

Fig A - Statistical power to detect associations with risk for genetic instruments explaining different proportions of a risk factor in a Mendelian randomization analysis based on 10,784 cases and 20,406 controls.

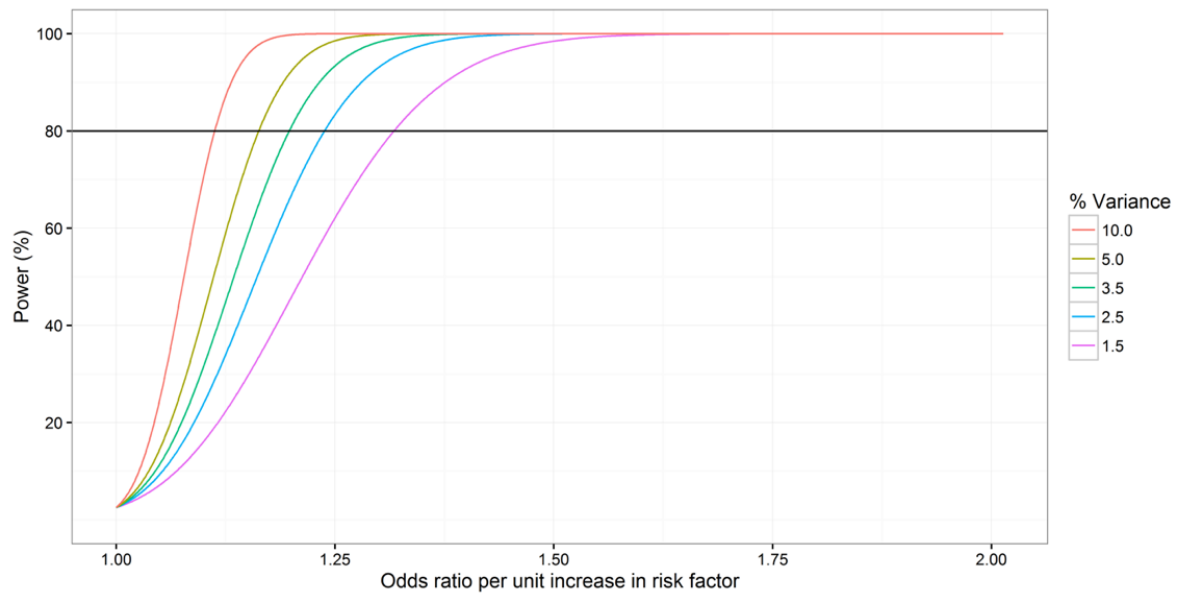


Fig B - Forest plot of RCC risk for each SD increment in BMI stratified by study. OR were estimated using likelihood-based MR approach. 95% CI: 95% Confidence Interval; P: P value. I^2 : between-strata heterogeneity (%). Phet: P value of between-strata heterogeneity.

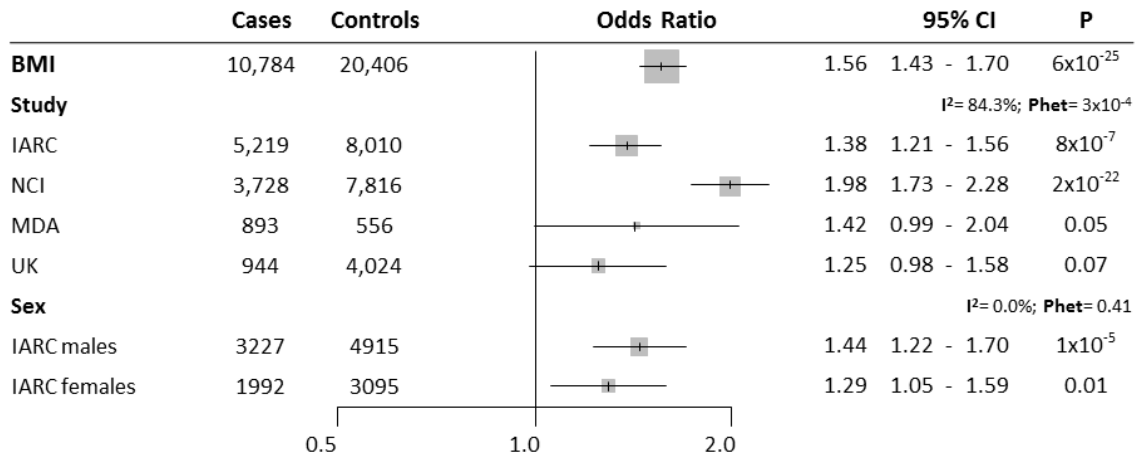


Fig C - Forest plot of RCC risk for each SD increment in waist-to-hip ratio stratified by study. OR were estimated using likelihood-based MR approach. 95% CI: 95% Confidence Interval; P: P value. I^2 : between-strata heterogeneity (%). Phet: P value of between-strata heterogeneity.

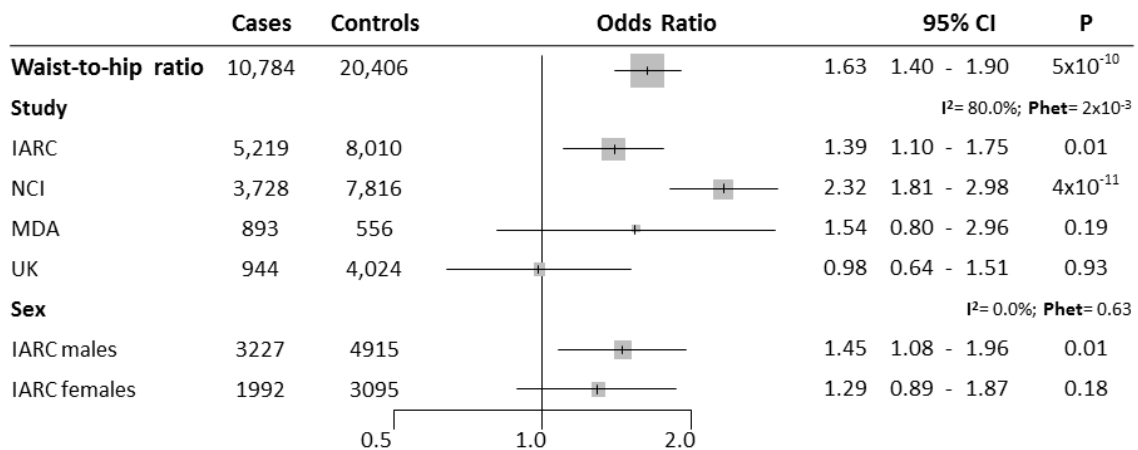


Fig D - Forest plot of RCC risk for each SD increment in body fat % stratified by study. OR were estimated using likelihood-based MR approach. 95% CI: 95% Confidence Interval; P: P value. I^2 : between-strata heterogeneity (%). Phet: P value of between-strata heterogeneity.

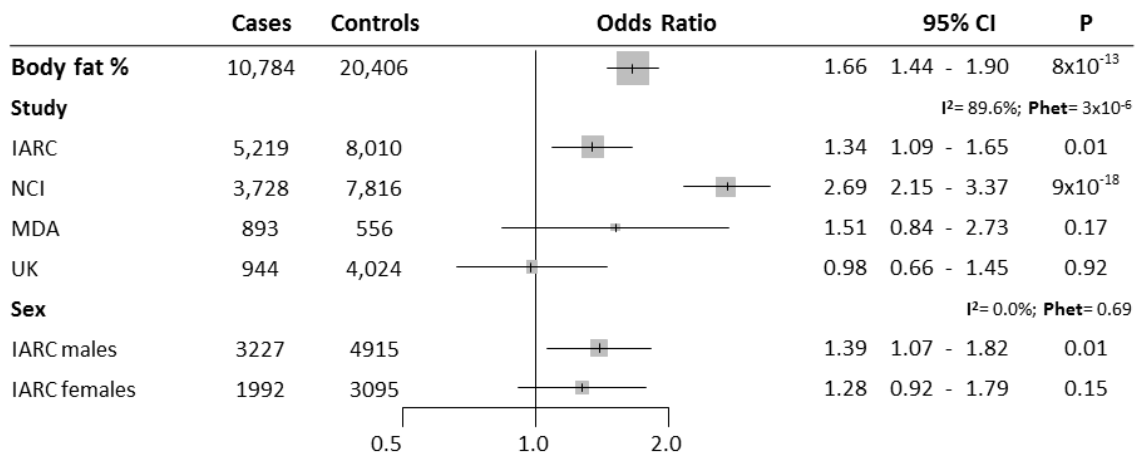


Fig E - The leave-one-out histogram reflects the distribution of the causal effect estimate of BMI instrument when one of the SNPs is removed. OR: odds ratio.

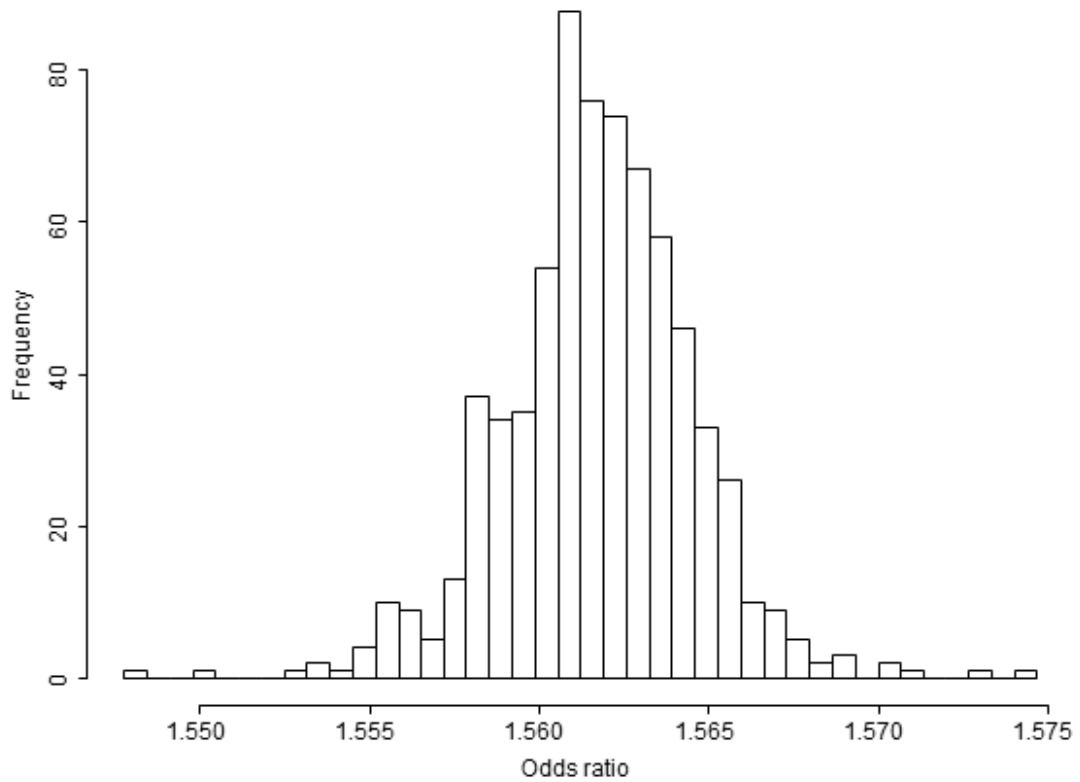


Fig F - The leave-one-out histogram reflects the distribution of the causal effect estimate of WHR instrument when one of the SNPs is removed. OR: odds ratio.

