

Supplementary

Table S1 Demographic characteristics of included Proteome GWASs used in the present MR analysis

GWAS	Sample size	Number of proteins	Measurement methods
YFS/FINRISK	8,293 Caucasians	41 cytokines	Bead-based immunoassays
IMPROVE	3,394 Caucasians	83 cardiovascular disease-related proteins	Modified antibodies conjugated to oligonucleotides
KORA F4/QMDiab	1,000 Caucasians	1,124 proteins	Slow off-rate modified aptamers (SOMAmers)
INTERVAL	3,301 Caucasians	2,994 proteins	SOMAmers
FHS	6,861 Caucasians	71 cardiovascular disease-related proteins	Modified enzyme-linked immunosorbent assay sandwich method
AGES	5,457 Caucasians	4,137 proteins	SOMAmers

Table S2 Demographic characteristics of included COVID-19 GWAS used in the present MR analysis (round 3)

GWAS	Sample information
Susceptibility	
C1	COVID (N=3,523) vs. lab/self-reported negative (N=36,634)
C2	COVID (N=6,696) vs. population (N=1,073,072)
D1	Predicted COVID from self-reported symptoms (N=1,865) vs. predicted or self-reported non-COVID (N=29,174)
Severity	
A2	Very severe respiratory confirmed COVID (N=536) vs. population (N=329,391)
B1	Hospitalized COVID (N=928) vs. not hospitalized COVID (N=2,028)
B2	Hospitalized COVID (N=3,199) vs. population (N=897,488)

