Title: Circulating polyunsaturated fatty acids and COVID-19: a prospective cohort study and Mendelian randomization analysis

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Supplementary Table 1. Notable Mendelian randomization studies of polyunsaturated fatty acids.

MR study	Exposure	Exposure data sources	Exposure unit	Outcome	Outcome data sources	Findings (increasing risk, decreasing risk, null)
Zhao, J.V., Schooling, C.M (1)	LA	CHARGE consortium	% total increase in total fatty acids	IHD, diabetes, HDL-C, LDL-C, TC, BP, and reticulocyte count	CARDIoGRAMplusC4D 1000 Genomes, the Myocardial Infarction Genetics and CARDIoGRAM Exome, the UK Biobank SOFT CAD GWAS, the DIAbetes Genetics Replication And Meta-analysis diabetes case study, Global Lipids Genetics Consortium, and the UK Biobank	Genetically predicted higher serum LA was associated with the lower diabetes risk, lower levels of HDL-C, LDL-C, and TC. Genetically predicted LA was not associated with IHD, SBP, or reticulocyte count.
Zhang, T. *et al.* (2)	AA	CHARGE consortium	SD	IHD, stroke, HDL-C, LDL-C, TG, ApoB, ApoA-I, BP, adiposity, and markers of inflammation and coagulation	The CARDIoGRAMplusC4D 1000 Genomes, MEGASTROKE consortium, the UK Biobank pan-ancestry summary statistics, GLGC, the Genetic Investigation of ANthropometric Traits Consortium and the UK Biobank meta-analysis, a GWAS of cytokines in 8293 Finnish individuals, the INTERVAL study in 3301 individuals of European ancestry, the CHARGE Inflammation Working Group, and the Biobank Japan.	Genetically predicted AA was associated with higher levels of ApoB, HDL-C, LDL-C, and a lower level of TG, but not associated with IHD, stroke, ApoA-I, BP, adiposity, or other markers of inflammation and coagulation.
Yuan, S. *et al.* (3)	ALA, EPA, DPA, DHA, LA, AA, POA, OA, PA, and SA	CHARGE consortium	SD	CAD, IS, AF, heart failure, aortic valve stenosis, abdominal and thoracic aortic aneurysms, transient ischemic attack, intracerebral and subarachnoid hemorrhages, VTE, and PAD	CARDIoGRAMplusC4D consortium, MEGASTROKE consortium, Atrial Fibrillation consortium, and UK Biobank	Genetically predicted plasma AA and SA levels were associated with the higher CVD risk. Genetically predicted higher plasma ALA, LA, and OA levels were associated with lower risks of large-vessel stroke and venous thromboembolism.
Yuan, T. *et al.* (4)	LA, AA, ALA, EPA,	CHARGE consortium	SD	IS, LDL-C, HDL-C, TC, SBP, and DBP	The International Stroke Genetics Consortium, the GLGC, and the UK Biobank	Genetically predicted AA was associated with higher IS risk, higher levels of LDL-C, HDL-C, and TC. Genetically predicted serum ALA was

	DHA, and DPA					associated with a lower IS risk, lower levels of LDL-C, HDL-C, and TC. Genetically predicted LA, EPA, DHA, and DPA were not associated with IS, lipids, or BP.
Liao, L. Z. *et al.* (5)	Omega-6 fatty acids	Large GWAS (n = 24,925) from 14 cohorts in people of European ancestry	SD	CHD, TC, LDL-C, HDL-C, and TG	CARDIoGRAMplusC4D and GLGC	Genetically predicted omega-6 was associated with a higher risk of CHD, which might be partially mediated by TC, LDL-C, and TG.
Mazidi, M. *et al.* (6)	10-heptadecenoate, MA, OA, and POA	A GWAS (including 7,824 adult samples of European ancestry)	SD	CHD, MI, CS, and IS	CARDIoGRAMplusC4D 1000 Genomes, UK Biobank SOFT CAD study, two small case (n = 4,120)–control (n = 3,910) studies from Germany and Greece, and METASTROKE	Genetically predicted serum 10-heptadecenoate, MA, OA, and POA were not associated with risks of CHD, MI, CS, or IS.
Zhang, T. *et al.* (7)	AA	CHARGE consortium	% total increase in fatty acid	ASCVD, IHD, PAD, VTE, and other CVD	CARDIoGRAMplusC4D 1000 Genomes, MEGASTROKE, Pan-UK Biobank, Atrial Fibrillation Consortium, HERMES consortium, and FinnGen.	Genetically predicted AA was associated with higher risks of ASCVD, IHD, PAD, and VTE, with possibly stronger associations in men than women.
Yuan, S., & Larsson, S. C. (8)	ALA, DHA, EPA, DPA, AA, and LA	CHARGE consortium	SD	AF	Atrial Fibrillation Consortium	Genetically predicted ALA, DHA, EPA, DPA, AA, and LA were not associated with the risk of AF.
Park, S. *et al.* (9)	DPA, EPA, DHA, LA, GLA, DGLA, AdrA, and AA	CHARGE consortium	SD	CAD and MI	UK Biobank and CARDIoGRAMplusC4D	Genetically predicted AA was associated with a higher risk of CAD. Genetically predicted higher EPA, LA, and DGLA levels were associated with a lower risk of CAD.
Wang, W *et al.* (10)	MUFA and omega-3 fatty acids	Large GWAS (n = 24,925) from 14 cohorts in people of European ancestry	SD	Incident heart failure and mortality of heart failure	Cohorts for Heart and Aging Research in Genomic Epidemiology-Heart Failure Working Group	Genetically predicted higher circulating MUFA levels were associated with increased risk of heart failure, but no association with mortality of heart failure. Genetically predicted omega-3 fatty acids were not associated with heart failure.
Chen, H. Y. *et al.* (11)	AA	FOS cohort (n = 1310, 492 cases of AVC) and European-ancestry participants in the MESA cohort (n = 2415)	SD	AVC and AS	Genetic Epidemiology Research on Adult Health and Aging cohort and CHARGE Consortium	Genetically predicted higher AA level was associated with higher risks of AS and AVC.

Yuan, S. *et al.* (12)	ALA, EPA, DHA, LA, AA, POA, OA, PA, and SA	CHARGE consortium	SD	T2DM	DIAGRAM consortium	Genetically predicted higher EPA, DPA, AA, and SA were associated with a higher risk of T2DM. Genetically predicted higher ALA, LA, POA, and OA levels were associated with a lower risk of T2DM.
Jäger, S. *et al.* (13)	D5D (AA/DGLA) and D6D (GLA/LA)	EPIC–Potsdam Study	SD	T2DM and CAD	DIAGRAM consortium and CARDIoGRAM.	Genetically predicted higher D6D and D5D were associated with higher risks of T2DM and CAD.
Adams, C. D., & Neuhausen, S. L. (14)	TOTFA, MUFA, omega-3 fatty acids, and PUFA	Large GWAS (n = 24,925) from 14 cohorts in people of European ancestry	SD	Chronotype and T2DM	UK Biobank and DIAGRAM consortium	Genetically predicted higher TOTFA and MUFA levels were associated with a lower risk of T2DM.
Zulyniak *et al.* (15)	AA	CHARGE consortium	SD	DI and T2DM	The Meta-Analysis of Glucose- and Insulin-Related Traits Consortium and the UK Biobank	Genetically predicted higher AA was associated with DI. Genetically predicted AA was not associated with T2DM.
Ma, M. *et al.* (16)	ALA, EPA, DPA, DHA, LA, and AA	CHARGE consortium	SD	BP, SBP, DBP, and PP	UK Biobank and International Consortium for Blood Pressure	Genetically predicted higher ALA was associated with higher DBP. Genetically predicted higher AA and EPA were associated with lower DBP. Genetically predicted ALA, EPA, DPA, DHA, LA, and AA were not associated with SBP. Genetically predicted DPA and DHA were not associated with DBP.
Zhao, J. V., & Schooling, C. M. (17)	LA	Large GWAS (n = 24,925) from 14 cohorts in people of European ancestry	SD	Asthma, eosinophil, neutrophil, and monocyte counts	Case-control study of asthma based on Trans-National Asthma Genetic Consortium and UK Biobank	Genetically predicted higher LA was associated with a lower risk of asthma, lower eosinophil count, and lower neutrophil count.
Liyanage, U. *et al.* (18)	EPA, ALA, LA, AA, DHA, and DPA	CHARGE consortium	SD	Overall cancer risk and cancer mortality	UK Biobank	Genetically predicted higher AA was associated with an increased risk for colorectal cancer. Genetically predicted EPA, ALA, LA, AA, DHA, and DPA were not associated with overall cancer risk or mortality.
Larsson, S. *et al.* (19)	AA, EPA, and DHA	CHARGE consortium	SD	Ten site-specific cancers (esophagus, stomach,	BioBank Japan, Breast Cancer Association Consortium, ILCCO, Ovarian Cancer Association Consortium, Prostate Cancer Association Group to Investigate Cancer	Genetically predicted higher plasma phospholipid AA concentrations were associated with increased risks of colorectal cancer, lung cancer, and esophageal cancer. Genetically predicted AA, EPA, and DHA were not

				colorectum, pancreas, lung, bladder, prostate, breast, uterus, and ovaries)	Associated Alterations in the Genome consortium	associated with cancers of the stomach, pancreas, bladder, prostate, breast, uterus, or ovary.
Liu, J. *et al.* (20)	DPA	CHARGE consortium	% total increase in fatty acid	Lung cancer risk	ILCCO	Genetically predicted higher DPA was associated with an increased risk for lung cancer.
Shen, J. *et al.* (21)	Other PUFA than 18:2 in blood, DHA, DPA, EPA, AA, DGLA, and LA	Large GWAS (n = 24,925) from 14 cohorts in people of European ancestry and a GWAS (including 7,824 adult samples of European ancestry)	SD	Lung cancer, LUAD, and LUSC	ILCCO	Genetically predicted higher other PUFA than 18:2, DPA, EPA, and AA were associated with an increased risk for lung cancer.
Yang, Z. *et al.* (22)	ALA, EPA, DPA, DHA, LA, AA, POA, OA, PA, and SA	CHARGE consortium	SD	Breast cancer and prostate cancer	Breast Cancer Association Consortium, Prostate Cancer Association Group to Investigate Cancer-Associated Alterations in the Genome consortium	Genetically predicted ALA, EPA, DPA, DHA, LA, AA, POA, OA, PA, and SA were not associated with breast cancer or prostate cancer.
Guo, F. *et al.* (23)	SFA, MUFA, and PUFA	Large GWAS (n = 24,925) from 14 cohorts in people of European ancestry	SD	Breast cancer	The National Health and Nutrition Examination Survey	Genetically predicted MUFA was associated with a reduced risk of breast cancer.
Khankari, N., Murff, H., Zeng, C. *et al.* (24)	LA, AA, ALA, EPA, DPA, and DHA	CHARGE consortium	SD	Prostate cancer	Prostate Cancer Association Group to Investigate Cancer Associated Alterations in the Genome	Genetically predicted LA, AA, ALA, EPA, DPA, and DHA were not associated with prostate cancer risk.
Ghoneim, D. H. *et al.* (25)	LA, AA, AdrA, GLA, and DGLA	CHARGE consortium	SD	Pancreatic cancer	Pancreatic Cancer Cohort Consortium and the Pancreatic Cancer Case-Control Consortium	Genetically predicted LA, AA, AdrA, GLA, and DGLA were not associated with pancreatic cancer risk.
Seviiri, M. *et al.* (26)	ALA, EPA, DPA, DHA, AA, and LA	CHARGE consortium	SD	Keratinocyte cancer, BCC, and SCC	UK Biobank, 23andMe, and QSkin Sun and Health Study cohort	Genetically predicted higher AA and EPA were associated with a higher BCC risk. Genetically predicted higher LA and ALA were associated with a reduced BCC risk.

Khankari, N. K. et al. (27)	LA, AA, ALA, EPA, DPA, and DHA	CHARGE Consortium	% total increase in fatty acid	CRC	Colorectal Cancer Consortium	Genetically predicted higher AA, EPA, and DPA were associated with an increased CRC risk. Genetically predicted higher LA and ALA were associated with a reduced CRC risk.
May-Wilson, S. *et al.* (28)	EPA, DPA, DHA, LA, AA, DGLA, OA, POA, PA, and SA	CHARGE consortium	% total increase in fatty acid	CRC	Colon Cancer Family Registry, COIN trial, Finnish Colorectal Cancer Predisposition Study, colorectal Tumour Gene Identification Consortium, Colorectal Cancer Susceptibility Study, and VQ58	Genetically predicted higher AA and SA were associated with an increased CRC risk. Genetically predicted higher LA, OA, and POA were associated with reduced CRC risk.
Isom, C.A. *et al.* (29)	AA	Tennessee Colorectal Polyps Study	% total increase in fatty acid	Colorectal adenoma	Tennessee Colorectal Polyps Study	Genetically predicted AA was not associated with colorectal adenoma risk.
Liyanage, U. *et al.* (30)	EPA, DPA, DHA, ALA, AA, and LA	CHARGE consortium	SD	Melanoma	Melanoma risk meta-analysis consisting of 11 GWAS	Genetically predicted plasma EPA, DPA, DHA, ALA, AA, and LA were not associated with melanoma risk.
Saunders, C. N. *et al.* (31)	MUFA, omega-3, and omega-6 fatty acids	Large GWAS (n = 24,925) from 14 cohorts in people of European ancestry	SD	Glioma	A GWAS of glioma	Genetically predicted higher MUFA and omega-3 fatty acids were associated with a reduced glioma sk.
Yuan, S. *et al.* (32)	ALA, EPA, DPA, DHA, LA, AA, POA, OA, PA, and SA	CHARGE Consortium	SD	Fracture and eBMD	UK Biobank	Genetically predicted higher plasma ALA, LA, PA, and OA levels were associated with an increased eBMD risk. Genetic predisposition to higher plasma AA, EPA, DPA, and SA levels were associated with an increased risk of fracture. Genetically predicted higher ALA, LA, PA, and OA levels were associated with a reduced risk of fracture. Genetically predicted higher plasma AA, EPA, DPA, and SA levels were associated with a lower risk of eBMD. Genetically predicted plasma DHA and PA were not associated with the risk of eBMD or fracture.
Zhao, J. V., & Schooling, C. M. (33)	LA	CHARGE consortium	NA	RA and SLE	UK Biobank, Rheumatoid Arthritis Consortium, and ImmunoBase Consortium	Genetically predicted higher LA was associated with reduced risks of RA and SLE.
Sun, L. *et al.* (34)	POA and OA	CHARGE consortium	SD	RA and osteoarthritis	A trans-ethnic GWASs and UK Biobank	Genetically predicted higher plasma levels of POA and OA were associated with a lower RA

