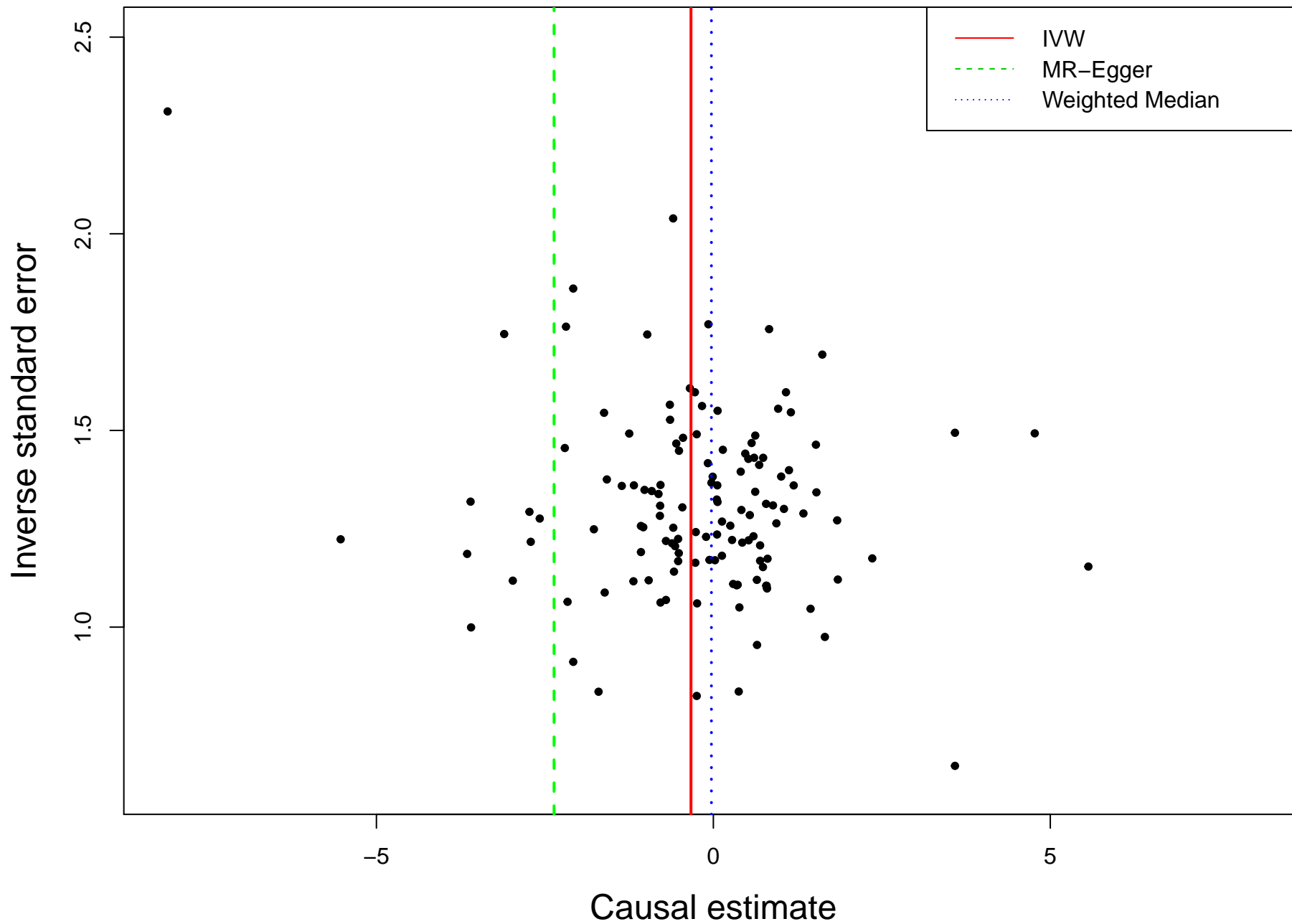
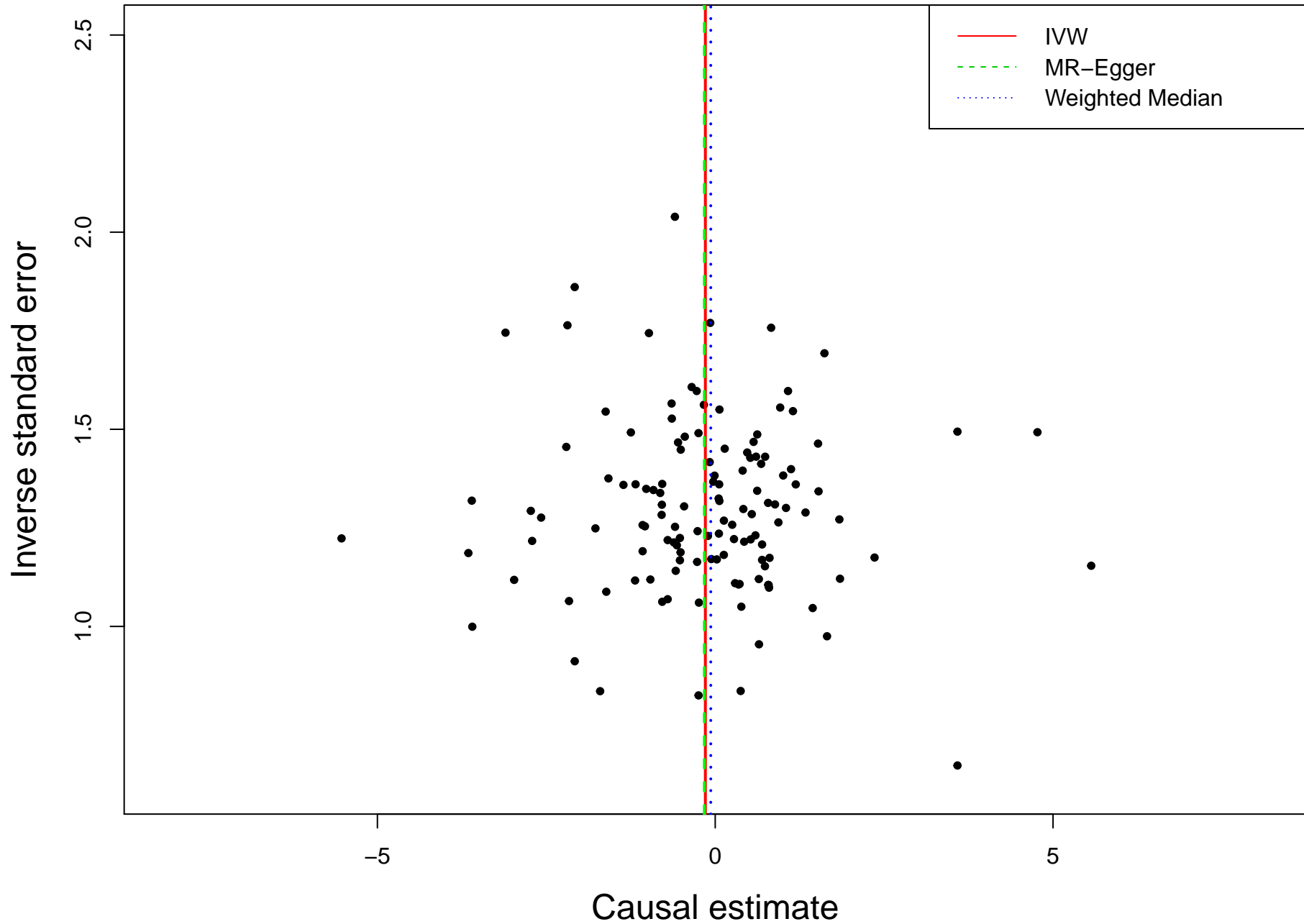


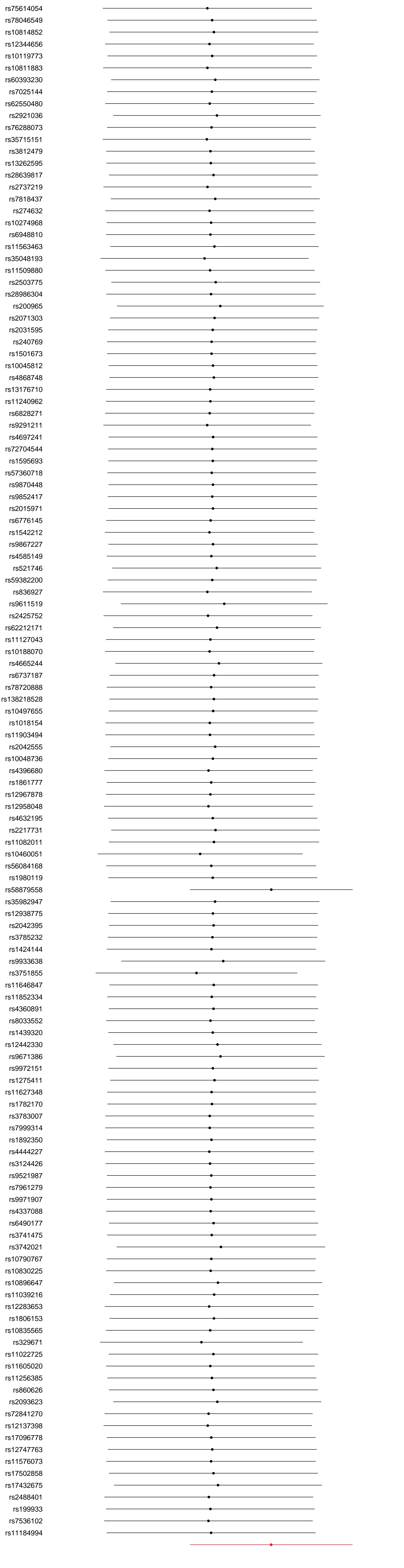
Supplementary figure 1. Funnel plot of Mendelian randomization analysis of neuroticism on PD risk, using all 129 SNPs. The x-axis shows the causal estimates (Wald ratios = β_Y/β_X) for each SNP in the MR analysis. The y-axis shows the inverse of standard errors for the effect sizes. The overall effect estimates using the IVW, MR-Egger and weighted median approaches are represented by vertical lines. Abbreviations: SNP = Single nucleotide polymorphism, MR= Mendelian randomization, IVW = inverse variance weighting



