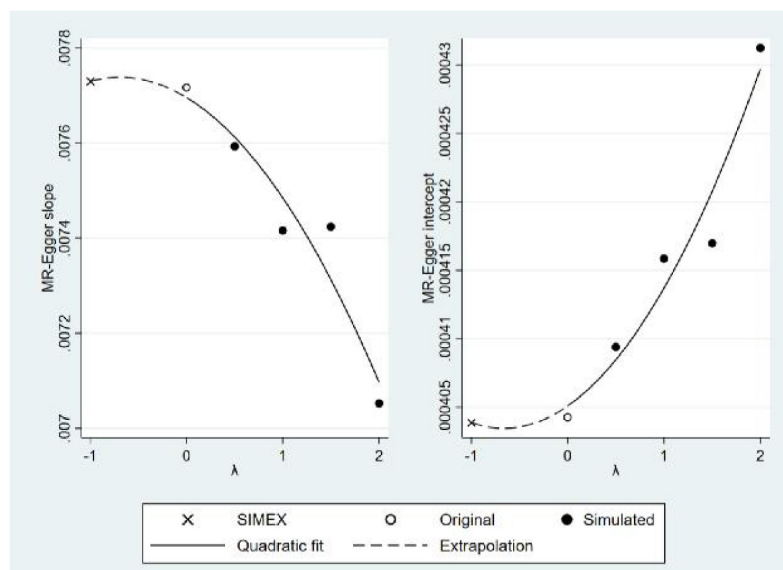


Figure S3-4: Myocardial Infarction

MR-Egger with multiplicative random effects

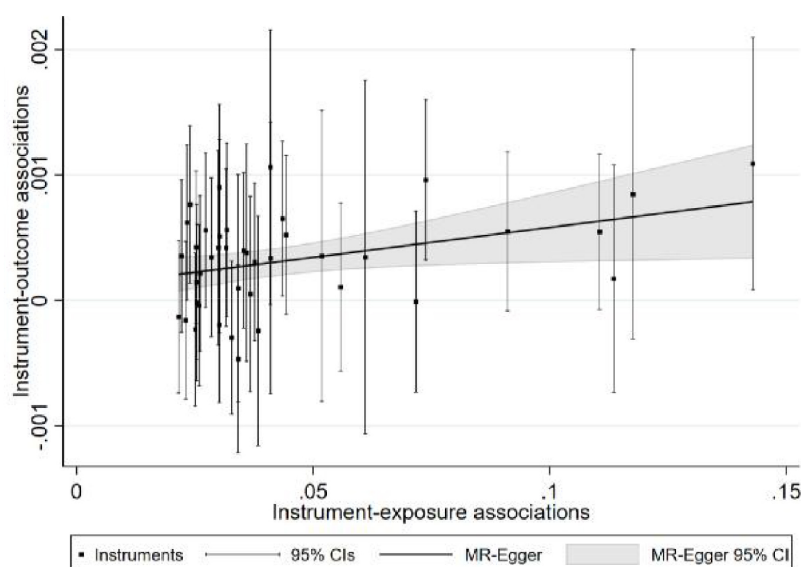
Variable	Coefficient	Standard Error	Z statistic	P value	95% CI
Slope	0.0047694	0.0021552	2.21	0.027	0.0005-0.009
Constant	0.0001055	0.0001042	1.01	0.312	-0.00009-0.0003

MR-Egger using a t-distribution for inference (P values) and CI limits

Variable	Coefficient	Standard Error	Z statistic	P value	95% CI
Slope	0.0047694	0.0021552	2.21	0.033	0.0004-0.009
Constant	0.0001055	0.0001042	1.01	0.318	-0.0001-0.0003

MR-Egger using the radial formulation

Variable	Coefficient	Standard Error	Z statistic	P value	95% CI
Slope	0.0046959	0.0023032	2.04	0.041	0.0001-0.009
Constant	0.3009743	0.3131872	0.96	0.337	-0.313-0.915



SIMEX suppressing bootstrapped SEs

Variable	Coefficient	Standard Error	Z statistic	P value	95% CI
Slope	0.0047254	0.0017359	2.72	0.006	0.001-0.008
Constant	0.0001073	0.0000788	1.36	0.173	-0.00004-0.0003

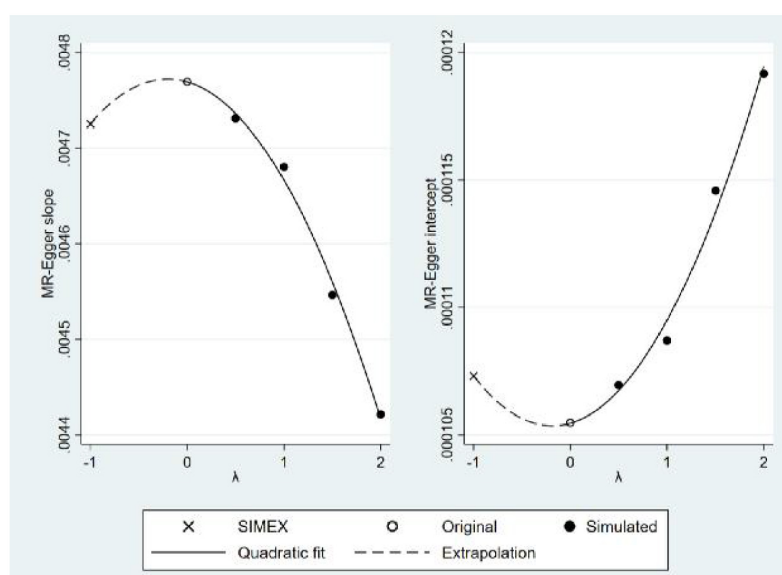


Figure S3-4: Myocardial Infarction

MR-Egger with multiplicative random effects

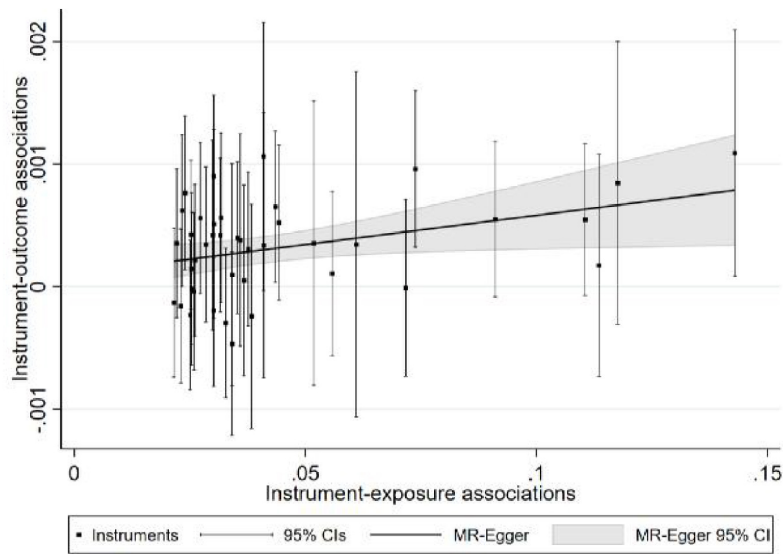
Variable	Coefficient	Standard Error	Z statistic	P value	95% CI
Slope	0.0047694	0.0021552	2.21	0.027	0.0005-0.009
Constant	0.0001055	0.0001042	1.01	0.312	-0.00009 -0.0003

MR-Egger using a t-distribution for inference (P values) and CI limits

Variable	Coefficient	Standard Error	Z statistic	P value	95% CI
Slope	0.0047694	0.0021552	2.21	0.033	0.0004 -0.009
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MR-Egger using the radial formulation

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SIMEX suppressing bootstrapped SEs

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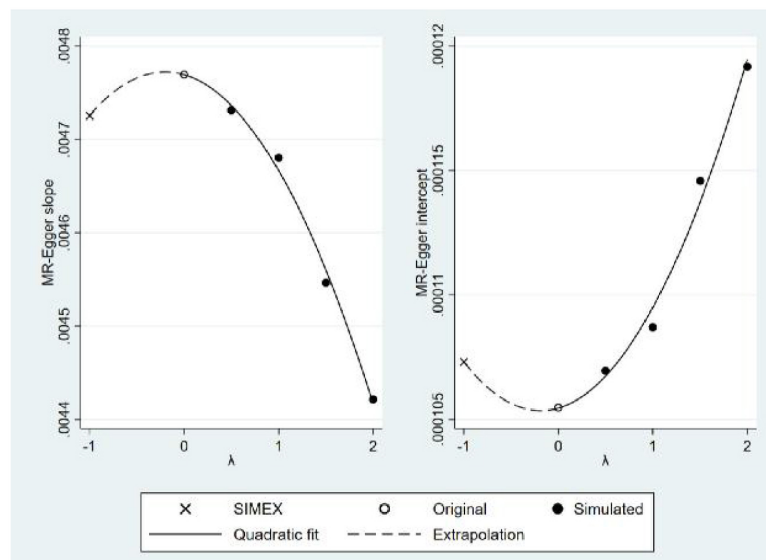
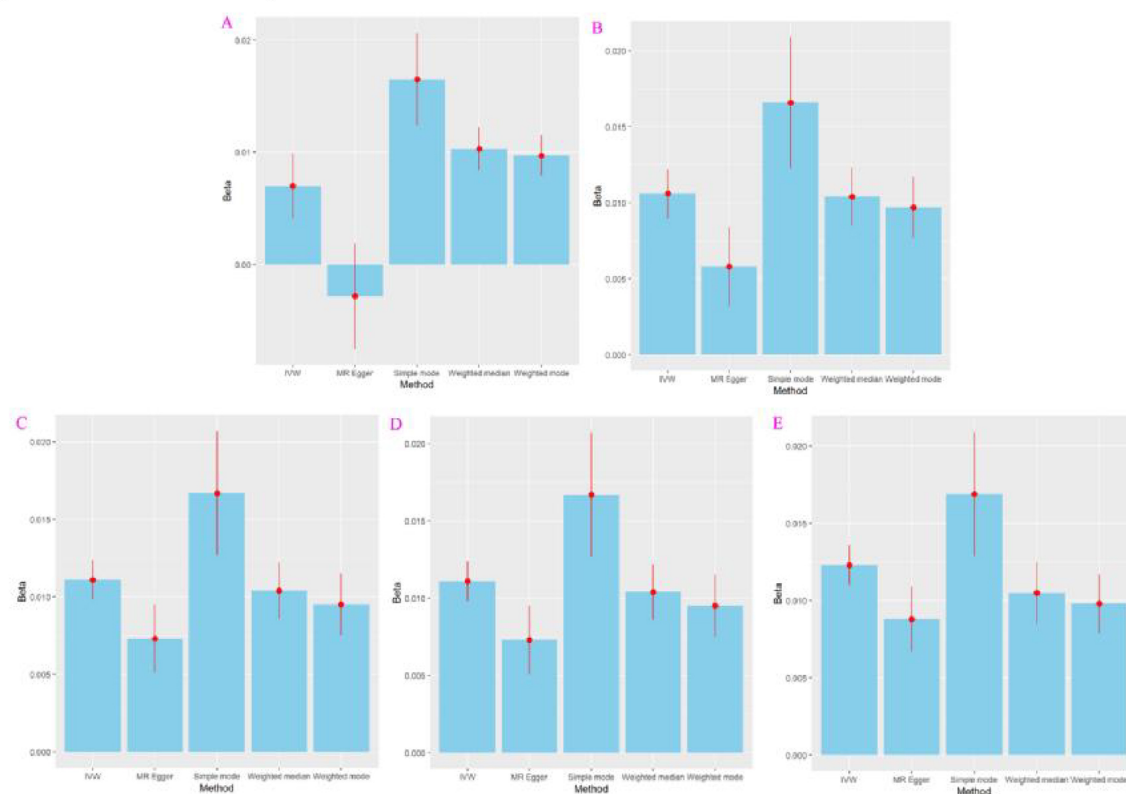


Figure S3: The scatter plot shows the genotype summary level data points and the fitted MR-Egger model.

