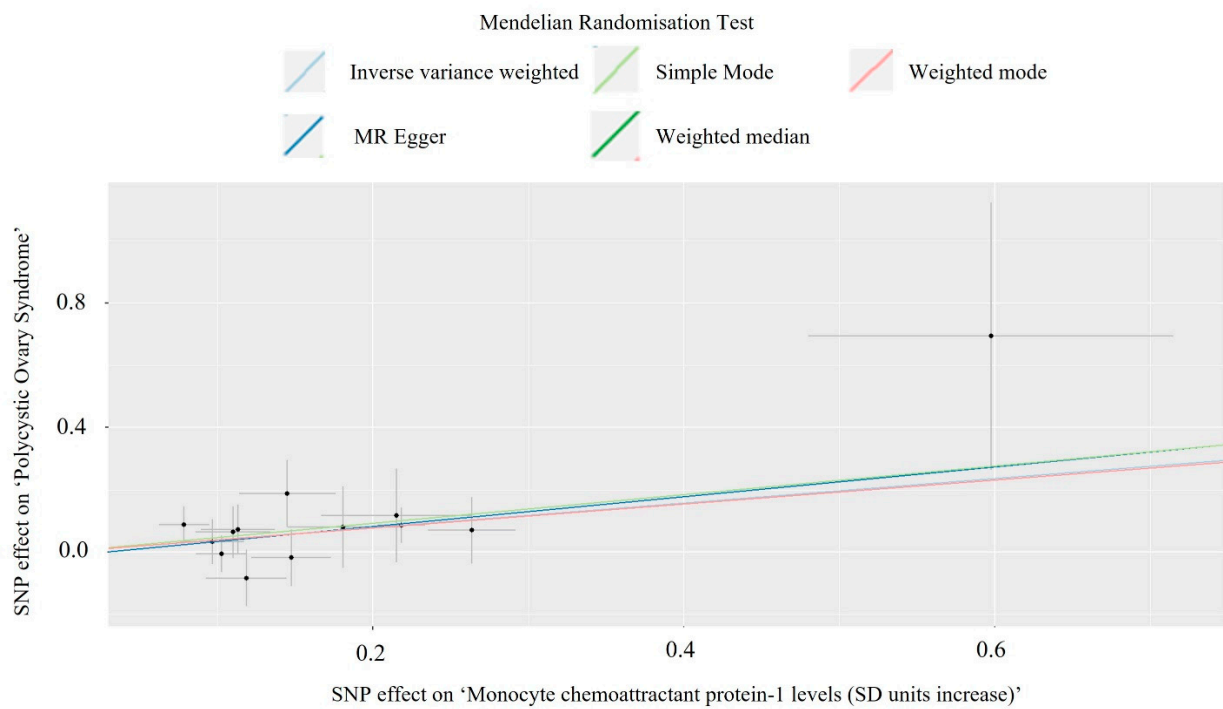
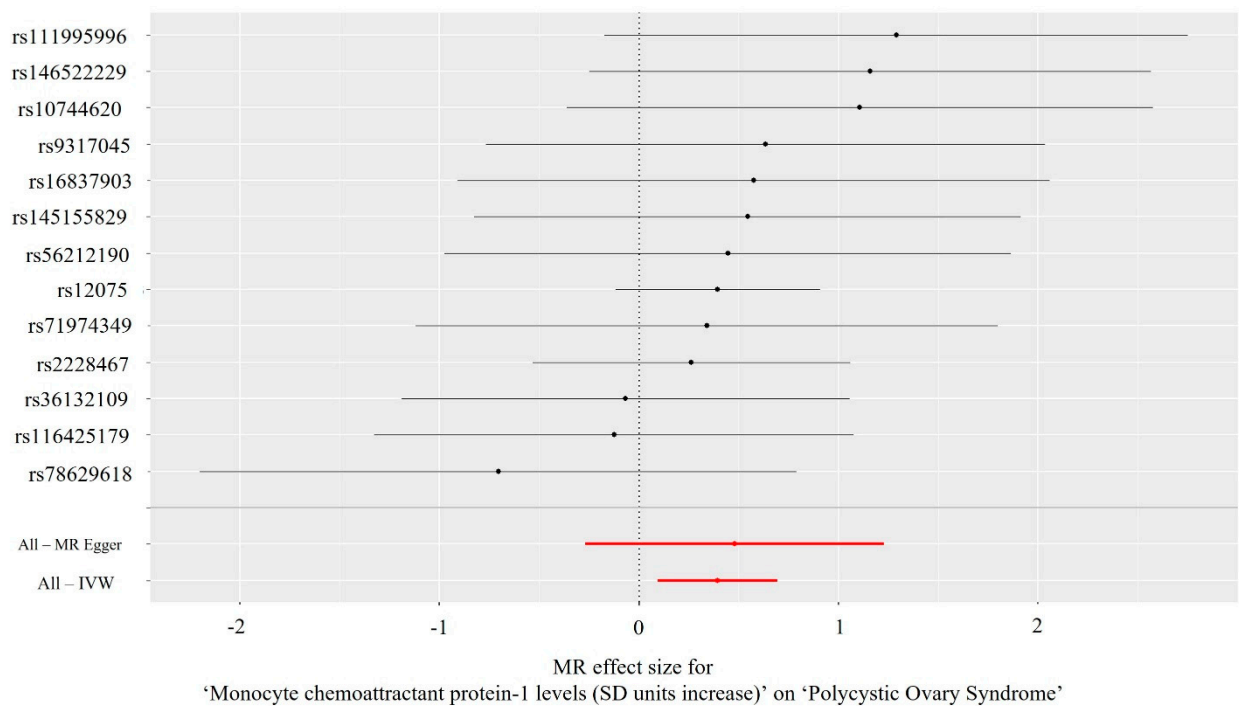


