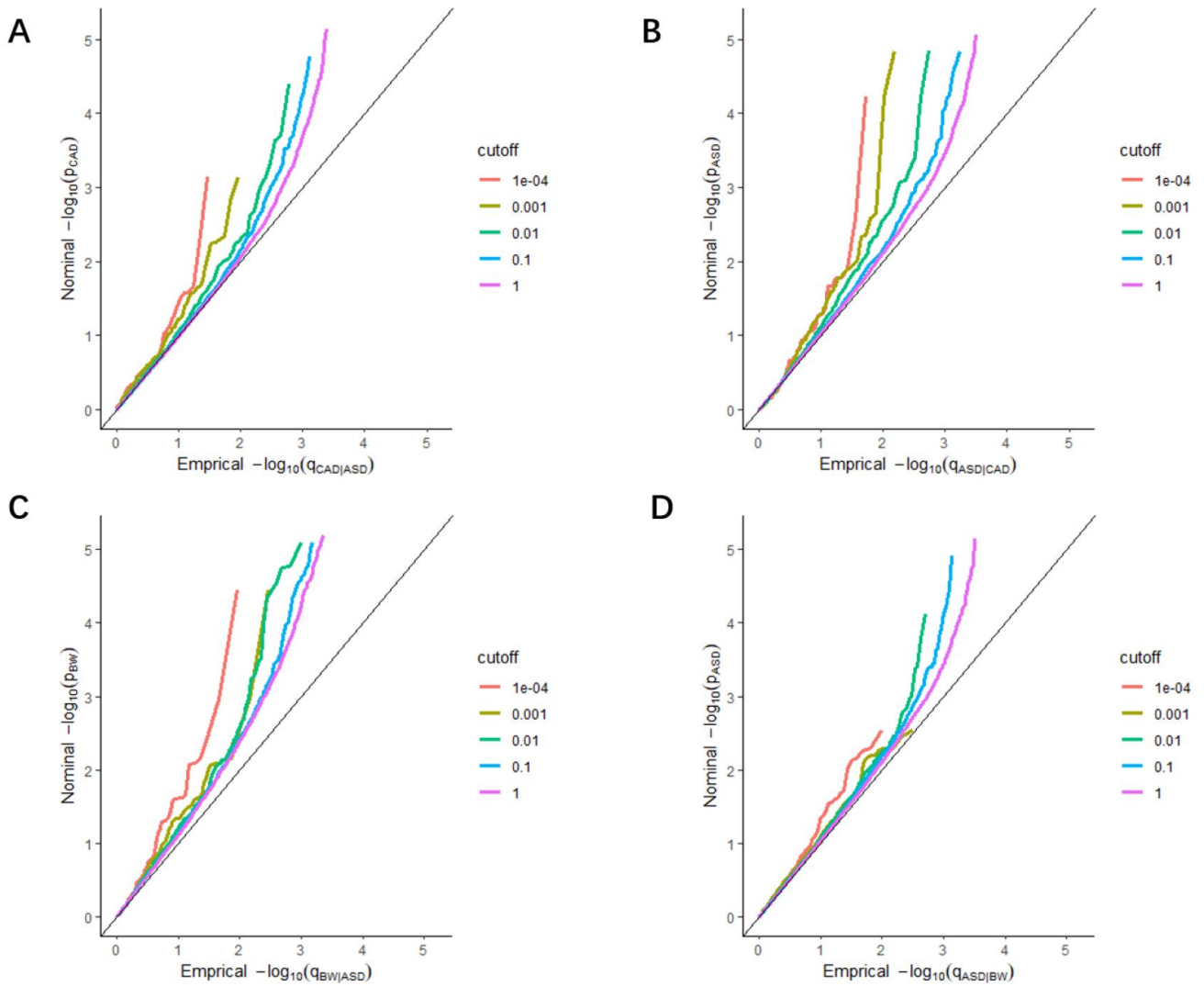
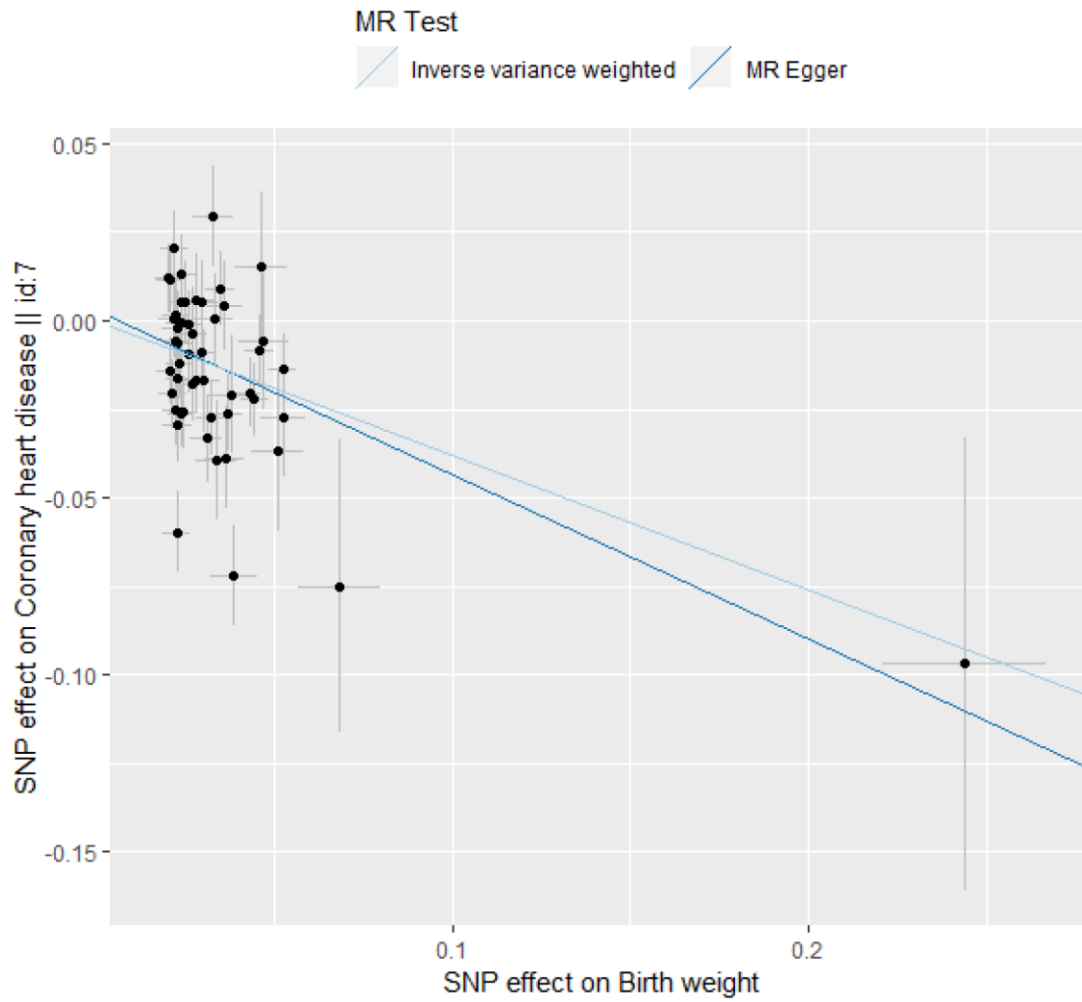


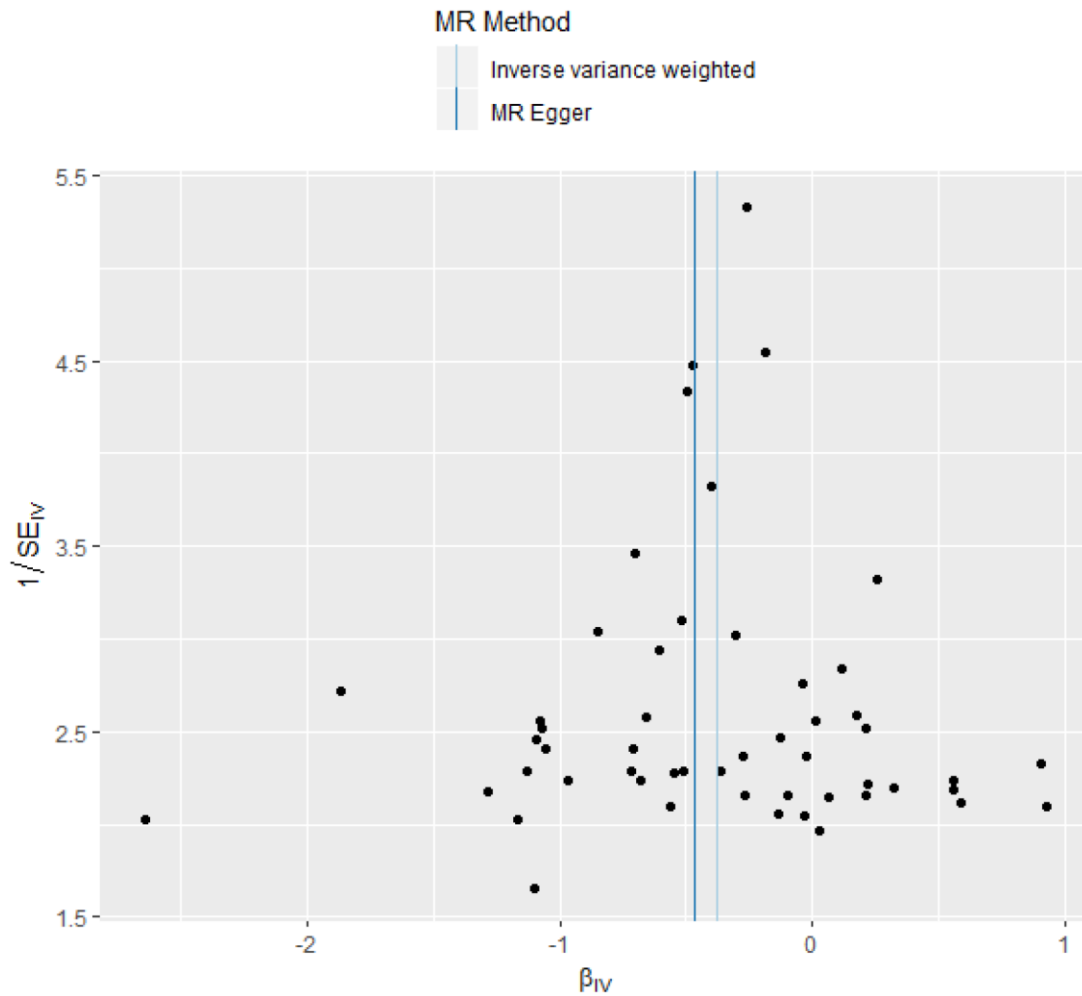
SUPPLEMENTARY FIGURES



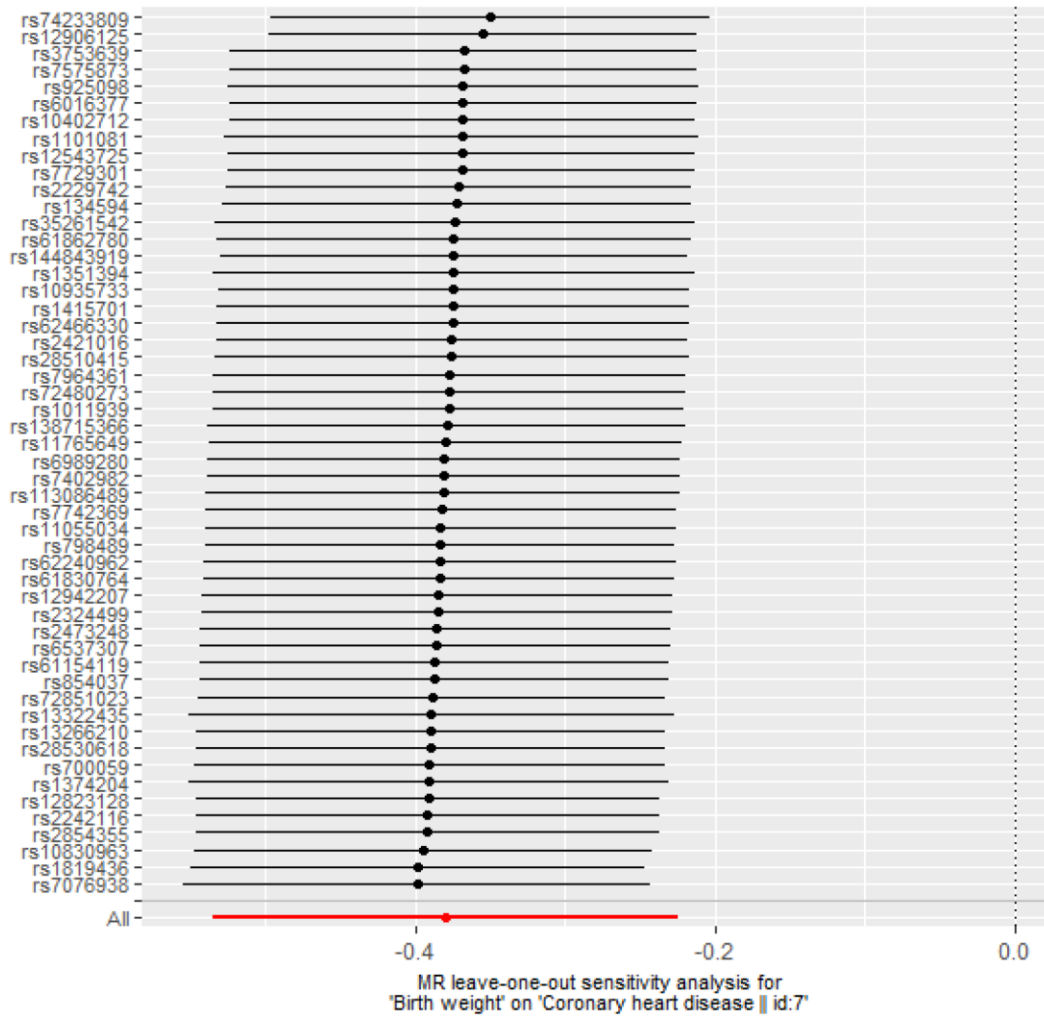
**Supplementary Figure 1. Stratified Q-Q plots.** Stratified Q-Q plots of nominal vs. empirical  $-\log_{10}(p)$  values in principal trait below the standard GWAS threshold of  $p \leq 5 \times 10^{-8}$  as a function of the significance of the association with conditional trait at the level of  $p \leq 1$ ,  $p \leq 0.1$ ,  $p \leq 0.01$ ,  $p \leq 0.001$ , and  $p \leq 0.0001$ , respectively. (A) CAD as a function of the significance of the association with ASD, (B) ASD as a function of the significance of the association with CAD, (C) BW as a function of the significance of the association with ASD, and (D) ASD as a function of the significance of the association with BW.