Figure S4-1: MUFA and Angina

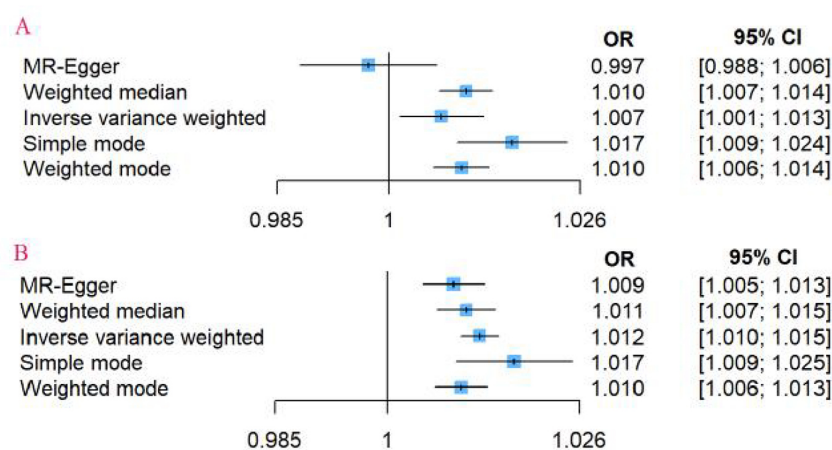
As seen, Residual and Cook's distance outperformed others. As a result, the Residual and Cook's distance were used to detect the potential outlier and influential point.



A: Initial analysis; B: After Phenoscanner; C: MR-PRESSO; D: Radial-MR; E: Residual and Cook's distance

When data contained the outlier and influential points, we observed that heterogeneity existed in the initial analysis ($Q_{IVW}=351.50$, $P=2.447131e-47$; $Q_{Egger}=308.24$, $P=1.103008e-39$; Egger intercept=0.0006, $P=0.012$). After the Phenoscanner, we obtained ($Q_{IVW}=90.82$, $P=0.00013$; $Q_{Egger}=81.64$, $P=0.00094$; Egger intercept=0.0003, $P=0.027$). After applying MR-PRESSO, Radial-MR, and Residual and Cook's distance, we found that these approaches could reduce the heterogeneity ($Q_{IVW}=61.89$, $P=0.047$; $Q_{Egger}=56.10$, $P=0.104$; Egger intercept=0.0002, $P=0.038$), ($Q_{IVW}=61.89$, $P=0.047$; $Q_{Egger}=56.10$, $P=0.104$; Egger intercept=0.0002, $P=0.038$), and ($Q_{IVW}=51.09$, $P=0.214$; $Q_{Egger}=46.81$, $P=0.318$; Egger intercept=0.0002, $P=0.053$), respectively.

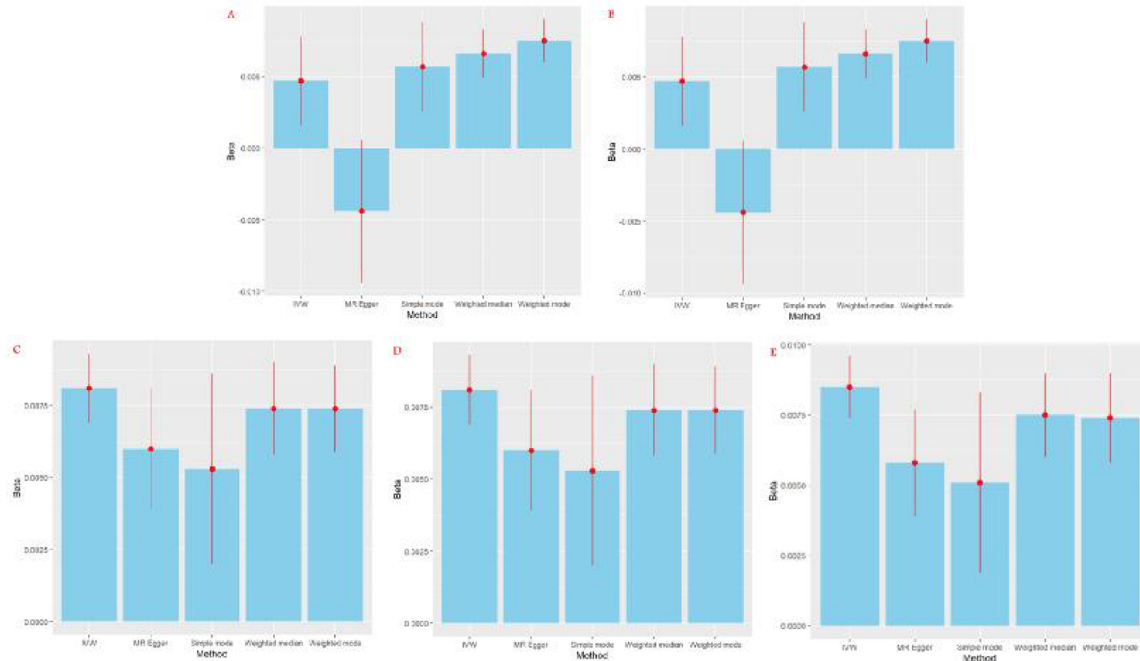
The following figure shows the main analysis (with potential outliers and influential points) and the analysis after using Residual and Cook's distance.



A: Main analysis (with potential outliers and influential points); B: After using Residual and Cook's distance (remove outliers); IVW: Inverse variance weighted; OR: Odds ratio; CI: Confidence interval

Figure S4-2: MUFA and Atherosclerotic

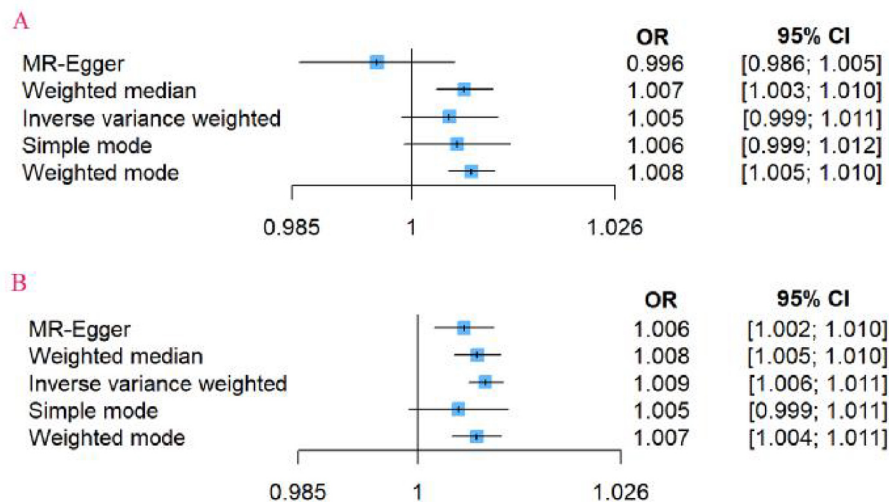
The following figure reveals the results of these methods. As seen, Residual and Cook's distance outperformed the others. As a result, we used Residual and Cook's distance to detect potential outliers and influential points.



A: Initial analysis; B: After Phenoscanner; C: MR-PRESSO; D: Radial-MR; E: Residual and Cook's distance

When data contained outlier and influential points, we observed that heterogeneity existed in the initial analysis ($Q_{IVW}=457.00$, $P=4.479277e-68$; $Q_{Egger}=411.65$, $P=9.657186e-60$; Egger intercept=0.0006, $P=0.027$). After Phenoscanner, we obtained ($Q_{IVW}=457.00$, $P=4.479277e-68$; $Q_{Egger}=411.65$, $P=9.657186e-60$; Egger intercept=0.0006, $P=0.027$). After applying MR-PRESSO, Radial-MR, and Residual and Cook's distance, we found that these approaches could reduce the heterogeneity ($Q_{IVW}=61.66$, $P=0.040$; $Q_{Egger}=59.61$, $P=0.047$; Egger intercept=0.0001, $P=0.230$), ($Q_{IVW}=61.66$, $P=0.040$; $Q_{Egger}=59.61$, $P=0.047$; Egger intercept=0.0001, $P=0.230$), and ($Q_{IVW}=51.14$, $P=0.157$; $Q_{Egger}=47.68$, $P=0.219$; Egger intercept=0.0001, $P=0.092$), respectively.

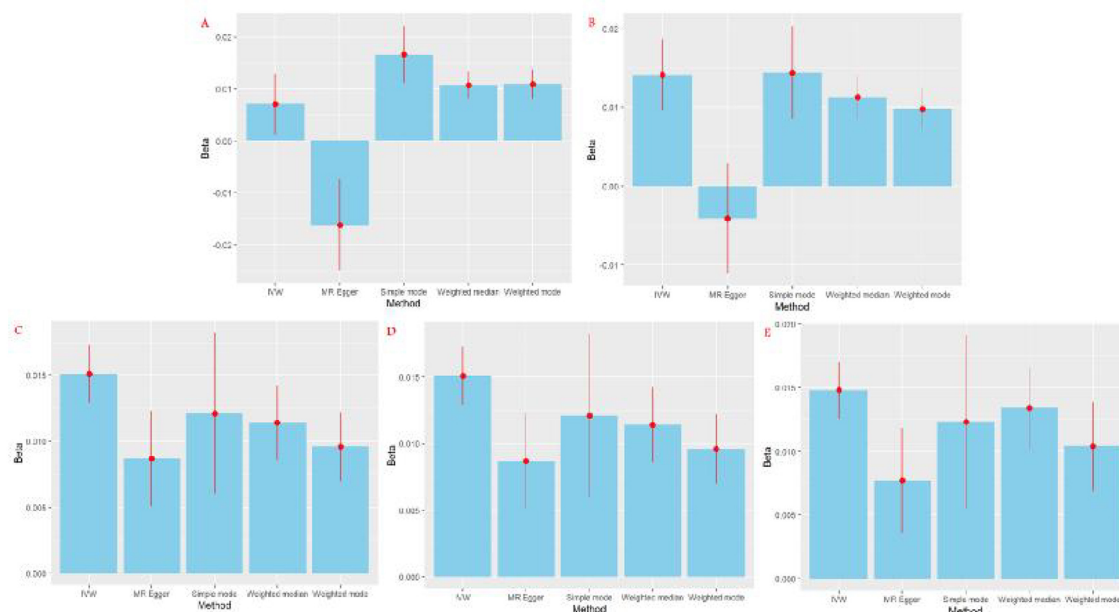
The following figure shows the main analysis (with potential outliers and influential points) and the analysis after using Residual and Cook's distance.



A: Main analysis (with potential outliers and influential points); B: After using Residual and Cook's distance (remove outliers); IVW: Inverse variance weighted; OR: Odds ratio; CI: Confidence interval

Figure S4-3: MUFA and Ischemic Heart Disease

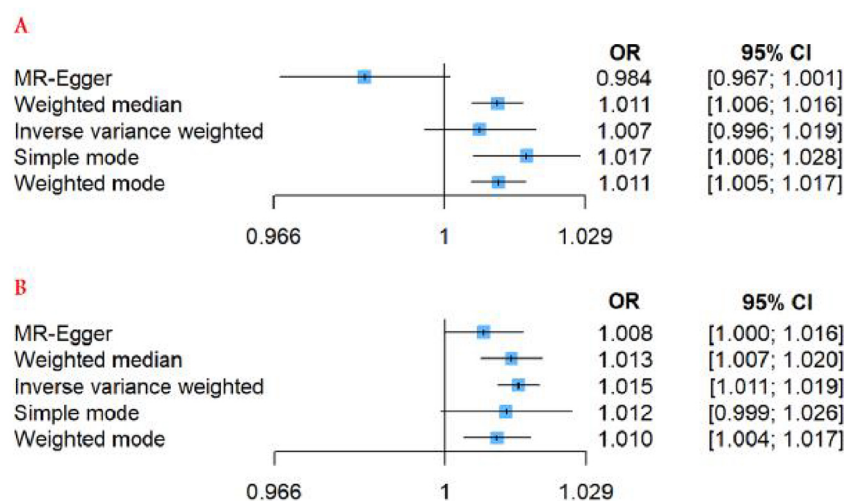
The following figure reveals the results of these methods. As seen, Residual and Cook's distance outperformed others. As a result, we used Residual and Cook's distance to detect potential outliers and influential points.