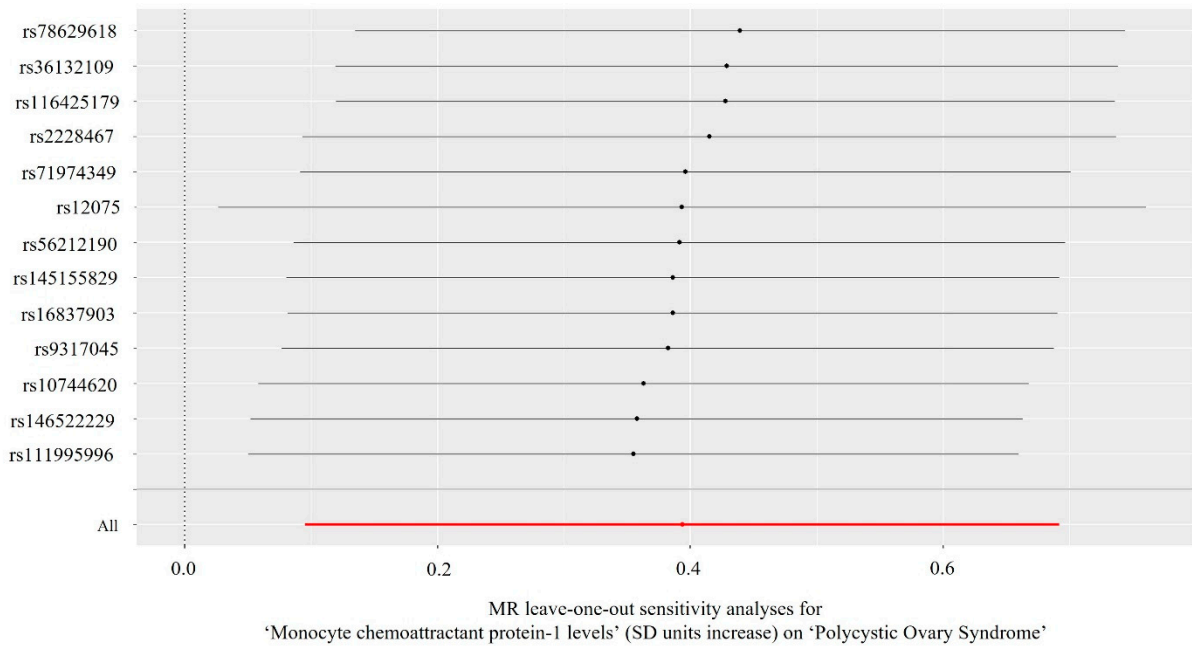
A)



