

Supplementary document and table list

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Mendelian randomization

In the forward Mendelian randomization (MR) analysis, COVID-19 is considered as the exposure variable, while MN is regarded as the outcome variable. Conversely, in the reverse MR analysis, the roles of COVID-19 and MN are interchanged, with COVID-19 now being treated as the outcome and MN as the exposure.

Selection of instrument variants

Relevance: It is essential to establish a strong correlation between the instrumental variables (IVs) and the exposure. We set a threshold of 1×10^{-5} for this purpose. Furthermore, we retained only those IVs that satisfied the condition $F > 10$ [$F = R^2(n - k - 1) / k(1 - R^2)$], ensuring a robust association between the IVs and COVID-19/ MN (exposure).

Independence: In order to ensure the independence of the variations used as IVs, we implemented a clumping process on Single Nucleotide Polymorphisms (SNPs). This was based on the Linkage Disequilibrium (LD) reference panel from the 1000 Genomes Project. The process involved associating any SNP within a 10000 kb window with $R^2 < 0.001$ and retaining the SNP with the lowest p-value at each locus.

Exclusion: To enhance our MR analysis's precision, we eliminated IVs that could potentially be associated with COVID-19/ MN (outcome) (outcome p-value $> 5e-05$). We employed “phenoscanner” to detect confounding factors (supplementary table). Any confounder that simultaneously influenced both the exposure and the outcome was subsequently excluded from further analysis.

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