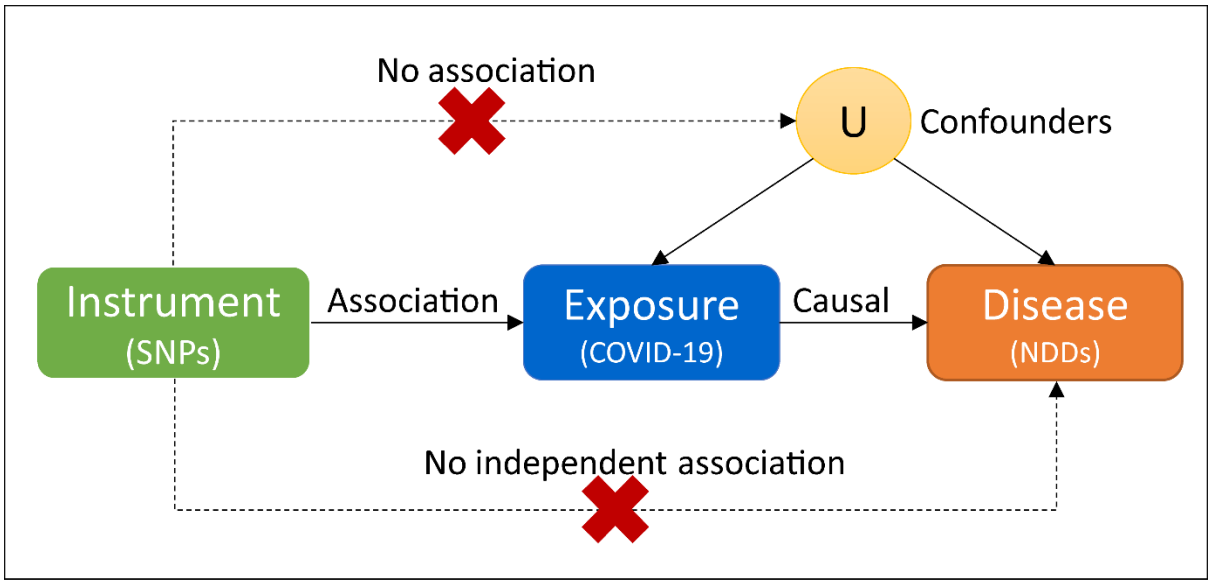
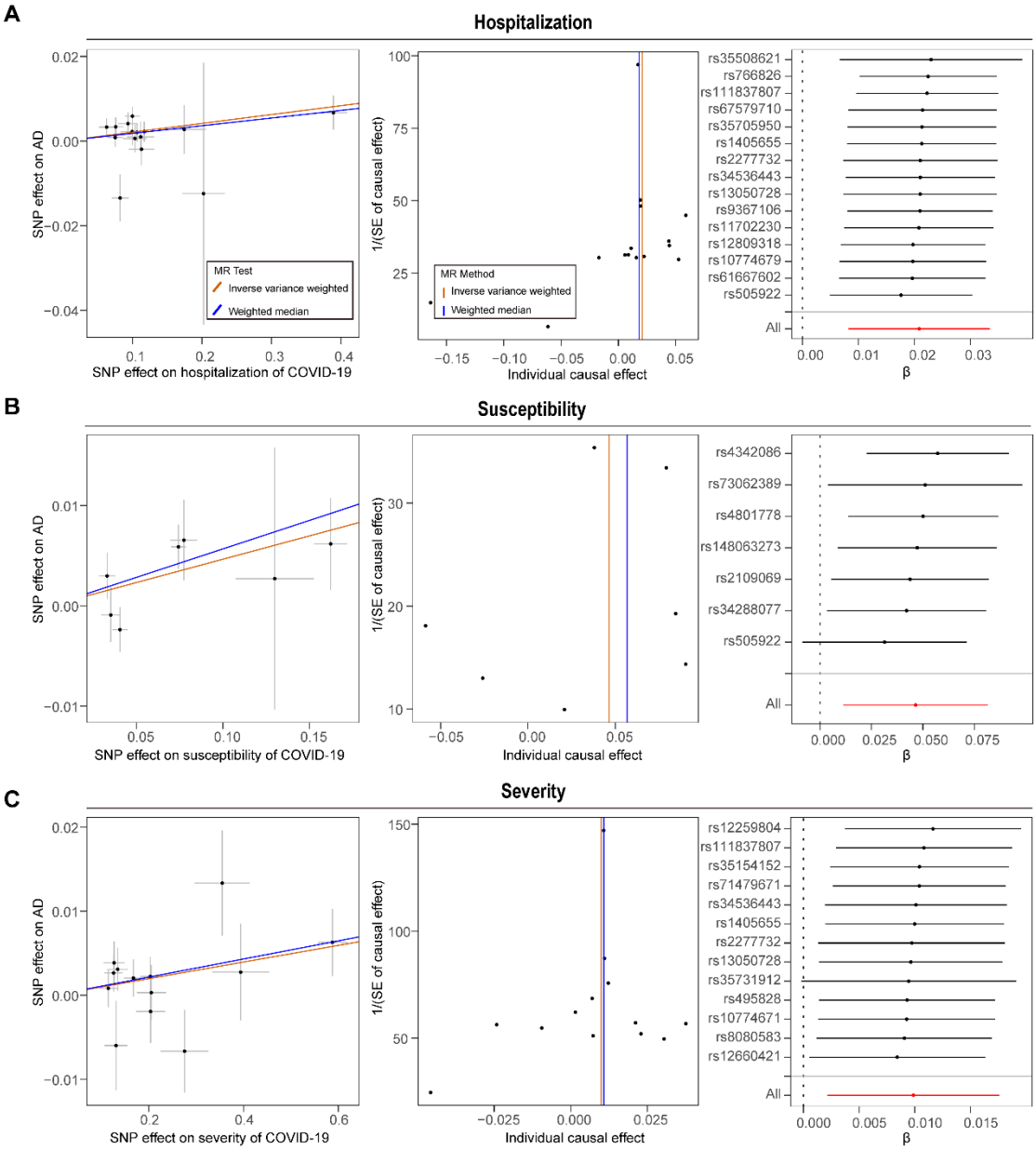
Supplementary Fig. 1. Assumptions in Mendelian randomization analysis



Broken lines represent potential pleiotropic or direct causal effects