A: Initial analysis; B: After Phenoscanner; C: MR-PRESSO; D: Radial-MR; E: Residual and Cook's distance

When data contained outlier and influential points, we observed that heterogeneity existed in the initial analysis ($Q_{IVW}=875.42$, $P=3.826891e-145$; $Q_{Egger}=735.38$, $P=1.785689e-117$; Egger intercept=0.0016, $P=0.001$). After the Phenoscanner, we obtained ($Q_{IVW}=504.34$, $P=5.894196e-72$; $Q_{Egger}=425.99$, $P=1.852011e-57$; Egger intercept=0.0012, $P=0.002$). After applying MR-PRESSO, Radial-MR, and Residual and Cook's distance, we found that these approaches could reduce the heterogeneity ($Q_{IVW}=93.97$, $P=0.00023$; $Q_{Egger}=85.86$, $P=0.0012$; Egger intercept=0.0002, $P=0.034$), ($Q_{IVW}=93.97$, $P=0.00023$; $Q_{Egger}=85.86$, $P=0.0012$; Egger intercept=0.0002, $P=0.034$), and ($Q_{IVW}=57.86$, $P=0.094$; $Q_{Egger}=53.12$, $P=0.162$; Egger intercept=0.0004, $P=0.054$), respectively.

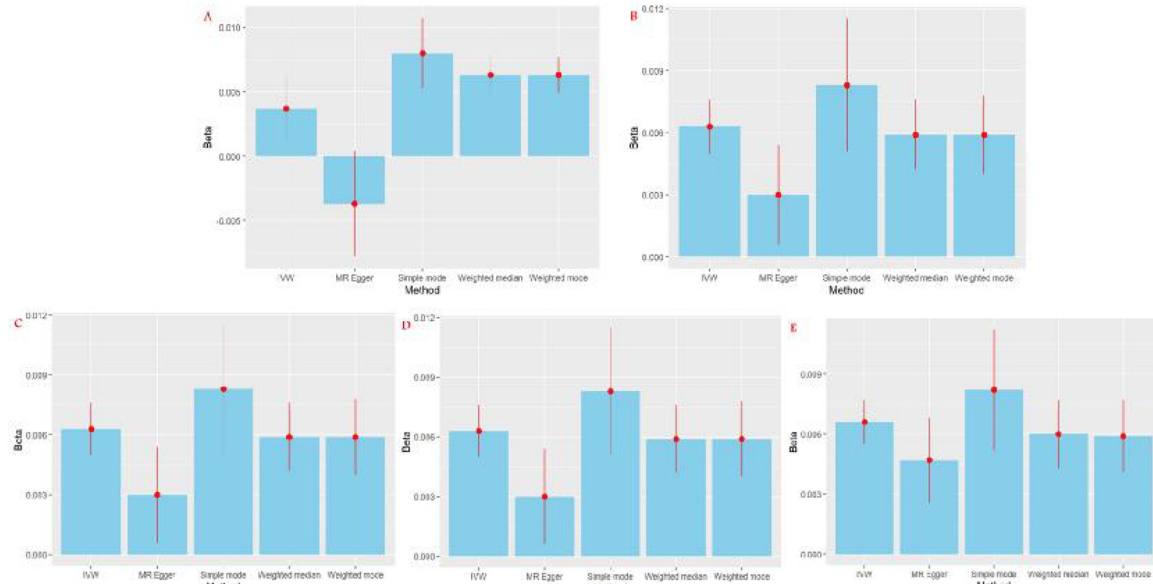
The following figure shows the main analysis (with potential outliers and influential points) and the analysis after using Residual and Cook's distance.



A: Main analysis (with potential outliers and influential points); B: After using Residual and Cook's distance (remove outliers); IVW: Inverse variance weighted; OR: Odds ratio; CI: Confidence interval

Figure S4-4: MUFA and Myocardial Infarction

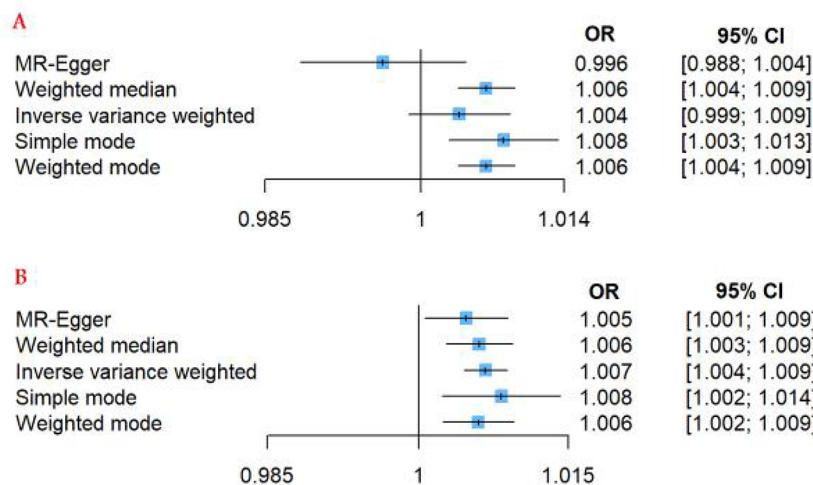
The following figure reveals the results of these methods. As seen, Residual and Cook's distance outperformed others. As a result, we used Residual and Cook's distance to detect potential outliers and influential points.



A: Initial analysis; B: After Phenoscanner; C: MR-PRESSO; D: Radial-MR; E: Residual and Cook's distance

When data contained the outlier and influential points, we observed that heterogeneity existed in the initial analysis ($Q_{IVW}=342.12$, $P=1.936199e-46$; $Q_{Egger}=308.51$, $P=1.462043e-40$; Egger intercept=0.0005, $P=0.030$). After the Phenoscanner, we obtained ($Q_{IVW}=59.20$, $P=0.051$; $Q_{Egger}=55.71$, $P=0.076$; Egger intercept=0.0002, $P=0.112$). After applying MR-PRESSO, Radial-MR, and Residual and Cook's distance, we found that these approaches could reduce the heterogeneity ($Q_{IVW}=59.20$, $P=0.051$; $Q_{Egger}=55.71$, $P=0.076$; Egger intercept=0.0002, $P=0.112$), ($Q_{IVW}=59.20$, $P=0.051$; $Q_{Egger}=55.71$, $P=0.076$; Egger intercept=0.0002, $P=0.112$), and ($Q_{IVW}=39.12$, $P=0.510$; $Q_{Egger}=38.10$, $P=0.511$; Egger intercept=0.0001, $P=0.318$), respectively.

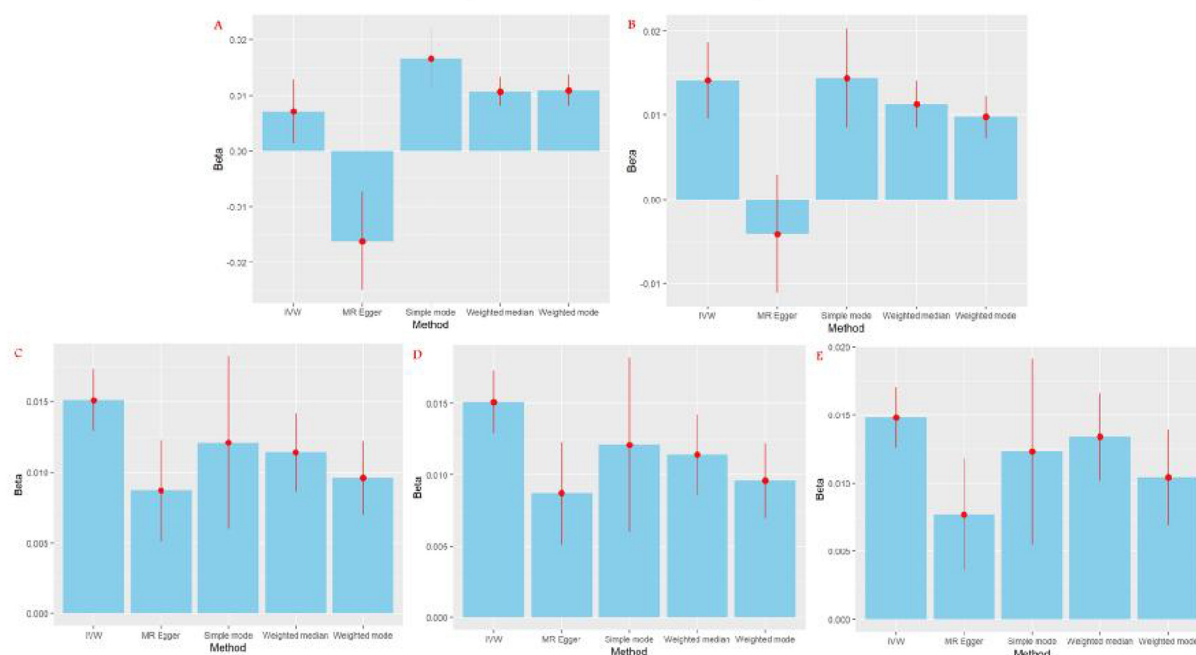
The following figure shows the main analysis (with potential outliers and influential points) and the analysis after using Residual and Cook's distance.



A: Main analysis (with potential outliers and influential points); B: After using Residual and Cook's distance (remove outliers); IVW: Inverse variance weighted; OR: Odds ratio; CI: Confidence interval.

Figure S4-5: MUFA and Hypertension

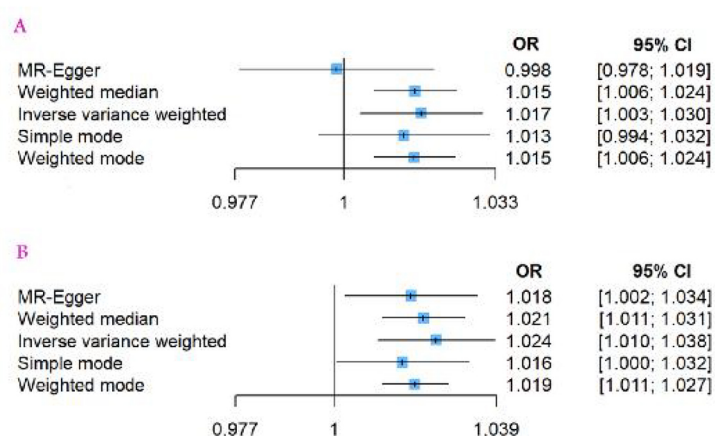
The following figure reveals the results of these methods. As seen, Residual and Cook's distance outperformed the others. As a result, we used Residual and Cook's distance to detect the potential outliers and influential points.