B)



C)



D)

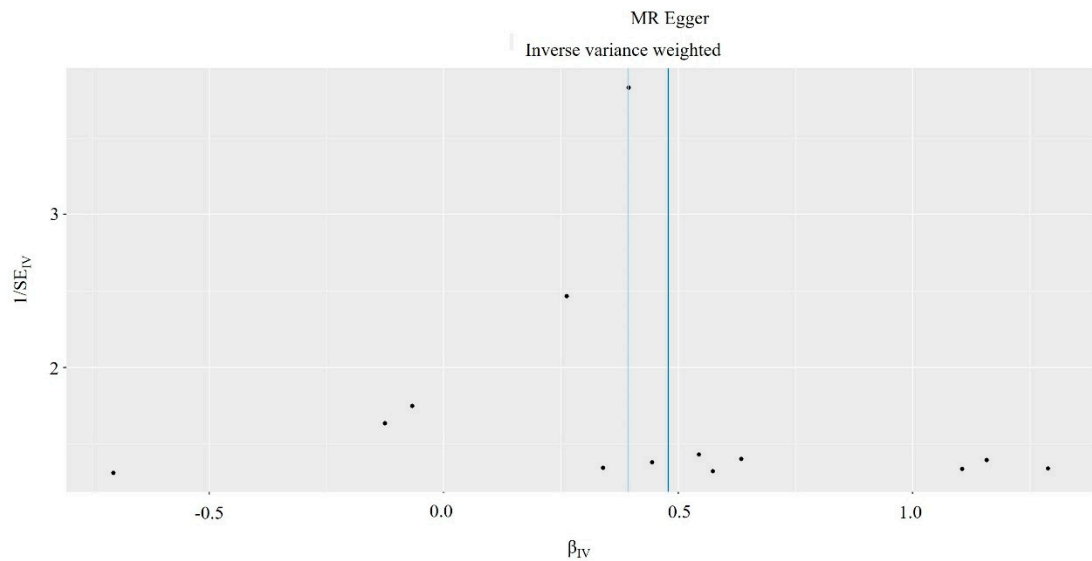
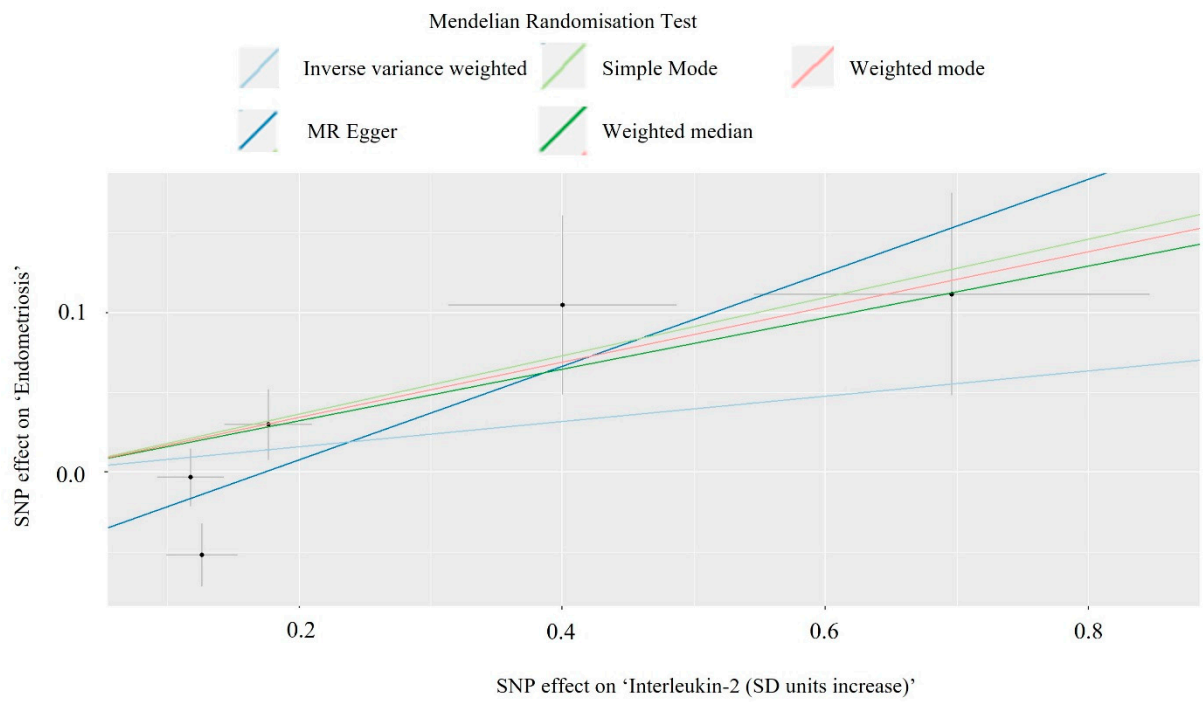
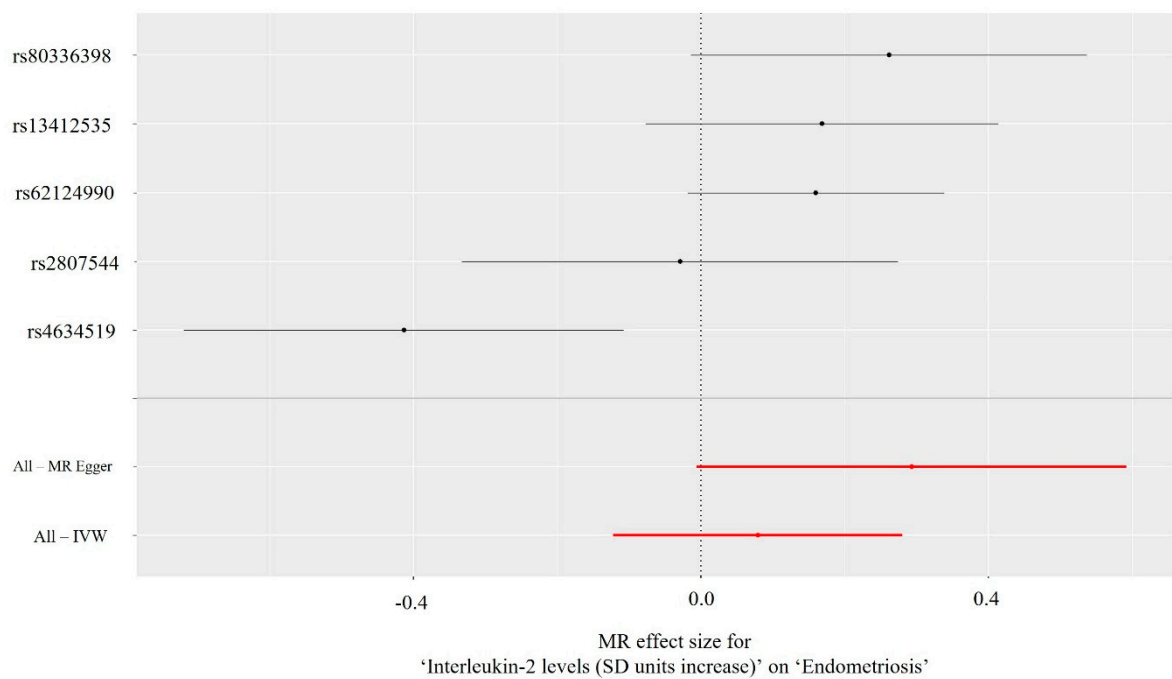