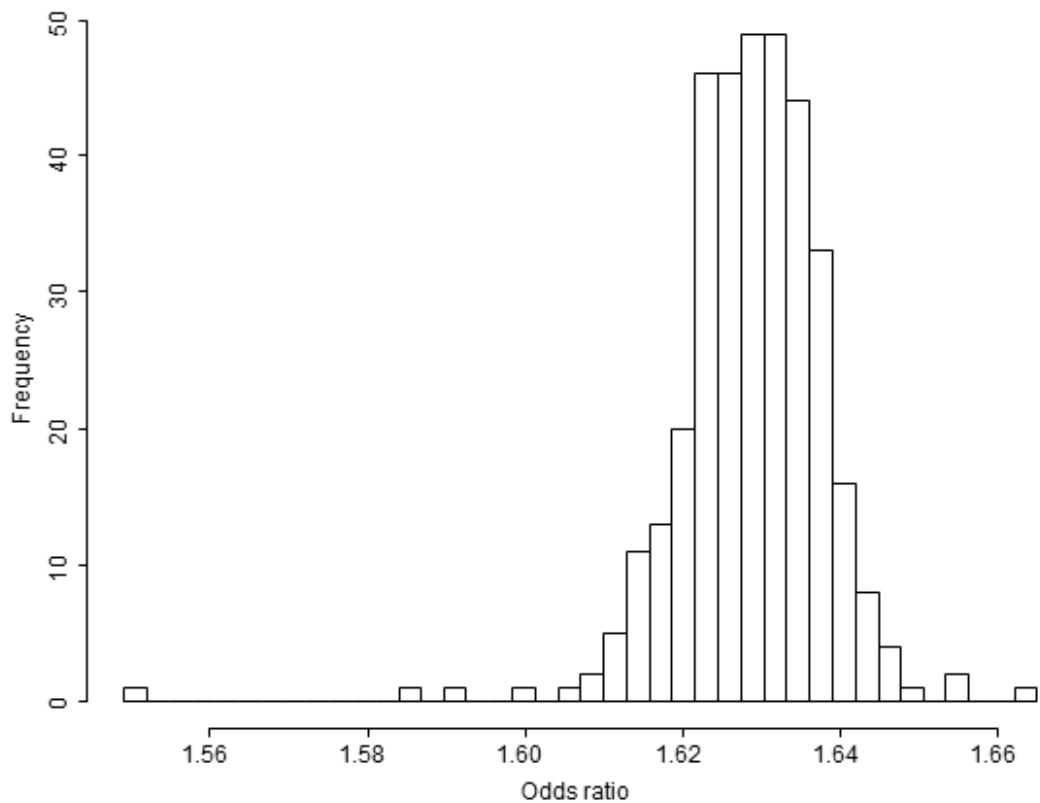
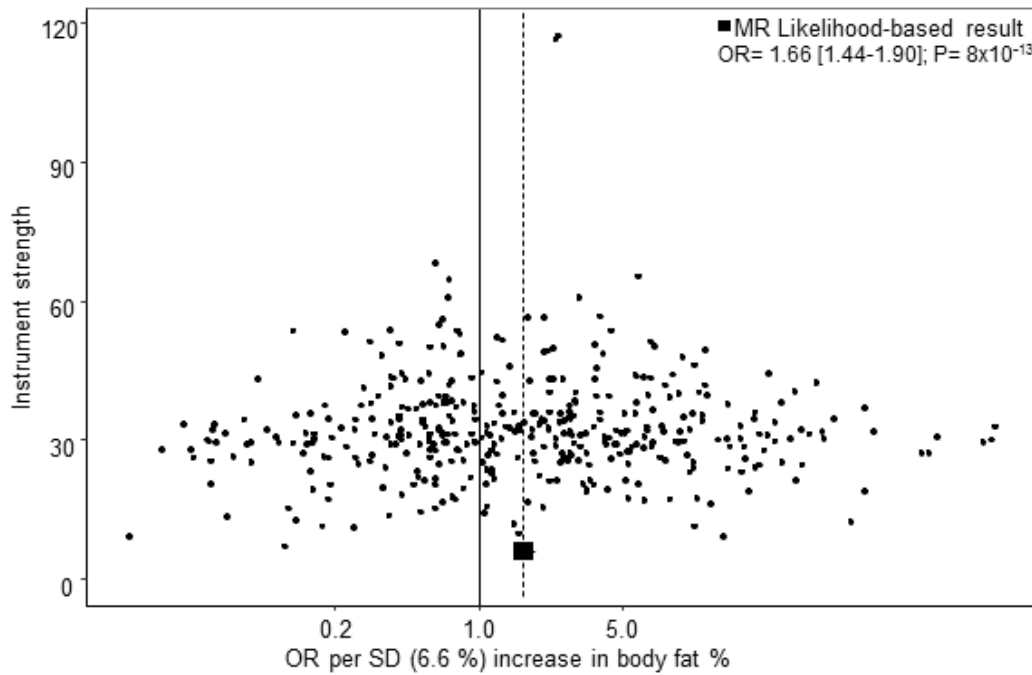


Fig G - For each SNP used in the genetic instrument of body fat %, the funnel plot (A) depicts the weight exerted into the causal effect estimate along the y-axis (β_{GP}/SE_{GD}), and estimates of the causal effect on RCC odds along the x-axis ($\exp(\beta_{GD}/\beta_{GP})$). The leave-one-out histogram (B) reflects the distribution of the causal effect estimate of body fat % instrument when one of the SNPs is removed. OR: odds ratio. Funnel plot X-axis is in logarithmic scale.

A- Funnel plot



B- Leave-one-out histogram

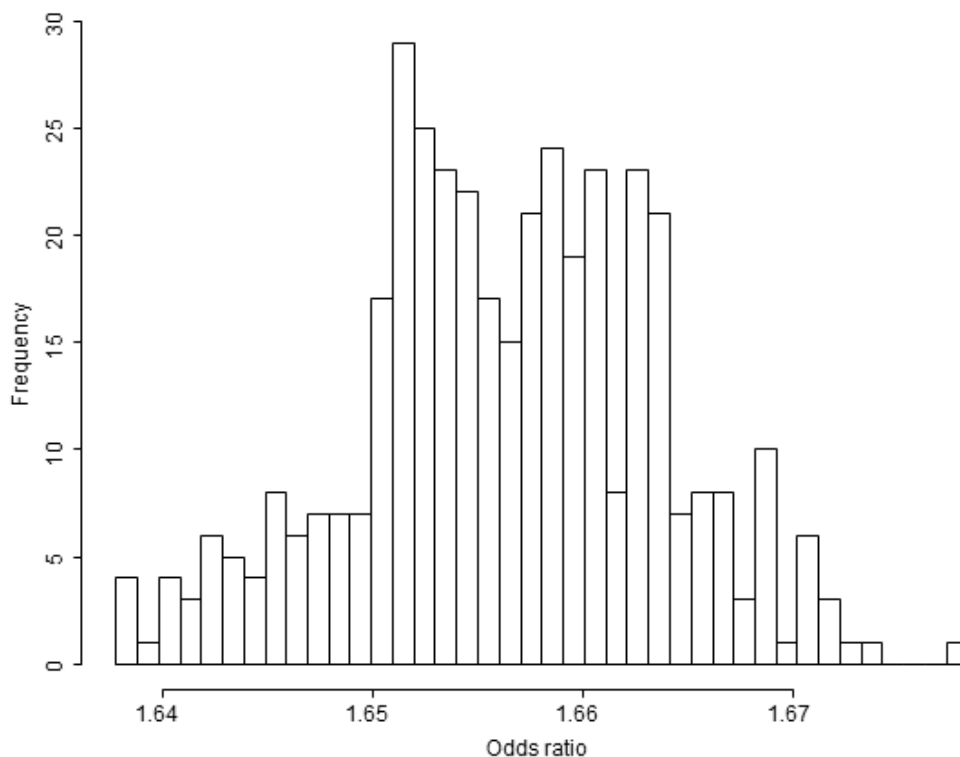


Fig H - Forest plot of RCC risk for each SD increment in DBP stratified by study. OR were estimated using likelihood-based MR approach. 95% CI: 95% Confidence Interval; P: P value. I²: between-strata heterogeneity (%). Phet: P value of between-strata heterogeneity.

