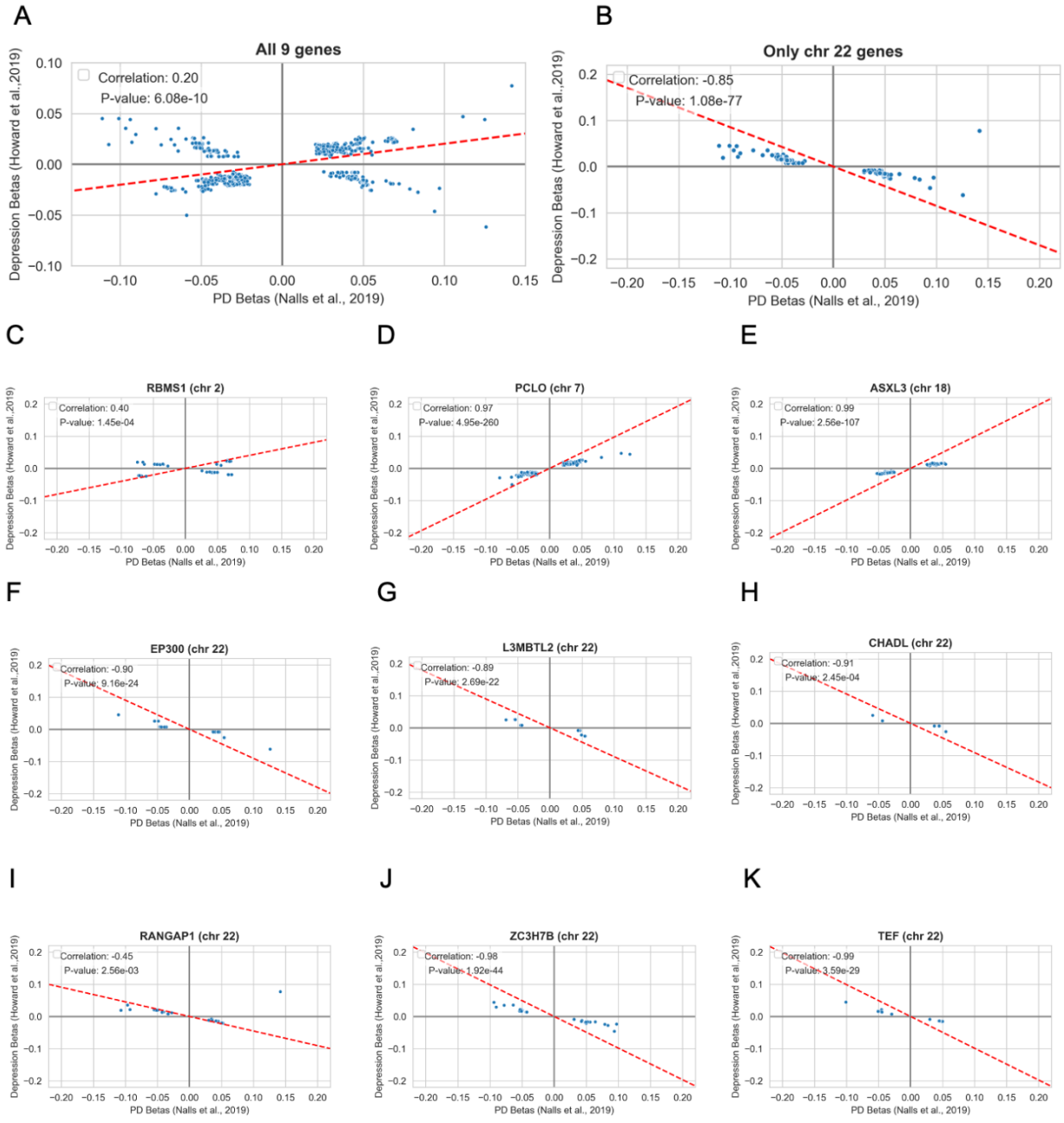
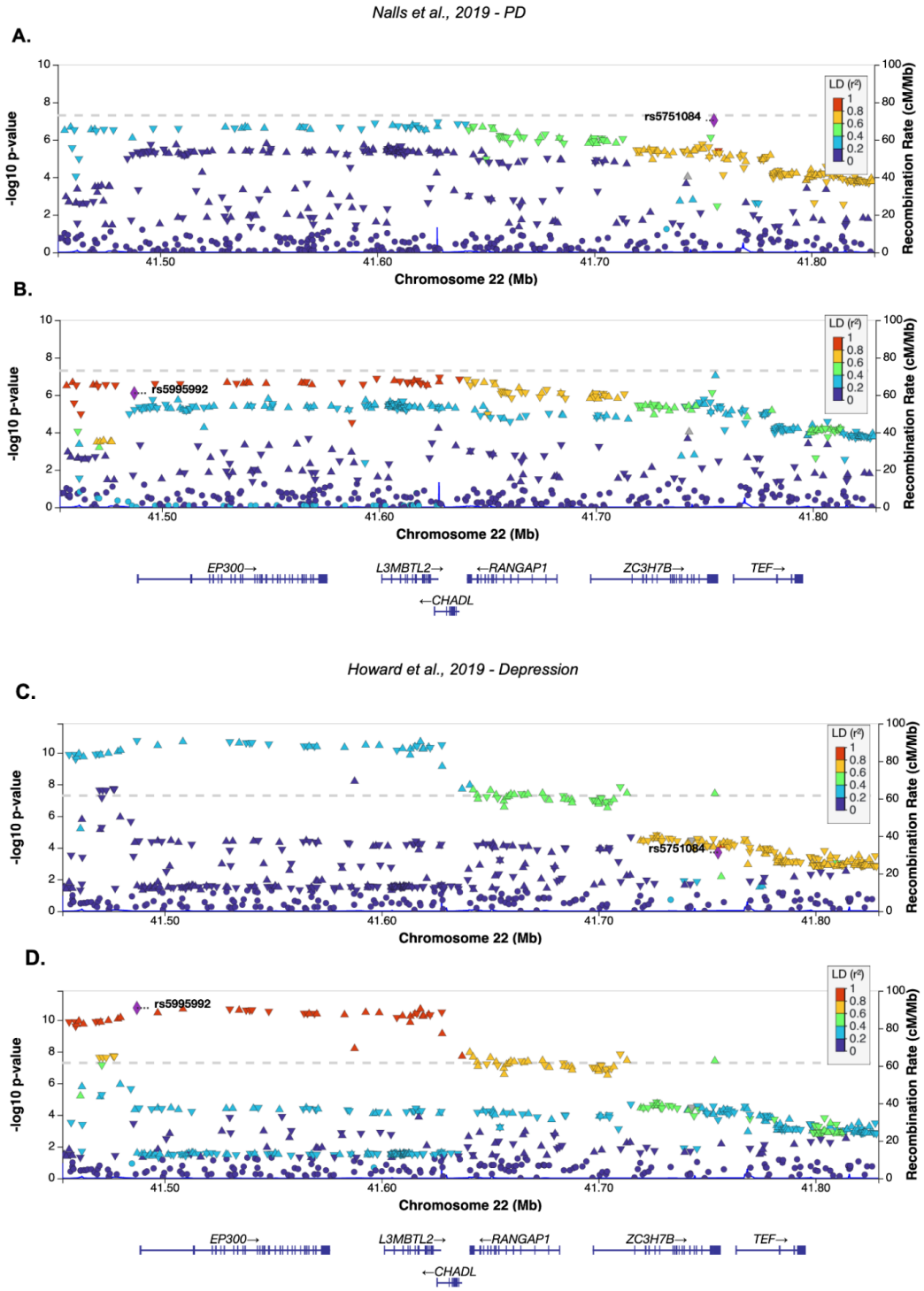
Supplementary Material

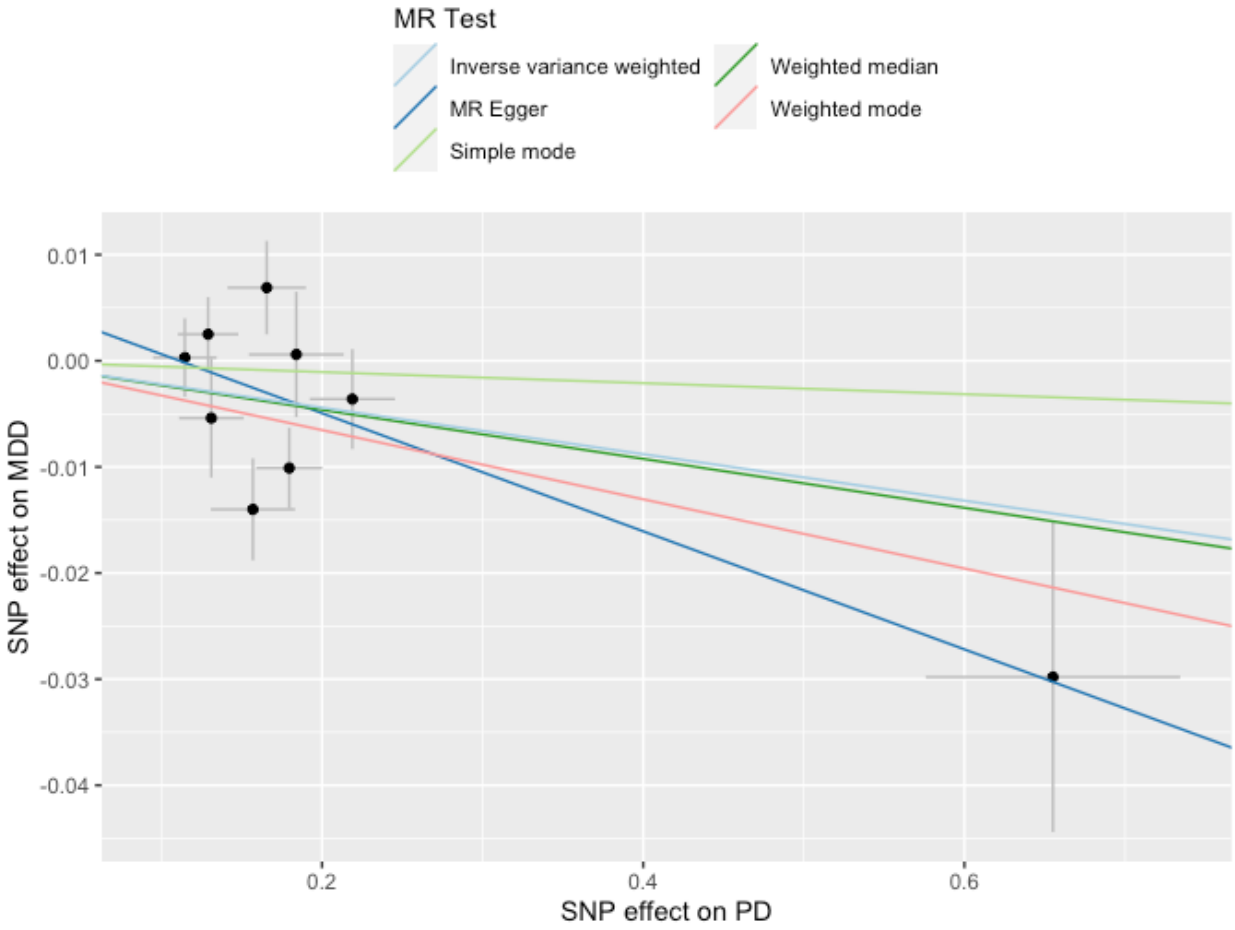
Investigating the Shared Genetic