Figure 1: The relationship between 'monocyte chemoattractant protein-1 (MCP-1/CCL2) (standard deviation units increase)' and the outcome of 'polycystic ovary syndrome', visualised by: **(A)** Scatter plot denoting the distribution of individual causal estimates, with lines indicating the trendlines of the causal estimate using each method; **(B)** Forest plot of the effects of individual single nucleotide polymorphisms (SNPs) and pooled estimates visualised via mendelian randomisation-egger (MRE) and inverse variance weighted (IVW) methods; **(C)** Leave-one-out analysis plot, where the dark points indicate the effect measure via IVW-mendelian randomisation (IVW-MR) analysis excluding the specific SNP. The red line indicates the pooled analysis encompassing all SNPs via IVW-MR; and **(D)** Funnel plot to assess heterogeneity.

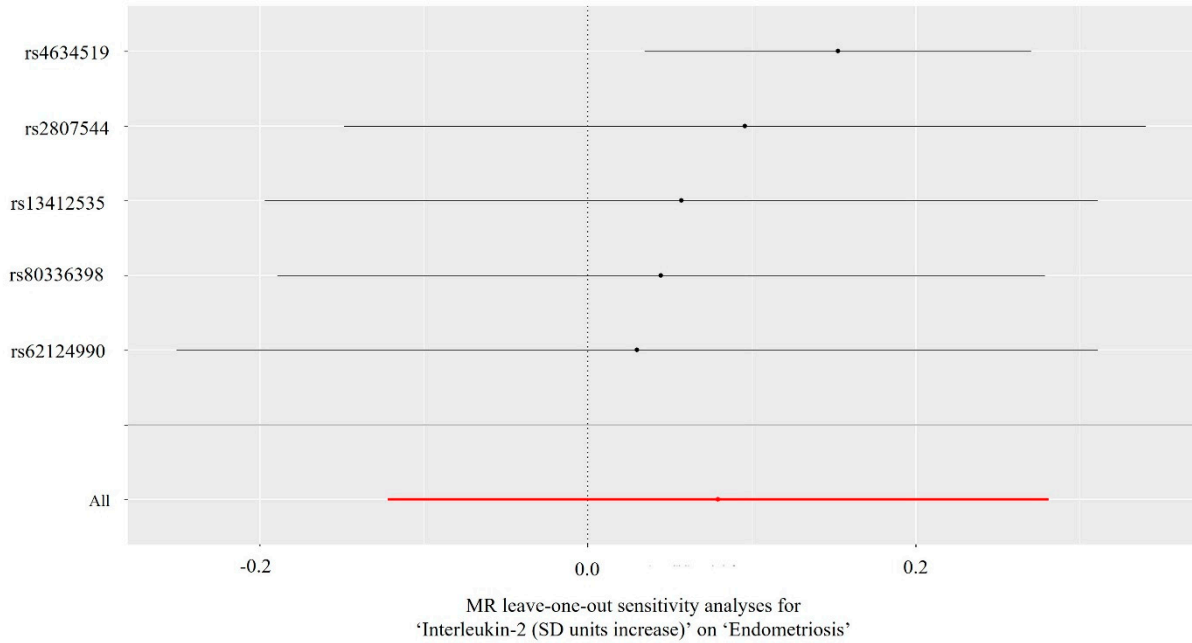
A)



B)



C)



D)