						risk. Genetically predicted plasma POA and OA were not associated with osteoarthritis risk.
Wang *et al.* (35)	LA and AA	CHARGE consortium	% total increase in total fatty acids	AMD	International AMD Genomics Consortium	Genetically predicted higher AA was associated with an increased AMD risk. Genetically predicted higher plasma LA was associated with a lower risk of AMD.
Carreras-Torres, R. *et al.* (36)	PUFA, omega-3 and omega-6 fatty acids, MUFA, and TFA	Large GWAS (n = 24,925) from 14 cohorts in people of European ancestry	SD	IBD, CD, and UC	IBD Genetics Consortium and the UK IBD Genetics Consortium	Genetically predicted higher omega-3 fatty acids levels were associated with a lower risk of CD.
Cheng, T. S. *et al.* (37)	DGLA and PA	EPIC–Potsdam Study	SD	Puberty timing	UK Biobank	Genetically predicted higher DGLA was associated with earlier menarche in girls.
Milaneschi, Y. *et al.* (38)	Omega-3 fatty acids	Large GWAS (n = 24,925) from 14 cohorts in people of European ancestry	SD	MDD	The Psychiatric Genomics Consortium	Genetically predicted omega-3 fatty acids were not associated with MDD risk.
Tomata *et al.* (39)	LA, AA, ALA, EPA, DPA, and DHA	CHARGE consortium	SD	Late-onset AD	Alzheimer Disease Genetics Consortium, CHARGE, The European Alzheimer's Disease Initiative, and Genetic and Environmental Risk in AD/Defining Genetic, Polygenic and Environmental Risk for Alzheimer's Disease Consortium	Genetically predicted LA, AA, ALA, EPA, DPA, and DHA were not associated with late-onset AD risk.
Wang, Z. *et al.* (40)	AA, cis-trans-18:2, DGLA, DPA, EPA, GLA, LA, PA, and SA	CHARGE consortium	SD	AD	International Genomics of Alzheimer's Project	Genetically predicted higher plasma LA was slightly associated with a lower risk of AD.
Jones, H. J. *et al.* (41)	ALA, EPA, DPA, DHA, LA, AA, and AdrA	CHARGE consortium	SD	Schizophrenia	Schizophrenia Working Group of the Psychiatric Genomics Consortium	Genetically predicted higher ALA was associated with the increased schizophrenia risk. Genetically predicted higher plasma DHA was associated with a lower risk of schizophrenia.
Sallis, H. *et al.* (42)	DHA and EPA	ALSPAC cohort	% total increase in total fatty acids	Perinatal onset depression, antenatal depression,	ALSPAC cohort	Genetically predicted EPA and DHA were not associated with depression risk.

				and postnatal depression.		
Thompson, A.D. *et al.* (43)	DHA, LA, omega-3, and omega-6 fatty acids	Large GWAS (n = 24,925) from 14 cohorts in people of European ancestry	SD	PE's and psychotic disorder	The Psychosis-LIKe Symptoms interview	Genetically predicted DHA, LA, omega-3, and omega-6 fatty acids were not associated with PE's or psychotic disorder.

LA: linoleic acid; AA, arachidonic acid; ALA, α-Linolenic acid; EPA, eicosapentaenoic acid; DPA, docosapentaenoic acid; DHA, docosahexaenoic acid; POA, palmitoleic acid; MA, myristoleic acid; OA, oleic acid; PA, palmitic acid; SA, stearic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AdrA, adrenic acid; MUFA, monounsaturated fatty acids; D5D, Δ5-desaturase; D6D, Δ6-desaturase; TOTFA, total fatty acids; PUFA, polyunsaturated fatty acids; SFA, saturated fatty acids; CHARGE, Cohorts for Heart and Aging Research in Genomic Epidemiology; FOS, Framingham Offspring Study; MESA, Multi-Ethnic Study of Atherosclerosis; EPIC, European Prospective Investigation into Cancer and Nutrition; ALSPAC, the Avon Longitudinal Study of Parents and Children; SD, standard deviation; IHD, ischemic heart disease; HDL-C, high-density lipoprotein cholesterol; LDL-C, low-density lipoprotein cholesterol; TC, total cholesterol; TG, triglycerides; BP, blood pressure; SBP, systolic blood pressure; DBP, diastolic blood pressure; ApoA-I, apolipoprotein A-I; ApoB, apolipoprotein B; CAD, coronary artery disease; AF, atrial fibrillation; IS, ischemic stroke; MI, myocardial infarction; CS, cardioembolic stroke; IS, ischemic stroke; ASCVD, atherosclerotic cardiovascular diseases; PAD, peripheral artery disease; CVD, cardiovascular diseases; VTE, venous thromboembolism; MI, myocardial infarction; AVC, aortic valve calcium; AS, aortic stenosis; T2DM, Type 2 diabetes; DI, insulin disposition index; PP, pulse pressure; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; BCC, basal cell carcinoma; SCC, squamous cell carcinoma; CRC, colorectal cancer; eBMD, estimated bone mineral density; RA, rheumatoid arthritis; SLE, systemic lupus erythematosus; AMD, age-related macular degeneration; IBD, inflammatory bowel diseases; CD, Crohn’s disease; UC, ulcerative colitis; MDD, major depressive disorder; AD, Alzheimer’s disease; PE's, later psychotic experiences; GLGC, Global Lipids Genetics Consortium; DIAGRAM, DIAbetes Genetics Replication And Meta-analysis; CARDIoGRAM, Coronary ARtery DIsease Genome wide Replication and Meta-analysis; ILCCO, International Lung Cancer Consortium.

Supplementary Table 2. STROBE Statement—checklist of items that should be included in reports of cohort studies.

	Item No.	Recommendation	Reported on page and line	Reported on section and paragraph
Title and abstract	1	(a) Indicate the study's design with a commonly used term in the title or the abstract	Page 1, lines 1-2; page 2, lines 25-26	Title: "Circulating polyunsaturated fatty acids and COVID-19: a prospective cohort study and Mendelian randomization analysis"; abstract, paragraph 3
		(b) Provide in the abstract an informative and balanced summary of what was done and what was found	Pages 2-3, lines 20-44	Abstract, paragraphs 1-5
Introduction				
Background/rationale	2	Explain the scientific background and rationale for the investigation being reported	Pages 4-5, lines 49-78	Introduction, paragraphs 1-2
Objectives	3	State specific objectives, including any prespecified hypotheses	Page 6, lines 93-97	Introduction, paragraph 4
Methods				
Study design	4	Present key elements of study design early in the paper	Page 7, lines 116-122	Methods, section of "Participants and study design"
Setting	5	Describe the setting, locations, and relevant dates, including periods of recruitment, exposure, follow-up, and data collection	Page 7, lines 116-122; pages 8-9, lines 134-147	Methods, section of "Participants and study design"; section of "Observational analysis"
Participants	6	(a) Give the eligibility criteria, and the sources and methods of selection of participants. Describe methods of follow-up	Page 7, lines 116-122; pages 8-9, lines 134-147	Methods, section of "Participants and study design"; section of "Observational analysis"; Figure 1
		(b) For matched studies, give matching criteria and number of exposed and unexposed	NA	NA
Variables	7	Clearly define all outcomes, exposures, predictors, potential confounders, and effect modifiers. Give diagnostic criteria, if applicable	Page 7, lines 116-122; pages 8-9, lines 147-156	Methods, section of "Participants and study design"; section of "Observational analysis"
Data sources/ measurement	8*	For each variable of interest, give sources of data and details of methods of assessment (measurement). Describe comparability of assessment methods if there is more than one group	Pages 8-9, lines 134-156	Methods, section of "Observational analysis"; Figure 1
Bias	9	Describe any efforts to address potential sources of bias	Page 8, lines 143-152	Methods, section of "Observational analysis"
Study size	10	Explain how the study size was arrived at	Pages 8-9, lines 134-152	Methods, section of "Observational analysis"; Figure 1

Quantitative variables	11	Explain how quantitative variables were handled in the analyses. If applicable, describe which groupings were chosen and why	Pages 9, lines 155-156	Methods, section of “Observational analysis”
Statistical methods	12	(a) Describe all statistical methods, including those used to control for confounding	Page 9, lines 152-156	Methods, section of “Observational analysis”
		(b) Describe any methods used to examine subgroups and interactions	Pages 8-9, lines 147-152	Methods, section of “Observational analysis”; Figure 1
		(c) Explain how missing data were addressed	Page 8, lines 156-157	Methods, section of “Observational analysis”; Figure 1
		(d) If applicable, explain how loss to follow-up was addressed	Pages 8-9, lines 134-138; 152-157	Methods, section of “Observational analysis”; Figure 1
		(e) Describe any sensitivity analyses	Pages 8-9, lines 147-152	Methods, section of “Observational analysis”
Results				
Participants	13*	(a) Report numbers of individuals at each stage of study—eg numbers potentially eligible, examined for eligibility, confirmed eligible, included in the study, completing follow-up, and analysed	Page 13, lines 229-239	Results, section of “Baseline characteristics”; Figure 1; Table 1
		(b) Give reasons for non-participation at each stage	Page 8, lines 156-157	Methods, section of “Observational analysis”
		(c) Consider use of a flow diagram	Page 13, lines 229-230	Results, section of “Baseline characteristics”; Figure 1
Descriptive data	14*	(a) Give characteristics of study participants (eg demographic, clinical, social) and information on exposures and potential confounders	Page 13, lines 229-239 and 241-245	Results, section of “Baseline characteristics” and “Observational association analysis”; Table 1
		(b) Indicate number of participants with missing data for each variable of interest	Page 8, lines 156-157; Page 13, lines 229-239 and 241-245	Methods, section of “Observational analysis” Results, section of “Baseline characteristics” and “Observational association analysis”; Figure 1; Table 1
		(c) Summarise follow-up time (eg, average and total amount)	NA	NA
Outcome data	15*	Report numbers of outcome events or summary measures over time	Page 13, lines 229-239; pages 13-14, lines 241-261	Results, section of “Baseline characteristics”; section of “Observational association analysis”; Figure 1; Tables 1-2
Main results	16	(a) Give unadjusted estimates and, if applicable, confounder-adjusted estimates and their precision (eg, 95%	Pages 13-14, lines 241-273	Results, section of “Observational association analysis”; Table 2

		confidence interval). Make clear which confounders were adjusted for and why they were included		
		(b) Report category boundaries when continuous variables were categorized	NA	NA
		(c) If relevant, consider translating estimates of relative risk into absolute risk for a meaningful time period	NA	NA
Other analyses	17	Report other analyses done—eg analyses of subgroups and interactions, and sensitivity analyses	Pages 13-14, lines 241-273	Results, section of "Observational association analysis"; Table 2
Discussion				
Key results	18	Summarise key results with reference to study objectives	Page 18, lines 331-335	Discussion, paragraph 1
Limitations	19	Discuss limitations of the study, taking into account sources of potential bias or imprecision. Discuss both direction and magnitude of any potential bias	Page 21, lines 413-421	Discussion, paragraph 5
Interpretation	20	Give a cautious overall interpretation of results considering objectives, limitations, multiplicity of analyses, results from similar studies, and other relevant evidence	Pages 18-19, lines 339-364	Discussion, paragraph 2
Generalisability	21	Discuss the generalisability (external validity) of the study results	Page 21, lines 418-419	Discussion, paragraph 5
Other information				
Funding	22	Give the source of funding and the role of the funders for the present study and, if applicable, for the original study on which the present article is based	Page 27, lines 604-609	Notes

*Give information separately for exposed and unexposed groups.

Note: An Explanation and Elaboration article discusses each checklist item and gives methodological background and published examples of transparent reporting. The STROBE checklist is best used in conjunction with this article (freely available on the Web sites of PLoS Medicine at http://www.plosmedicine.org/, Annals of Internal Medicine at http://www.annals.org/, and Epidemiology at http://www.epidem.com/). Information on the STROBE Initiative is available at http://www.strobe-statement.org.

Supplementary Table 3. STROBE-MR checklist.

Item	Complete/location
1. **Title and Abstract:** "Mendelian randomization" is named both in the title and the abstract	Title and abstract
Introduction	
2. **Background:** Explain the scientific background and rationale for the reported study. Is causality between exposure and outcome plausible? Justify why MR is a helpful method to address the study question.	Introduction, paragraphs 1-3
3. **Objectives:** State specific objectives clearly, including pre-specified causal hypotheses (if any).	Introduction, paragraph 4
Methods	
4. **Study design and data sources:** Present key elements of study design early in the paper. Consider including a table listing sources of data for all phases of the study. For each data source contributing to the analysis, describe the following: a) Describe the study design and the underlying population from which it was drawn. Describe also the setting, locations, and relevant dates, including periods of recruitment, exposure, follow-up, and data collection, if available. b) Give the eligibility criteria, and the sources and methods of selection of participants. c) Explain how the analyzed sample size was arrived at. d) Describe measurement, quality and selection of genetic variants. e) For each exposure, outcome and other relevant variables, describe methods of assessment and, in the case of diseases, the diagnostic criteria used. f) Provide details of ethics committee approval and participant informed consent, if relevant.	a) Methods, section of “Participants and study design” b) Methods, section of “Participants and study design” c) Methods, section of “Participants and study design”; section of “Genetic associations with PUFAs”; section of “Genetic associations with COVID-19” d) Methods, section of “Genetic associations with PUFAs”; section of “Genetic associations with COVID-19” e) Methods, section of “Genetic associations with PUFAs”; section of “Genetic associations with COVID-19” f) Methods, section of “Ethical considerations”
5. **Assumptions:** Explicitly state assumptions for the main analysis (e.g. relevance, exclusion, independence, homogeneity) as well assumptions for any additional or sensitivity analysis.	Methods, section of “Genetic associations with PUFAs”; section of “Genetic associations with COVID-19”; section of “MR analyses”
6. **Statistical methods main analysis** Describe statistical methods and statistics used. a) Describe how quantitative variables were handled in the analyses (i.e., scale, units, model). b) Describe the process for identifying genetic variants and weights to be included in the analyses (i.e, independence and model). Consider a flow diagram.	a) Methods, section of “Genetic associations with PUFAs”; section of “Genetic associations with COVID-19”