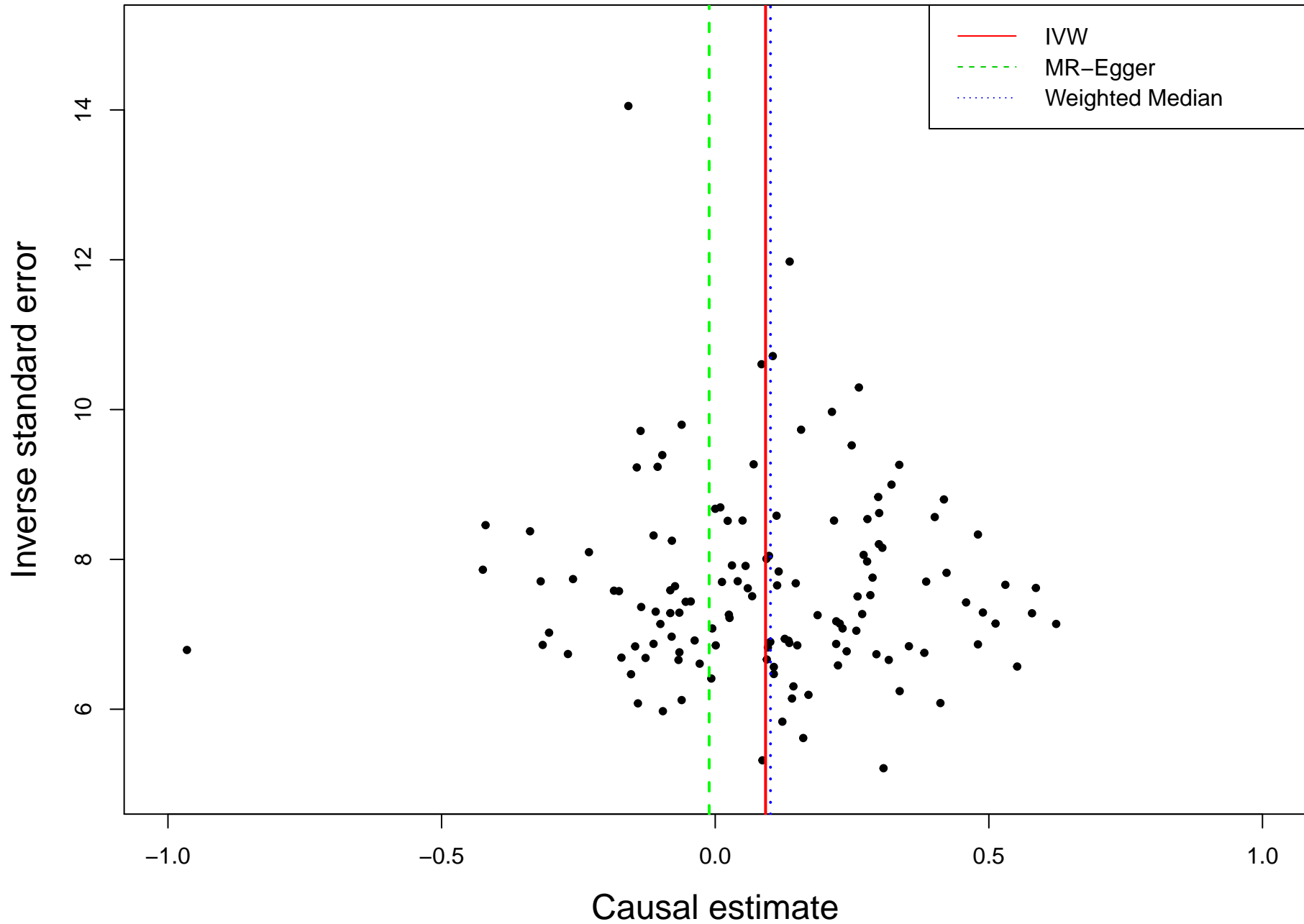
Supplementary figure 2. Funnel plot of Mendelian randomization analysis of neuroticism on PD risk, using 128 SNPs (outlier removed). The x-axis shows the causal estimates (Wald ratios = β_Y/β_X) for each SNP in the MR analysis. The y-axis shows the inverse of standard errors for the effect sizes. The overall effect estimates using the IVW, MR-Egger and weighted median approaches are represented by vertical lines. Abbreviations: SNP = Single nucleotide polymorphism, MR= Mendelian randomization, IVW = inverse variance weighting



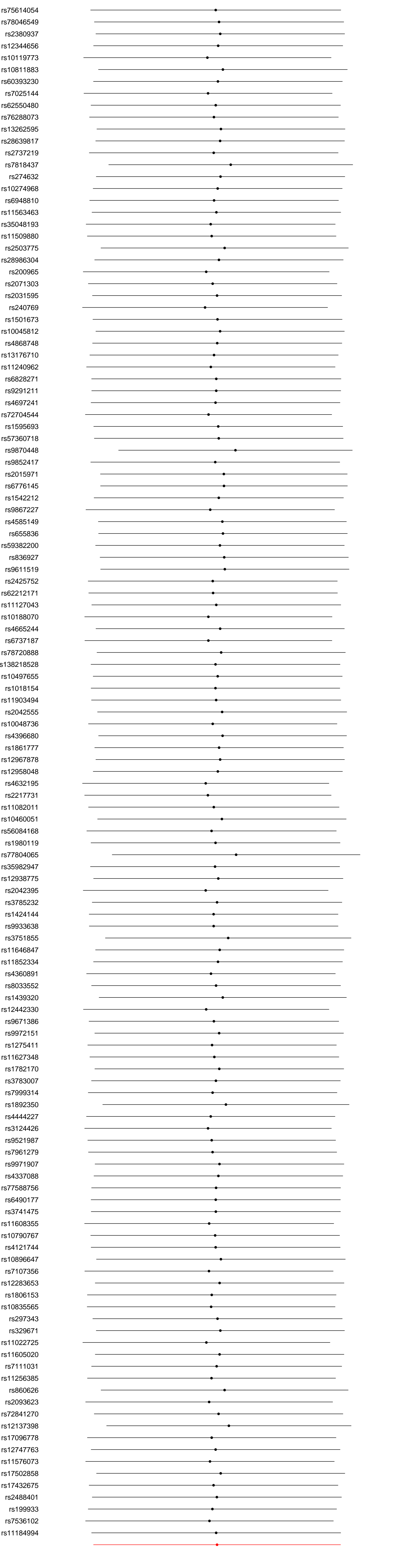