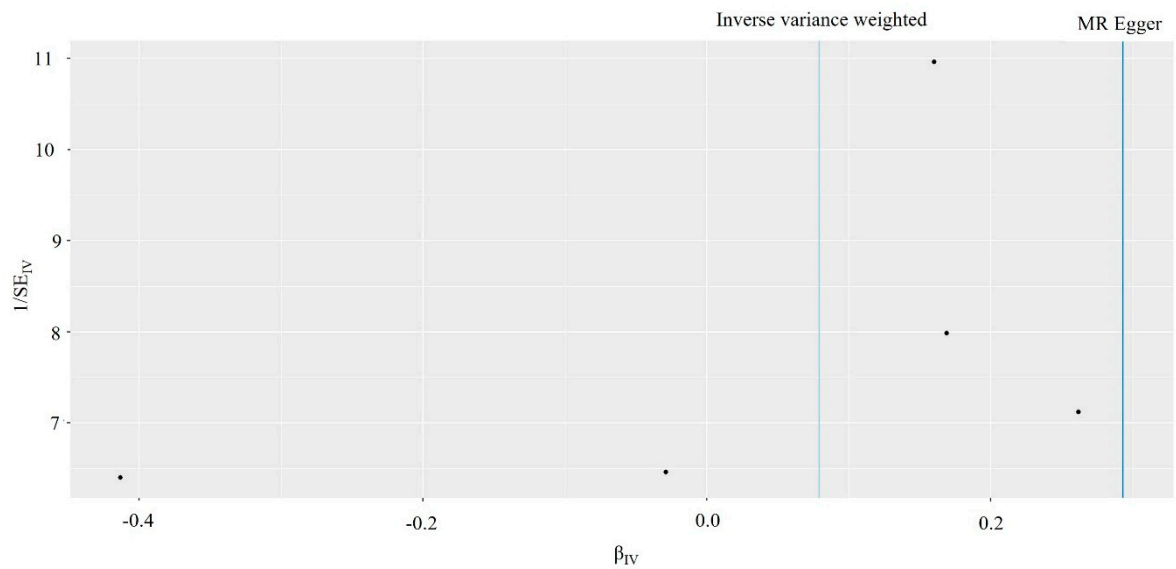
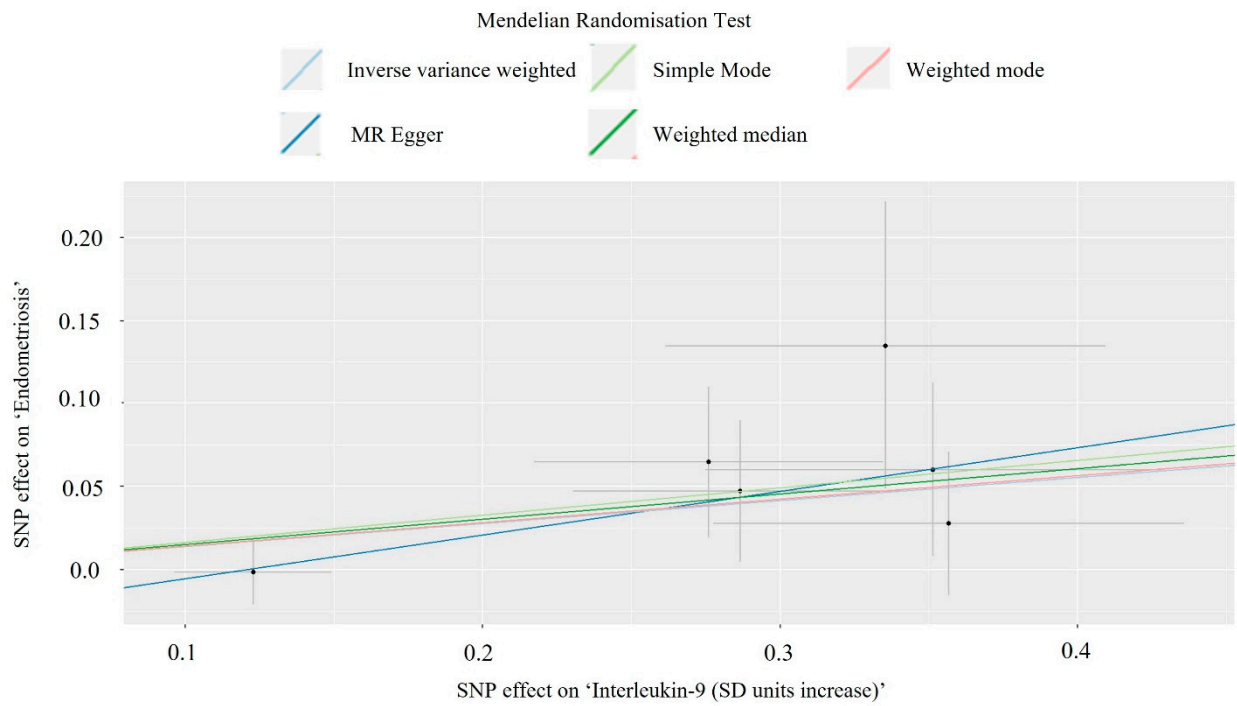