A: Initial analysis; B: After Phenoscanner; C: MR-PRESSO; D: Radial-MR; E: Residual and Cook's distance

When data contained the outlier and influential points, we observed that heterogeneity existed in the initial analysis ($Q_{IVW}=360.91$, $P=1.483769e-46$; $Q_{Egger}=331.88$, $P=1.314358e-41$; Egger intercept=0.0013, $P=0.034$). After the Phenoscanner, we obtained ($Q_{IVW}=212.62$, $P=6.077566e-22$; $Q_{Egger}=196.54$, $P=1.445449e-19$; Egger intercept=0.0005, $P=0.0507$). After applying MR-PRESSO, Radial-MR and Residual and Cook's distance, we found that these approaches could reduce the heterogeneity ($Q_{IVW}=120.92$, $P=7.107560e-09$; $Q_{Egger}=119.78$, $P=6.137456e-09$; Egger intercept=0.0002, $P=0.520$), ($Q_{IVW}=110.05$, $P=1.403757e-07$; $Q_{Egger}=108.78$, $P=1.288251e-07$; Egger intercept=0.0003, $P=0.482$), and ($Q_{IVW}=86.02$, $P=2.101390e-05$; $Q_{Egger}=87.78$, $P=1.964347e-05$; Egger intercept=0.0004, $P=0.387$), respectively.

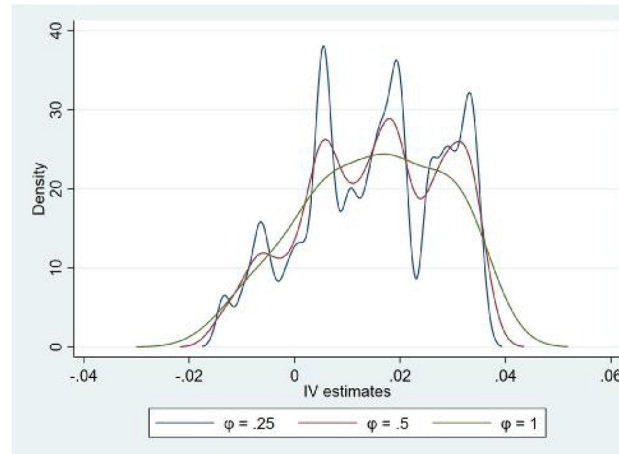
The following figure shows the main analysis (with potential outliers and influential points) and the analysis after using Residual and Cook's distance.



A: Main analysis (with potential outliers and influential points); B: After using Residual and Cook's distance (remove outliers); IVW: Inverse variance weighted; OR: Odds ratio; CI: Confidence interval.

Figure S4: The figure shows outliers based on MR-PRESSO, RadialMR, and Cook's distance.

Figure S5-1: Angina



Densities of the IV estimates using different values of the phi parameter.

Estimates using different values of the phi parameter

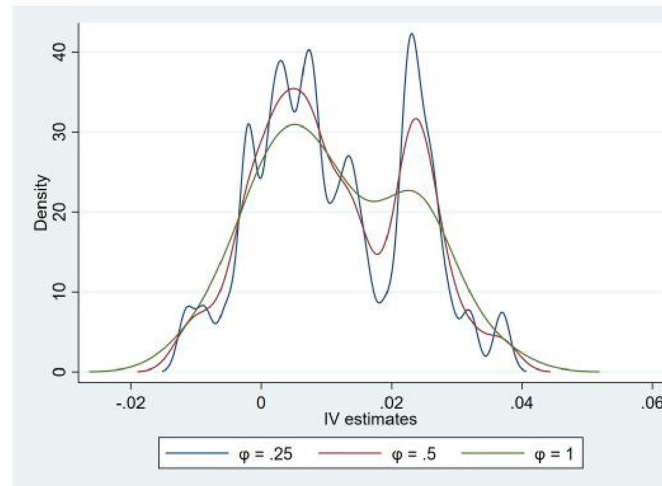
Phi	Beta	Standard Error	Z Statistic	P value	95% CI
0.25	0.0055035	0.0067975	0.081	0.418	-0.008-0.019
0.05	0.0179922	0.0059752	3.01	0.003	0.006-0.029
1.00	0.0169183	0.004576	3.70	<0.001	0.008-0.026

Mode estimator with $\phi=1$

Method	Beta	Standard Error	Z Statistic	P value	95% CI
SM	0.0169183	0.0044367	3.81	<0.001	0.008-0.026
WM	0.0098626	0.0019013	5.19	<0.001	0.006-0.013
SM with NOME	0.0169183	0.0045142	3.75	<0.001	0.008-0.026

SM: Simple mode; WM: Weighted mode; SM with NOME: Simple mode estimator with NOME assumption

Figure S5-2: Atherosclerotic



Densities of the IV estimates using different values of the phi parameter.

Estimates using different values of the phi parameter.

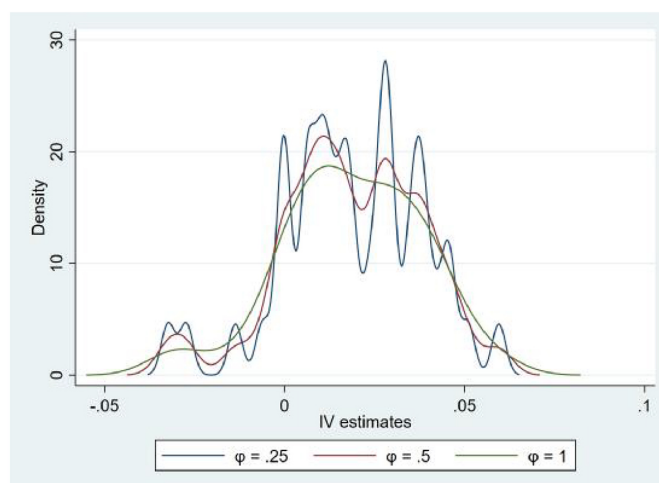
Phi	Beta	Standard Error	Z Statistic	P value	95% CI
0.25	0.0230629	0.0056914	4.05	<0.001	0.012-0.034
0.05	0.0049771	0.0049212	1.01	0.312	-0.005-0.015
1.00	0.0051419	0.003707	1.39	0.165	-0.002-0.012

Mode estimator with $\phi=1$

Method	Beta	Standard Error	Z Statistic	P value	95% CI
SM	0.0051419	0.0036237	1.42	0.156	-0.002-0.012
WM	0.0074403	0.0017178	4.33	<0.001	0.004-0.011
SM with NOME	0.0051419	0.0036718	1.40	0.161	-0.002-0.012

SM: Simple mode; WM: Weighted mode; SM with NOME: Simple mode estimator with NOME assumption

Figure S5-3: Ischemic Heart Disease



Densities of the IV estimates using different values of the phi parameter.

Estimates using different values of the phi parameter.

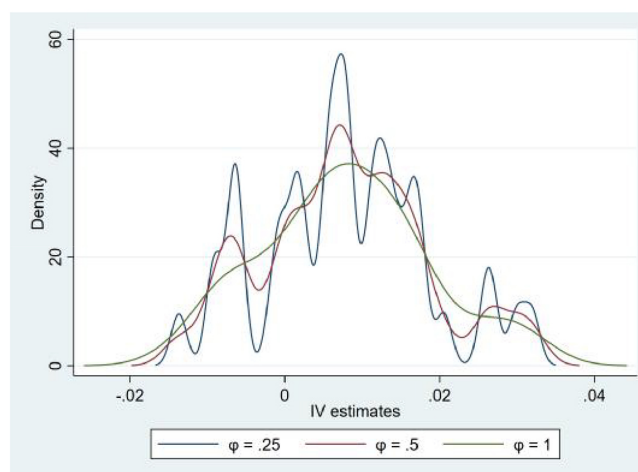
Phi	Beta	Standard Error	Z Statistic	P value	95% CI
0.25	0.0280196	0.0107344	2.61	0.009	0.007-0.049
0.05	0.0107682	0.0093947	1.15	0.252	-0.008-0.029
1.00	0.0123624	0.0071088	1.74	0.082	-0.001-0.026

Mode estimator with $\varphi=1$

Method	Beta	Standard Error	Z Statistic	P value	95% CI
SM	0.0123624	0.0070729	1.75	0.080	-0.001-0.026
WM	0.0104804	0.004163	2.52	0.012	0.002-0.019
SM with NOME	0.0123624	0.0072871	1.70	0.090	-0.002-0.027

SM: Simple mode; WM: Weighted mode; SM with NOME: Simple mode estimator with NOME assumption

Figure S5-4: Myocardial Infarction



Densities of the IV estimates using different values of the phi parameter.

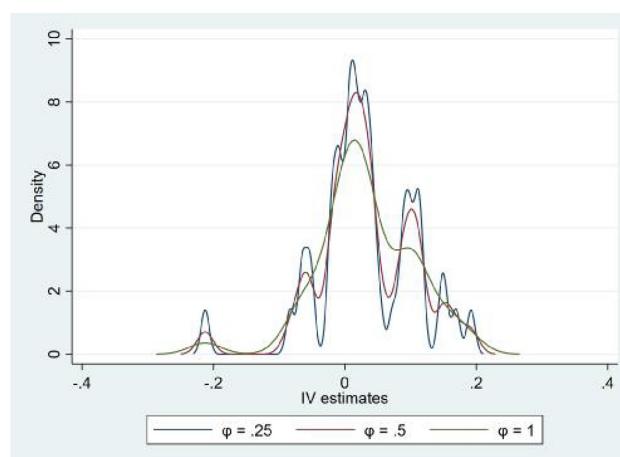
Estimates using different values of the phi parameter.

Phi	Beta	Standard Error	Z Statistic	P value	95% CI
0.25	0.0072589	0.0053183	1.36	0.172	-0.003-0.018
0.05	0.0071504	0.0045992	1.55	0.120	-0.002-0.016
1.00	0.0082399	0.0034194	2.41	0.016	0.001-0.015

Mode estimator with $\varphi=1$

Method	Beta	Standard Error	Z Statistic	P value	95% CI
SM	0.0082399	0.0034355	2.40	0.016	0.001-0.015
WM	0.0059076	0.001846	3.20	0.001	0.002-0.009
SM with NOME	0.0082399	0.0034271	2.40	0.016	0.001-0.015

SM: Simple mode; WM: Weighted mode; SM with NOME: Simple mode estimator with NOME assumption

Figure S5-5: Hypertension

Densities of the IV estimates using different values of the phi parameter.

Estimates using different values of the phi parameter.

Phi	Beta	Standard Error	Z Statistic	P value	95% CI
0.25	0.0117454	0.0205172	0.57	0.567	-0.028-0.052
0.05	0.0173461	0.0142013	1.22	0.222	-0.010-0.045
1.00	0.0151371	0.0099997	1.51	0.130	-0.004-0.035

Mode estimator with $\phi=1$

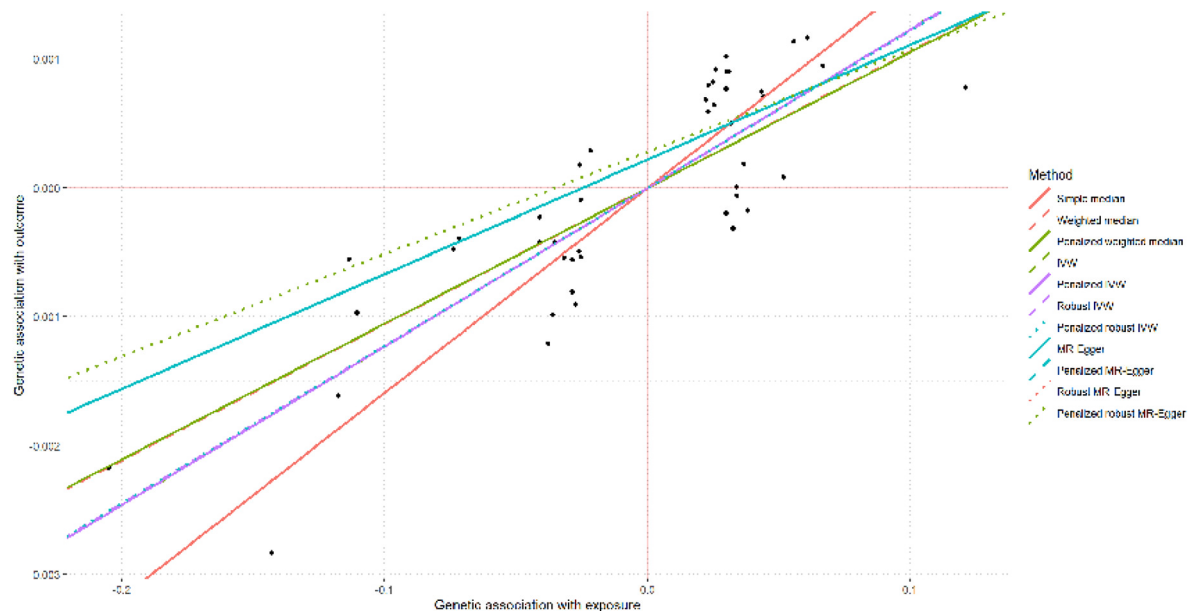
Method	Beta	Standard Error	Z Statistic	P	95% CI
SM	0.0151371	0.0099997	1.51	0.130	-0.004-0.035
WM	0.0194667	0.0042677	4.56	<0.001	0.011-0.028
SM with NOME	0.0151371	0.010542	1.44	0.151	-0.005-0.036

SM: Simple mode; WM: Weighted mode; SM with NOME: Simple mode estimator with NOME assumption

Figure S5: The figure shows the densities of the IV estimates using different values of the phi parameter.