c) Describe the MR estimator, e.g. two-stage least squares, Wald ratio, and related statistics. Detail the included covariates and, in case of two-sample MR, whether the same covariate set was used for adjustment in the two samples. d) Explain how missing data were addressed. e) If applicable, say how multiple testing was dealt with.	b) Methods, section of "Genetic associations with PUFAs"; section of "Genetic associations with COVID-19" c) Methods, section of "MR analyses" d) NA e) Methods, section of "MR analyses"
7. Assessment of assumptions: Describe any methods used to assess the assumptions or justify their validity.	Methods, section of "MR analyses"
8. Sensitivity analyses: Describe any sensitivity analyses or additional analyses performed.	Methods, section of "MR analyses"
9. Software and pre-registration a) Name statistical software and package(s), including version and settings used. b) State whether the study protocol and details were pre-registered (as well as when and where).	a) Methods, section of section of "MR analyses" b) Data availability
Results	
10. Descriptive data a) Report the numbers of individuals at each stage of included studies and reasons for exclusion. Consider use of a flow-diagram. b) Report summary statistics for phenotypic exposure(s), outcome(s) and other relevant variables (e.g. means, standard deviations, proportions). c) If the data sources include meta-analyses of previous studies, provide the number of studies, their reported ancestry, if available, and assessments of heterogeneity across these studies. Consider using a supplementary table for each data source. d) For two-sample Mendelian randomization: i. Provide information on the similarity of the genetic variant-exposure associations between the exposure and outcome samples. ii. Provide information on extent of sample overlap between the exposure and outcome data sources.	a) Results, section of "Bidirectional MR analyses" b) Results, section of "Bidirectional MR analyses"; Supplementary Tables 4-5 c) Results, section of "Bidirectional MR analyses" d) Results, section of "Bidirectional MR analyses"
11. Main results a) Report the associations between genetic variant and exposure, and between genetic variant and outcome, preferably on an interpretable scale (e.g. comparing 25th and 75th percentile of allele count or genetic risk score, if individual-level data available). b) Report causal effect estimate between exposure and outcome, and the measures of uncertainty from the MR analysis. Use an intuitive scale, such as odds ratio, or relative risk, per standard deviation difference.	a) Results, section of "Bidirectional MR analyses" b) Results, section of "Bidirectional MR analyses"; Supplementary Tables 6-29 c) NA d) Figures 2-3

c) If relevant, consider translating estimates of relative risk into absolute risk for a meaningful time-period. d) Consider any plots to visualize results (e.g. forest plot, scatterplot of associations between genetic variants and outcome versus between genetic variants and exposure).	
12. Assessment of assumptions a) Assess the validity of the assumptions. b) Report any additional statistics (e.g., assessments of heterogeneity, such as I2, Q statistic).	a) Results, section of "Bidirectional MR analyses"; Supplementary Tables 6-29 b) Results, section of "Bidirectional MR analyses"; Supplementary Tables 6-29
13. Sensitivity and additional analyses a) Use sensitivity analyses to assess the robustness of the main results to violations of the assumptions. b) Report results from other sensitivity analyses (e.g., replication study with different dataset, analyses of subgroups, validation of instrument(s), simulations, etc.). c) Report any assessment of direction of causality (e.g., bidirectional MR). d) When relevant, report and compare with estimates from non-MR analyses. e) Consider any additional plots to visualize results (e.g., leave-one-out analyses).	a) Results, section of "Bidirectional MR analyses"; Supplementary Tables 6-29 b) Results, section of "Bidirectional MR analyses"; Supplementary Tables 6-29 c) Results, section of "Bidirectional MR analyses"; Supplementary Tables 14-29 d) Results, section of "Observational analysis"; Table 2 e) Figures 2-3
Discussion	
14. Key results	Discussion, paragraph 1
15. Limitations Discuss limitations of the study, taking into account the validity of the MR assumptions, other sources of potential bias, and imprecision. Discuss both direction and magnitude of any potential bias, and any efforts to address them.	Discussion, paragraph 5
16. Interpretations a) Give a cautious overall interpretation of results considering objectives and limitations. Compare with results from other relevant studies. b) Discuss underlying biological mechanisms that could be modelled by using the genetic variants to assess the relationship between the exposure and the outcome. c) Discuss whether the results have clinical or policy relevance, and whether interventions could have the same size effect.	a) Discussion, paragraphs 2-3 b) Discussion, paragraphs 2-3 c) Discussion, paragraph 2
17. Generalizability:	Discussion, paragraph 5
18. Funding:	Notes

19. Data and data sharing:	Data availability
20. Conflicts of Interest:	Acknowledgments

Supplementary Table 4. Genetic instruments for plasma polyunsaturated fatty acids.

PUFA	SNP	Chr	Position (BP)	Nearest gene	Effect allele	Non effect allele	EAF	Beta	SE	P-value
ALA	rs174547	11	61570783	*FADS1*	C	T	0.33124	0.016	0.001	3.50×10^{-641}
LA	rs10740118	10	65101207	*JMJD1C*	C	G	0.407725	-0.248	0.043	8.10×10^{-9}
LA	rs174547	11	61570783	*FADS1*	C	T	0.33124	1.474	0.042	5.00×10^{-274}
LA	rs16966952	16	15135943	*NTAN1*	A	G	0.279871	-0.351	0.044	1.20×10^{-15}
GLA	rs174547	11	61570783	*FADS1*	C	T	0.33124	-0.016	0.001	2.30×10^{-72}
GLA	rs16966952	16	15135943	*PDXDC1*	A	G	0.279871	-0.0061	0.001	5.00×10^{-11}
DGLA	rs174547	11	61570783	*FADS1*	C	T	0.33124	0.36	0.01	2.60×10^{-151}
DGLA	rs16966952	16	15135943	*PDXDC1*	A	G	0.279871	-0.22	0.02	7.60×10^{-15}
AA	rs174547	11	61570783	*FADS1*	C	T	0.33124	-1.691	0.025	3×10^{-971}
AA	rs16966952	16	15135943	*NTAN1*	A	G	0.279871	-0.199	0.031	2.40×10^{-10}
DPA-n3	rs780094	2	27741237	*GCKR*	T	C	0.447679	0.017	0.003	9.04×10^{-9}
DPA-n3	rs3734398	6	10982973	*ELOVL2*	C	T	0.434361	0.04	0.003	9.60×10^{-44}
DPA-n3	rs174547	11	61570783	*FADS1*	T	C	0.66876	0.075	0.003	3.80×10^{-154}
DHA	rs2236212	6	10995015	*ELOVL2*	G	C	0.569	0.113	0.014	1.30×10^{-15}

PUFA, polyunsaturated fatty acid; SNP, single nucleotide polymorphism; Chr, chromosome; EAF, Effect allele frequency; SE, standard error. For each PUFA, we selected SNPs that reached genome-wide significance level ($P < 5 \times 10^{-8}$) and were restricted by linkage disequilibrium (LD) clumping to ensure independence ($R^2 < 0.001$ within a 10 Mb window).

Supplementary Table 5. Significant SNPs for red blood cell polyunsaturated fatty acids.

PUFA	SNP	Chr	Position (BP)	Nearest gene	Effect allele	Non effect allele	EAF	Beta	SE	P-value
ALA	rs174548	11	61571348	*FADS1*	C	G	0.69996	-0.031079453	0.005544021	2.10×10^{-8}
ALA	rs1535	11	61597972	*FADS2*	A	G	0.66595	-0.030344391	0.005554751	4.70×10^{-8}
ALA	rs174574	11	61600342	*FADS2*	C	A	0.63796	-0.030961912	0.005666031	4.60×10^{-8}
LA	rs174550	11	61571478	*FADS1*	T	C	0.67143	-0.025923175	0.001983862	$<1\times10^{-16}$
LA	rs174547	11	61570783	*FADS1*	T	C	0.67136	-0.025924923	0.001983583	$<1\times10^{-16}$
LA	rs174546	11	61569830	*FADS1*	C	T	0.67116	-0.02592704	0.001984449	$<1\times10^{-16}$
LA	rs174545	11	61569306	*FADS1*	C	G	0.6711	-0.025927951	0.001984711	$<1\times10^{-16}$
LA	rs174541	11	61565908		T	C	0.65148	-0.026187705	0.002005041	$<1\times10^{-16}$
LA	rs4246215	11	61564299	*FEN1*	G	T	0.65088	-0.02618057	0.002007268	$<1\times10^{-16}$
LA	rs174549	11	61571382	*FADS1*	G	A	0.70775	-0.026380702	0.002034896	$<1\times10^{-16}$
LA	rs174555	11	61579760	*FADS1*	T	C	0.70764	-0.026513764	0.002047489	$<1\times10^{-16}$
LA	rs174556	11	61580635	*FADS1*	C	T	0.70764	-0.026518518	0.002048022	$<1\times10^{-16}$
LA	rs174548	11	61571348	*FADS1*	C	G	0.69996	-0.026169921	0.0020244	$<1\times10^{-16}$
LA	rs1535	11	61597972	*FADS2*	A	G	0.66595	-0.02613899	0.002025075	$<1\times10^{-16}$
LA	rs174537	11	61552680	*C11orf9*	G	T	0.66488	-0.025442966	0.00200945	$<1\times10^{-16}$
LA	rs174576	11	61603510	*FADS2*	C	A	0.65841	-0.025850504	0.0020428	$<1\times10^{-16}$
LA	rs174535	11	61551356	*C11orf9*	T	C	0.65839	-0.025365057	0.002007878	$<1\times10^{-16}$
LA	rs174536	11	61551927	*C11orf9*	A	C	0.66386	-0.025322394	0.002009214	$<1\times10^{-16}$
LA	rs174577	11	61604814	*FADS2*	C	A	0.6524	-0.025577242	0.002040915	$<1\times10^{-16}$
LA	rs174574	11	61600342	*FADS2*	C	A	0.63796	-0.025861826	0.002072471	$<1\times10^{-16}$
LA	rs174578	11	61605499	*FADS2*	T	A	0.65154	-0.025095132	0.002039835	$<1\times10^{-16}$
LA	rs102275	11	61557803	*C11orf10*	T	C	0.62686	-0.02551658	0.002076206	$<1\times10^{-16}$
LA	rs174583	11	61609750	*FADS2*	C	T	0.65299	-0.025052255	0.002052984	$<1\times10^{-16}$
LA	rs174538	11	61560081	*C11orf10*	G	A	0.69487	-0.024581334	0.002023435	$<1\times10^{-16}$
LA	rs174528	11	61543499	*C11orf9*	T	C	0.61669	-0.023670615	0.002054035	$<1\times10^{-16}$
LA	rs174601	11	61623140	*FADS2*	C	T	0.61373	-0.024275521	0.002151782	$<1\times10^{-16}$
LA	rs108499	11	61547237	*C11orf9*	C	T	0.67142	-0.021955949	0.002013526	$<1\times10^{-16}$
LA	rs174534	11	61549458	*C11orf9*	A	G	0.66316	-0.020878982	0.001958043	$<1\times10^{-16}$
LA	rs174575	11	61602003	*FADS2*	C	G	0.7332	-0.02085927	0.002270508	$<1\times10^{-16}$
LA	rs174593	11	61618831	*FADS2*	T	C	0.7208	-0.019803494	0.002267427	$<1\times10^{-16}$
LA	rs174579	11	61605613	*FADS2*	C	T	0.78402	-0.019710352	0.002352998	$<1\times10^{-16}$
LA	rs174591	11	61617676	*FADS2*	T	A	0.71832	-0.019329175	0.002308087	$<1\times10^{-16}$
LA	rs968567	11	61595564	*FADS2*	C	T	0.83527	-0.022516292	0.002717439	1.10×10^{-16}

LA	rs174585	11	61611694	*FADS2*	G	A	0.78304	-0.019280656	0.002340284	2.20×10^{-16}
LA	rs174448	11	61639573		A	G	0.64303	-0.01629102	0.002011707	5.60×10^{-16}
LA	rs174570	11	61597212	*FADS2*	C	T	0.86422	-0.023734742	0.002960526	1.10×10^{-15}
LA	rs174589	11	61615803	*FADS2*	C	G	0.78765	-0.018654832	0.002330472	1.20×10^{-15}
LA	rs422249	11	61639488		C	T	0.67098	-0.016220448	0.002071517	4.90×10^{-15}
LA	rs174605	11	61626921	*FADS2*	G	T	0.71151	-0.016218161	0.002074222	5.30×10^{-15}
LA	rs174597	11	61621040	*FADS2*	G	C	0.74735	-0.018547979	0.002373894	5.60×10^{-15}
LA	rs174611	11	61627881	*FADS2*	T	C	0.71039	-0.01626599	0.002083075	5.80×10^{-15}
LA	rs174449	11	61640379		A	G	0.63271	-0.015007949	0.001941676	1.10×10^{-14}
LA	rs509360	11	61548559	*C11orf9*	G	A	0.649	0.019146856	0.002509696	2.40×10^{-14}
LA	rs2269928	11	61537529	*C11orf9*	T	G	0.77978	-0.020839115	0.002805667	1.10×10^{-13}
LA	rs2727270	11	61603237	*FADS2*	C	T	0.89029	-0.022241527	0.002996633	1.20×10^{-13}
LA	rs2727271	11	61603358	*FADS2*	A	T	0.89	-0.022240948	0.002998407	1.20×10^{-13}
LA	rs174627	11	61637466		G	A	0.835	-0.019385566	0.002750477	1.80×10^{-12}
LA	rs2524299	11	61604782	*FADS2*	A	T	0.88064	-0.021077959	0.003019821	3.00×10^{-12}
LA	rs174479	11	61678754	*RAB3IL1*	C	G	0.81614	-0.019966658	0.002868303	3.40×10^{-12}
LA	rs2845573	11	61601908	*FADS2*	A	G	0.92668	-0.025076609	0.003623849	4.50×10^{-12}
LA	rs2072114	11	61605215	*FADS2*	A	G	0.8814	-0.020285664	0.002962778	7.50×10^{-12}
LA	rs174455	11	61656117	*FADS3*	G	A	0.36538	0.013278008	0.001944147	8.50×10^{-12}
LA	rs2851682	11	61616012	*FADS2*	A	G	0.92129	-0.026018	0.003862008	1.60×10^{-11}
LA	rs174616	11	61629122	*FADS2*	G	A	0.52756	-0.012926856	0.001927302	2.00×10^{-11}
LA	rs174532	11	61548874	*C11orf9*	G	A	0.72114	0.017458535	0.002616894	2.50×10^{-11}
LA	rs174626	11	61637057		A	G	0.52886	-0.01304876	0.001959376	2.70×10^{-11}
LA	rs174450	11	61641542	*FADS3*	G	T	0.47314	0.013061701	0.001993513	5.70×10^{-11}
LA	rs198462	11	61524119	*C11orf9*	G	A	0.48644	0.012838099	0.001984777	9.90×10^{-11}
LA	rs198476	11	61525730	*C11orf9*	G	A	0.47167	0.01298316	0.002038935	1.90×10^{-10}
LA	rs198464	11	61521621		G	A	0.48411	0.012173434	0.001915542	2.10×10^{-10}
LA	rs412334	11	61560261	*FEN1*	C	T	0.85305	0.026964394	0.004252483	2.30×10^{-10}
LA	rs174634	11	61647387	*FADS3*	C	G	0.72588	-0.013223298	0.002151382	7.90×10^{-10}
LA	rs174464	11	61657926	*FADS3*	G	A	0.72982	-0.013261427	0.002186526	1.30×10^{-9}
LA	rs1000778	11	61655305	*FADS3*	G	A	0.72904	-0.012692579	0.00211719	2.00×10^{-9}
LA	rs174456	11	61656182	*FADS3*	A	C	0.72918	-0.012665509	0.002115463	2.10×10^{-9}
LA	rs2526678	11	61623793	*FADS2*	G	A	0.93057	-0.026337496	0.004428129	2.70×10^{-9}
LA	rs149803	11	61539020	*C11orf9*	C	G	0.74636	0.015625177	0.002763177	1.60×10^{-8}
LA	rs12580543	12	7100973	*MBOAT5*	A	C	0.93596	-0.045842834	0.0039947	$<1\times10^{-16}$
LA	rs4394918	12	7110335	*MBOAT5*	C	A	0.93926	-0.04537712	0.004016596	$<1\times10^{-16}$