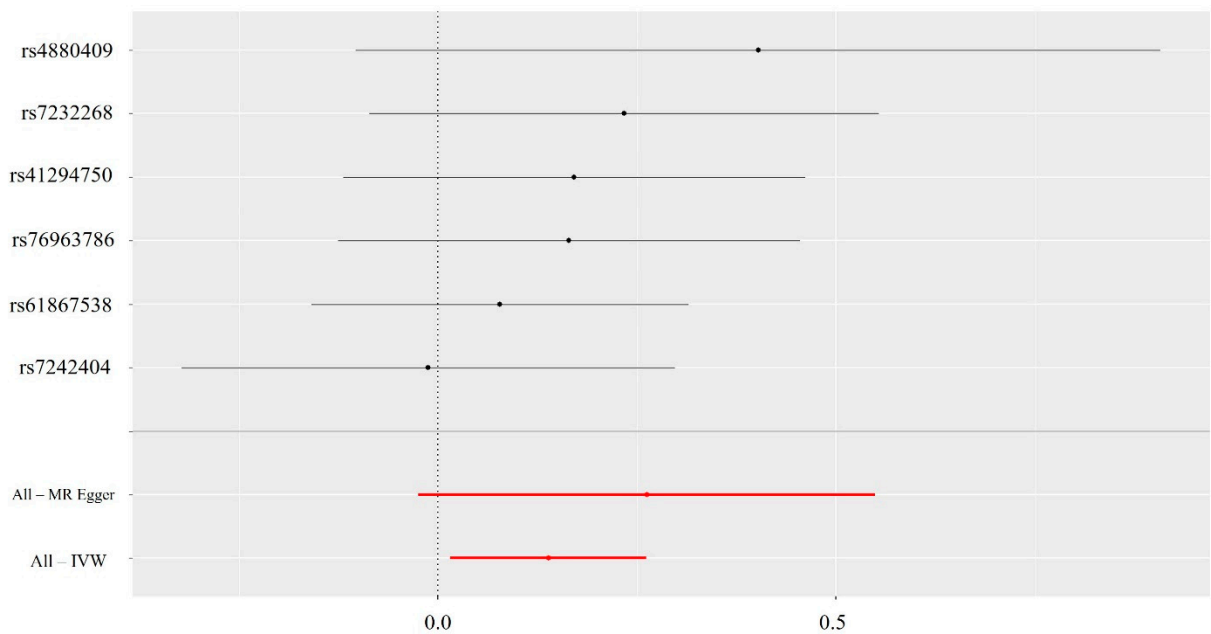