Figure S6-1: Angina

The following figures show the several Mendelian randomization methods, including Simple median, Weighted median, Penalized weighted median, Inverse variance weighted, Penalized Inverse variance weighted, Robust inverse variance weighted, Penalized robust inverse variance weighted, MR-Egger, Penalized MR-Egger, Robust MR-Egger, Penalized robust MR-Egger, Maximum likelihood estimate, and Mode-based method.



The plot shows the positive causality of MUFA on angina.

The following figure displays a scatter plot, which represents a genetic association. The X-axis represents the genetic association of exposure (MUFA), and the Y-axis represents the genetic association of the outcome (angina). The linear line corresponds to the inverse variance weighted method. As seen, the slope is positive.

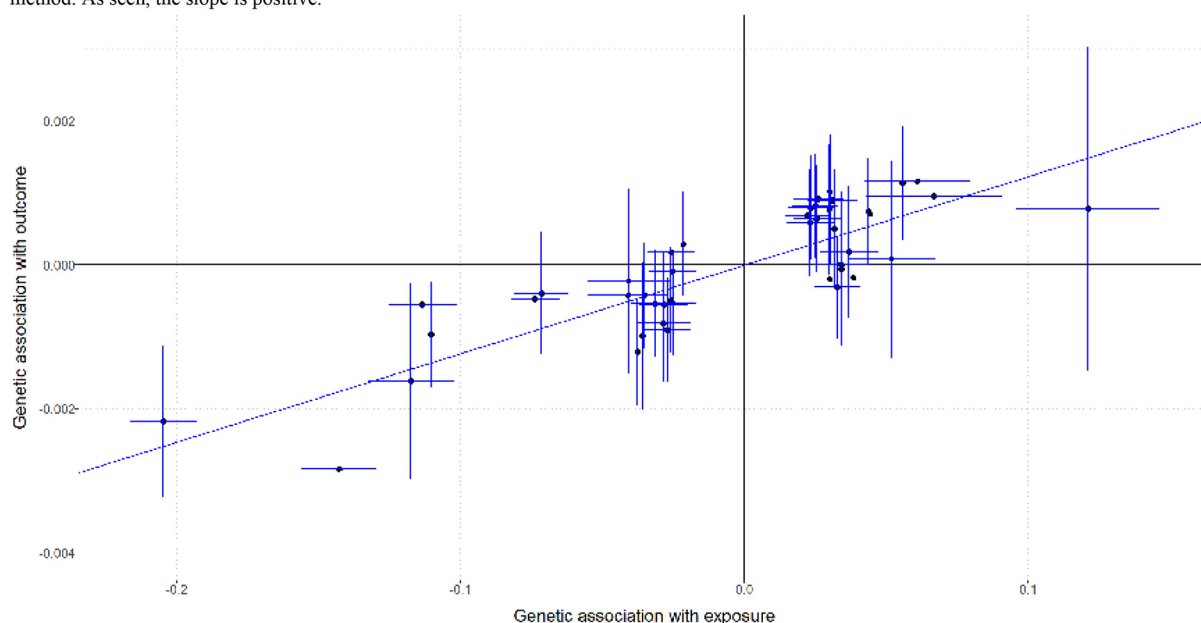
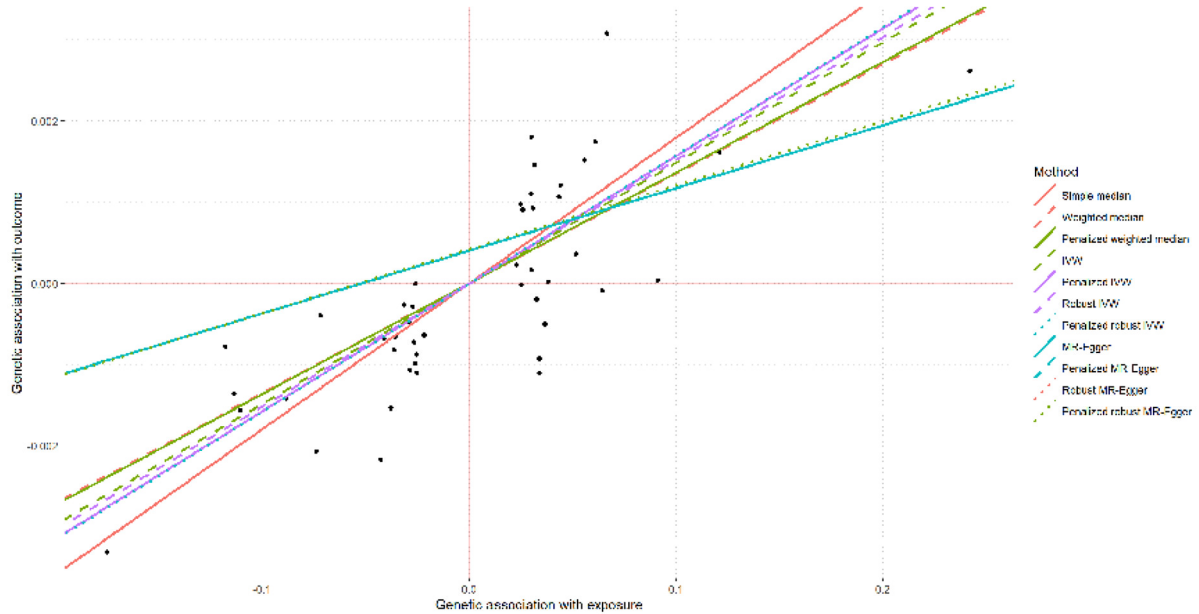


Figure S6-2: Atherosclerotic

The following figures show the several Mendelian randomization methods, including Simple median, Weighted median, Penalized weighted median, Inverse variance weighted, Penalized Inverse variance weighted, Robust inverse variance weighted, Penalized robust inverse variance weighted, MR-Egger, Penalized MR-Egger, Robust MR-Egger, Penalized robust MR-Egger, Maximum likelihood estimate, and Mode-based method.



The following figure displays a scatter plot, which shows a genetic association. The X-axis represents the genetic association of the exposure (MUFA), and the Y-axis represents the genetic association of the outcome (atherosclerotic heart disease). The linear line corresponds to the inverse variance weighted method. As seen, the slope is positive.

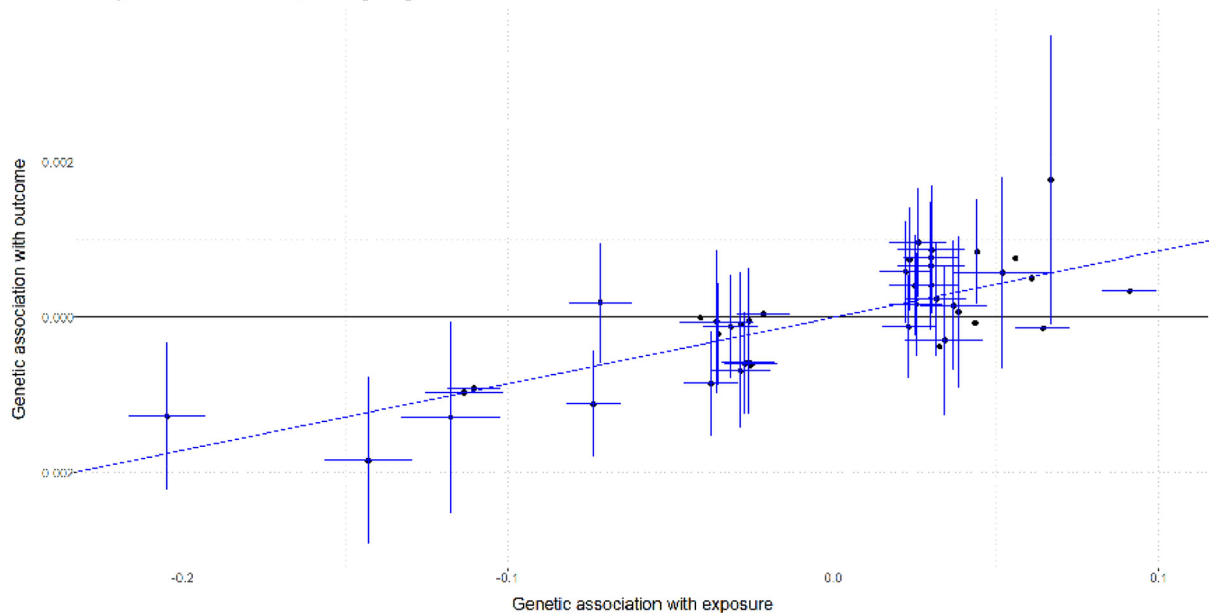
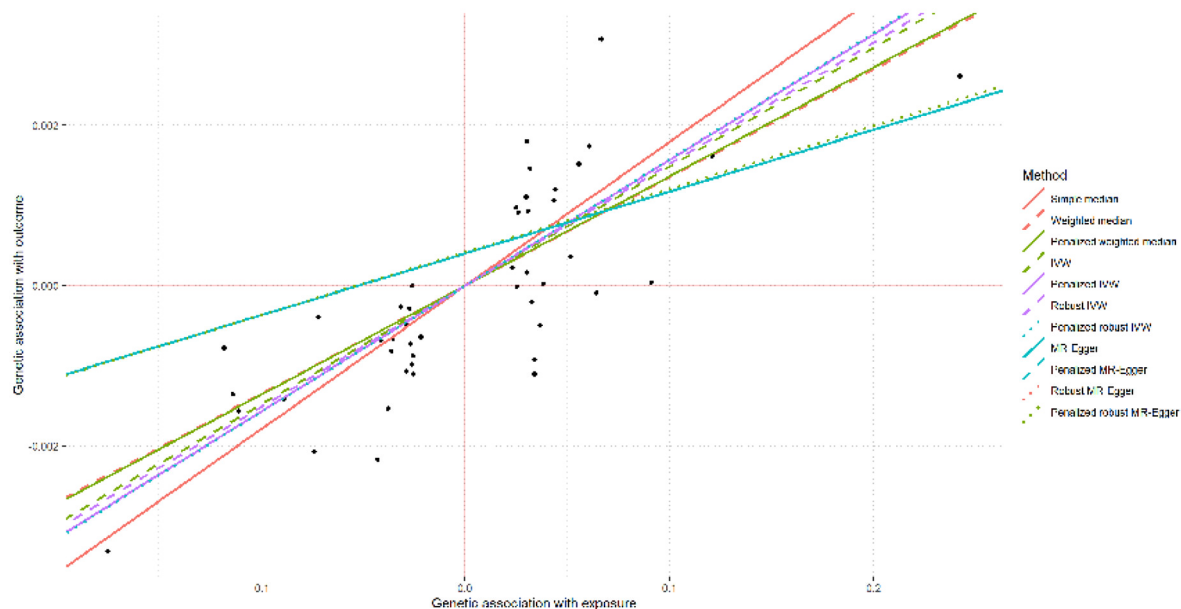


Figure S6-3: Ischemic Heart Disease

The following figures show the several Mendelian randomization methods, including Simple median, Weighted median, Penalized weighted median, Inverse variance weighted, Penalized Inverse variance weighted, Robust inverse variance weighted, Penalized robust inverse variance weighted, MR-Egger, Penalized MR-Egger, Robust MR-Egger, Penalized robust MR-Egger, Maximum likelihood estimate, and Mode-based method.