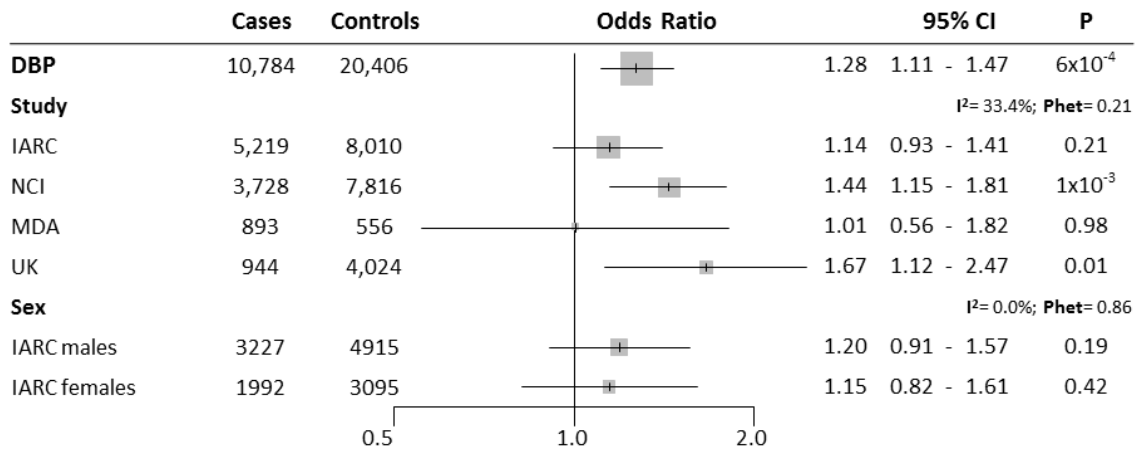


Fig I - Forest plot of RCC risk for each SD increment in SBP stratified by study. OR were estimated using likelihood-based MR approach. 95% CI: 95% Confidence Interval; P: P value. I²: between-strata heterogeneity (%). Phet: P value of between-strata heterogeneity.

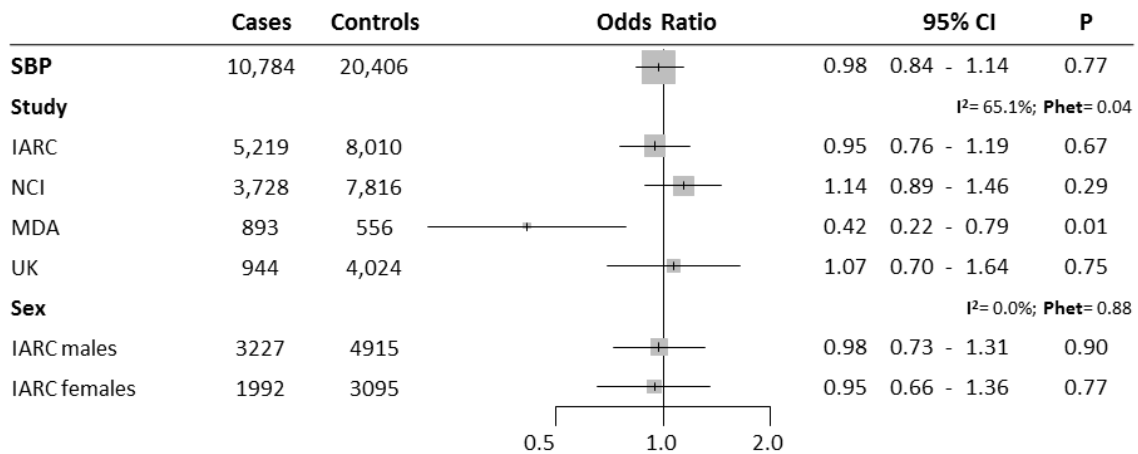


Fig J - Forest plot of RCC risk for each SD increment in PP stratified by study. OR were estimated using likelihood-based MR approach. 95% CI: 95% Confidence Interval; P: P value. I²: between-strata heterogeneity (%). Phet: P value of between-strata heterogeneity.

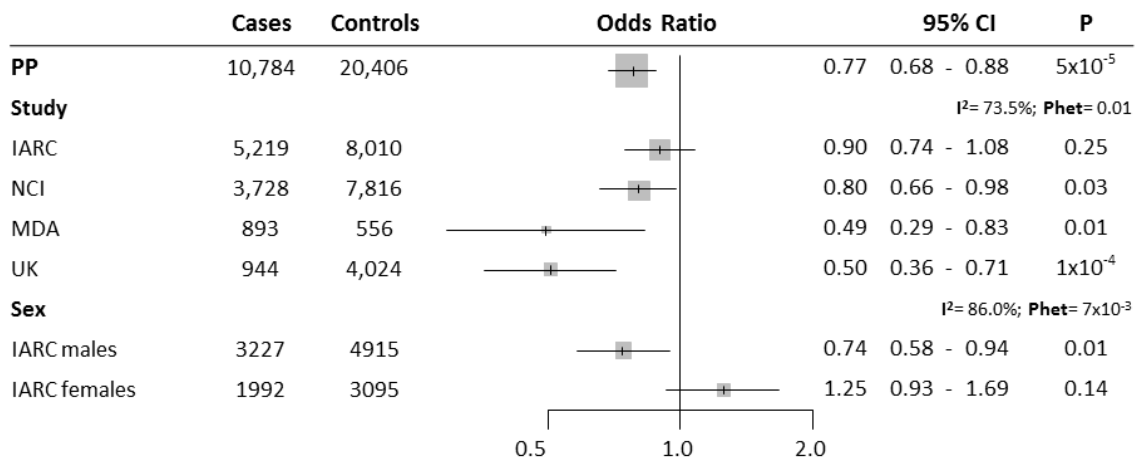


Fig K - The leave-one-out histogram reflects the distribution of the causal effect estimate of DBP instrument when one of the SNPs is removed. OR: odds ratio.

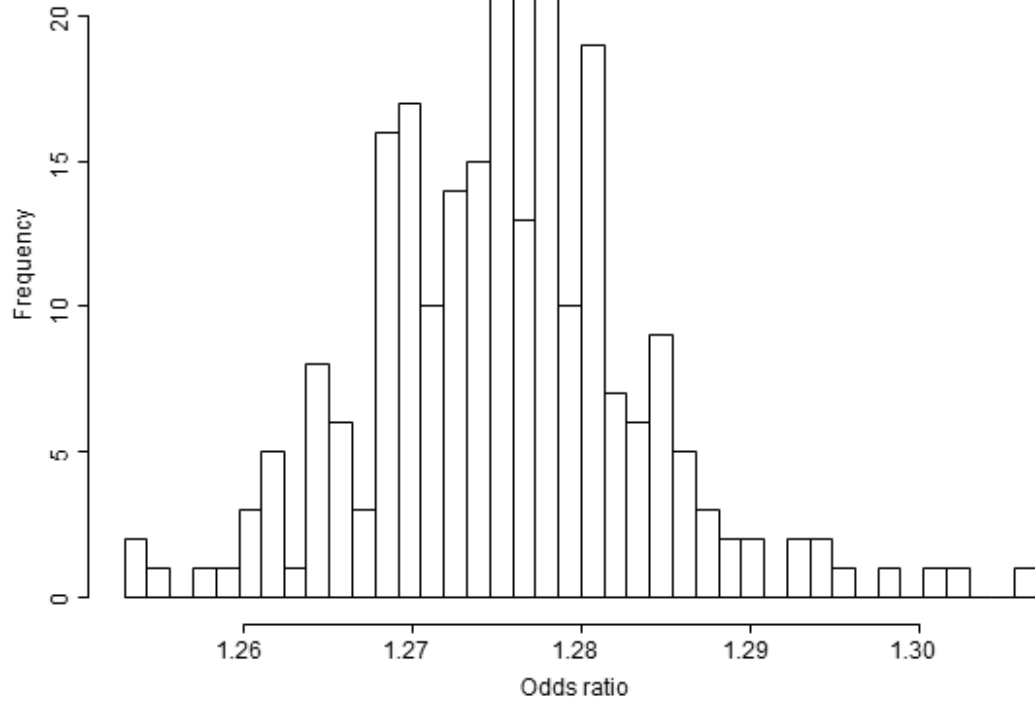
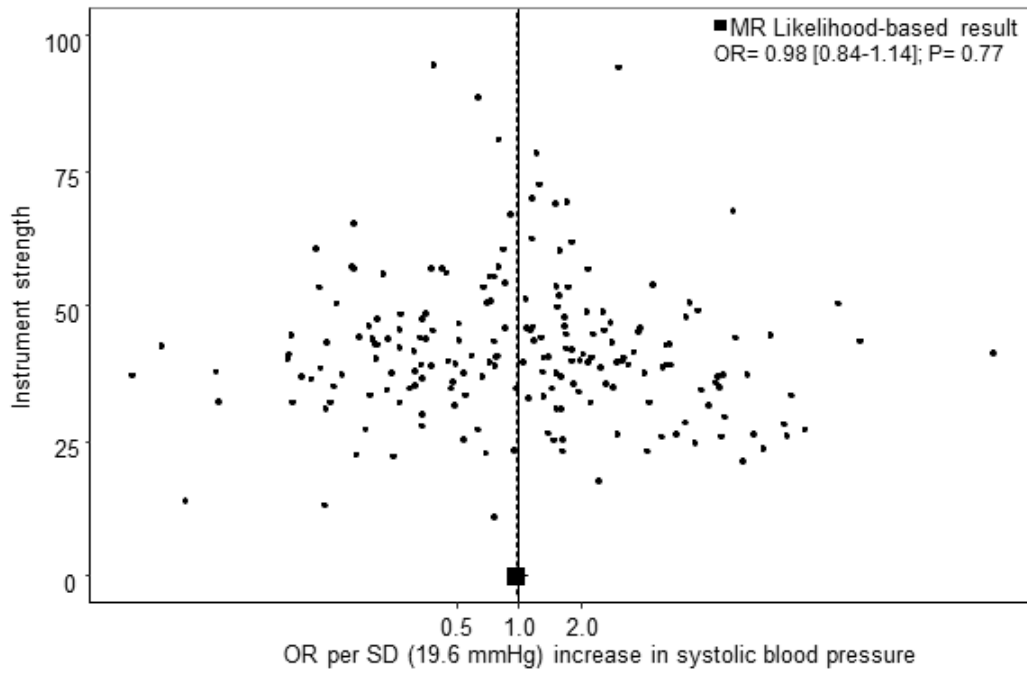


Fig L - For each SNP used in the genetic instrument of SBP, the funnel plot (A) depicts the weight exerted into the causal effect estimate along the y-axis (β_{GP}/SE_{GD}), and estimates of the causal effect on RCC odds along the x-axis ($\exp(\beta_{GD}/\beta_{GP})$). The leave-one-out histogram (B) reflects the distribution of the causal effect estimate of SBP instrument when one of the SNPs is removed. OR: odds ratio. Funnel plot X-axis is in logarithmic scale.