Supplementary figure 3. MR leave-one-out analysis for neuroticism on PD risk. Each black dot and bar represent the effect estimate and 95% confidence interval for neuroticism on PD risk using IVW method if the indicated SNP was omitted. The red dot and bar represent the final IVW estimate when using 128 SNPs (outlier removed).
 Abbreviations: MR = Mendelian randomization, PD = Parkinson's disease; IVW = Inverse variance weighted, SNP = single nucleotide polymorphism



Supplementary figure 4. Funnel plot of Mendelian randomization analysis of neuroticism on risk of smoking initiation, using 129 SNPs. The x-axis shows the causal estimates (Wald ratios = β_Y/β_X) for each SNP in the MR analysis. The y-axis shows the inverse of standard errors for the effect sizes. The overall effect estimates using the IVW, MR-Egger and weighted median approaches are represented by vertical lines. Abbreviations: SNP = Single nucleotide polymorphism, MR= Mendelian randomization, IVW = inverse variance weighting

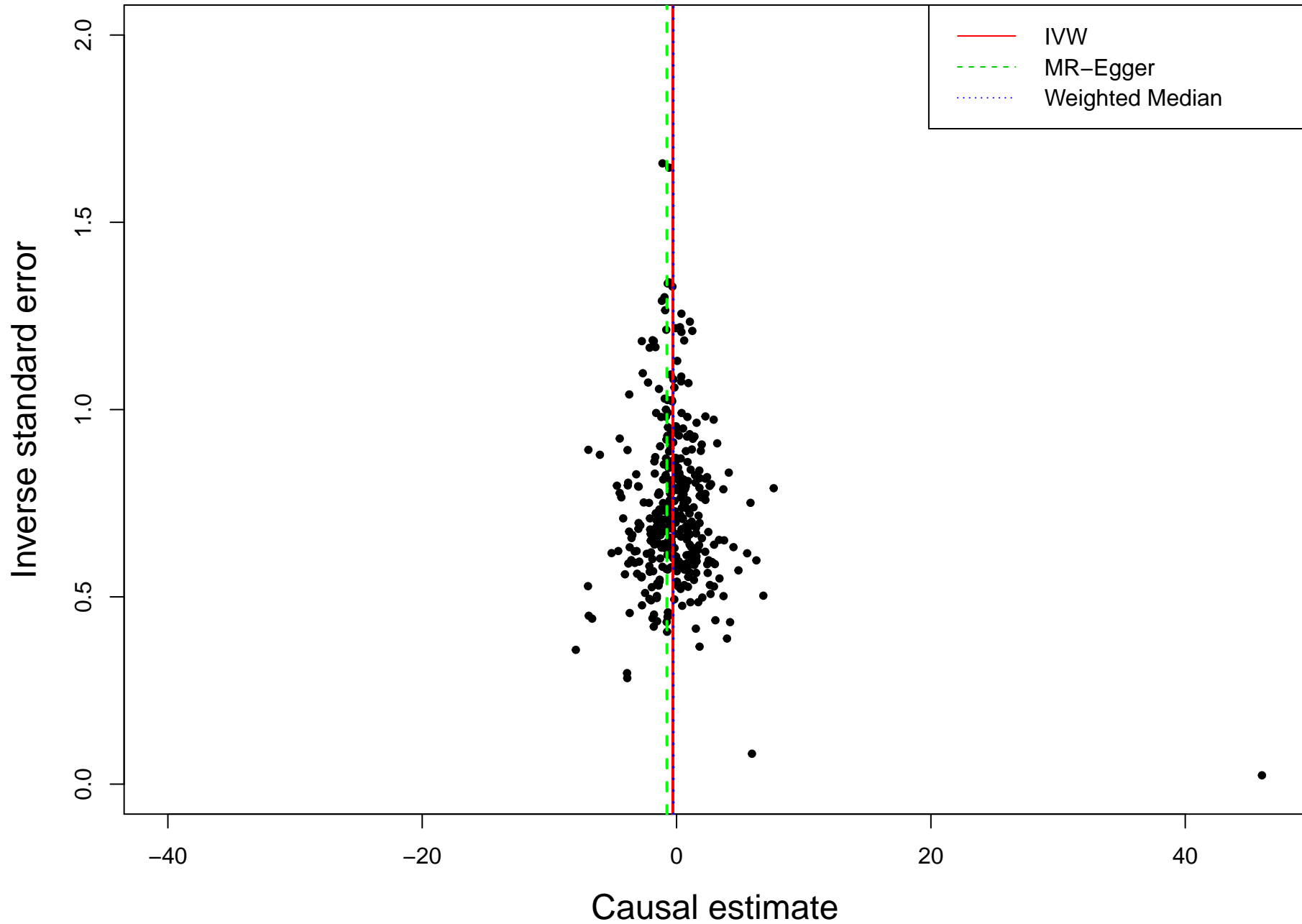


Supplementary figure 5. MR leave-one-out analysis for neuroticism on smoking initiation risk. Each black dot and bar represent the effect estimate (beta) and 95% confidence interval for neuroticism on PD risk using IVW method if the indicated SNP was omitted. The red dot and bar represent the final IVW estimate when using all 129 SNPs. Abbreviations: MR = Mendelian randomization, PD = Parkinson's disease; IVW = Inverse variance weighted, SNP = single nucleotide polymorphism



0.04 0.06 0.08 0.1
IV Estimate and 95% CI

Supplementary figure 6. Funnel plot of Mendelian randomization analysis of smoking initiation on PD risk, using 365 SNPs. The x-axis shows the causal estimates (Wald ratios = β_Y/β_X) for each SNP in the MR analysis. The y-axis shows the inverse of standard errors for the effect sizes. The overall effect estimates using the IVW, MR-Egger and weighted median approaches are represented by vertical lines. Abbreviations: SNP = Single nucleotide polymorphism, MR= Mendelian randomization, IVW = inverse variance weighting



Supplementary figure 7. MR leave-one-out analysis for smoking initiation on PD risk. Each black dot and bar represent the effect estimate (beta) and 95% confidence interval for smoking initiation on PD risk using IVW method if the indicated SNP was omitted. The red dot and bar represent the final IVW estimate when using all 365 SNPs. Abbreviations: MR = Mendelian randomization, PD = Parkinson's disease; IVW = Inverse variance weighted, SNP = single nucleotide polymorphism