Etiology Between Parkinson's Disease and Depression



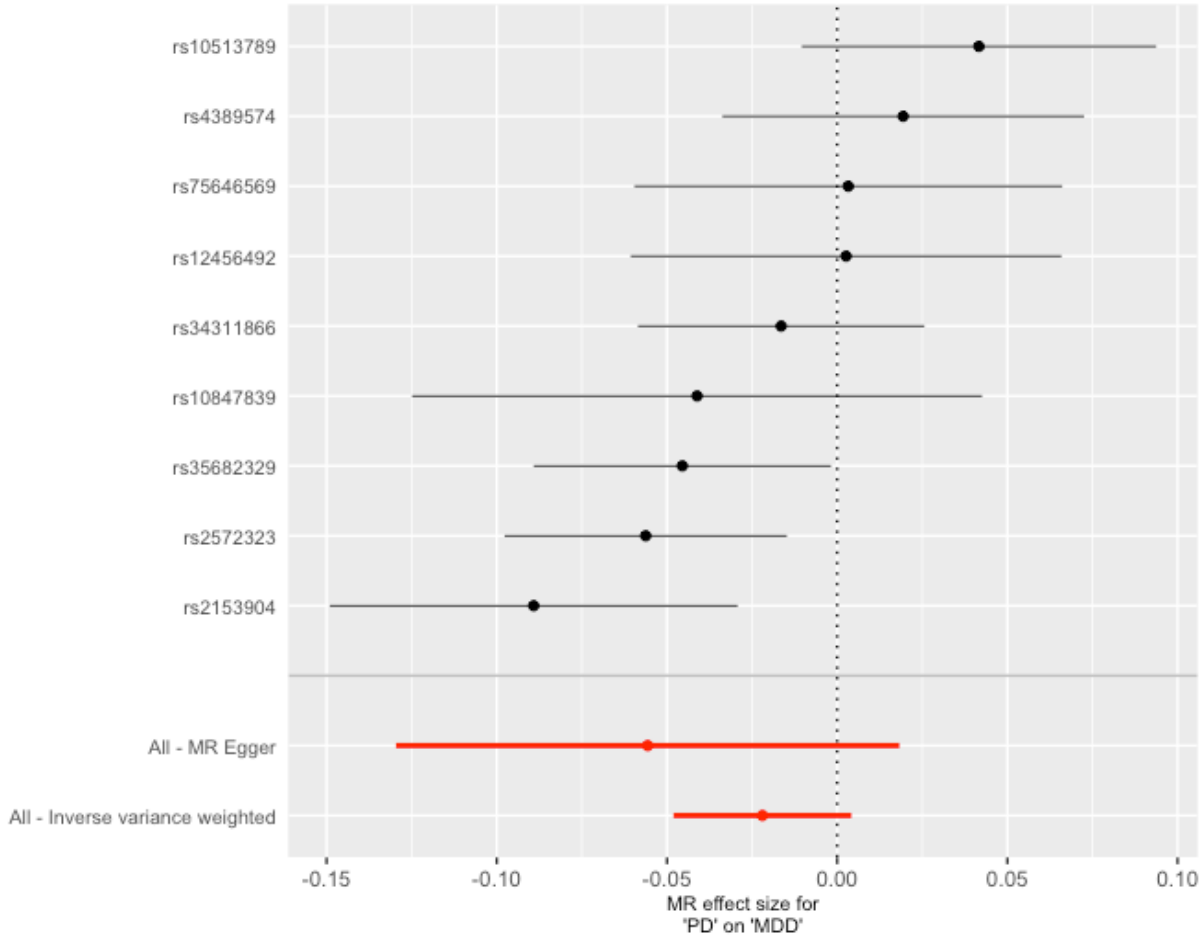
Supplementary Figure 1. Beta-beta plots showing the correlation between effect sizes derived from the PD GWAS (x-axis) and the depression GWAS (y-axis) nominally significant ($p < 0.05$) SNPs within identified gene loci plotted altogether (A), for genes located in chromosome 22 (B), and individually for genes located in chromosomes 2, 7,18 (C-E) and 22 (F-K). Only variants with a significance level of $p < 0.05$ were considered.