that would violate Mendelian randomization assumptions. Assumption 1: Genetic variants are associated with the COVID-19; Assumption 2: Genetic variants are not associated with confounders; Assumption 3: Genetic variants influence risk of neurodegenerative disorders (NDDs) only through the exposure.

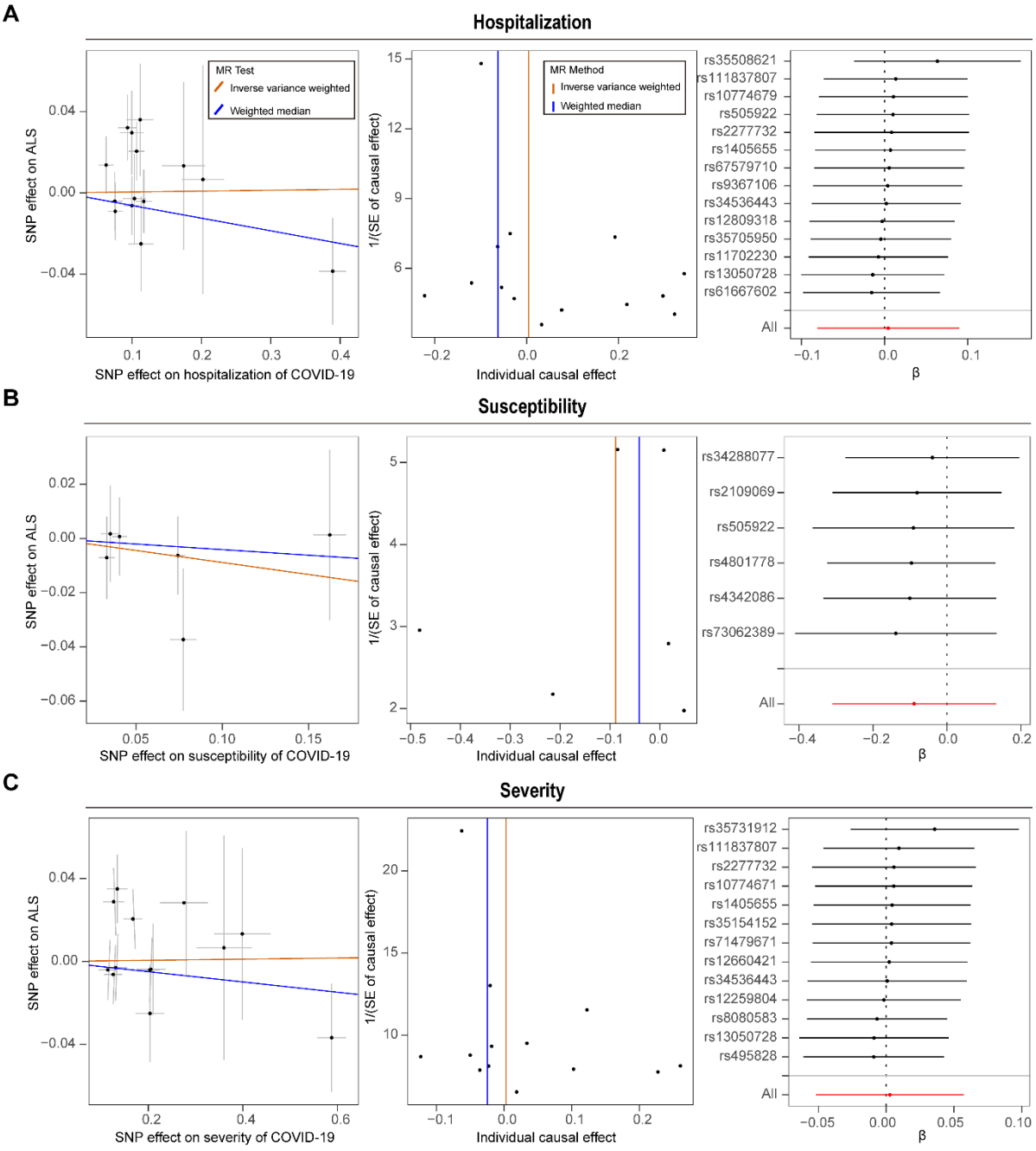
Supplementary Fig. 2. Mendelian randomization analysis results for COVID-19 on risk of Alzheimer's disease.