The plot shows positive causality between MUFA and IHD.

The following figure displays a scatter plot, which shows a genetic association. The X-axis represents the genetic association of exposure (MUFA), and the Y-axis represents the genetic association of the outcome (IHD). The linear line corresponds to the inverse variance weighted method. As seen, the slope is positive.

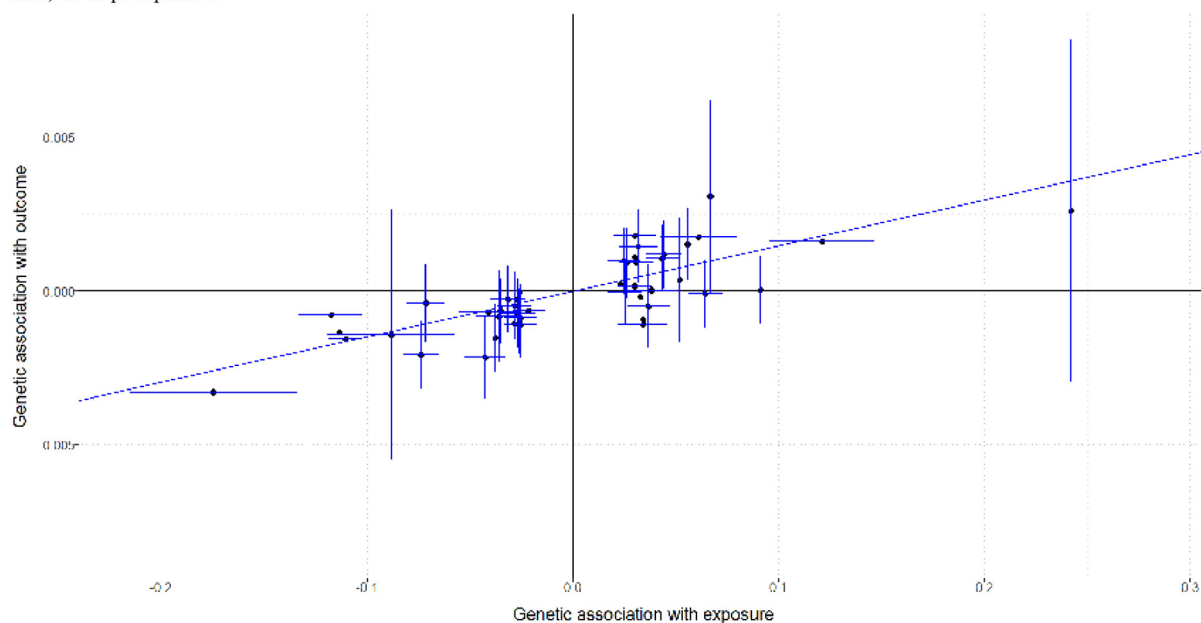
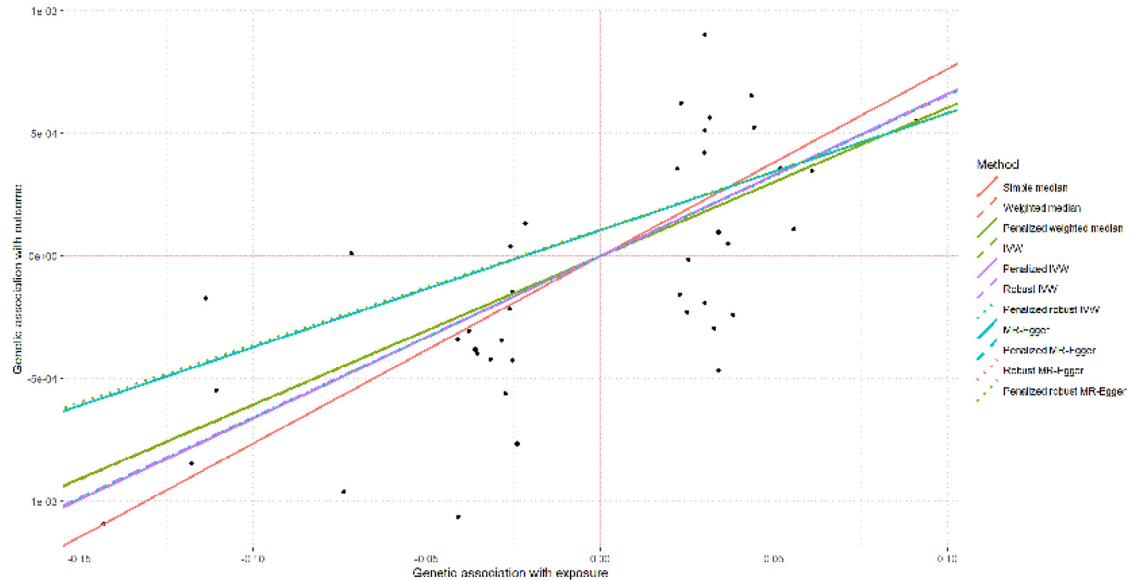


Figure S6-4: Myocardial Infarction

The following figures show the several Mendelian randomization methods, including Simple median, Weighted median, Penalized weighted median, Inverse variance weighted, Penalized Inverse variance weighted, Robust inverse variance weighted, Penalized robust inverse variance weighted, MR-Egger, Penalized MR-Egger, Robust MR-Egger, Penalized robust MR-Egger, Maximum likelihood estimate, and Mode-based method.



The plot shows positive causality between MUFA and MI.

The following figure displays a scatter plot, which shows a genetic association. The X-axis represents the genetic association of exposure (MUFA), and the Y-axis represents the genetic association of outcome (MI). The linear line corresponds to the inverse variance weighted method. As seen, the slope is positive.

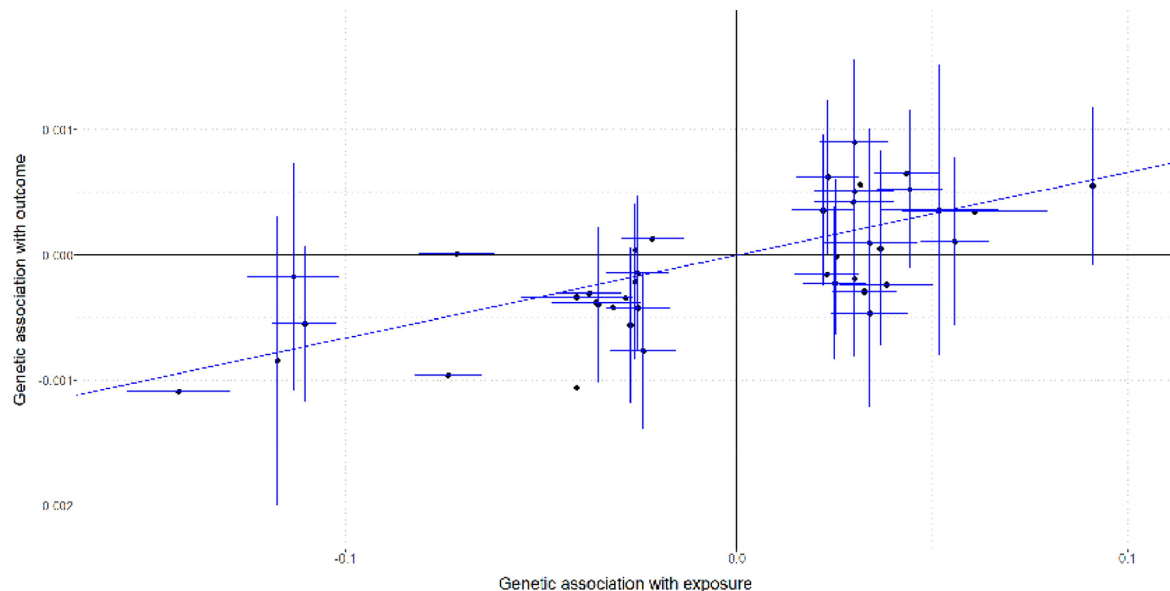
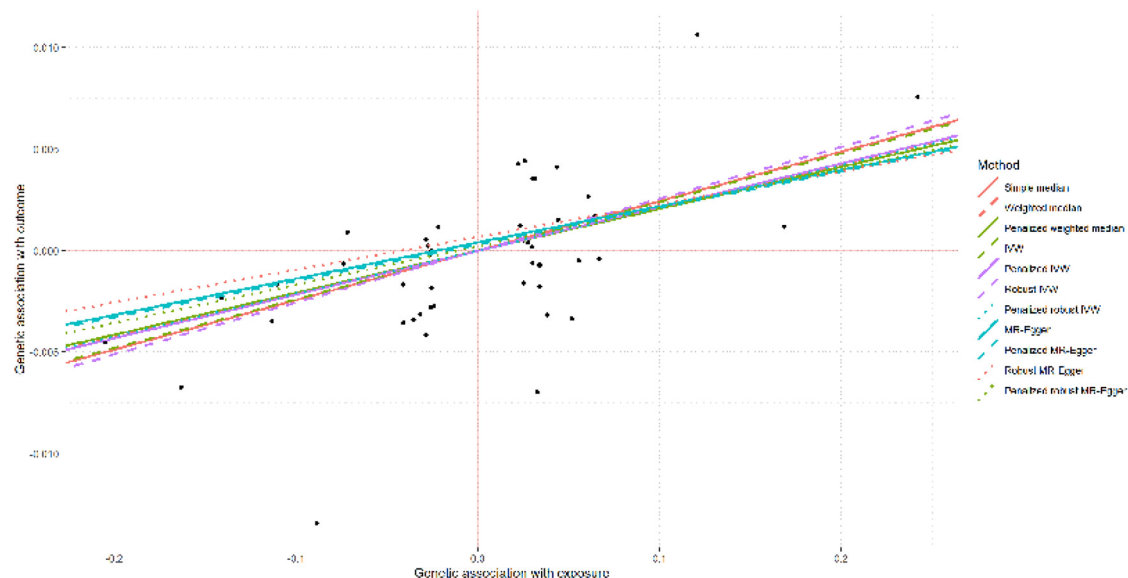


Figure S6-5: Hypertension

The following figures show the several Mendelian randomization methods, including Simple median, Weighted median, Penalized weighted median, Inverse variance weighted, Penalized Inverse variance weighted, Robust inverse variance weighted, Penalized robust inverse variance weighted, MR-Egger, Penalized MR-Egger, Robust MR-Egger, Penalized robust MR-Egger, Maximum likelihood estimate, and Mode-based method.



The plot shows positive causality between MUFA and hypertension.

The following figure displays a scatter plot, which shows a genetic association. The X-axis represents the genetic association of exposure (MUFA), and the Y-axis represents the genetic association of outcome (hypertension). The linear line corresponds to the inverse variance weighted method. As seen, the slope is positive.

