

Supplemental information

Cystatin C is associated with adverse COVID-19 outcomes in diverse populations

Sam O. Kleeman, Mattia Cordioli, Paul R.H. J. Timmers, Atlas Khan, Pinkus Tober-Lau, Florian Kurth, Vadim Demichev, Hannah V. Meyer, James F. Wilson, Markus Ralser, Krzysztof Kiryluk, Andrea Ganna, Kenneth Baillie, and Tobias Janowitz

Supplemental material

Supplemental Figures

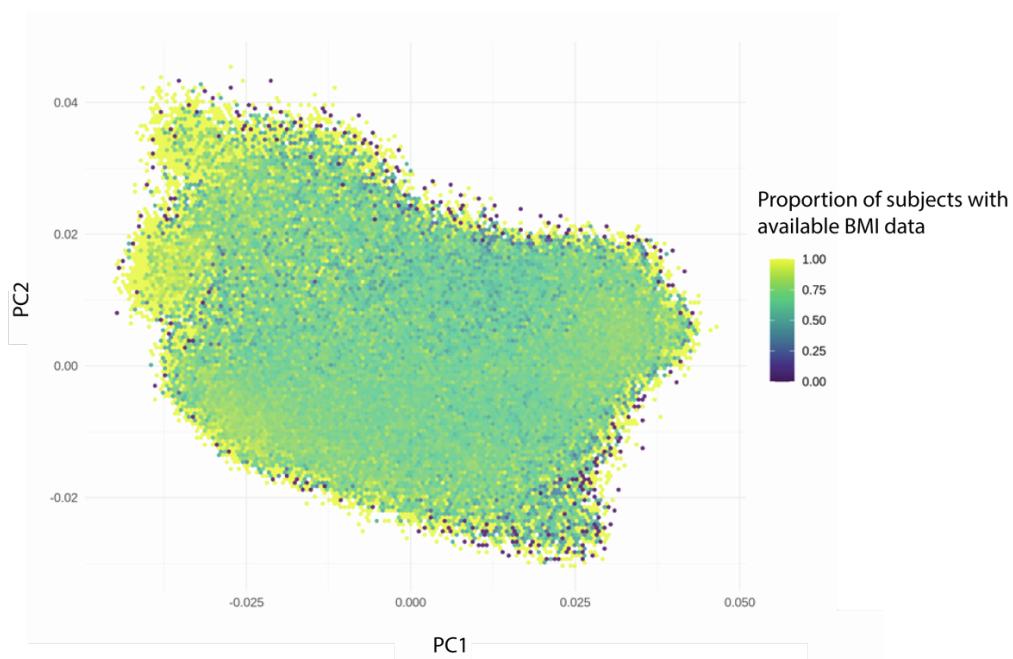


Figure S1, Related to Figure 1: Principal component analysis of linkage disequilibrium-pruned directly genotyped SNPs in FinnGen demonstrating no evidence of population stratification between FinnGen participants with BMI recorded versus not recorded. As individual-level PCA coordinates cannot be shared for FinnGen participants, data are displayed as a histogram where the color of each hexagon reflects the proportion of subjects with available BMI data.

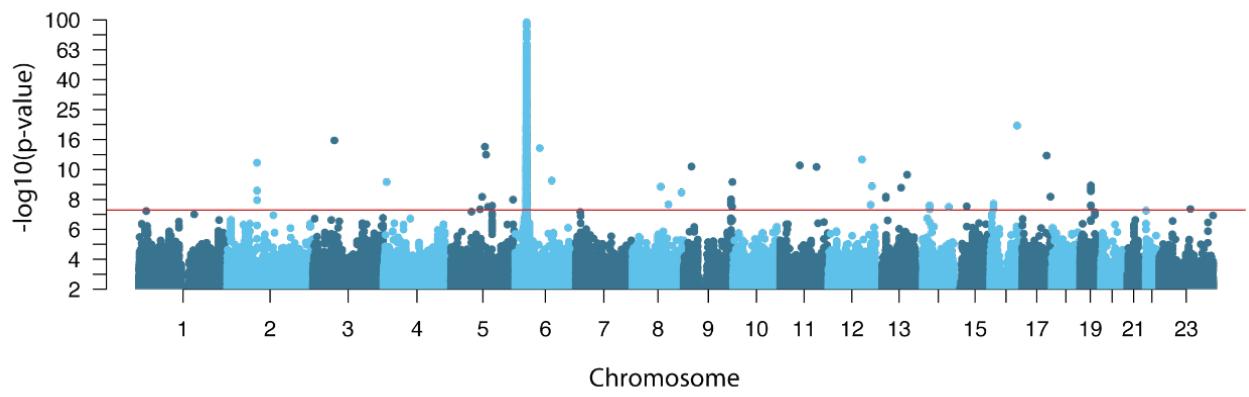


Figure S2, Related to Figure 1: Manhattan plot summarizing results of genome-wide association study for GWAS recorded/not recorded in FinnGen.