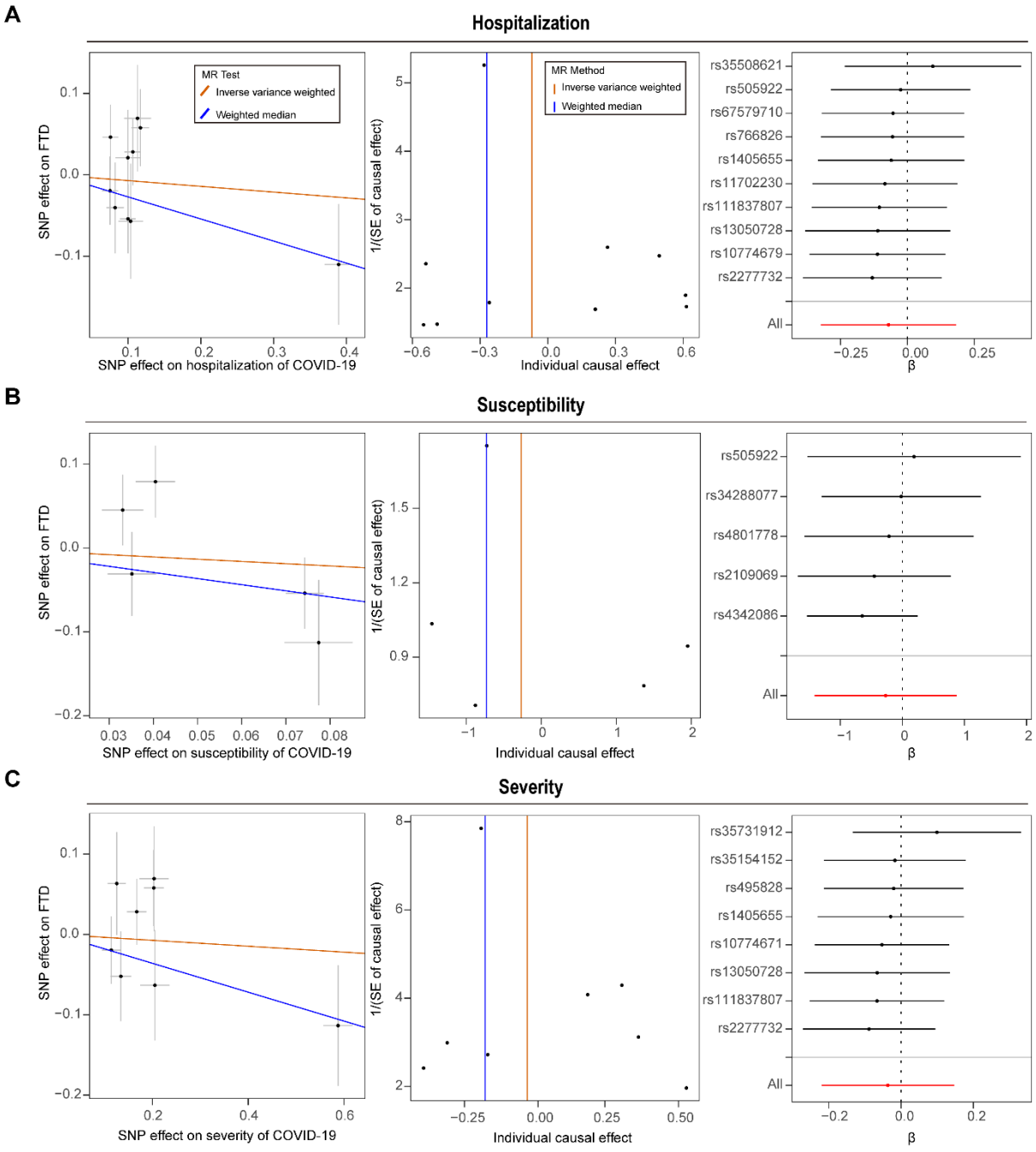
Column 1: Scatter plot of single nucleotide polymorphism (SNP) potential effects on COVID-19 and Alzheimer's disease. The 95% CI for the effect size on Alzheimer's disease is shown as vertical lines, while the 95% CI for the effect size on COVID-19 is shown as horizontal lines. The slope of fitted lines represents the estimated MR effect per method. Column 2: Funnel plot for COVID-19 shows the estimation using the inverse of the standard error of the causal

estimate with each individual SNP as a tool. The vertical line represents the estimated causal effect obtained using IVW and MR-Egger methods. Column 3: Forest plot of the results of the leave-one-out sensitivity analysis, where each SNP in the instrument was iteratively removed from the instrument variables.