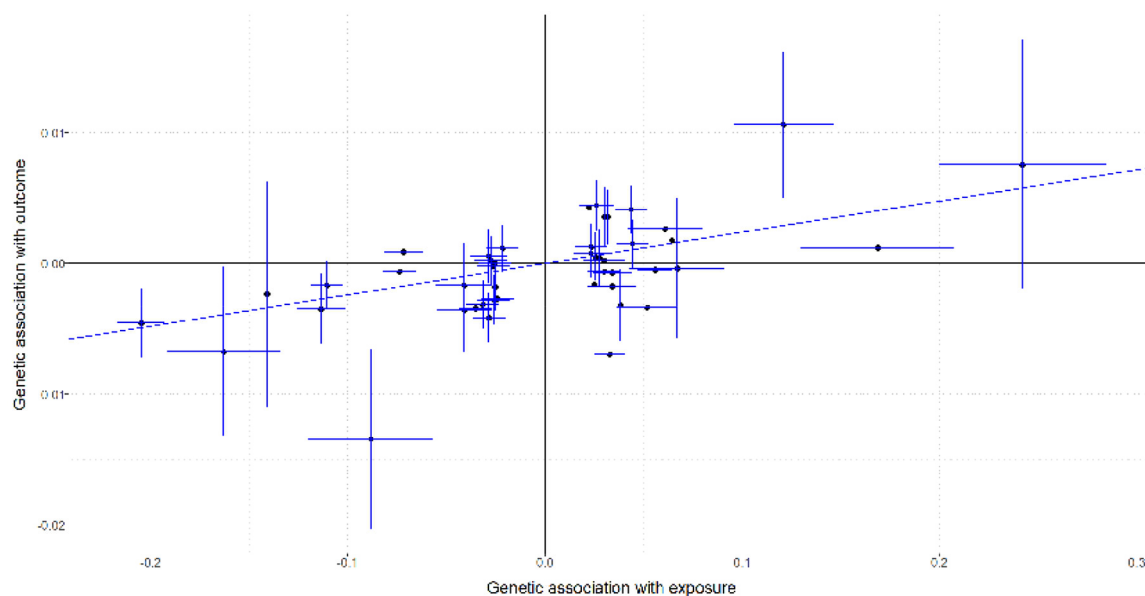


Figure S6: The figure shows the comparison of the causal estimates from the various Mendelian randomization methods and a scatter plot of the potential effects of MUFA-associated SNPs on cardiovascular diseases.

Figure S7-1: Angina

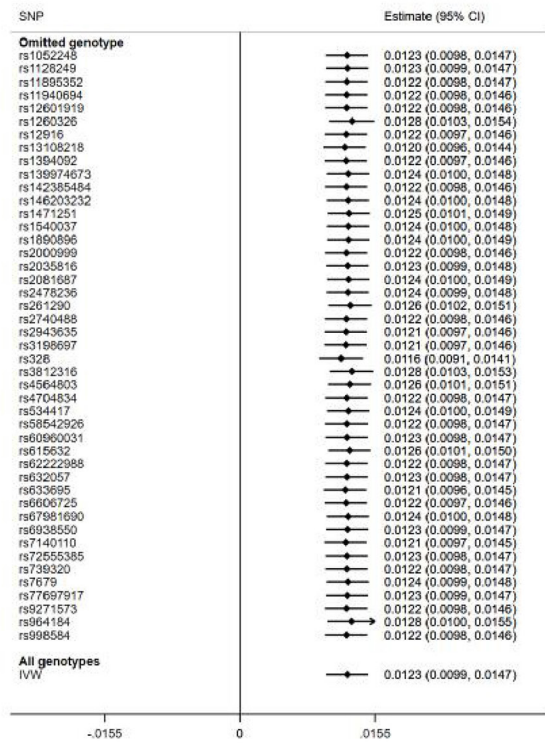


Figure S7-3: Ischemic Heart Disease

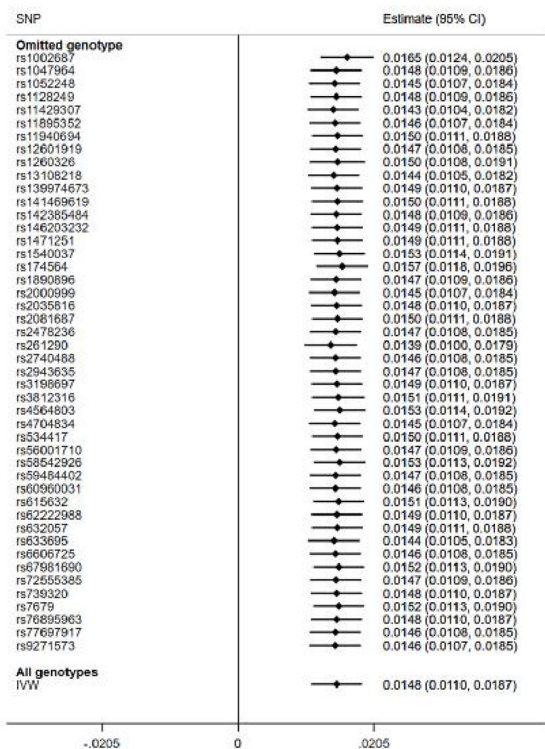


Figure S7-2: Atherosclerotic

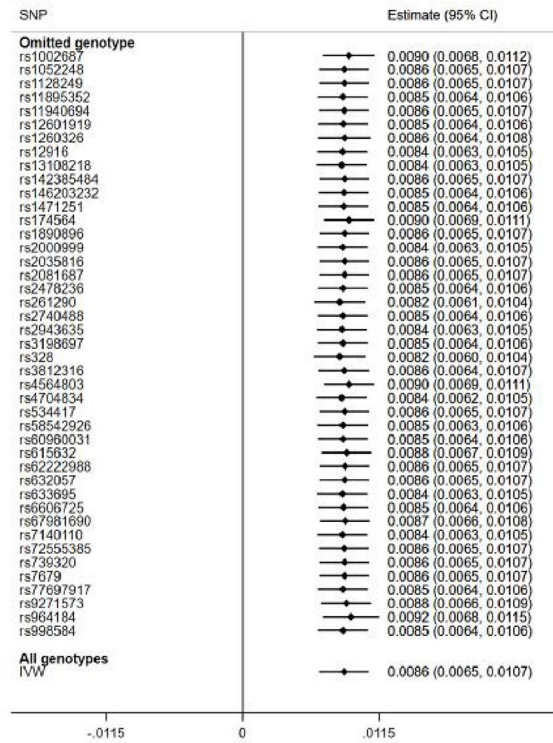


Figure S7-4: Myocardial Infarction

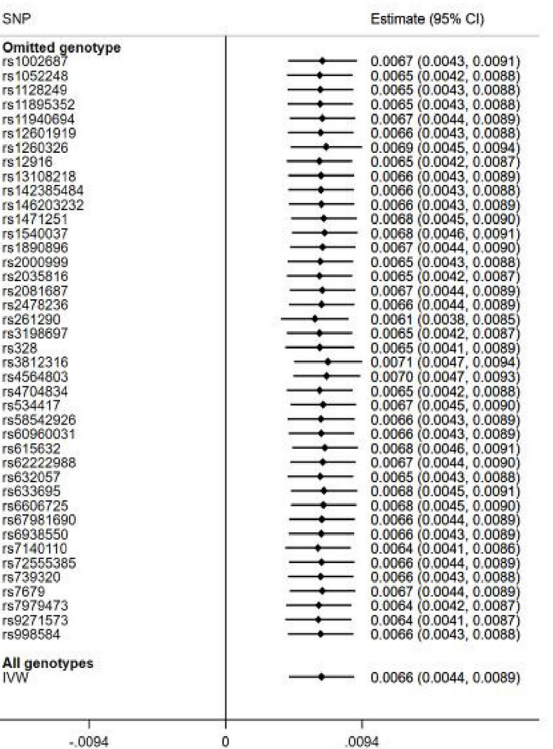


Figure S7-5: Hypertension

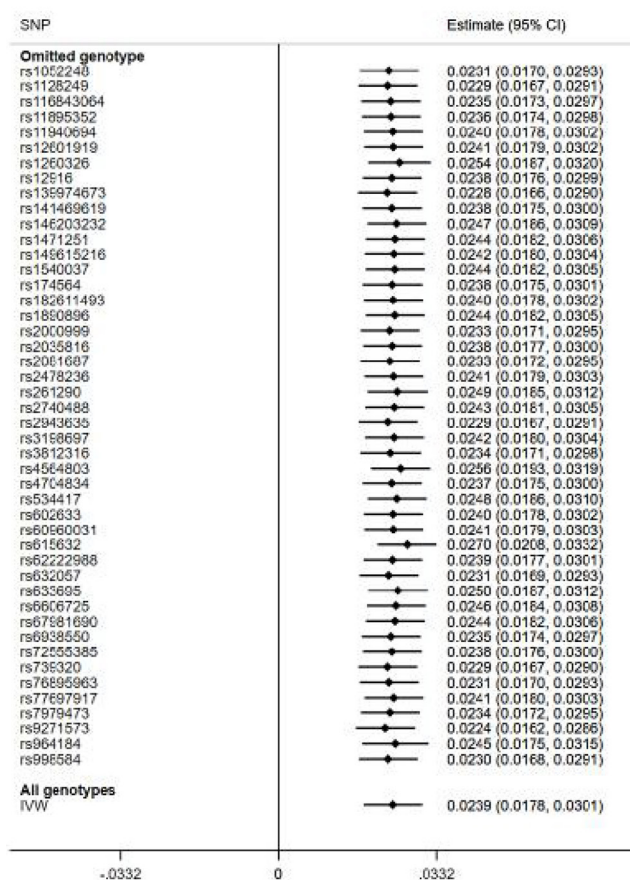


Figure S7: The figure shows the leave-one-out plot to assess whether a single variant is driving the association between MUFA and cardiovascular diseases.