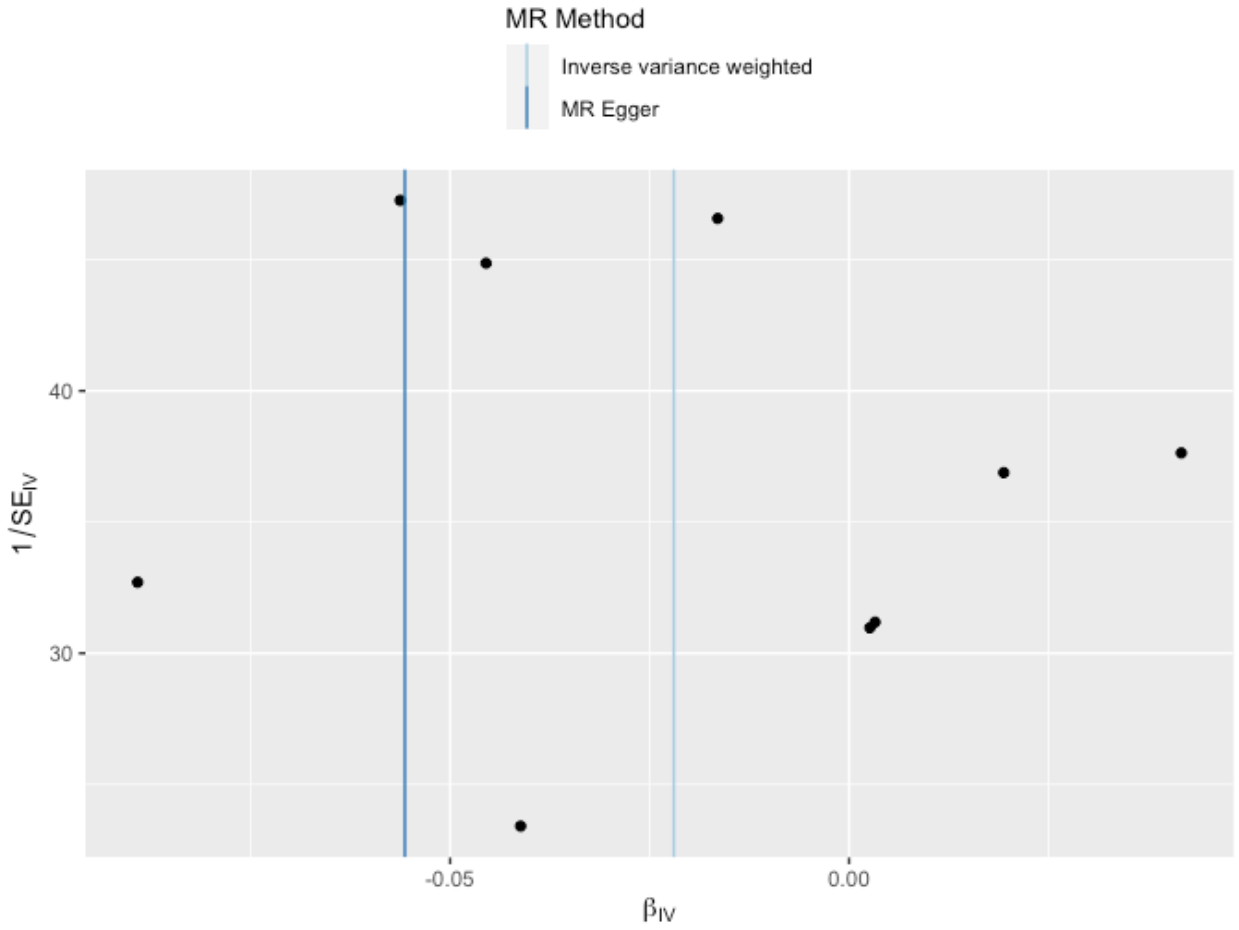
Supplementary Figure 2. Regional association plots for the chr22:41452876-41829000 region in GWAS summary statistics showing SNPs associated with Parkinson's disease (A, B) and Depression (C, D). The statistical significance (−log10 p-value) of the SNPs for the association results for each trait is plotted on the y-axis. The color bar shows the linkage disequilibrium (r^2) between the highlighted SNP and the rest of SNPs within the region. Panels A and C highlight the most significant SNP in the PD GWAS (rs5751084), and the remaining SNPs. Panels B and D highlight the most significant SNP in the Depression GWAS (rs5995992), and the remaining SNPs in the chr22:41452876-41829000 region. The plots were generated by the LocusZoom website (https://my.locuszoom.org).



Supplementary Figure 3. Scatter plot describing Mendelian randomization effect estimates of Parkinson's disease (PD) on depression. The plot displays findings from various methods, including inverse variance weighted, MR Egger, simple mode, weighted median, and weighted mode.



Supplementary Figure 4. Forest plot describing Mendelian randomization causal effect estimates for all Parkinson's disease SNPs on depression risk.



Supplementary Figure 5. Funnel plot showing Parkinson's disease Mendelian randomization effect estimates against the inverse standard error.