Supplemental Tables

Table S1, Related to Figure 1: Summary statistics from logistic regression between Z-scored CyC-production PGS in four cohorts (UK Biobank, FinnGen, GenOMICC and Columbia COVID-19 Biobank). Tables summarizes the features of each regression, including case/control cohorts, numbers of cases/controls, patient ancestry, number of SNPs matched between the CyC-production PGS and the relevant cohort, the covariates included in the analysis and the summary statistics for the mild-moderate control and population control analyses. Black cells refer to missing data.

Non BMI-adjusted analyses																
Case cohort	Control cohort	n_cases_hosp	n_cases_critical	n_cases_death	n_controls_mildmod	n_controls_pop	Ancestry	Matched SNPs	Covariates	Mild-moderate COVID-19 controls			Population controls			
										Hospitalization	Critical illness	Death	Hospitalization	Critical illness	Death	
UKB	UKB	245	43	109	1513	48208	EUR	1031527	PC1-10, sex, year of birth, recruitment centre, array	OR 1.21 (95% CI 1.04-1.40), p=0.01297	OR 2.15 (95% CI 1.55-3.03), p=7.17e-6	OR 1.16 (95% CI 0.93-1.46), p=0.183	OR 1.24 (95% CI 1.09-1.41), p=0.000766	OR 2.13 (95% CI 1.58-2.87), p=7.12e-7	OR 1.20 (95% CI 1.00-1.45), p=0.0529	
GenOMICC	UKB			2018		11837	318280	EUR	980733	PC1-10, age, sex, Townsend deprivation index, local authority	OR 1.16 (95% CI 1.11-1.21), p=4.69e-8			OR 1.20 (95% CI 1.16-1.25), p=2.49e-16		
FinnGen	FinnGen	319	165		2835	305996	EUR	1016675	PC1-4, age, sex	OR 1.09 (95% CI 0.96-1.25), p=0.164	OR 1.22 (95% CI 1.02-1.46), p=0.0298		OR 1.04 (95% CI 0.93-1.16), p=0.538	OR 1.10 (95% CI 0.94-1.28), p=0.233		
Columbia	Columbia	201	93			2341	AFR	957602	PC1-3, sex				OR 1.05 (95% CI 1.05-1.34), p=0.0175	OR 1.44 (95% CI 1.22-1.65), p=0.000956		
Columbia	UKB	184	84			2334	AFR	957602	PC1-8, age, sex				OR 1.16 (95% CI 0.98-1.33), p=0.102	OR 1.31 (95% CI 1.02-1.57), p=0.053		
BMI-adjusted analyses																
Case cohort	Control cohort	n_cases_hosp	n_cases_critical	n_cases_death	n_controls_mildmod	n_controls_pop	Ancestry	Matched SNPs	Covariates	Mild-moderate COVID-19 controls			Population controls			
										OR 1.14 (95% CI 0.98-1.33), p=0.0918	OR 2.02 (95% CI 1.45-2.85), p=4.17e-5	OR 1.07 (95% CI 0.86-1.35), p=0.531	OR 1.15 (95% CI 1.01-1.31), p=0.0277	OR 1.94 (95% CI 1.44-2.63), p=1.55e-5	OR 1.12 (95% CI 0.93-1.36), p=0.23	
UKB	UKB	245	43	109	1513	48208	EUR	1031527	PC1-10, sex, year of birth, recruitment centre, array, BMI	OR 0.99 (95% CI 0.84-1.16), p=0.898	OR 1.01 (95% CI 0.82-1.25), p=0.163		OR 0.97 (95% CI 0.85-1.10), p=0.639	OR 1.08 (95% CI 0.90-1.29), p=0.397		
FinnGen	FinnGen	239	123		1939	220475	EUR	1016675	PC1-4, age, sex, BMI							