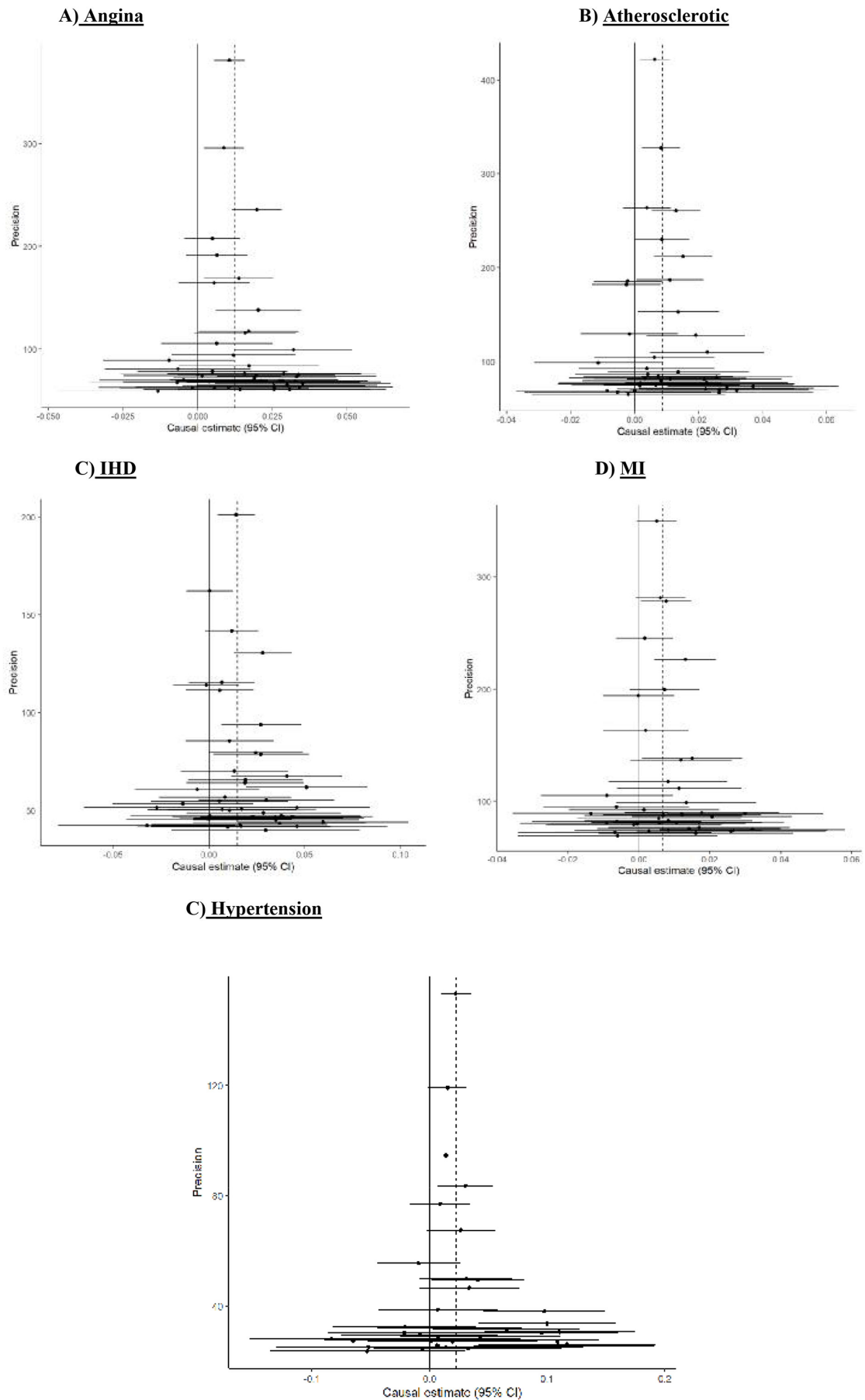


Figure S8: The figure shows the funnel plot of the causal association between MUFA and cardiovascular diseases.

Figure S9-1: Angina

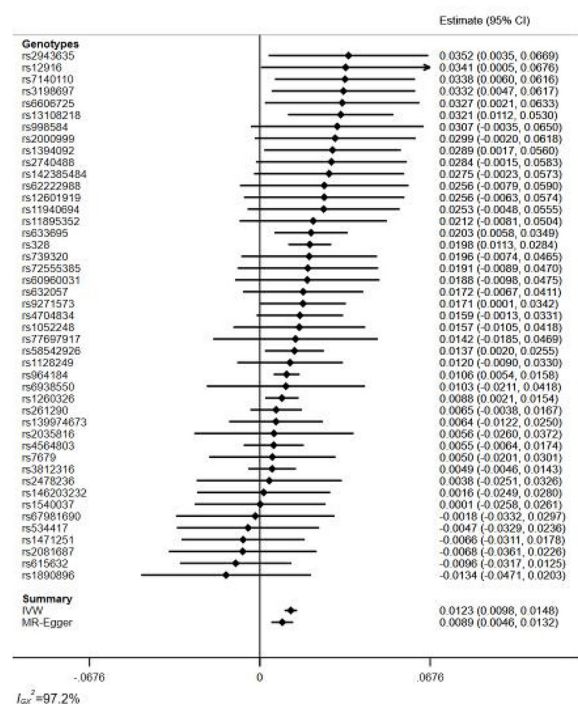


Figure S9-2: Atherosclerotic

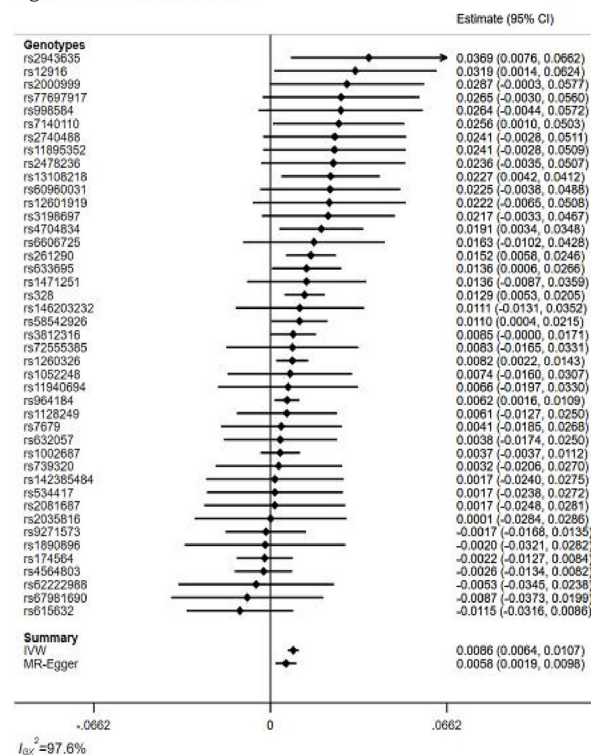


Figure S9-3: Ischemic Heart Disease

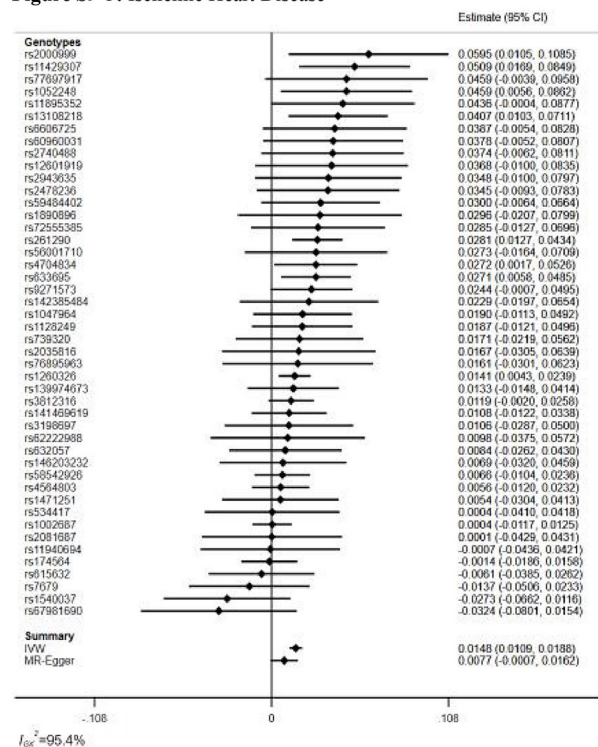


Figure S9-4: Myocardial Infarction

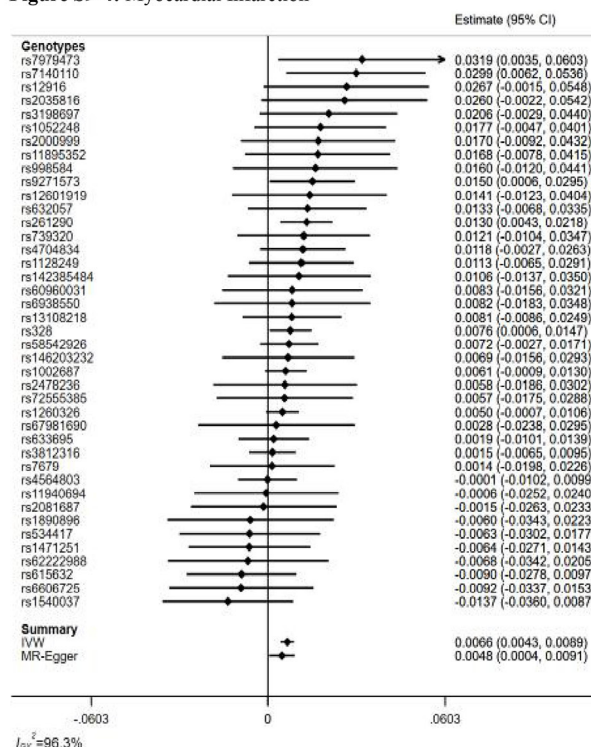


Figure S9-5: Hypertension

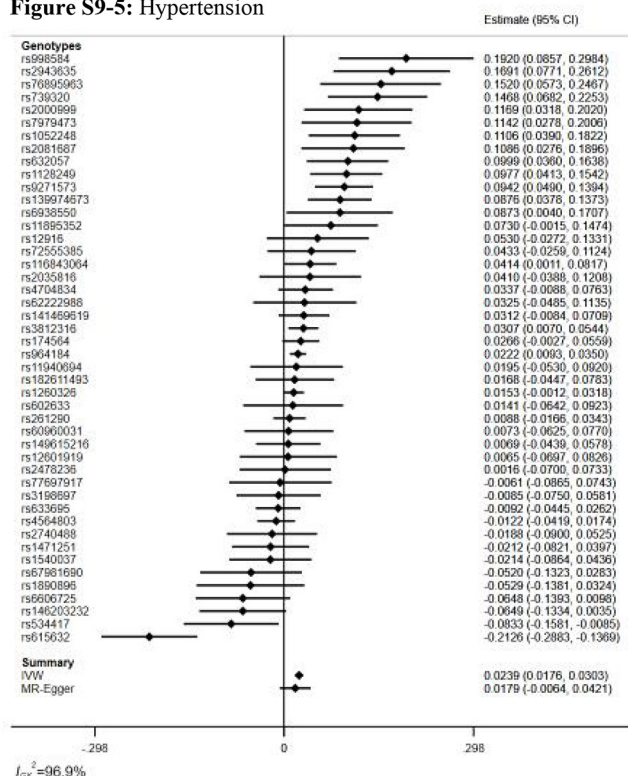


Figure S9: The figure shows the forest plot of variant-specific inverse variance estimates for the causal association between MUFA and cardiovascular diseases.

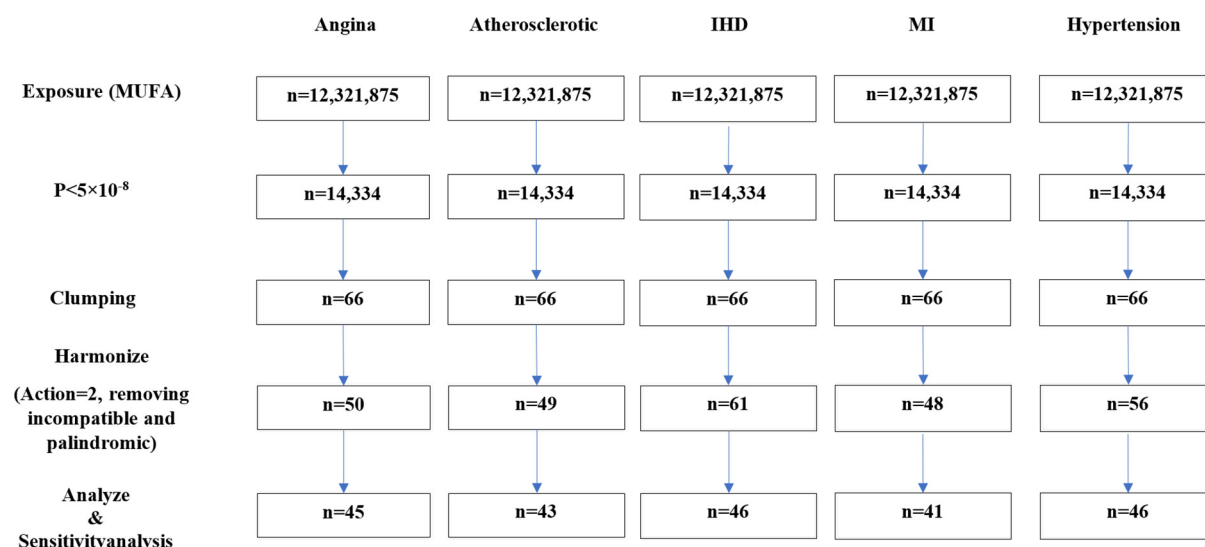


Figure S10: The figure shows the steps of two-sample Mendelian randomization.