A- Funnel plot



B- Leave-one-out histogram

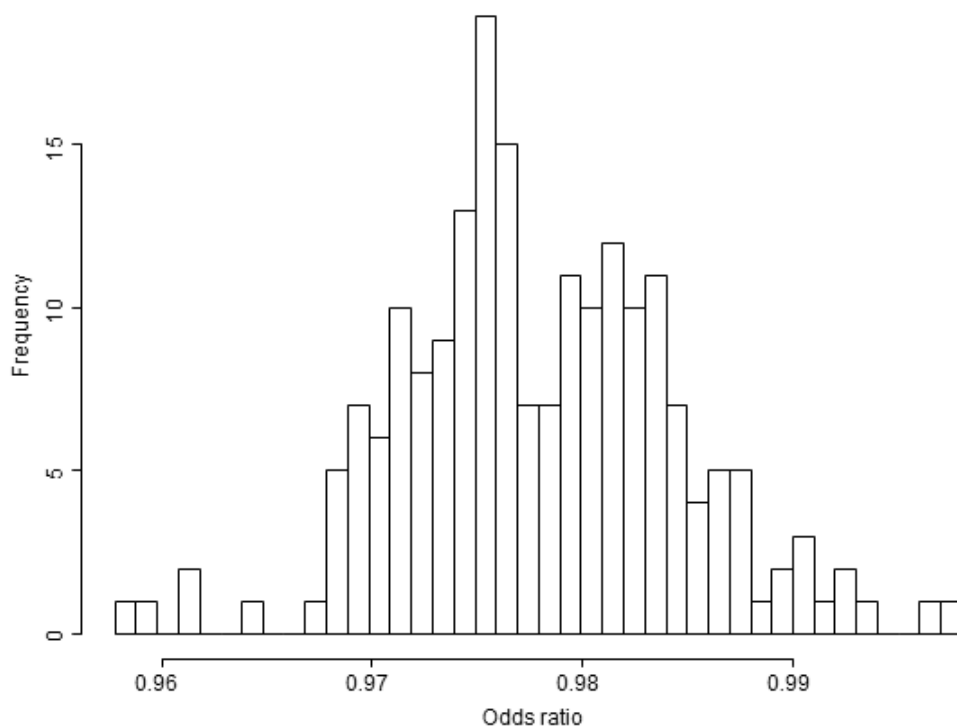
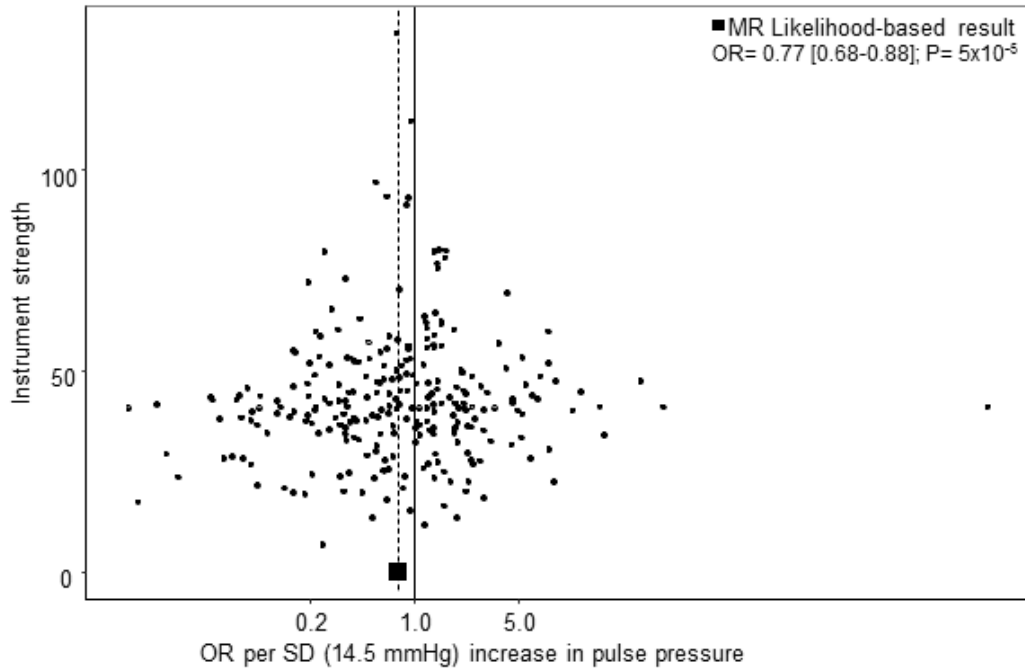


Fig M - For each SNP used in the genetic instrument of PP, the funnel plot (A) depicts the weight exerted into the causal effect estimate along the y-axis (β_{GP}/SE_{GD}), and estimates of the causal effect on RCC odds along the x-axis ($\exp(\beta_{GD}/\beta_{GP})$). The leave-one-out histogram (B) reflects the distribution of the causal effect estimate of PP instrument when one of the SNPs is removed. OR: odds ratio. Funnel plot X-axis is in logarithmic scale.

A- Funnel plot



B- Leave-one-out histogram

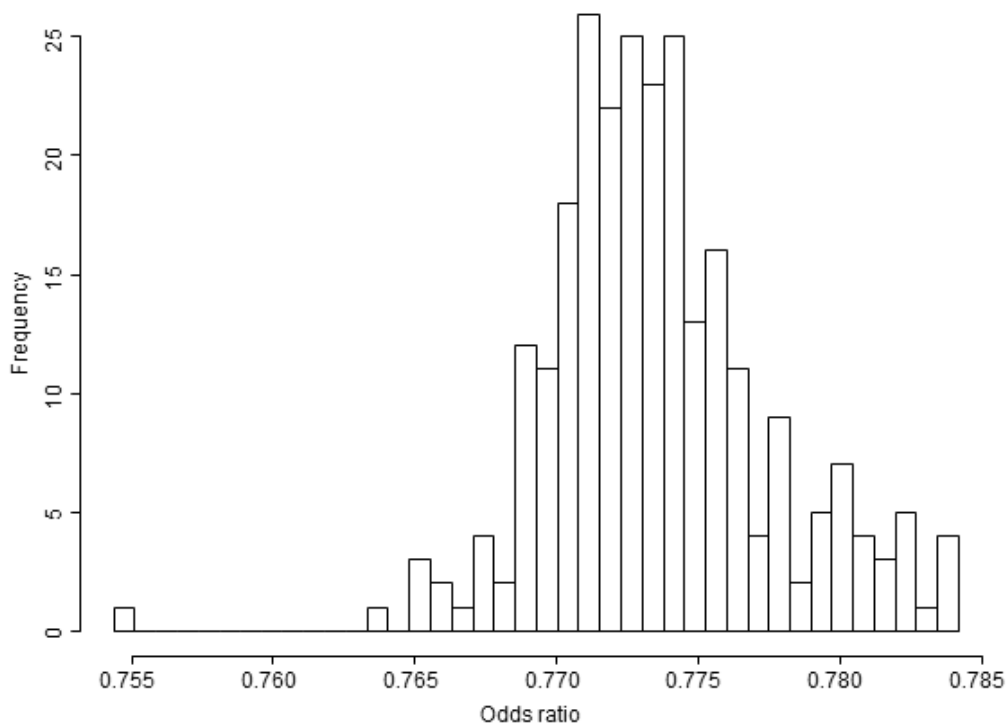


Fig N - Forest plot of RCC risk for each SD increment in HDL stratified by study. OR were estimated using likelihood-based MR approach. 95% CI: 95% Confidence Interval; P: P value. I²: between-strata heterogeneity (%). Phet: P value of between-strata heterogeneity.

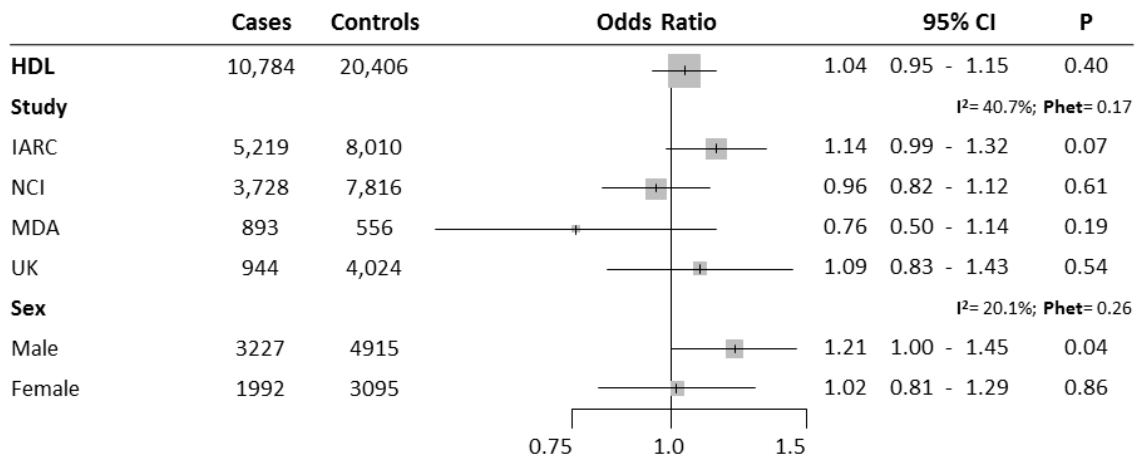


Fig O - Forest plot of RCC risk for each SD increment in LDL stratified by study. OR were estimated using likelihood-based MR approach. 95% CI: 95% Confidence Interval; P: P value. I²: between-strata heterogeneity (%). Phet: P value of between-strata heterogeneity.

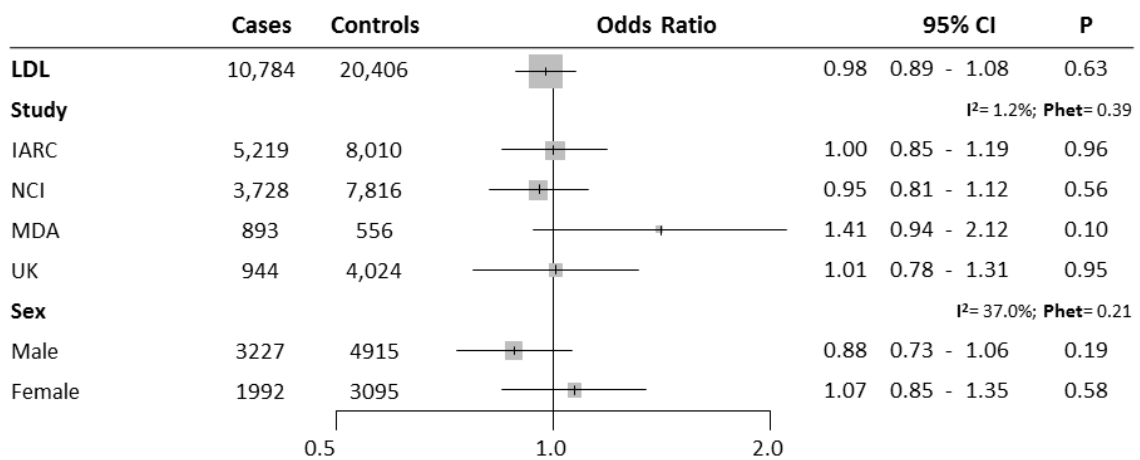


Fig P - Forest plot of RCC risk for each SD increment in total cholesterol stratified by study. OR were estimated using likelihood-based MR approach. 95% CI: 95% Confidence Interval; P: P value. I²: between-strata heterogeneity (%). Phet: P value of between-strata heterogeneity.