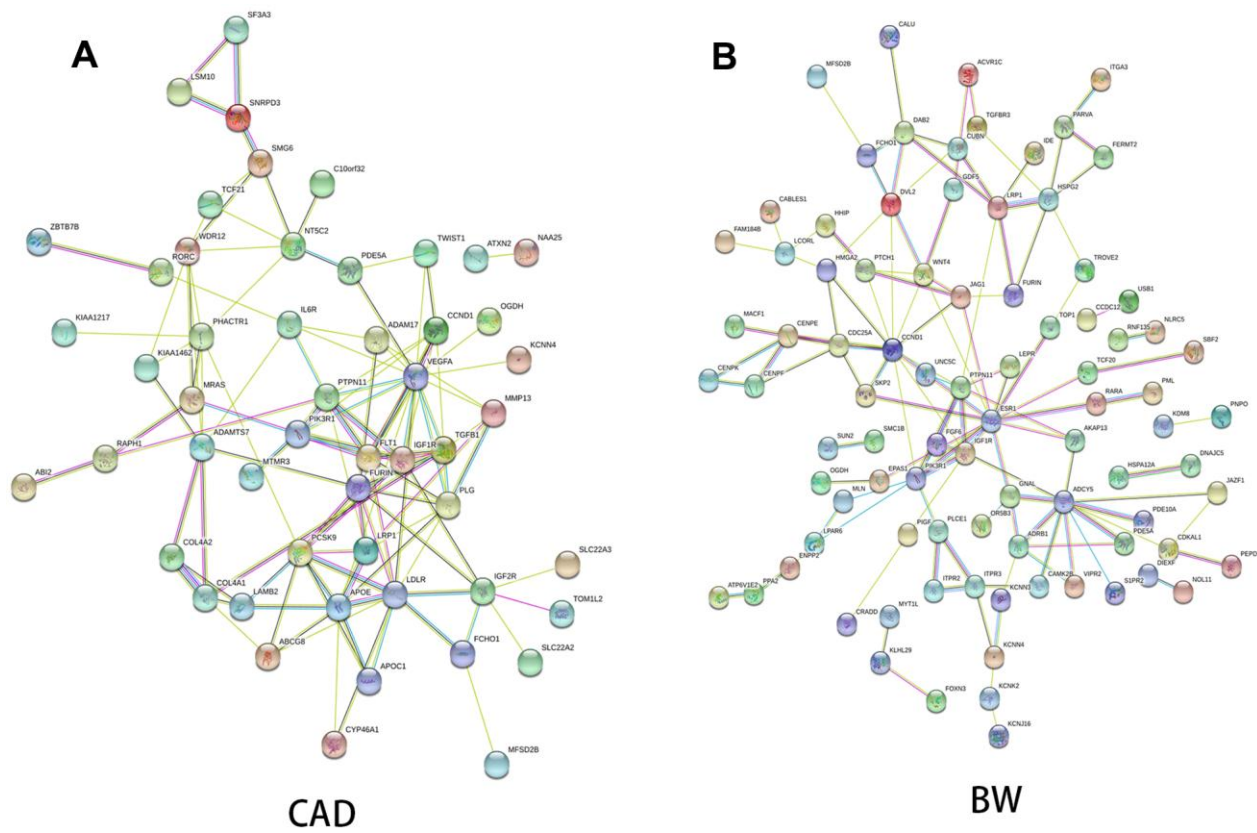
**Supplementary Figure 2. MR regression scatter plot.** The relationship of the SNP effects on the exposure against the SNP effects on the outcome was depicted using a scatter plot. The different color lines show the results of corresponding MR analysis methods.



**Supplementary Figure 3. MR regression funnel plot.** Asymmetry in a funnel plot is useful for gauging the reliability of a particular MR analysis. Each SNP's MR estimate is plotted against its minor allele frequency (MAF) corrected association with BW. A MAF correction proportional to the BW related SNP standard error is used since a low-frequency allele is likely to be measured with low precision. Similar to the use of funnel plots in the meta-analysis literature, this plot can be used for visual inspection of symmetry, where any deviation can be suggestive of pleiotropy.



**Supplementary Figure 4. Leave-one-out plot.** The leave-one-out analysis result was visualized by the forest plot. Each black dot and line correspond to the effect size and 95% confidence interval (95%CI), and the bottom red dot and line is the overall effect size and 95%CI.



**Supplementary Figure 5. Functional protein association network analysis.** Connections are based on co-expression and experimental evidence with a STRING 10.5 summary score above 0.4. Each filled node denotes a gene; edges between nodes indicate protein-protein interactions between protein products of the corresponding genes in **(A)** CAD and **(B)** BW. Different edge colors represent the types of evidence for the association.