LA	rs16928105	12	7114196	*MBOAT5*	C	T	0.93917	-0.045109814	0.00400763	$<1\times10^{-16}$
LA	rs1984564	12	7090193	*MBOAT5*	A	G	0.91021	-0.036294608	0.003302183	$<1\times10^{-16}$
LA	rs7952839	12	7110571	*MBOAT5*	G	A	0.90923	-0.036105147	0.003312813	$<1\times10^{-16}$
LA	rs12582990	12	7145853		T	C	0.90538	-0.037264689	0.003452779	$<1\times10^{-16}$
LA	rs16933023	12	7107348	*MBOAT5*	C	G	0.9166	-0.037045099	0.003512866	$<1\times10^{-16}$
LA	rs12580233	12	7124522	*MBOAT5*	T	C	0.91542	-0.036368727	0.003485457	$<1\times10^{-16}$
LA	rs16933011	12	7073805		G	T	0.91316	-0.036528813	0.003541195	$<1\times10^{-16}$
LA	rs3764031	12	7091918	*MBOAT5*	C	T	0.91377	-0.035061406	0.003409011	$<1\times10^{-16}$
LA	rs7311050	12	7120836	*MBOAT5*	C	T	0.91388	-0.03495796	0.003409288	$<1\times10^{-16}$
LA	rs2110073	12	7075882	*PHB2*	C	T	0.89587	-0.031198306	0.003100397	$<1\times10^{-16}$
LA	rs7962738	12	7166672	*C1S*	T	A	0.94463	-0.040285903	0.004311937	$<1\times10^{-16}$
LA	rs12579775	12	7085171		G	A	0.90521	-0.030763165	0.003293403	$<1\times10^{-16}$
LA	rs759052	12	7069620	*PTPN6*	C	T	0.8603	-0.029867787	0.003337284	$<1\times10^{-16}$
LA	rs11064497	12	7169661	*C1S*	C	T	0.86151	-0.017528017	0.002841673	6.90×10^{-10}
LA	rs12368181	12	7181105		A	G	0.86823	-0.017538707	0.002862766	9.00×10^{-10}
LA	rs12366520	12	7181162		C	A	0.8682	-0.017532536	0.002863014	9.10×10^{-10}
LA	rs12146727	12	7170336	*C1S*	G	A	0.86979	-0.017143651	0.002814623	1.10×10^{-9}
LA	rs16933078	12	7171338	*C1S*	T	A	0.86831	-0.017158756	0.002818129	1.10×10^{-9}
LA	rs16933084	12	7172084	*C1S*	A	T	0.86906	-0.017078607	0.002814758	1.30×10^{-9}
LA	rs11838267	12	7175872	*C1S*	T	C	0.86788	-0.017089309	0.002813916	1.30×10^{-9}
LA	rs12368783	12	7179400		G	T	0.86858	-0.017239953	0.002841371	1.30×10^{-9}
LA	rs7962629	12	7166770	*C1S*	A	G	0.86456	-0.017224081	0.002842693	1.40×10^{-9}
LA	rs11064501	12	7179822		A	C	0.86691	-0.017250584	0.002845788	1.30×10^{-9}
LA	rs10849546	12	7176204	*C1S*	G	A	0.86876	-0.01702788	0.002813537	1.40×10^{-9}
LA	rs12371227	12	7176978	*C1S*	C	T	0.86834	-0.017016845	0.002810648	1.40×10^{-9}
LA	rs7183	12	7178019	*C1S*	G	T	0.86851	-0.017045684	0.002816664	1.40×10^{-9}
LA	rs11064498	12	7171507	*C1S*	A	G	0.85324	-0.016734174	0.002842967	4.00×10^{-9}
LA	rs3919533	12	7162801		T	C	0.83695	-0.015492514	0.002653374	5.30×10^{-9}
LA	rs7311672	12	7165114		G	A	0.83872	-0.014988034	0.002629557	1.20×10^{-8}
GLA	rs174548	11	61571348	*FADS1*	C	G	0.69996	0.056093204	0.008052263	3.30×10^{-12}
GLA	rs174549	11	61571382	*FADS1*	G	A	0.70775	0.05399605	0.008102706	2.70×10^{-11}
GLA	rs174555	11	61579760	*FADS1*	T	C	0.70764	0.054235078	0.008152221	2.90×10^{-11}
GLA	rs174556	11	61580635	*FADS1*	C	T	0.70764	0.054246393	0.008154209	2.90×10^{-11}
GLA	rs4246215	11	61564299	*FEN1*	G	T	0.65088	0.051586938	0.008006419	1.20×10^{-11}
GLA	rs174541	11	61565908		T	C	0.65148	0.051462442	0.007998025	1.20×10^{-10}
GLA	rs174535	11	61551356	*C11orf9*	T	C	0.65839	0.051333021	0.007993626	1.30×10^{-10}

GLA	rs102275	11	61557803	*C11orf10*	T	C	0.62686	0.052391657	0.008240345	2.00×10^{-10}
GLA	rs174574	11	61600342	*FADS2*	C	A	0.63796	0.05204465	0.00824537	2.80×10^{-10}
GLA	rs1535	11	61597972	*FADS2*	A	G	0.66595	0.050795864	0.008081966	3.30×10^{-10}
GLA	rs174577	11	61604814	*FADS2*	C	A	0.6524	0.050837053	0.008124732	3.90×10^{-10}
GLA	rs174578	11	61605499	*FADS2*	T	A	0.65154	0.050440978	0.008113275	5.10×10^{-10}
GLA	rs174536	11	61551927	*C11orf9*	A	C	0.66386	0.049696809	0.008001506	5.30×10^{-10}
GLA	rs174537	11	61552680	*C11orf9*	G	T	0.66488	0.049704656	0.008006979	5.40×10^{-10}
GLA	rs174550	11	61571478	*FADS1*	T	C	0.67143	0.049090576	0.007921297	5.70×10^{-10}
GLA	rs174545	11	61569306	*FADS1*	C	G	0.6711	0.049037087	0.007925609	6.10×10^{-10}
GLA	rs174546	11	61569830	*FADS1*	C	T	0.67116	0.049019012	0.007924646	6.20×10^{-10}
GLA	rs174547	11	61570783	*FADS1*	T	C	0.67136	0.048973853	0.007921437	6.30×10^{-10}
GLA	rs174576	11	61603510	*FADS2*	C	A	0.65841	0.050172662	0.008139624	7.10×10^{-10}
GLA	rs174583	11	61609750	*FADS2*	C	T	0.65299	0.049850145	0.00816299	1.00×10^{-9}
GLA	rs174528	11	61543499	*C11orf9*	T	C	0.61669	0.049271281	0.008126065	1.30×10^{-9}
DGLA	rs174555	11	61579760	*FADS1*	T	C	0.70764	-0.093383417	0.002276368	$<1\times10^{-16}$
DGLA	rs174556	11	61580635	*FADS1*	C	T	0.70764	-0.093407652	0.002276937	$<1\times10^{-16}$
DGLA	rs174549	11	61571382	*FADS1*	G	A	0.70775	-0.092786816	0.002263023	$<1\times10^{-16}$
DGLA	rs174548	11	61571348	*FADS1*	C	G	0.69996	-0.092279425	0.002252042	$<1\times10^{-16}$
DGLA	rs174538	11	61560081	*C11orf10*	G	A	0.69487	-0.089612614	0.002277243	$<1\times10^{-16}$
DGLA	rs174545	11	61569306	*FADS1*	C	G	0.6711	-0.087925132	0.002250125	$<1\times10^{-16}$
DGLA	rs174550	11	61571478	*FADS1*	T	C	0.67143	-0.087877368	0.002249418	$<1\times10^{-16}$
DGLA	rs174546	11	61569830	*FADS1*	C	T	0.67116	-0.087912789	0.002249869	$<1\times10^{-16}$
DGLA	rs174547	11	61570783	*FADS1*	T	C	0.67136	-0.087868043	0.002249103	$<1\times10^{-16}$
DGLA	rs1535	11	61597972	*FADS2*	A	G	0.66595	-0.089394544	0.002298171	$<1\times10^{-16}$
DGLA	rs174537	11	61552680	*C11orf9*	G	T	0.66488	-0.088477735	0.0022804	$<1\times10^{-16}$
DGLA	rs174536	11	61551927	*C11orf9*	A	C	0.66386	-0.088243053	0.002282768	$<1\times10^{-16}$
DGLA	rs174535	11	61551356	*C11orf9*	T	C	0.65839	-0.08813322	0.00228418	$<1\times10^{-16}$
DGLA	rs174541	11	61565908		T	C	0.65148	-0.08718654	0.002300447	$<1\times10^{-16}$
DGLA	rs4246215	11	61564299	*FEN1*	G	T	0.65088	-0.087265838	0.002302899	$<1\times10^{-16}$
DGLA	rs174574	11	61600342	*FADS2*	C	A	0.63796	-0.089774642	0.002372438	$<1\times10^{-16}$
DGLA	rs174577	11	61604814	*FADS2*	C	A	0.6524	-0.088450038	0.002337515	$<1\times10^{-16}$
DGLA	rs174576	11	61603510	*FADS2*	C	A	0.65841	-0.088521769	0.002340525	$<1\times10^{-16}$
DGLA	rs102275	11	61557803	*C11orf10*	T	C	0.62686	-0.089486222	0.002382655	$<1\times10^{-16}$
DGLA	rs174578	11	61605499	*FADS2*	T	A	0.65154	-0.08766831	0.002343702	$<1\times10^{-16}$
DGLA	rs174583	11	61609750	*FADS2*	C	T	0.65299	-0.087686767	0.002364368	$<1\times10^{-16}$
DGLA	rs108499	11	61547237	*C11orf9*	C	T	0.67142	-0.083095987	0.002342602	$<1\times10^{-16}$

DGLA	rs174528	11	61543499	*C11orf9*	T	C	0.61669	-0.084062886	0.002413168	$<1\times10^{-16}$
DGLA	rs174534	11	61549458	*C11orf9*	A	G	0.66316	-0.079069068	0.002300709	$<1\times10^{-16}$
DGLA	rs968567	11	61595564	*FADS2*	C	T	0.83527	-0.108510323	0.003158099	$<1\times10^{-16}$
DGLA	rs174601	11	61623140	*FADS2*	C	T	0.61373	-0.084828533	0.002568194	$<1\times10^{-16}$
DGLA	rs174579	11	61605613	*FADS2*	C	T	0.78402	-0.08787706	0.00282469	$<1\times10^{-16}$
DGLA	rs174585	11	61611694	*FADS2*	G	A	0.78304	-0.086669437	0.002816734	$<1\times10^{-16}$
DGLA	rs174575	11	61602003	*FADS2*	C	G	0.7332	-0.083882013	0.002750669	$<1\times10^{-16}$
DGLA	rs174589	11	61615803	*FADS2*	C	G	0.78765	-0.084379029	0.002825277	$<1\times10^{-16}$
DGLA	rs174591	11	61617676	*FADS2*	T	A	0.71832	-0.080976985	0.002834895	$<1\times10^{-16}$
DGLA	rs174593	11	61618831	*FADS2*	T	C	0.7208	-0.077790899	0.002813594	$<1\times10^{-16}$
DGLA	rs174597	11	61621040	*FADS2*	G	C	0.74735	-0.079166265	0.002959683	$<1\times10^{-16}$
DGLA	rs174627	11	61637466		G	A	0.835	-0.081359634	0.003515982	$<1\times10^{-16}$
DGLA	rs2269928	11	61537529	*C11orf9*	T	G	0.77978	-0.080790453	0.003623491	$<1\times10^{-16}$
DGLA	rs509360	11	61548559	*C11orf9*	G	A	0.649	0.070454333	0.003264146	$<1\times10^{-16}$
DGLA	rs174611	11	61627881	*FADS2*	T	C	0.71039	-0.057047069	0.002721521	$<1\times10^{-16}$
DGLA	rs174605	11	61626921	*FADS2*	G	T	0.71151	-0.056782086	0.002710525	$<1\times10^{-16}$
DGLA	rs174448	11	61639573		A	G	0.64303	-0.052877561	0.002655524	$<1\times10^{-16}$
DGLA	rs422249	11	61639488		C	T	0.67098	-0.053451571	0.00273317	$<1\times10^{-16}$
DGLA	rs174449	11	61640379		A	G	0.63271	-0.050106436	0.002567625	$<1\times10^{-16}$
DGLA	rs174469	11	61667443	*RAB3IL1*	C	T	0.82555	-0.067713817	0.00367945	$<1\times10^{-16}$
DGLA	rs174479	11	61678754	*RAB3IL1*	C	G	0.81614	-0.06773423	0.003816048	$<1\times10^{-16}$
DGLA	rs174634	11	61647387	*FADS3*	C	G	0.72588	-0.050487213	0.00286443	$<1\times10^{-16}$
DGLA	rs526126	11	61624885	*FADS2*	C	G	0.76593	-0.072444969	0.004129038	$<1\times10^{-16}$
DGLA	rs174464	11	61657926	*FADS3*	G	A	0.72982	-0.04998859	0.002920249	$<1\times10^{-16}$
DGLA	rs1000778	11	61655305	*FADS3*	G	A	0.72904	-0.048000579	0.002829881	$<1\times10^{-16}$
DGLA	rs174456	11	61656182	*FADS3*	A	C	0.72918	-0.047889577	0.002828034	$<1\times10^{-16}$
DGLA	rs174532	11	61548874	*C11orf9*	G	A	0.72114	0.058842315	0.003511758	$<1\times10^{-16}$
DGLA	rs174455	11	61656117	*FADS3*	G	A	0.36538	0.042120936	0.002625943	$<1\times10^{-16}$
DGLA	rs412334	11	61560261	*FEN1*	C	T	0.85305	0.084373277	0.005760646	$<1\times10^{-16}$
DGLA	rs174616	11	61629122	*FADS2*	G	A	0.52756	-0.038302878	0.002618867	$<1\times10^{-16}$
DGLA	rs174626	11	61637057		A	G	0.52886	-0.038773801	0.002662012	$<1\times10^{-16}$
DGLA	rs174450	11	61641542	*FADS3*	G	T	0.47314	0.038438145	0.002713908	$<1\times10^{-16}$
DGLA	rs149803	11	61539020	*C11orf9*	C	G	0.74636	0.051444004	0.003767124	$<1\times10^{-16}$
DGLA	rs174570	11	61597212	*FADS2*	C	T	0.86422	-0.054262313	0.004080799	$<1\times10^{-16}$
DGLA	rs198462	11	61524119	*C11orf9*	G	A	0.48644	0.032261333	0.00275405	$<1\times10^{-16}$
DGLA	rs198464	11	61521621		G	A	0.48411	0.030068552	0.002661756	$<1\times10^{-16}$