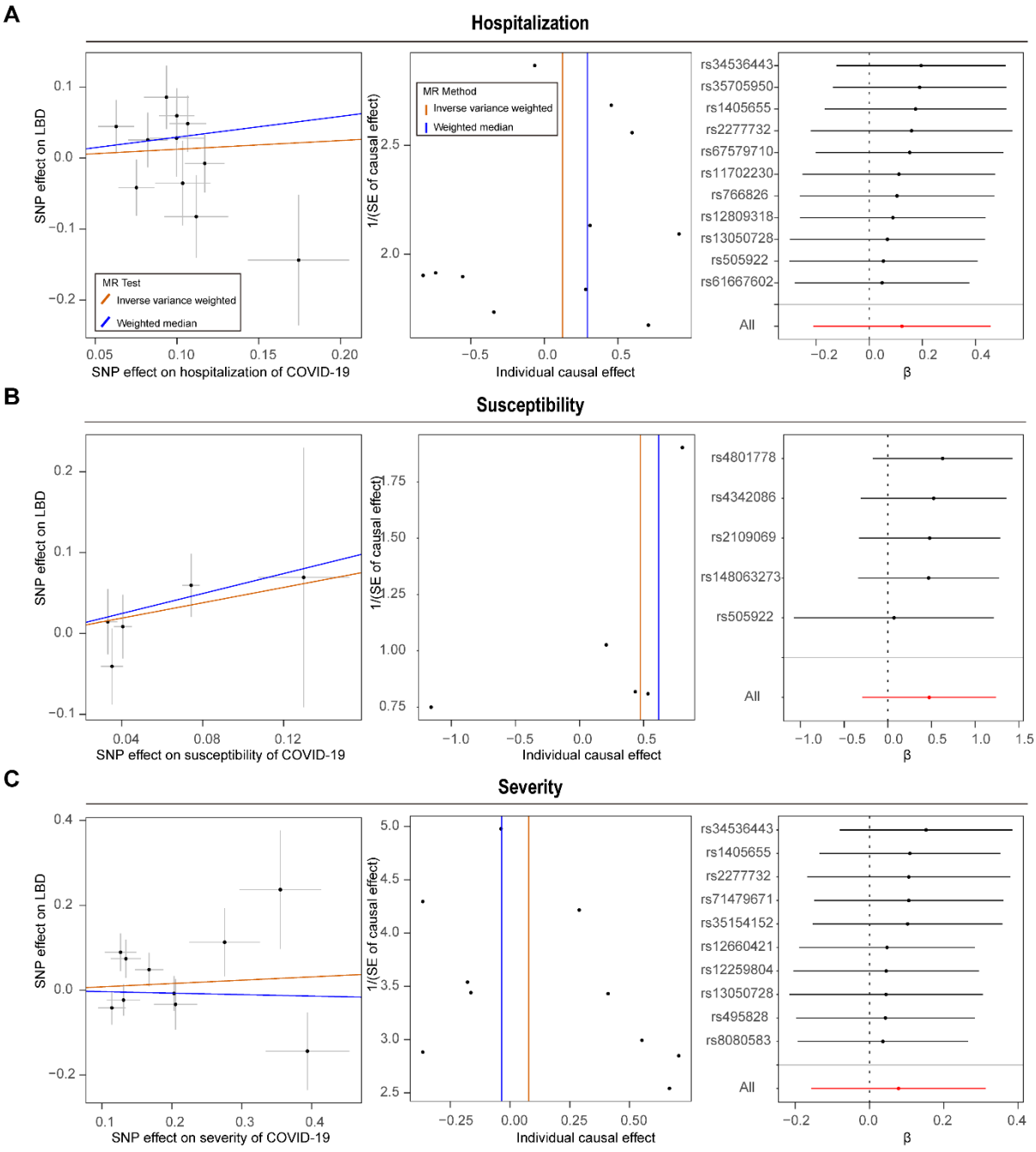
Supplementary Fig. 3. Mendelian randomization analysis results for COVID-19 on risk of amyotrophic lateral sclerosis.