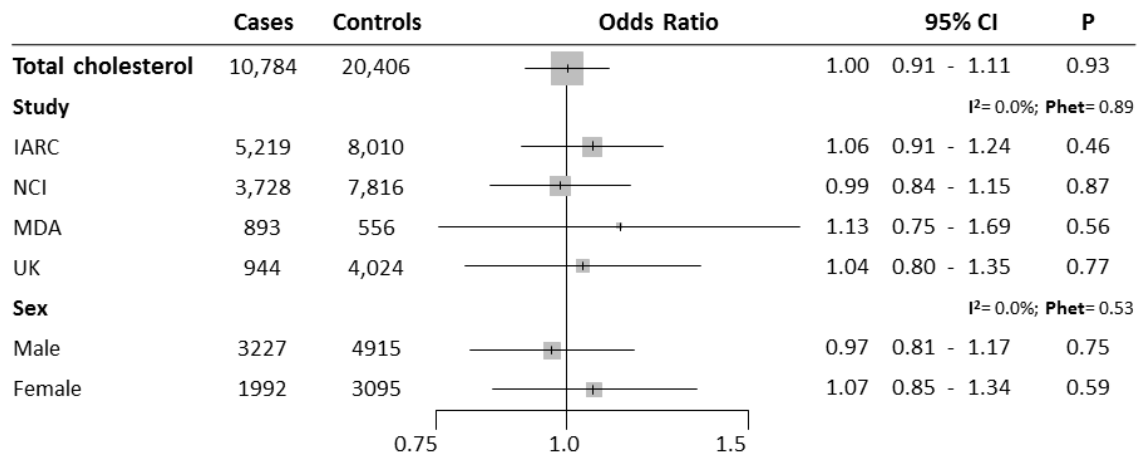


Fig Q - Forest plot of RCC risk for each SD increment in triglycerides stratified by study. OR were estimated using likelihood-based MR approach. 95% CI: 95% Confidence Interval; P: P value. I²: between-strata heterogeneity (%). Phet: P value of between-strata heterogeneity.

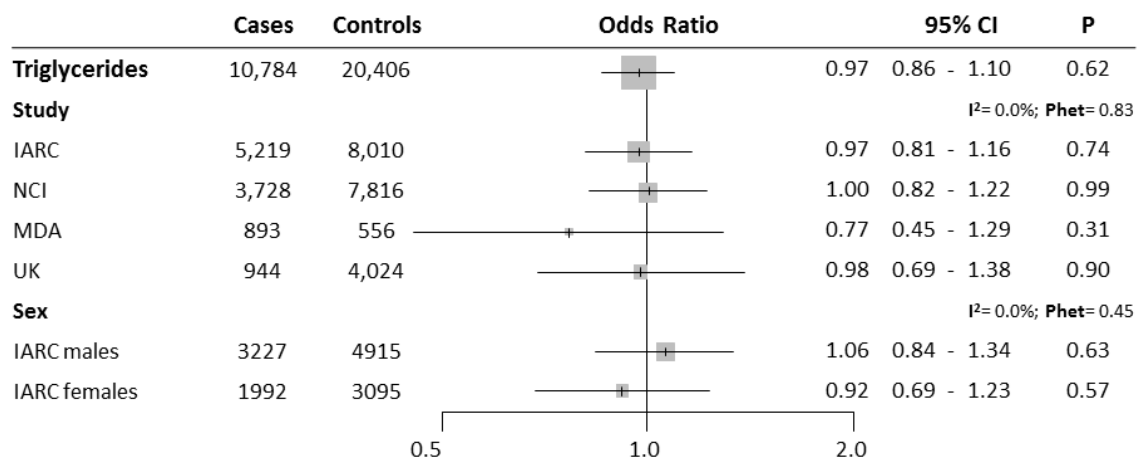
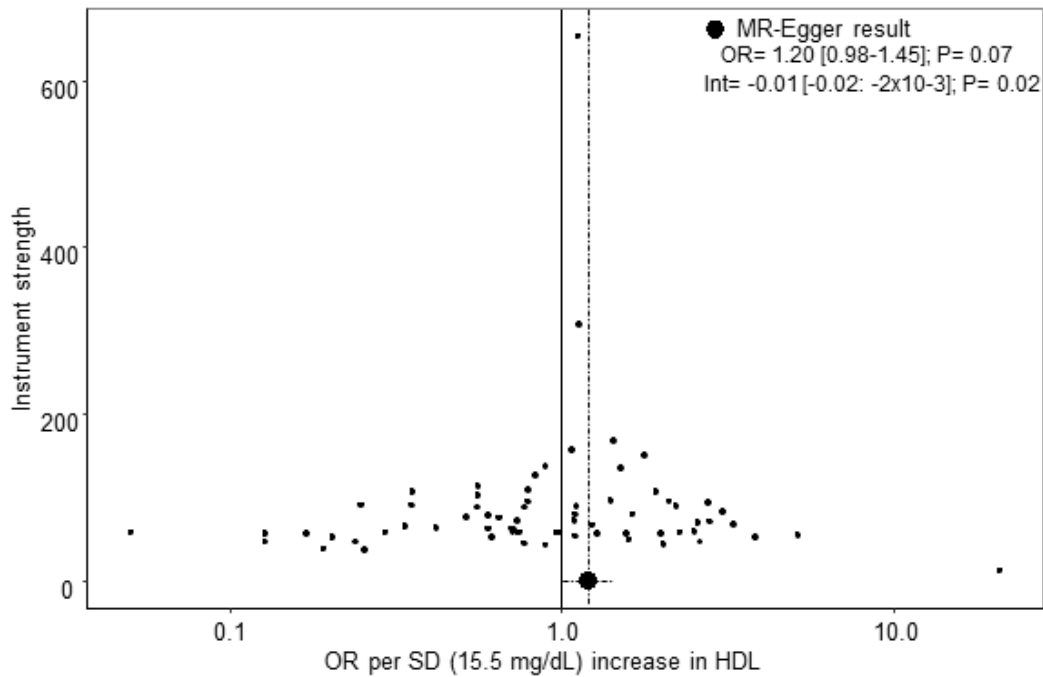


Fig R - For each SNP used in the genetic instrument of HDL, the funnel plot (A) depicts the weight exerted into the causal effect estimate along the y-axis (β_{GP}/SE_{GD}), and estimates of the causal effect on RCC odds along the x-axis ($\exp(\beta_{GD}/\beta_{GP})$). The leave-one-out histogram (B) reflects the distribution of the causal effect estimate of HDL instrument when one of the SNPs is removed. OR: odds ratio. Funnel plot X-axis is in logarithmic scale.

A- Funnel plot



B- Leave-one-out histogram

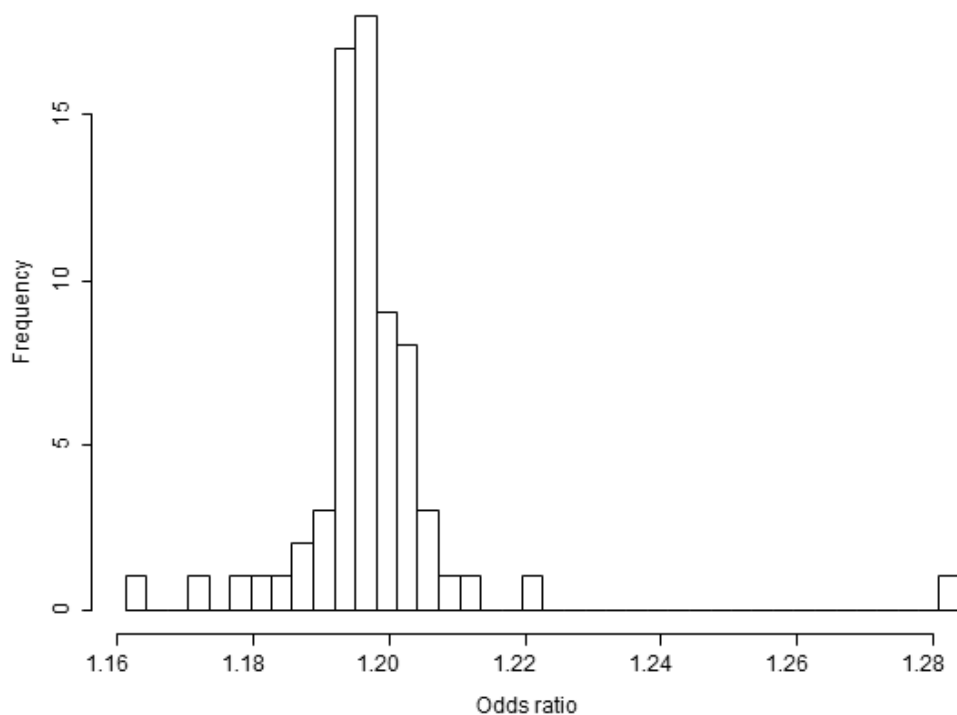
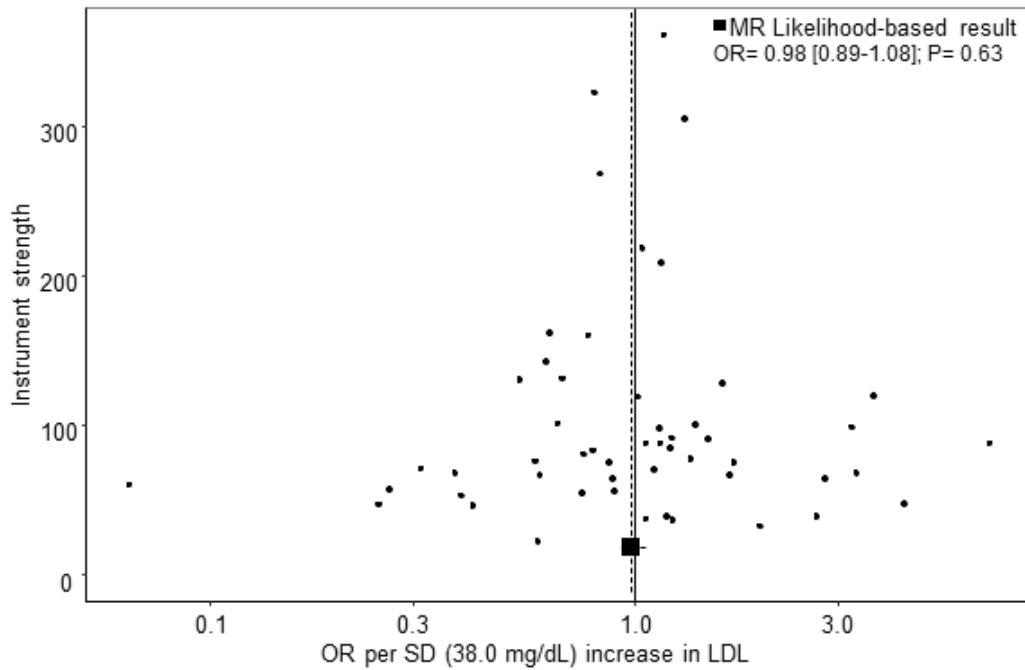