DGLA	rs7102974	11	61560035	*C11orf10*	C	T	0.97886	-0.125814384	0.011223658	$<1\times10^{-16}$
DGLA	rs198476	11	61525730	*C11orf9*	G	A	0.47167	0.031434935	0.002835967	$<1\times10^{-16}$
DGLA	rs498793	11	61624705	*FADS2*	C	T	0.60008	0.045940115	0.004146446	$<1\times10^{-16}$
DGLA	rs174468	11	61663691		G	A	0.60365	0.034164486	0.003117167	$<1\times10^{-16}$
DGLA	rs2845573	11	61601908	*FADS2*	A	G	0.92668	-0.054916984	0.005041632	$<1\times10^{-16}$
DGLA	rs2851682	11	61616012	*FADS2*	A	G	0.92129	-0.057949708	0.00537644	$<1\times10^{-16}$
DGLA	rs198473	11	61526556	*C11orf9*	A	G	0.74785	-0.035487193	0.003376086	$<1\times10^{-16}$
DGLA	rs174476	11	61674118	*RAB3IL1*	C	T	0.60208	0.033121705	0.00318768	$<1\times10^{-16}$
DGLA	rs174478	11	61678576	*RAB3IL1*	T	G	0.60099	0.033154421	0.003200503	$<1\times10^{-16}$
DGLA	rs174602	11	61624414	*FADS2*	T	C	0.76774	-0.045141254	0.004359976	$<1\times10^{-16}$
DGLA	rs666870	11	61677479	*RAB3IL1*	G	A	0.6013	0.033122844	0.003199448	$<1\times10^{-16}$
DGLA	rs198475	11	61526071	*C11orf9*	C	T	0.75215	-0.034406845	0.003339929	$<1\times10^{-16}$
DGLA	rs13966	11	61664992	*RAB3IL1*	C	T	0.54676	0.031902864	0.003191463	$<1\times10^{-16}$
DGLA	rs2235093	11	61665122	*RAB3IL1*	G	A	0.54967	0.031732481	0.003194219	$<1\times10^{-16}$
DGLA	rs579383	11	61536583	*C11orf9*	A	G	0.57529	0.030046342	0.00304175	$<1\times10^{-16}$
DGLA	rs2727270	11	61603237	*FADS2*	C	T	0.89029	-0.041144884	0.004187134	$<1\times10^{-16}$
DGLA	rs2727271	11	61603358	*FADS2*	A	T	0.89	-0.041055738	0.004190331	$<1\times10^{-16}$
DGLA	rs650436	11	61536430	*C11orf9*	C	T	0.57937	0.029706454	0.003050024	$<1\times10^{-16}$
DGLA	rs2526678	11	61623793	*FADS2*	G	A	0.93057	-0.059961422	0.006165896	$<1\times10^{-16}$
DGLA	rs198446	11	61503381	*DAGLA*	G	A	0.74811	-0.03169164	0.003313523	$<1\times10^{-16}$
DGLA	rs2072114	11	61605215	*FADS2*	A	G	0.8814	-0.039457728	0.004132432	$<1\times10^{-16}$
DGLA	rs1692120	11	61417472		G	A	0.56219	0.03328641	0.003663514	$<1\times10^{-16}$
DGLA	rs174472	11	61671956	*RAB3IL1*	G	A	0.45428	0.0295229	0.00325842	$<1\times10^{-16}$
DGLA	rs740006	11	61557868	*C11orf10*	T	C	0.91448	0.059024656	0.006536418	$<1\times10^{-16}$
DGLA	rs1800009	11	61730234	*BEST1*	C	T	0.3478	0.026452212	0.002951664	$<1\times10^{-16}$
DGLA	rs2524299	11	61604782	*FADS2*	A	T	0.88064	-0.037770077	0.004228786	$<1\times10^{-16}$
DGLA	rs198418	11	61496272	*DAGLA*	A	C	0.73879	-0.028012495	0.003145658	$<1\times10^{-16}$
DGLA	rs198425	11	61491431	*DAGLA*	A	T	0.7406	-0.027561243	0.003129851	$<1\times10^{-16}$
DGLA	rs2453710	11	61406542	*RPLP0P2*	A	G	0.58218	0.034261295	0.003928726	$<1\times10^{-16}$
DGLA	rs3758977	11	61737244	*LOC399900*	G	T	0.3436	0.025007725	0.002869771	$<1\times10^{-16}$
DGLA	rs81658	11	61487944	*DAGLA*	G	A	0.74192	-0.026810422	0.003098609	$<1\times10^{-16}$
DGLA	rs198430	11	61487690	*DAGLA*	G	A	0.74192	-0.026799632	0.003098162	$<1\times10^{-16}$
DGLA	rs17633020	11	61744881		G	A	0.76205	-0.026458923	0.003117735	$<1\times10^{-16}$
DGLA	rs17185574	11	61745694		T	C	0.76159	-0.026226638	0.003098671	$<1\times10^{-16}$
DGLA	rs198432	11	61484981	*DAGLA*	C	A	0.73843	-0.026339822	0.003116762	$<1\times10^{-16}$

DGLA	rs1791785	11	61442813		C	T	0.7418	-0.029047122	0.003440297	$<1\times10^{-16}$
DGLA	rs2028062	11	61745953		A	G	0.34067	0.023546253	0.002808945	$<1\times10^{-16}$
DGLA	rs10792320	11	61746291		C	A	0.34095	0.023443942	0.002812546	1.10×10^{-16}
DGLA	rs198453	11	61464550	*DAGLA*	C	T	0.73648	-0.027339291	0.003359827	4.40×10^{-16}
DGLA	rs472031	11	61638420		G	A	0.90451	0.039188093	0.004829156	4.40×10^{-16}
DGLA	rs482548	11	61633182	*FADS2*	C	T	0.90592	0.03821008	0.004845138	3.10×10^{-15}
DGLA	rs2521568	11	61700933	*RAB3IL1*	G	C	0.92845	-0.039959378	0.005208729	1.70×10^{-14}
DGLA	rs3825036	11	61516476		G	A	0.81744	0.030058234	0.003918162	1.70×10^{-14}
DGLA	rs2727266	11	61704334	*RAB3IL1*	A	G	0.92849	-0.039999915	0.005295094	4.20×10^{-14}
DGLA	rs2521572	11	61711475	*RAB3IL1*	G	T	0.96168	-0.050851342	0.006866003	1.30×10^{-13}
DGLA	rs2240287	11	61505583	*DAGLA*	G	A	0.82919	0.028707876	0.003943812	3.40×10^{-13}
DGLA	rs2238001	11	61524507	*C11orf9*	T	C	0.8425	0.031498283	0.004338058	3.80×10^{-13}
DGLA	rs879486	11	61475233	*DAGLA*	C	T	0.6649	-0.022341409	0.003125355	8.80×10^{-13}
DGLA	rs9735635	11	61490880	*DAGLA*	C	A	0.83017	0.027813027	0.003894957	9.30×10^{-13}
DGLA	rs12274157	11	61477647	*DAGLA*	A	C	0.82525	0.027112706	0.003823371	1.30×10^{-12}
DGLA	rs2727261	11	61712131	*RAB3IL1*	C	T	0.90126	-0.037934632	0.005412819	2.40×10^{-12}
DGLA	rs198435	11	61483324	*DAGLA*	G	C	0.84649	0.028753775	0.004101929	2.40×10^{-12}
DGLA	rs4963243	11	61494327	*DAGLA*	G	A	0.84942	0.029374573	0.004225089	3.60×10^{-12}
DGLA	rs4423188	11	61766418		T	A	0.72099	-0.021455644	0.003103223	4.70×10^{-12}
DGLA	rs10736716	11	61765133		G	C	0.63697	-0.019460274	0.00292327	2.80×10^{-11}
DGLA	rs569258	11	61520668	*MYRF*	T	C	0.65011	0.020504387	0.003093989	3.40×10^{-11}
DGLA	rs174552	11	61574999	*FADS1*	C	T	0.99468	-0.200839135	0.030353866	3.70×10^{-11}
DGLA	rs11827215	11	61458595	*DAGLA*	G	A	0.83972	0.024691446	0.003732647	3.70×10^{-11}
DGLA	rs198746	11	61376970		G	A	0.81159	0.057831365	0.008769685	4.30×10^{-11}
DGLA	rs4963308	11	61456426	*DAGLA*	G	A	0.83996	0.024468091	0.003719449	4.80×10^{-11}
DGLA	rs883724	11	61457857	*DAGLA*	C	T	0.84031	0.024428044	0.003715425	4.90×10^{-11}
DGLA	rs1109748	11	61722645	*BEST1*	C	A	0.92539	-0.036466281	0.005670758	1.30×10^{-10}
DGLA	rs17762402	11	61553201	*C11orf9*	G	A	0.94147	0.046143991	0.007250444	2.00×10^{-10}
DGLA	rs4313591	11	61766569		T	C	0.62638	-0.018246733	0.002906377	3.40×10^{-10}
DGLA	rs4963441	11	61768639		C	G	0.62575	-0.01808825	0.002903362	4.70×10^{-10}
DGLA	rs6591657	11	61434532		G	T	0.88788	0.028180673	0.004523613	4.70×10^{-10}
DGLA	rs7937198	11	61768973		A	G	0.62364	-0.018037627	0.002900861	5.00×10^{-10}
DGLA	rs4963442	11	61768706		T	C	0.62445	-0.018054672	0.002905273	5.20×10^{-10}
DGLA	rs7925523	11	61442492		G	A	0.83567	0.023437215	0.003773306	5.30×10^{-10}
DGLA	rs198745	11	61376680		T	C	0.8253	0.055397405	0.008959375	6.30×10^{-10}
DGLA	rs198428	11	61489705	*DAGLA*	T	A	0.61775	0.018459334	0.003019546	9.80×10^{-10}

DGLA	rs198426	11	61490486	*DAGLA*	C	T	0.67872	0.019104342	0.003140967	1.20×10^{-9}
DGLA	rs11230749	11	61362978	*LOC101927495*	C	T	0.87613	-0.069231534	0.011822452	4.70×10^{-9}
AA	rs2581624	3	142633869		G	C	0.79336	0.009754995	0.001589181	8.30×10^{-10}
AA	rs2248811	3	142606942	*PCOLCE2*	G	C	0.78715	0.008693928	0.001593601	4.90×10^{-9}
AA	rs174545	11	61569306	*FADS1*	C	G	0.6711	0.024581721	0.001250655	$<1\times10^{-16}$
AA	rs174546	11	61569830	*FADS1*	C	T	0.67116	0.024577777	0.001250506	$<1\times10^{-16}$
AA	rs174547	11	61570783	*FADS1*	T	C	0.67136	0.024564543	0.001250019	$<1\times10^{-16}$
AA	rs174550	11	61571478	*FADS1*	T	C	0.67143	0.024550948	0.001250319	$<1\times10^{-16}$
AA	rs174537	11	61552680	*C11orf9*	G	T	0.66488	0.024690364	0.001264599	$<1\times10^{-16}$
AA	rs1535	11	61597972	*FADS2*	A	G	0.66595	0.024866869	0.00127604	$<1\times10^{-16}$
AA	rs174536	11	61551927	*C11orf9*	A	C	0.66386	0.024631536	0.001264481	$<1\times10^{-16}$
AA	rs174535	11	61551356	*C11orf9*	T	C	0.65839	0.024623865	0.001264411	$<1\times10^{-16}$
AA	rs4246215	11	61564299	*FEN1*	G	T	0.65088	0.024433841	0.001268673	$<1\times10^{-16}$
AA	rs174541	11	61565908		T	C	0.65148	0.024407299	0.001267406	$<1\times10^{-16}$
AA	rs102275	11	61557803	*C11orf10*	T	C	0.62686	0.024886779	0.001309693	$<1\times10^{-16}$
AA	rs174576	11	61603510	*FADS2*	C	A	0.65841	0.024507775	0.001290441	$<1\times10^{-16}$
AA	rs174574	11	61600342	*FADS2*	C	A	0.63796	0.024829465	0.001307902	$<1\times10^{-16}$
AA	rs174577	11	61604814	*FADS2*	C	A	0.6524	0.024440279	0.001288954	$<1\times10^{-16}$
AA	rs174578	11	61605499	*FADS2*	T	A	0.65154	0.024219492	0.001288197	$<1\times10^{-16}$
AA	rs174583	11	61609750	*FADS2*	C	T	0.65299	0.024199448	0.001296296	$<1\times10^{-16}$
AA	rs174555	11	61579760	*FADS1*	T	C	0.70764	0.024018629	0.001301119	$<1\times10^{-16}$
AA	rs174556	11	61580635	*FADS1*	C	T	0.70764	0.024026422	0.001301439	$<1\times10^{-16}$
AA	rs174548	11	61571348	*FADS1*	C	G	0.69996	0.023714033	0.001287432	$<1\times10^{-16}$
AA	rs174549	11	61571382	*FADS1*	G	A	0.70775	0.023812139	0.001293691	$<1\times10^{-16}$
AA	rs174538	11	61560081	*C11orf10*	G	A	0.69487	0.023462625	0.001279837	$<1\times10^{-16}$
AA	rs174528	11	61543499	*C11orf9*	T	C	0.61669	0.023234781	0.001300411	$<1\times10^{-16}$
AA	rs174601	11	61623140	*FADS2*	C	T	0.61373	0.023990221	0.001361246	$<1\times10^{-16}$
AA	rs108499	11	61547237	*C11orf9*	C	T	0.67142	0.021386038	0.001279824	$<1\times10^{-16}$
AA	rs174534	11	61549458	*C11orf9*	A	G	0.66316	0.020499565	0.001244953	$<1\times10^{-16}$
AA	rs174570	11	61597212	*FADS2*	C	T	0.86422	0.025409935	0.001896779	$<1\times10^{-16}$
AA	rs174575	11	61602003	*FADS2*	C	G	0.7332	0.018928681	0.00146665	$<1\times10^{-16}$
AA	rs174593	11	61618831	*FADS2*	T	C	0.7208	0.018203337	0.001464843	$<1\times10^{-16}$
AA	rs174579	11	61605613	*FADS2*	C	T	0.78402	0.018337051	0.001519732	$<1\times10^{-16}$
AA	rs174591	11	61617676	*FADS2*	T	A	0.71832	0.017953589	0.001491899	$<1\times10^{-16}$
AA	rs174585	11	61611694	*FADS2*	G	A	0.78304	0.018018992	0.001511651	$<1\times10^{-16}$