Figure 2: The relationship between 'interleukin-2 (IL-2) (standard deviation units increase)' and the outcome of 'endometriosis', visualised by: **(A)** Scatter plot denoting the distribution of individual causal estimates, with lines indicating the trendlines of the causal estimate using each method; **(B)** Forest plot of the effects of individual single nucleotide polymorphisms (SNPs) and pooled estimates visualised via mendelian randomisation-egger (MRE) and inverse variance weighted (IVW) methods; **(C)** Leave-one-out analysis plot, where the dark points indicate the effect measure via IVW-mendelian randomisation (IVW-MR) analysis excluding the specific SNP. The red line indicates the pooled analysis encompassing all SNPs via IVW-MR; and **(D)** Funnel plot to assess heterogeneity.

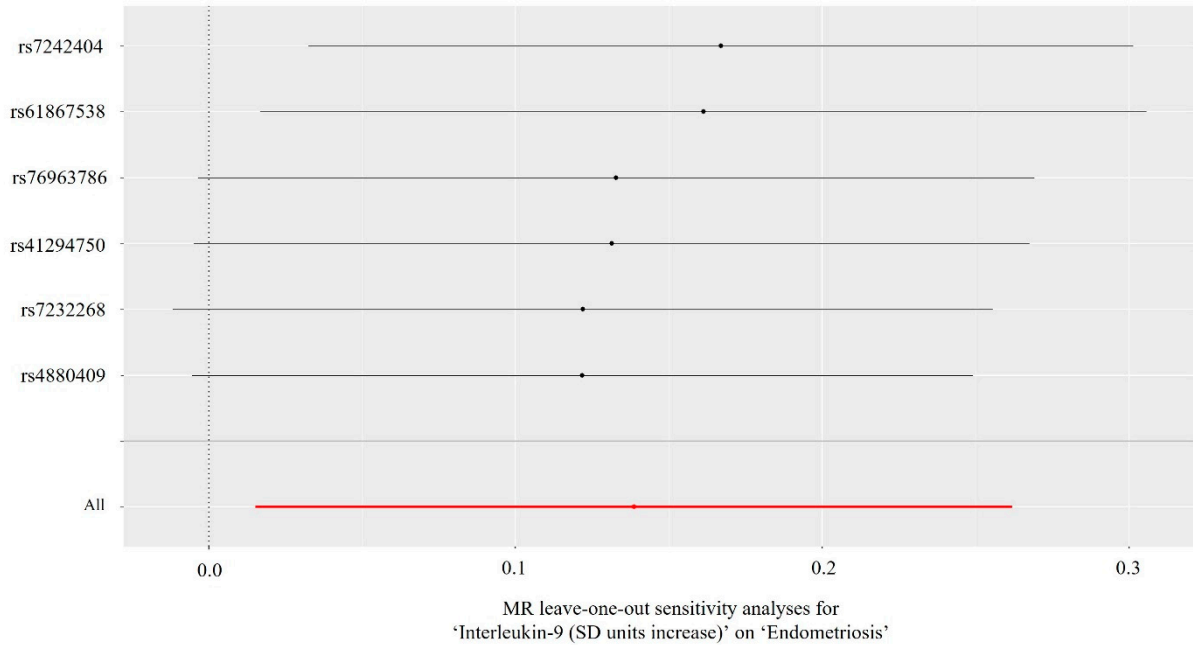
A)