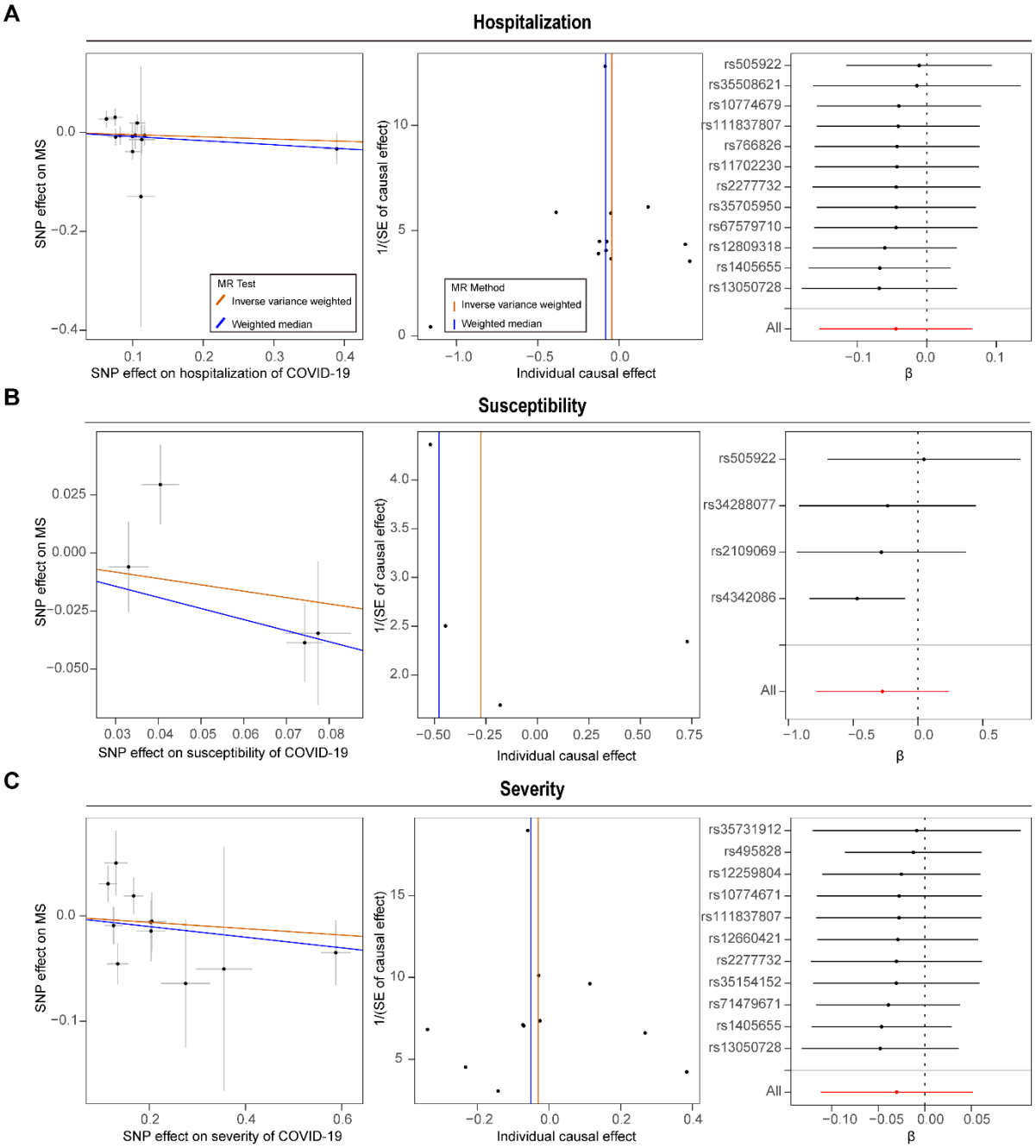
Supplementary Fig. 4. Mendelian randomization analysis results for COVID-19 on risk of frontotemporal dementia.



Supplementary Fig. 5. Mendelian randomization analysis results for COVID-19 on risk of Lewy body dementia.



Supplementary Fig. 6. Mendelian randomization analysis results for COVID-19 on risk of multiple sclerosis.



Supplementary Fig. 7. Mendelian randomization analysis results for COVID-19 on risk of Parkinson's disease.