AA	rs174448	11	61639573		A	G	0.64303	0.015302061	0.00129954	$<1\times10^{-16}$
AA	rs174589	11	61615803	*FADS2*	C	G	0.78765	0.017527017	0.001505997	$<1\times10^{-16}$
AA	rs2727270	11	61603237	*FADS2*	C	T	0.89029	0.022375137	0.001932447	$<1\times10^{-16}$
AA	rs2727271	11	61603358	*FADS2*	A	T	0.89	0.022344776	0.001933855	$<1\times10^{-16}$
AA	rs509360	11	61548559	*C11orf9*	G	A	0.649	-0.018655647	0.001621963	$<1\times10^{-16}$
AA	rs2851682	11	61616012	*FADS2*	A	G	0.92129	0.028410035	0.002486314	$<1\times10^{-16}$
AA	rs2845573	11	61601908	*FADS2*	A	G	0.92668	0.026552235	0.002334587	$<1\times10^{-16}$
AA	rs174449	11	61640379		A	G	0.63271	0.01413323	0.001255778	$<1\times10^{-16}$
AA	rs2524299	11	61604782	*FADS2*	A	T	0.88064	0.021480109	0.001949754	$<1\times10^{-16}$
AA	rs174597	11	61621040	*FADS2*	G	C	0.74735	0.016773041	0.001538603	$<1\times10^{-16}$
AA	rs968567	11	61595564	*FADS2*	C	T	0.83527	0.019099505	0.001763269	$<1\times10^{-16}$
AA	rs422249	11	61639488		C	T	0.67098	0.014503632	0.001342686	$<1\times10^{-16}$
AA	rs2072114	11	61605215	*FADS2*	A	G	0.8814	0.020548561	0.00191428	$<1\times10^{-16}$
AA	rs2269928	11	61537529	*C11orf9*	T	G	0.77978	0.019499261	0.001818698	$<1\times10^{-16}$
AA	rs174532	11	61548874	*C11orf9*	G	A	0.72114	-0.017638345	0.001693061	$<1\times10^{-16}$
AA	rs174611	11	61627881	*FADS2*	T	C	0.71039	0.014014928	0.00135256	$<1\times10^{-16}$
AA	rs174605	11	61626921	*FADS2*	G	T	0.71151	0.013918115	0.001347101	$<1\times10^{-16}$
AA	rs174455	11	61656117	*FADS3*	G	A	0.36538	-0.012877611	0.001259959	$<1\times10^{-16}$
AA	rs2526678	11	61623793	*FADS2*	G	A	0.93057	0.028878715	0.002861908	$<1\times10^{-16}$
AA	rs412334	11	61560261	*FEN1*	C	T	0.85305	-0.027620235	0.002751166	$<1\times10^{-16}$
AA	rs174616	11	61629122	*FADS2*	G	A	0.52756	0.012524792	0.001249924	$<1\times10^{-16}$
AA	rs174626	11	61637057		A	G	0.52886	0.012688919	0.001270477	$<1\times10^{-16}$
AA	rs174450	11	61641542	*FADS3*	G	T	0.47314	-0.012731387	0.001293061	$<1\times10^{-16}$
AA	rs149803	11	61539020	*C11orf9*	C	G	0.74636	-0.015835817	0.001793894	$<1\times10^{-16}$
AA	rs174627	11	61637466		G	A	0.835	0.015374786	0.001793824	$<1\times10^{-16}$
AA	rs174468	11	61663691		G	A	0.60365	-0.012450023	0.001468168	$<1\times10^{-16}$
AA	rs666870	11	61677479	*RAB3IL1*	G	A	0.6013	-0.0125676	0.001503774	1.10×10^{-16}
AA	rs174478	11	61678576	*RAB3IL1*	T	G	0.60099	-0.012569856	0.001504329	1.10×10^{-16}
AA	rs174634	11	61647387	*FADS3*	C	G	0.72588	0.011703135	0.001401397	1.10×10^{-16}
AA	rs174479	11	61678754	*RAB3IL1*	C	G	0.81614	0.01555274	0.001871898	1.10×10^{-16}
AA	rs174464	11	61657926	*FADS3*	G	A	0.72982	0.011685088	0.001424754	2.20×10^{-16}
AA	rs174476	11	61674118	*RAB3IL1*	C	T	0.60208	-0.012249595	0.001499231	3.30×10^{-16}
AA	rs1000778	11	61655305	*FADS3*	G	A	0.72904	0.011228085	0.001379677	4.40×10^{-16}
AA	rs174469	11	61667443	*RAB3IL1*	C	T	0.82555	0.014755401	0.001813425	4.40×10^{-16}
AA	rs174456	11	61656182	*FADS3*	A	C	0.72918	0.011202139	0.001378583	4.40×10^{-16}
AA	rs526126	11	61624885	*FADS2*	C	G	0.76593	0.016088208	0.00202466	1.90×10^{-15}

AA	rs174602	11	61624414	*FADS2*	T	C	0.76774	0.016117955	0.00204734	3.40×10^{-15}
AA	rs198462	11	61524119	*C11orf9*	G	A	0.48644	-0.010170448	0.001297982	4.70×10^{-15}
AA	rs198476	11	61525730	*C11orf9*	G	A	0.47167	-0.010063125	0.001334135	4.60×10^{-14}
AA	rs198464	11	61521621		G	A	0.48411	-0.009390417	0.001253592	6.90×10^{-14}
AA	rs1692120	11	61417472		G	A	0.56219	-0.011385056	0.001721542	3.80×10^{-11}
AA	rs650436	11	61536430	*C11orf9*	C	T	0.57937	-0.009229438	0.00143508	1.30×10^{-10}
AA	rs2453710	11	61406542	*RPLP0P2*	A	G	0.58218	-0.011508617	0.0018469	4.60×10^{-10}
DPA-n3	rs8523	6	10981053	*ELOVL2*	A	G	0.44465	0.011293305	0.002041436	3.20×10^{-8}
DPA-n3	rs3798707	6	10991935	*ELOVL2*	T	C	0.44596	0.011325177	0.002047072	3.20×10^{-8}
DPA-n3	rs4532436	6	10983971	*ELOVL2*	G	C	0.44571	0.011295698	0.002047548	3.50×10^{-8}
DPA-n3	rs4713103	6	10969141	*SYCP2L*	T	G	0.46298	0.01132793	0.002057244	3.70×10^{-8}
DPA-n3	rs1225717	6	10978240		G	A	0.46545	0.011529213	0.002095265	3.70×10^{-8}
DPA-n3	rs3798711	6	11002810	*ELOVL2*	C	T	0.44625	0.01120606	0.002047701	4.40×10^{-8}
DPA-n3	rs2295602	6	11005842	*ELOVL2*	C	T	0.44643	0.011203922	0.002047984	4.50×10^{-8}
DPA-n3	rs174549	11	61571382	*FADS1*	G	A	0.70775	0.01248346	0.002243944	2.60×10^{-8}
DPA-n3	rs174555	11	61579760	*FADS1*	T	C	0.70764	0.012503236	0.002257835	3.10×10^{-8}
DPA-n3	rs174556	11	61580635	*FADS1*	C	T	0.70764	0.01250357	0.002258417	3.10×10^{-8}
DTA	rs174546	11	61569830	*FADS1*	C	T	0.67116	0.028954763	0.003208542	$<1\times10^{-16}$
DTA	rs174545	11	61569306	*FADS1*	C	G	0.6711	0.028960669	0.003208942	$<1\times10^{-16}$
DTA	rs174547	11	61570783	*FADS1*	T	C	0.67136	0.02893559	0.003207219	$<1\times10^{-16}$
DTA	rs174550	11	61571478	*FADS1*	T	C	0.67143	0.028901207	0.00320778	$<1\times10^{-16}$
DTA	rs174537	11	61552680	*C11orf9*	G	T	0.66488	0.029222614	0.003242213	$<1\times10^{-16}$
DTA	rs174536	11	61551927	*C11orf9*	A	C	0.66386	0.029169235	0.00324112	$<1\times10^{-16}$
DTA	rs174535	11	61551356	*C11orf9*	T	C	0.65839	0.028930165	0.003242579	$<1\times10^{-16}$
DTA	rs1535	11	61597972	*FADS2*	A	G	0.66595	0.029022244	0.003272799	$<1\times10^{-16}$
DTA	rs174538	11	61560081	*C11orf10*	G	A	0.69487	0.028802552	0.003253572	$<1\times10^{-16}$
DTA	rs4246215	11	61564299	*FEN1*	G	T	0.65088	0.028385671	0.003248709	$<1\times10^{-16}$
DTA	rs174541	11	61565908		T	C	0.65148	0.028344796	0.003245402	$<1\times10^{-16}$
DTA	rs174576	11	61603510	*FADS2*	C	A	0.65841	0.027746738	0.003302934	$<1\times10^{-16}$
DTA	rs174574	11	61600342	*FADS2*	C	A	0.63796	0.028012059	0.00334974	1.10×10^{-16}
DTA	rs174555	11	61579760	*FADS1*	T	C	0.70764	0.027768362	0.003322717	1.10×10^{-16}
DTA	rs174556	11	61580635	*FADS1*	C	T	0.70764	0.027778084	0.003323559	1.10×10^{-16}
DTA	rs174549	11	61571382	*FADS1*	G	A	0.70775	0.027546529	0.003302683	1.10×10^{-16}
DTA	rs102275	11	61557803	*C11orf10*	T	C	0.62686	0.027917164	0.003355333	1.10×10^{-16}
DTA	rs174577	11	61604814	*FADS2*	C	A	0.6524	0.02741364	0.00330046	1.10×10^{-16}
DTA	rs174548	11	61571348	*FADS1*	C	G	0.69996	0.027024764	0.003288992	2.20×10^{-16}

DTA	rs174578	11	61605499	*FADS2*	T	A	0.65154	0.026865055	0.003296302	3.30×10^{-16}
DTA	rs174583	11	61609750	*FADS2*	C	T	0.65299	0.026853695	0.003314948	5.60×10^{-16}
DTA	rs174534	11	61549458	*C11orf9*	A	G	0.66316	0.0246155	0.003138156	4.30×10^{-15}
DTA	rs108499	11	61547237	*C11orf9*	C	T	0.67142	0.025336206	0.003231711	4.60×10^{-15}
DTA	rs174528	11	61543499	*C11orf9*	T	C	0.61669	0.025454057	0.003314775	1.60×10^{-14}
DTA	rs174601	11	61623140	*FADS2*	C	T	0.61373	0.025711832	0.003466068	1.20×10^{-13}
DTA	rs174579	11	61605613	*FADS2*	C	T	0.78402	0.024832406	0.003742543	3.20×10^{-11}
DTA	rs174585	11	61611694	*FADS2*	G	A	0.78304	0.024103702	0.003722047	9.40×10^{-11}
DTA	rs174589	11	61615803	*FADS2*	C	G	0.78765	0.023079185	0.003705559	4.70×10^{-10}
DTA	rs174575	11	61602003	*FADS2*	C	G	0.7332	0.022193588	0.00363031	9.80×10^{-10}
DTA	rs174570	11	61597212	*FADS2*	C	T	0.86422	0.028406585	0.004715405	1.70×10^{-9}
DTA	rs968567	11	61595564	*FADS2*	C	T	0.83527	0.025899899	0.004325846	2.10×10^{-9}
DTA	rs2269928	11	61537529	*C11orf9*	T	G	0.77978	0.026124322	0.004452842	4.40×10^{-9}
DTA	rs174593	11	61618831	*FADS2*	T	C	0.7208	0.020456431	0.003622509	1.60×10^{-8}

PUFA, polyunsaturated fatty acid; SNP, single nucleotide polymorphism; Chr, chromosome; EAF, Effect allele frequency; SE, standard error. For the 413 genome-wide significant associations (188 unique SNPs) reported by Tintle *et al.* 2015, a total of 369 associations (171 unique SNPs) remained significant at $p < 5.0\times10^{-8}$ in our repeating analysis with the Framingham Heart Study. Their summary statistics were reported in this table. Among them, genetic instruments were further selected based on different LD cutoffs.

Supplementary Table 6. Forward Mendelian randomization estimates of associations of genetically predicted polyunsaturated fatty acids with COVID-19 severity based on the release 5 HGI A2.