Fig S - For each SNP used in the genetic instrument of LDL, the funnel plot (A) depicts the weight exerted into the causal effect estimate along the y-axis (β_{GP}/SE_{GD}), and estimates of the causal effect on RCC odds along the x-axis ($\exp(\beta_{GD}/\beta_{GP})$). The leave-one-out histogram (B) reflects the distribution of the causal effect estimate of LDL instrument when one of the SNPs is removed. OR: odds ratio. Funnel plot X-axis is in logarithmic scale.

A- Funnel plot



B- Leave-one-out histogram

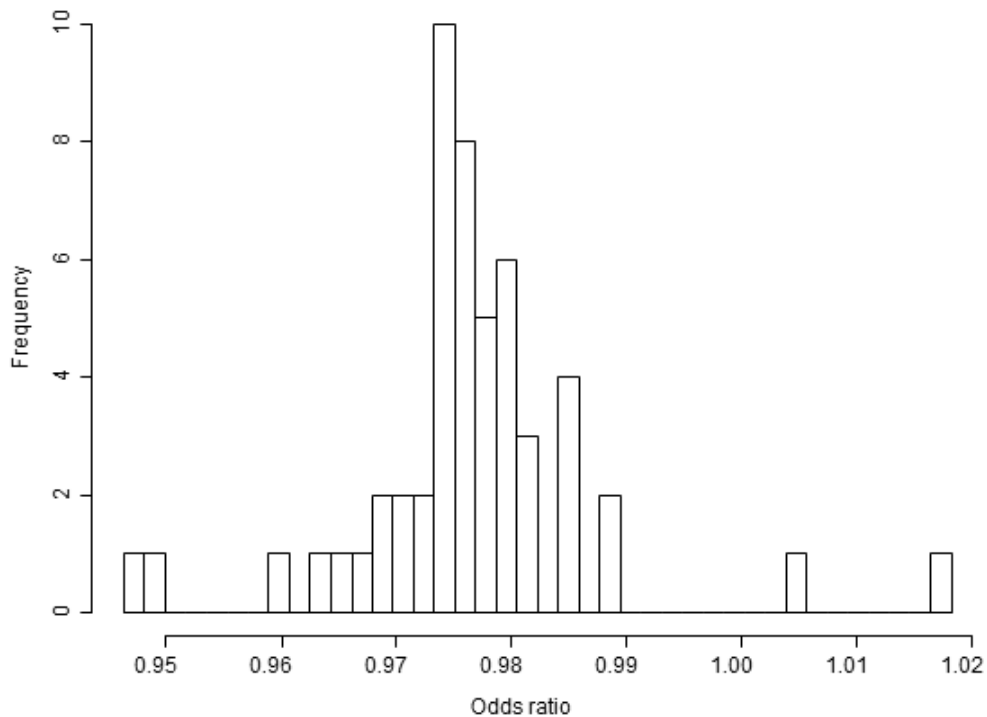
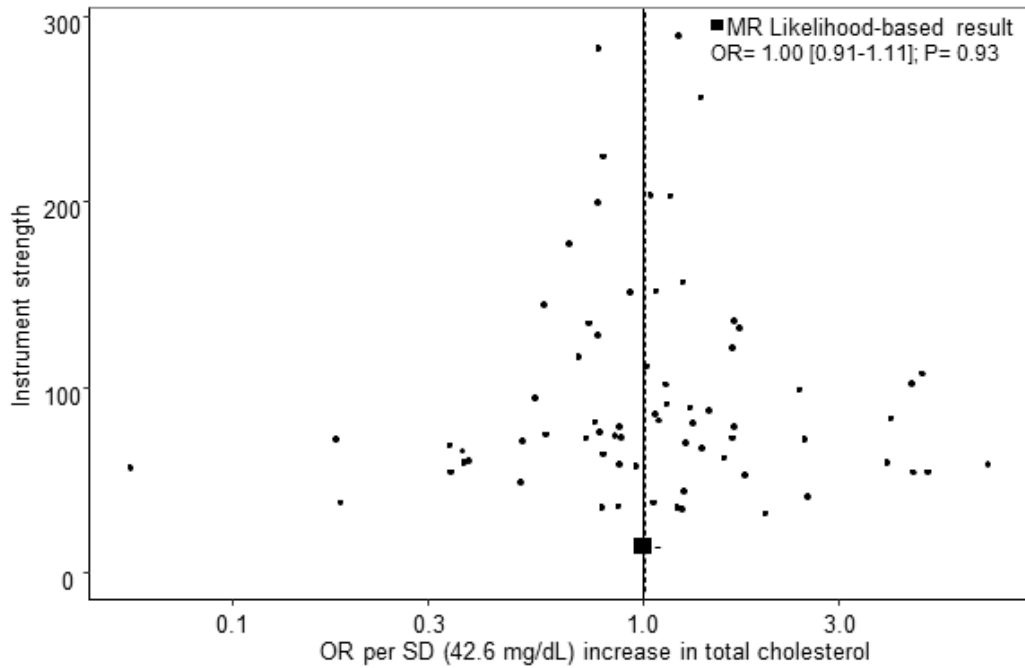


Fig T - For each SNP used in the genetic instrument of total cholesterol, the funnel plot (A) depicts the weight exerted into the causal effect estimate along the y-axis (β_{GP}/SE_{GD}), and estimates of the causal effect on RCC odds along the x-axis ($\exp(\beta_{GD}/\beta_{GP})$). The leave-one-out histogram (B) reflects the distribution of the causal effect estimate of total cholesterol instrument when one of the SNPs is removed. OR: odds ratio. Funnel plot X-axis is in logarithmic scale.

A- Funnel plot



B- Leave-one-out histogram

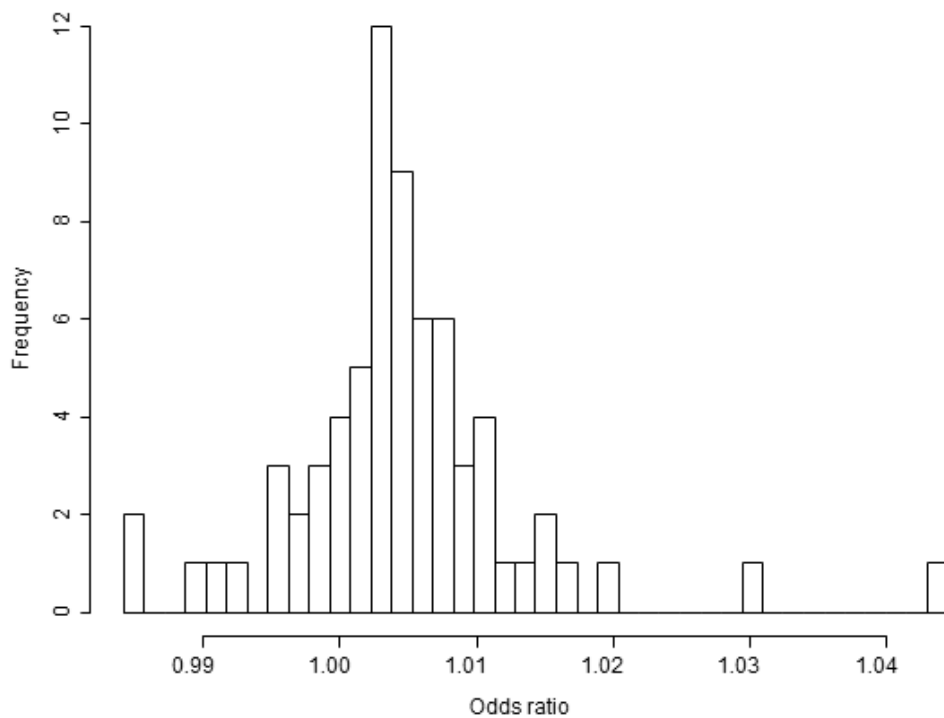
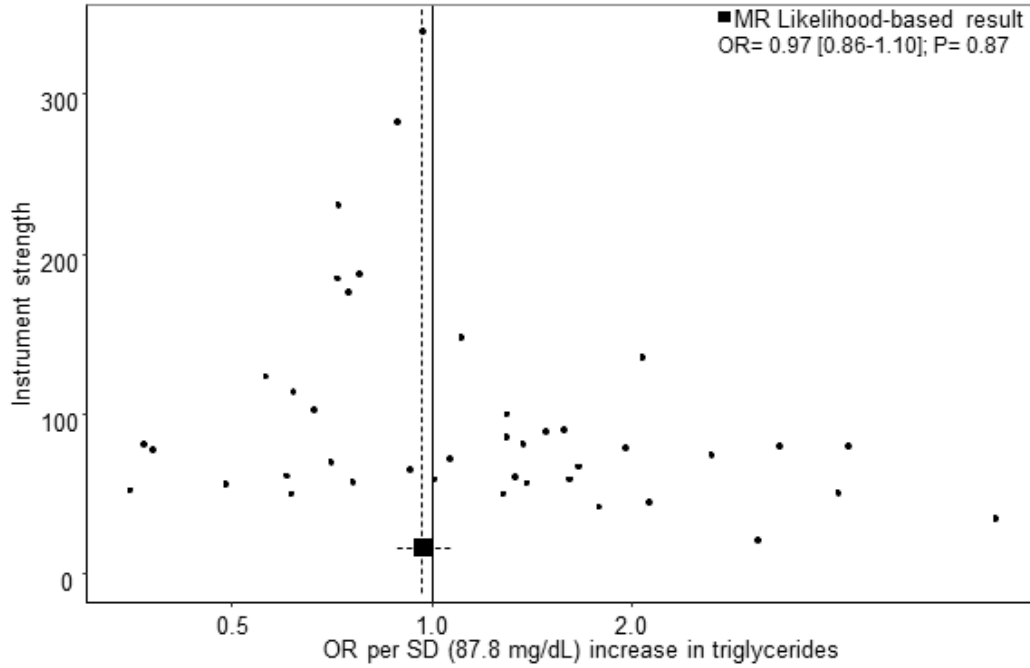