B)



C)



D)

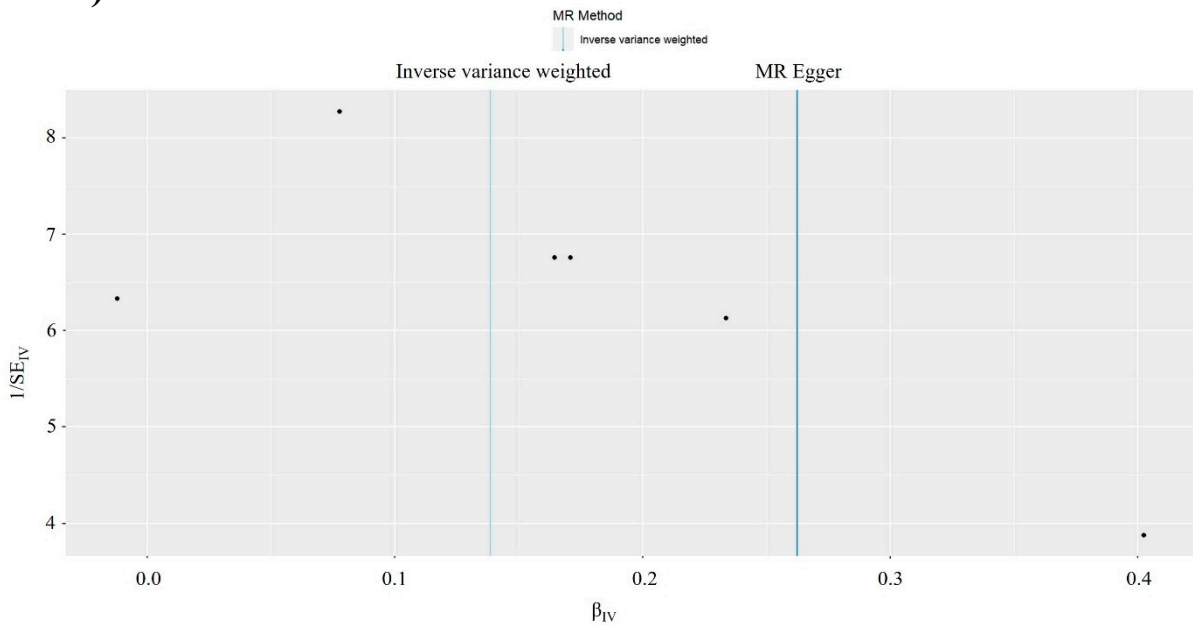


Figure 3: The relationship between 'interleukin-9 (IL-9) (standard deviation units increase)' and the outcome of 'endometriosis', visualised by: (A) Scatter plot denoting the distribution of individual causal estimates, with lines indicating the trendlines of the causal estimate using each method; (B) Forest plot of the effects of individual single nucleotide polymorphisms (SNPs) and pooled estimates visualised via mendelian randomisation-egger (MRE) and inverse variance weighted (IVW) methods; (C) Leave-one-out analysis plot, where the dark points indicate the effect measure via IVW-mendelian randomisation (IVW-MR) analysis excluding the specific SNP. The red line indicates the pooled analysis encompassing all SNPs via IVW-MR; and (D) Funnel plot to assess heterogeneity.