			IVW_MRE			MR-Egger			Wald ratio			MR-Egger intercept		Heterogeneity test		Weighted median				
Group name	**PUFA**	**R^2**	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	***P***	***P*_IVW**	***P*_Egger**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	0.001	-	-	-	-	-	-	0.107	0.089	0.23	-	-	-	-	-	-	-	1	256
Plasma	ALA	0.01	-	-	-	-	-	-	0.108	0.09	0.23	-	-	-	-	-	-	-	1	312
Plasma	ALA	0.1	0.099	0.027	2.00E-04	0.042	0.17	0.828	-	-	-	0.016	0.745	0.935	0.866	0.108	0.078	0.164	4	436
Plasma	ALA	0.3	0.125	0.046	0.006	-0.075	0.132	0.58	-	-	-	0.05	0.134	0.441	0.582	0.103	0.063	0.104	13	1107
RBC	ALA	0.001	-	-	-	-	-	-	0.048	0.172	0.78	-	-	-	-	-	-	-	1	31
RBC	ALA	0.01	-	-	-	-	-	-	0.048	0.172	0.78	-	-	-	-	-	-	-	1	31
RBC	ALA	0.1	-	-	-	-	-	-	0.048	0.172	0.78	-	-	-	-	-	-	-	1	31
RBC	ALA	0.3	-	-	-	-	-	-	0.048	0.172	0.78	-	-	-	-	-	-	-	1	31
Plasma	LA	0.001	0.073	0.038	0.053	0.013	0.081	0.899	-	-	-	0.027	0.517	0.574	0.645	0.065	0.051	0.204	3	1329
RBC	LA	0.001	-	-	-	-	-	-	0.04	0.079	0.611	-	-	-	-	-	-	-	1	133
RBC	LA	0.01	-	-	-	-	-	-	0.04	0.079	0.611	-	-	-	-	-	-	-	1	133
RBC	LA	0.1	0.057	0.03	0.054	-	-	-	-	-	-	-	-	-	-	-	-	-	2	175
RBC	LA	0.3	0.072	0.037	0.053	-0.099	0.2	0.635	-	-	-	0.05	0.414	0.534	0.509	0.042	0.051	0.406	9	566
Plasma	GLA	0.001	-0.11	0.066	0.094	-	-	-	-	-	-	-	-	-	-	-	-	-	2	293
RBC	GLA	0.001	-	-	-	-	-	-	-0.038	0.138	0.78	-	-	-	-	-	-	-	1	49
RBC	GLA	0.01	-	-	-	-	-	-	-0.038	0.138	0.78	-	-	-	-	-	-	-	1	49
RBC	GLA	0.1	-	-	-	-	-	-	-0.038	0.138	0.78	-	-	-	-	-	-	-	1	49
RBC	GLA	0.3	-	-	-	-	-	-	-0.038	0.138	0.78	-	-	-	-	-	-	-	1	49
Plasma	DGLA	0.001	0.069	0.011	7.00E-11	-	-	-	-	-	-	-	-	-	-	-	-	-	2	1417
RBC	DGLA	0.001	0.017	0.103	0.87	-	-	-	-	-	-	-	-	-	-	-	-	-	2	542
RBC	DGLA	0.01	0.044	0.056	0.436	-0.103	0.125	0.498	-	-	-	0.085	0.329	0.042	0.104	0.059	0.047	0.201	4	788
RBC	DGLA	0.1	0.045	0.019	0.017	0.015	0.045	0.747	-	-	-	0.02	0.464	0.488	0.453	0.01	0.026	0.708	14	2375
RBC	DGLA	0.3	0.041	0.012	0.001	-3.00E-04	0.032	0.992	-	-	-	0.027	0.168	0.672	0.733	0.016	0.019	0.408	26	5970
Plasma	AA	0.001	-0.039	0.014	0.007	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4616
RBC	AA	0.001	-0.029	0.015	0.048	-0.089	0.182	0.712	-	-	-	0.024	0.788	0.938	0.927	-0.035	0.066	0.599	3	268
RBC	AA	0.01	-0.041	0.021	0.049	-0.114	0.166	0.616	-	-	-	0.031	0.72	0.872	0.816	-0.044	0.065	0.493	3	287
RBC	AA	0.1	-0.111	0.038	0.003	-0.038	0.129	0.782	-	-	-	-0.029	0.575	0.429	0.352	-0.081	0.05	0.109	7	584
RBC	AA	0.3	-0.078	0.024	0.001	-0.015	0.076	0.842	-	-	-	-0.026	0.4	0.345	0.33	-0.051	0.033	0.118	14	1440
Plasma	DPA-n3	0.001	-0.114	0.051	0.026	-0.066	0.157	0.746	-	-	-	-0.016	0.792	0.426	0.216	-0.113	0.058	0.051	3	835
Plasma	DPA-n3	0.01	-0.115	0.051	0.024	-0.069	0.157	0.736	-	-	-	-0.016	0.801	0.434	0.219	-0.114	0.058	0.05	3	937
Plasma	DPA-n3	0.1	-0.116	0.027	2.00E-05	-0.047	0.082	0.578	-	-	-	-0.021	0.358	0.954	0.963	-0.087	0.054	0.108	14	1506
Plasma	DPA-n3	0.3	-0.119	0.025	1.00E-06	-0.02	0.062	0.744	-	-	-	-0.03	0.084	0.77	0.869	-0.084	0.041	0.039	29	3466
RBC	DPA-n3	0.001	-0.237	0.116	0.041	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.01	-0.237	0.116	0.041	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.1	-0.237	0.116	0.041	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.3	-0.237	0.116	0.041	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DTA	0.001	-	-	-	-	-	-	-0.091	0.104	0.382	-	-	-	-	-	-	-	1	80
RBC	DTA	0.01	-	-	-	-	-	-	-0.091	0.104	0.382	-	-	-	-	-	-	-	1	80
RBC	DTA	0.1	-	-	-	-	-	-	-0.091	0.104	0.382	-	-	-	-	-	-	-	1	80
RBC	DTA	0.3	-0.081	0.016	7.00E-07	-	-	-	-	-	-	-	-	-	-	-	-	-	2	114
Plasma	DHA	0.001	-	-	-	-	-	-	0.47	0.212	0.026	-	-	-	-	-	-	-	1	65
Plasma	DHA	0.01	-	-	-	-	-	-	0.469	0.211	0.026	-	-	-	-	-	-	-	1	64
Plasma	DHA	0.1	-	-	-	-	-	-	0.469	0.211	0.026	-	-	-	-	-	-	-	1	64
Plasma	DHA	0.3	0.393	0.137	0.004	-	-	-	-	-	-	-	-	-	-	-	-	-	2	95

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 7. Forward Mendelian randomization estimates of associations of genetically predicted polyunsaturated fatty acids with COVID-19 severity based on the release 5 HGI B2.

			IVW_MRE			MR-Egger			Wald ratio			MR-Egger intercept		Heterogeneity test		Weighted median				
Group name	PUFA	R^2	β	SE	*P*	β	SE	*P*	β	SE	*P*	β	*P*	*P*_IVW	*P*_Egger	β	SE	*P*	nsnps	*F*-statistic
Plasma	ALA	0.001	-	-	-	-	-	-	0.101	0.061	0.098	-	-	-	-	-	-	-	1	256
Plasma	ALA	0.01	-	-	-	-	-	-	0.101	0.061	0.098	-	-	-	-	-	-	-	1	312
Plasma	ALA	0.1	0.109	0.083	0.192	-0.090	0.195	0.689	-	-	-	0.057	0.380	0.020	0.049	0.118	0.056	0.034	4	436
Plasma	ALA	0.3	0.101	0.038	0.008	-0.108	0.096	0.284	-	-	-	0.052	0.041	0.042	0.203	0.094	0.039	0.016	13	1107
RBC	ALA	0.001	-	-	-	-	-	-	0.122	0.116	0.291	-	-	-	-	-	-	-	1	31
RBC	ALA	0.01	-	-	-	-	-	-	0.122	0.116	0.291	-	-	-	-	-	-	-	1	31
RBC	ALA	0.1	-	-	-	-	-	-	0.122	0.116	0.291	-	-	-	-	-	-	-	1	31
RBC	ALA	0.3	-	-	-	-	-	-	0.122	0.116	0.291	-	-	-	-	-	-	-	1	31
Plasma	LA	0.001	0.058	0.024	0.015	0.052	0.055	0.517	-	-	-	0.003	0.915	0.617	0.331	0.057	0.036	0.108	3	1329
RBC	LA	0.001	-	-	-	-	-	-	0.082	0.053	0.126	-	-	-	-	-	-	-	1	133
RBC	LA	0.01	-	-	-	-	-	-	0.082	0.053	0.126	-	-	-	-	-	-	-	1	133
RBC	LA	0.1	0.109	0.048	0.024	-	-	-	-	-	-	-	-	-	-	-	-	-	2	175
RBC	LA	0.3	0.076	0.023	0.001	-0.045	0.136	0.752	-	-	-	0.036	0.397	0.622	0.610	0.074	0.034	0.030	9	566
Plasma	GLA	0.001	-0.117	0.013	6.60e-20	-	-	-	-	-	-	-	-	-	-	-	-	-	2	293
RBC	GLA	0.001	-	-	-	-	-	-	-0.098	0.093	0.291	-	-	-	-	-	-	-	1	49
RBC	GLA	0.01	-	-	-	-	-	-	-0.098	0.093	0.291	-	-	-	-	-	-	-	1	49
RBC	GLA	0.1	-	-	-	-	-	-	-0.098	0.093	0.291	-	-	-	-	-	-	-	1	49
RBC	GLA	0.3	-	-	-	-	-	-	-0.098	0.093	0.291	-	-	-	-	-	-	-	1	49
Plasma	DGLA	0.001	0.048	0.040	0.231	-	-	-	-	-	-	-	-	-	-	-	-	-	2	1417
RBC	DGLA	0.001	0.010	0.044	0.828	-	-	-	-	-	-	-	-	-	-	-	-	-	2	542
RBC	DGLA	0.01	0.006	0.022	0.774	-0.069	0.054	0.328	-	-	-	0.044	0.266	0.332	0.582	-0.007	0.024	0.760	4	788
RBC	DGLA	0.1	0.029	0.017	0.080	0.039	0.040	0.353	-	-	-	-0.006	0.795	0.091	0.065	0.023	0.017	0.177	13	2341
RBC	DGLA	0.3	0.033	0.010	0.001	0.006	0.024	0.819	-	-	-	0.017	0.238	0.089	0.106	0.026	0.011	0.021	25	5936
Plasma	AA	0.001	-0.038	0.004	3.23e-20	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4616
RBC	AA	0.001	-0.049	0.011	1.32e-05	-0.097	0.123	0.574	-	-	-	0.019	0.753	0.912	0.894	-0.053	0.041	0.189	3	268
RBC	AA	0.01	-0.056	0.015	1.78e-04	-0.112	0.113	0.502	-	-	-	0.024	0.694	0.844	0.795	-0.059	0.039	0.135	3	287
RBC	AA	0.1	-0.069	0.015	3.89e-06	-0.056	0.082	0.528	-	-	-	-0.005	0.871	0.888	0.807	-0.059	0.030	0.047	7	584
RBC	AA	0.3	-0.055	0.012	9.17e-06	-0.039	0.048	0.425	-	-	-	-0.006	0.736	0.791	0.734	-0.052	0.021	0.012	14	1440
Plasma	DPA-n3	0.001	-0.069	0.007	4.73e-20	-0.089	0.082	0.475	-	-	-	0.007	0.827	0.962	0.977	-0.070	0.038	0.067	3	835
Plasma	DPA-n3	0.01	-0.069	0.008	6.21e-20	-0.089	0.083	0.475	-	-	-	0.007	0.826	0.961	0.990	-0.070	0.039	0.073	3	937
Plasma	DPA-n3	0.1	-0.076	0.028	0.007	0.012	0.053	0.830	-	-	-	-0.027	0.081	0.302	0.491	-0.070	0.034	0.042	14	1506
Plasma	DPA-n3	0.3	-0.072	0.019	1.65e-04	0.015	0.040	0.710	-	-	-	-0.026	0.022	0.188	0.401	-0.065	0.026	0.012	29	3466
RBC	DPA-n3	0.001	-0.130	0.033	9.30e-05	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.01	-0.130	0.033	9.30e-05	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.1	-0.130	0.033	9.30e-05	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.3	-0.130	0.033	9.30e-05	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DTA	0.001	-	-	-	-	-	-	-0.102	0.071	0.148	-	-	-	-	-	-	-	1	80
RBC	DTA	0.01	-	-	-	-	-	-	-0.102	0.071	0.148	-	-	-	-	-	-	-	1	80
RBC	DTA	0.1	-	-	-	-	-	-	-0.102	0.071	0.148	-	-	-	-	-	-	-	1	80
RBC	DTA	0.3	-0.098	0.006	3.04e-60	-	-	-	-	-	-	-	-	-	-	-	-	-	2	114
Plasma	DHA	0.001	-	-	-	-	-	-	0.161	0.146	0.269	-	-	-	-	-	-	-	1	65
Plasma	DHA	0.01	-	-	-	-	-	-	0.161	0.146	0.269	-	-	-	-	-	-	-	1	64
Plasma	DHA	0.1	-	-	-	-	-	-	0.161	0.146	0.269	-	-	-	-	-	-	-	1	64
Plasma	DHA	0.3	0.170	0.014	5.32e-34	-	-	-	-	-	-	-	-	-	-	-	-	-	2	95

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 8. Forward Mendelian randomization estimates of associations of genetically predicted polyunsaturated fatty acids with COVID-19 severity based on the release 5 HGI B1.