Fig U - For each SNP used in the genetic instrument of triglycerides, the funnel plot (A) depicts the weight exerted into the causal effect estimate along the y-axis (β_{GP}/SE_{GD}), and estimates of the causal effect on RCC odds along the x-axis ($\exp(\beta_{GD}/\beta_{GP})$). The leave-one-out histogram (B) reflects the distribution of the causal effect estimate of triglycerides instrument when one of the SNPs is removed. OR: odds ratio. Funnel plot X-axis is in logarithmic scale.

A- Funnel plot



B- Leave-one-out histogram

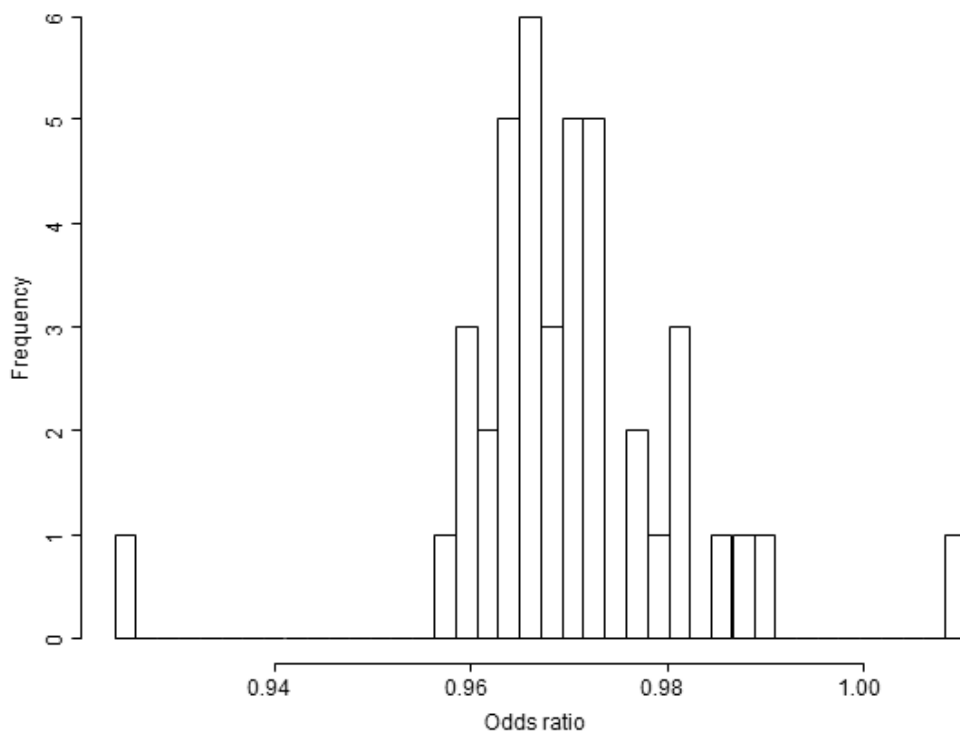


Fig V - Forest plot of RCC risk for each SD increment in type 2 diabetes stratified by study. OR were estimated using likelihood-based MR approach. 95% CI: 95% Confidence Interval; P: P value. I²: between-strata heterogeneity (%). Phet: P value of between-strata heterogeneity.

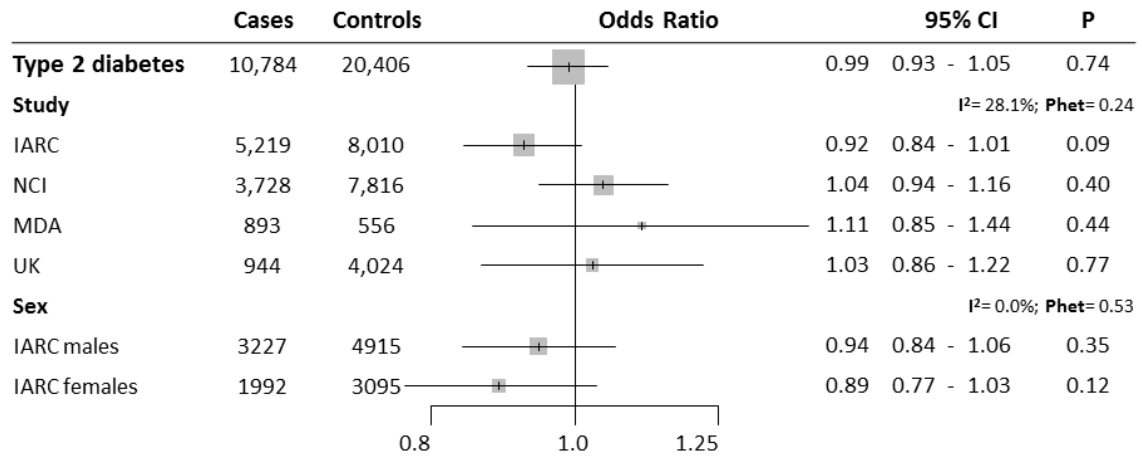


Fig W - Forest plot of RCC risk for each SD increment in fasting insulin stratified by study. OR were estimated using likelihood-based MR approach. 95% CI: 95% Confidence Interval; P: P value. I²: between-strata heterogeneity (%). Phet: P value of between-strata heterogeneity.

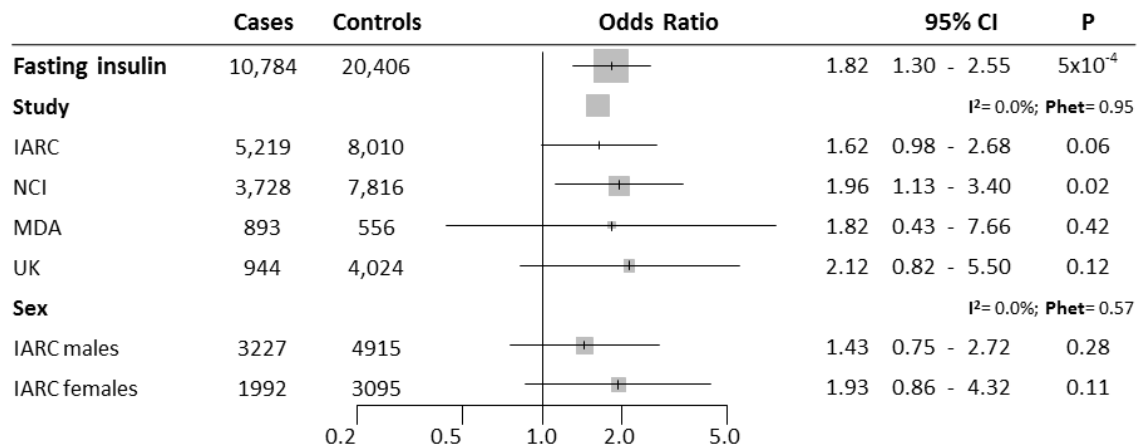


Fig X - Forest plot of RCC risk for each SD increment in fasting glucose stratified by study. OR were estimated using likelihood-based MR approach. 95% CI: 95% Confidence Interval; P: P value. I²: between-strata heterogeneity (%). Phet: P value of between-strata heterogeneity.

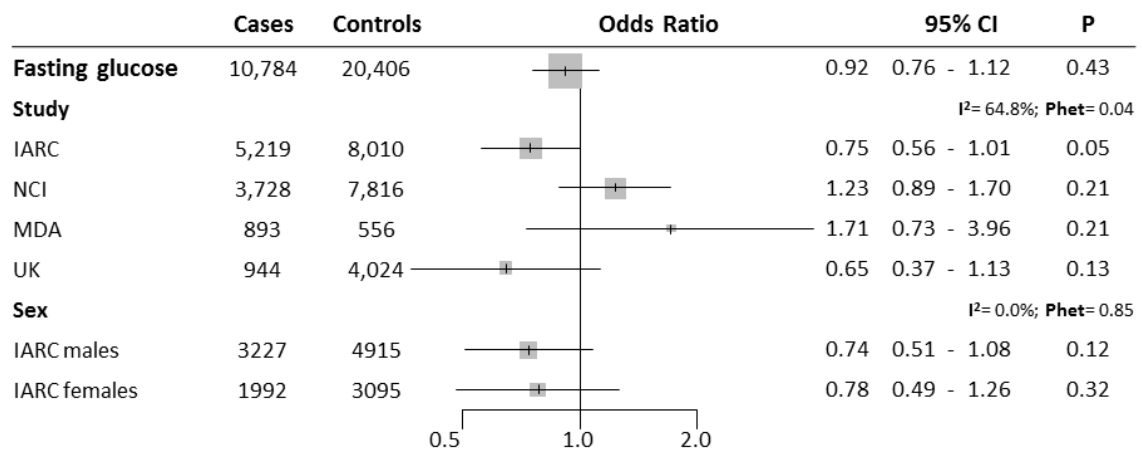
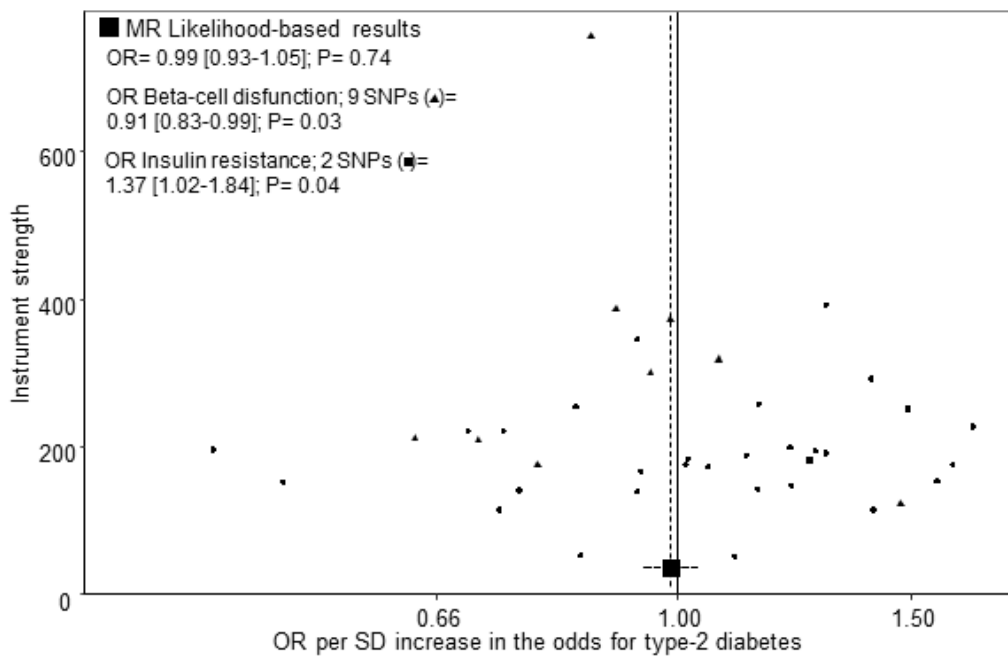


Fig Y - For each SNP used in the genetic instrument of type 2 diabetes, the funnel plot (A) depicts the weight exerted into the causal effect estimate along the y-axis (β_{GP}/SE_{GD}), and estimates of the causal effect on RCC odds along the x-axis ($\exp(\beta_{GD}/\beta_{GP})$)*. The leave-one-out histogram (B) reflects the distribution of the causal effect estimate of type 2 diabetes instrument when one of the SNPs is removed. OR: odds ratio. Funnel plot X-axis is in logarithmic scale. Beta-cell dysfunction SNPs and insulin resistance SNPs are depicted as triangles and squares, respectively.

A- Funnel plot



B- Leave-one-out histogram

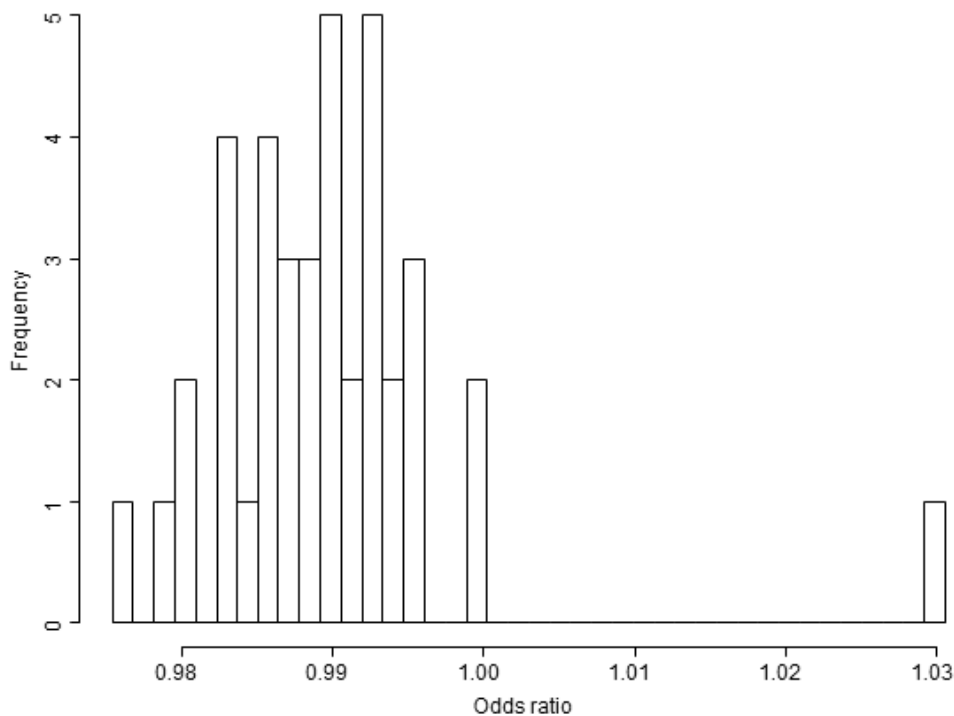


Fig Z - The leave-one-out histogram reflects the distribution of the causal effect estimate of fasting insulin instrument when one of the SNPs is removed. OR: odds ratio.

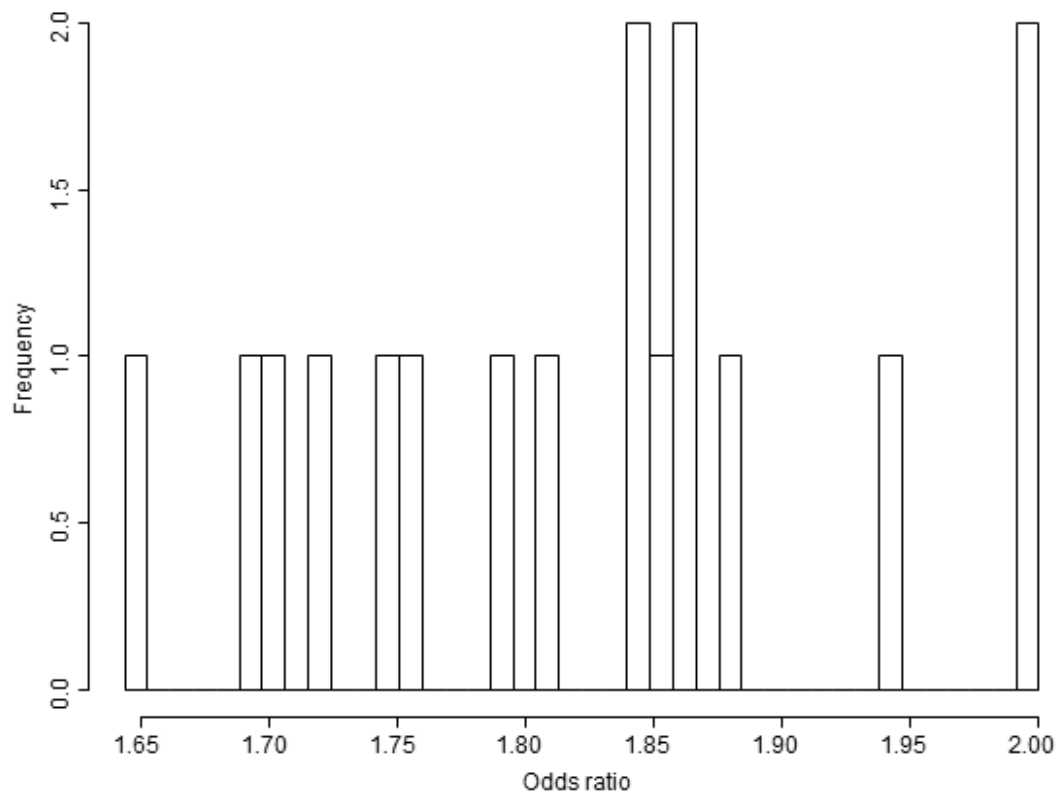
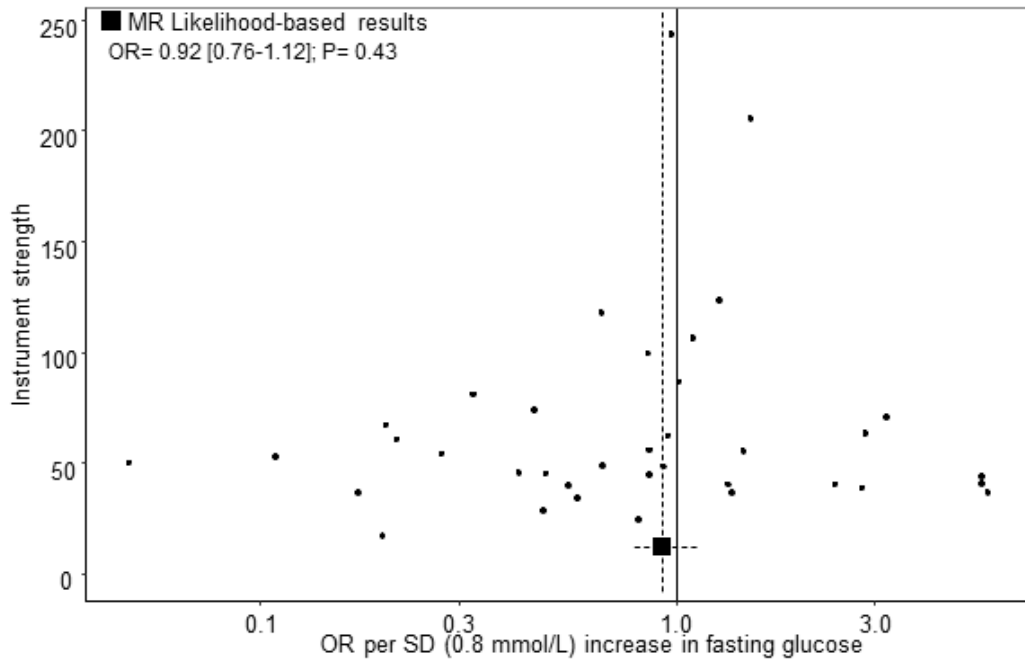


Fig AA - For each SNP used in the genetic instrument of fasting glucose, the funnel plot (A) depicts the weight exerted into the causal effect estimate along the y-axis (β_{GP}/SE_{GD}), and estimates of the causal effect on RCC odds along the x-axis ($\exp(\beta_{GD}/\beta_{GP})$). The leave-one-out histogram (B) reflects the distribution of the causal effect estimate of fasting glucose instrument when one of the SNPs is removed. OR: odds ratio. Funnel plot X-axis is in logarithmic scale.

A- Funnel plot



B- Leave-one-out histogram