			IVW_MRE			MR-Egger			Wald ratio			MR-Egger intercept		Heterogeneity test		Weighted median				
Group name	**PUFA**	**R^2**	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	***P***	***P*_IVW**	***P*_Egger**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	0.001	-	-	-	-	-	-	0.211	0.102	0.038	-	-	-	-	-	-	-	1	256
Plasma	ALA	0.01	-	-	-	-	-	-	0.213	0.102	0.038	-	-	-	-	-	-	-	1	312
Plasma	ALA	0.1	0.224	0.179	0.211	-0.174	0.45	0.737	-	-	-	0.115	0.437	0.001	0.002	0.229	0.097	0.018	4	436
Plasma	ALA	0.3	0.183	0.07	0.009	-0.053	0.204	0.8	-	-	-	0.058	0.245	0.004	0.007	0.209	0.065	0.001	13	1107
RBC	ALA	0.001	-	-	-	-	-	-	0.362	0.193	0.061	-	-	-	-	-	-	-	1	31
RBC	ALA	0.01	-	-	-	-	-	-	0.362	0.193	0.061	-	-	-	-	-	-	-	1	31
RBC	ALA	0.1	-	-	-	-	-	-	0.362	0.193	0.061	-	-	-	-	-	-	-	1	31
RBC	ALA	0.3	-	-	-	-	-	-	0.362	0.193	0.061	-	-	-	-	-	-	-	1	31
Plasma	LA	0.001	0.112	0.071	0.117	0.138	0.159	0.545	-	-	-	-0.011	0.868	0.213	0.085	0.113	0.058	0.05	3	1329
RBC	LA	0.001	-	-	-	-	-	-	0.227	0.09	0.011	-	-	-	-	-	-	-	1	133
RBC	LA	0.01	-	-	-	-	-	-	0.227	0.09	0.011	-	-	-	-	-	-	-	1	133
RBC	LA	0.1	0.27	0.076	3.90E-04	-	-	-	-	-	-	-	-	-	-	-	-	-	2	175
RBC	LA	0.3	0.183	0.038	1.75E-06	0.057	0.228	0.81	-	-	-	0.037	0.592	0.55	0.476	0.216	0.056	1.04E-04	9	566
Plasma	GLA	0.001	-0.265	0.031	2.82E-17	-	-	-	-	-	-	-	-	-	-	-	-	-	2	293
RBC	GLA	0.001	-	-	-	-	-	-	-0.29	0.155	0.061	-	-	-	-	-	-	-	1	49
RBC	GLA	0.01	-	-	-	-	-	-	-0.29	0.155	0.061	-	-	-	-	-	-	-	1	49
RBC	GLA	0.1	-	-	-	-	-	-	-0.29	0.155	0.061	-	-	-	-	-	-	-	1	49
RBC	GLA	0.3	-	-	-	-	-	-	-0.29	0.155	0.061	-	-	-	-	-	-	-	1	49
Plasma	DGLA	0.001	0.074	0.118	0.528	-	-	-	-	-	-	-	-	-	-	-	-	-	2	1417
RBC	DGLA	0.001	0.005	0.025	0.84	-	-	-	-	-	-	-	-	-	-	-	-	-	2	542
RBC	DGLA	0.01	-0.015	0.027	0.591	-0.014	0.086	0.886	-	-	-	-4.98E-04	0.993	0.55	0.348	-0.006	0.036	0.876	4	788
RBC	DGLA	0.1	0.048	0.029	0.101	0.087	0.07	0.24	-	-	-	-0.025	0.551	0.029	0.024	0.053	0.029	0.069	13	2341
RBC	DGLA	0.3	0.059	0.017	0.001	0.049	0.044	0.279	-	-	-	0.007	0.804	0.02	0.014	0.054	0.02	0.007	25	5936
Plasma	AA	0.001	-0.082	0.031	0.008	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4616
RBC	AA	0.001	-0.171	0.007	8.57E-130	-0.139	0.204	0.621	-	-	-	-0.013	0.895	0.986	0.998	-0.167	0.067	0.013	3	268
RBC	AA	0.01	-0.167	0.009	4.60E-80	-0.13	0.188	0.615	-	-	-	-0.016	0.871	0.978	0.956	-0.164	0.066	0.012	3	287
RBC	AA	0.1	-0.109	0.031	4.43E-04	-0.185	0.137	0.234	-	-	-	0.03	0.587	0.687	0.61	-0.113	0.05	0.025	7	584
RBC	AA	0.3	-0.1	0.025	5.99E-05	-0.137	0.083	0.126	-	-	-	0.015	0.652	0.418	0.358	-0.114	0.032	3.62E-04	14	1440
Plasma	DPA-n3	0.001	-0.131	0.028	3.59E-06	-0.164	0.132	0.431	-	-	-	0.011	0.82	0.818	0.573	-0.149	0.064	0.021	3	835
Plasma	DPA-n3	0.01	-0.131	0.029	6.00E-06	-0.164	0.132	0.433	-	-	-	0.011	0.824	0.811	0.561	-0.15	0.067	0.025	3	937
Plasma	DPA-n3	0.1	-0.138	0.058	0.018	-0.017	0.115	0.887	-	-	-	-0.038	0.244	0.02	0.031	-0.153	0.064	0.017	14	1506
Plasma	DPA-n3	0.3	-0.121	0.034	3.48E-04	-0.028	0.075	0.718	-	-	-	-0.028	0.178	0.034	0.048	-0.15	0.041	2.88E-04	29	3466
RBC	DPA-n3	0.001	-0.274	0.131	0.036	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.01	-0.274	0.131	0.036	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.1	-0.274	0.131	0.036	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.3	-0.274	0.131	0.036	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DTA	0.001	-	-	-	-	-	-	-0.25	0.118	0.034	-	-	-	-	-	-	-	1	80
RBC	DTA	0.01	-	-	-	-	-	-	-0.25	0.118	0.034	-	-	-	-	-	-	-	1	80
RBC	DTA	0.1	-	-	-	-	-	-	-0.25	0.118	0.034	-	-	-	-	-	-	-	1	80
RBC	DTA	0.3	-0.271	0.027	2.21E-23	-	-	-	-	-	-	-	-	-	-	-	-	-	2	114
Plasma	DHA	0.001	-	-	-	-	-	-	0.103	0.246	0.674	-	-	-	-	-	-	-	1	65
Plasma	DHA	0.01	-	-	-	-	-	-	0.103	0.245	0.674	-	-	-	-	-	-	-	1	64
Plasma	DHA	0.1	-	-	-	-	-	-	0.103	0.245	0.674	-	-	-	-	-	-	-	1	64
Plasma	DHA	0.3	-0.005	0.158	0.974	-	-	-	-	-	-	-	-	-	-	-	-	-	2	95

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 9. Forward Mendelian randomization estimates of associations of genetically predicted polyunsaturated fatty acids with COVID-19 susceptibility based on the release 5 HGI C2.

			IVW_MRE			MR-Egger			Wald ratio			MR-Egger intercept		Heterogeneity test		Weighted median				
Group name	**PUFA**	**R^2**	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	***P***	***P*_IVW**	***P*_Egger**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	0.001	-	-	-	-	-	-	0.012	0.031	0.697	-	-	-	-	-	-	-	1	256
Plasma	ALA	0.01	-	-	-	-	-	-	0.012	0.031	0.697	-	-	-	-	-	-	-	1	312
Plasma	ALA	0.1	0.010	0.008	0.211	0.031	0.056	0.636	-	-	-	-0.006	0.728	0.938	0.882	0.010	0.025	0.693	4	436
Plasma	ALA	0.3	0.012	0.009	0.200	-0.012	0.041	0.770	-	-	-	0.006	0.545	0.943	0.930	0.012	0.017	0.477	13	1107
RBC	ALA	0.001	-	-	-	-	-	-	-4.57e-04	0.059	0.994	-	-	-	-	-	-	-	1	31
RBC	ALA	0.01	-	-	-	-	-	-	-4.57e-04	0.059	0.994	-	-	-	-	-	-	-	1	31
RBC	ALA	0.1	-	-	-	-	-	-	-4.57e-04	0.059	0.994	-	-	-	-	-	-	-	1	31
RBC	ALA	0.3	-	-	-	-	-	-	-4.57e-04	0.059	0.994	-	-	-	-	-	-	-	1	31
Plasma	LA	0.001	0.007	0.009	0.430	0.010	0.028	0.779	-	-	-	-0.001	0.914	0.761	0.468	0.008	0.018	0.669	3	1329
RBC	LA	0.001	-	-	-	-	-	-	2.25e-04	0.028	0.993	-	-	-	-	-	-	-	1	133
RBC	LA	0.01	-	-	-	-	-	-	2.25e-04	0.028	0.993	-	-	-	-	-	-	-	1	133
RBC	LA	0.1	-0.004	0.008	0.594	-	-	-	-	-	-	-	-	-	-	-	-	-	2	175
RBC	LA	0.3	-0.005	0.005	0.245	0.012	0.070	0.872	-	-	-	-0.005	0.812	0.998	0.996	-0.009	0.017	0.593	9	566
Plasma	GLA	0.001	-0.006	0.023	0.775	-	-	-	-	-	-	-	-	-	-	-	-	-	2	293
RBC	GLA	0.001	-	-	-	-	-	-	3.67e-04	0.047	0.994	-	-	-	-	-	-	-	1	49
RBC	GLA	0.01	-	-	-	-	-	-	3.67e-04	0.047	0.994	-	-	-	-	-	-	-	1	49
RBC	GLA	0.1	-	-	-	-	-	-	3.67e-04	0.047	0.994	-	-	-	-	-	-	-	1	49
RBC	GLA	0.3	-	-	-	-	-	-	3.67e-04	0.047	0.994	-	-	-	-	-	-	-	1	49
Plasma	DGLA	0.001	0.011	0.005	0.031	-	-	-	-	-	-	-	-	-	-	-	-	-	2	1417
RBC	DGLA	0.001	0.010	0.004	0.007	-	-	-	-	-	-	-	-	-	-	-	-	-	2	542
RBC	DGLA	0.01	0.007	0.006	0.284	0.017	0.026	0.579	-	-	-	-0.006	0.702	0.786	0.647	0.009	0.012	0.438	4	788
RBC	DGLA	0.1	0.001	0.005	0.793	0.001	0.015	0.943	-	-	-	1.23e-04	0.989	0.850	0.792	-0.002	0.008	0.767	14	2375
RBC	DGLA	0.3	3.29e-04	0.003	0.896	0.002	0.010	0.854	-	-	-	-0.001	0.869	0.997	0.996	-0.002	0.005	0.702	26	5970
Plasma	AA	0.001	-0.004	0.007	0.576	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4616
RBC	AA	0.001	0.016	0.008	0.050	-0.021	0.063	0.793	-	-	-	0.015	0.648	0.821	0.914	0.013	0.020	0.527	3	268
RBC	AA	0.01	0.011	0.010	0.294	-0.031	0.058	0.684	-	-	-	0.018	0.582	0.711	0.767	0.008	0.020	0.670	3	287
RBC	AA	0.1	-0.004	0.008	0.580	-0.024	0.042	0.599	-	-	-	0.008	0.651	0.876	0.821	-0.012	0.014	0.399	7	584
RBC	AA	0.3	0.001	0.004	0.754	-0.002	0.024	0.946	-	-	-	0.001	0.899	0.991	0.983	0.002	0.010	0.873	14	1440
Plasma	DPA-n3	0.001	-0.005	0.009	0.579	-0.027	0.041	0.628	-	-	-	0.007	0.650	0.809	0.828	-0.007	0.020	0.716	3	835
Plasma	DPA-n3	0.01	-0.005	0.009	0.577	-0.027	0.041	0.627	-	-	-	0.007	0.648	0.809	0.836	-0.007	0.019	0.708	3	937
Plasma	DPA-n3	0.1	-0.009	0.009	0.293	-0.035	0.026	0.202	-	-	-	0.008	0.273	0.949	0.970	-0.006	0.016	0.731	14	1506
Plasma	DPA-n3	0.3	-0.009	0.007	0.224	-0.006	0.019	0.741	-	-	-	-0.001	0.900	0.883	0.852	-0.006	0.012	0.582	29	3466
RBC	DPA-n3	0.001	-0.014	0.001	6.05e-136	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.01	-0.014	0.001	6.05e-136	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.1	-0.014	0.001	6.05e-136	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.3	-0.014	0.001	6.05e-136	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DTA	0.001	-	-	-	-	-	-	-0.009	0.036	0.794	-	-	-	-	-	-	-	1	80
RBC	DTA	0.01	-	-	-	-	-	-	-0.009	0.036	0.794	-	-	-	-	-	-	-	1	80
RBC	DTA	0.1	-	-	-	-	-	-	-0.009	0.036	0.794	-	-	-	-	-	-	-	1	80
RBC	DTA	0.3	0.003	0.017	0.858	-	-	-	-	-	-	-	-	-	-	-	-	-	2	114
Plasma	DHA	0.001	-	-	-	-	-	-	0.042	0.075	0.574	-	-	-	-	-	-	-	1	65
Plasma	DHA	0.01	-	-	-	-	-	-	0.042	0.075	0.574	-	-	-	-	-	-	-	1	64
Plasma	DHA	0.1	-	-	-	-	-	-	0.042	0.075	0.574	-	-	-	-	-	-	-	1	64
Plasma	DHA	0.3	0.049	0.010	1.56e-06	-	-	-	-	-	-	-	-	-	-	-	-	-	2	95

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 10. Forward Mendelian randomization estimates of associations of genetically predicted polyunsaturated fatty acids with COVID-19 severity based on the release 4 HGI A2.

			IVW_MRE			MR-Egger			Wald ratio			MR-Egger intercept		Heterogeneity test		Weighted median				
Group name	**PUFA**	**R^2**	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	***P***	***P*_IVW**	***P*_Egger**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	0.001	-	-	-	-	-	-	0.067	0.092	0.467	-	-	-	-	-	-	-	1	256
Plasma	ALA	0.01	-	-	-	-	-	-	0.067	0.093	0.467	-	-	-	-	-	-	-	1	312
Plasma	ALA	0.1	0.056	0.049	0.247	-0.092	0.177	0.653	-	-	-	0.041	0.451	0.739	0.820	0.045	0.084	0.596	4	436
Plasma	ALA	0.3	0.087	0.049	0.075	-0.130	0.137	0.364	-	-	-	0.054	0.120	0.398	0.551	0.069	0.066	0.295	13	1107
RBC	ALA	0.001	-	-	-	-	-	-	-0.070	0.173	0.687	-	-	-	-	-	-	-	1	31
RBC	ALA	0.01	-	-	-	-	-	-	-0.070	0.173	0.687	-	-	-	-	-	-	-	1	31
RBC	ALA	0.1	-	-	-	-	-	-	-0.070	0.173	0.687	-	-	-	-	-	-	-	1	31
RBC	ALA	0.3	-	-	-	-	-	-	-0.070	0.173	0.687	-	-	-	-	-	-	-	1	31
Plasma	LA	0.001	0.050	0.030	0.093	0.001	0.083	0.993	-	-	-	0.021	0.590	0.725	0.777	0.048	0.052	0.351	3	1329
RBC	LA	0.001	-	-	-	-	-	-	0.037	0.081	0.645	-	-	-	-	-	-	-	1	133
RBC	LA	0.01	-	-	-	-	-	-	0.037	0.081	0.645	-	-	-	-	-	-	-	1	133
RBC	LA	0.1	0.059	0.038	0.121	-	-	-	-	-	-	-	-	-	-	-	-	-	2	175
RBC	LA	0.3	0.059	0.045	0.185	-0.177	0.221	0.448	-	-	-	0.070	0.311	0.312	0.332	0.041	0.057	0.468	9	566
Plasma	GLA	0.001	-0.051	0.102	0.614	-	-	-	-	-	-	-	-	-	-	-	-	-	2	293
RBC	GLA	0.001	-	-	-	-	-	-	0.056	0.139	0.687	-	-	-	-	-	-	-	1	49
RBC	GLA	0.01	-	-	-	-	-	-	0.056	0.139	0.687	-	-	-	-	-	-	-	1	49
RBC	GLA	0.1	-	-	-	-	-	-	0.056	0.139	0.687	-	-	-	-	-	-	-	1	49
RBC	GLA	0.3	-	-	-	-	-	-	0.056	0.139	0.687	-	-	-	-	-	-	-	1	49
Plasma	DGLA	0.001	0.057	0.024	0.016	-	-	-	-	-	-	-	-	-	-	-	-	-	2	1417
RBC	DGLA	0.001	-0.003	0.109	0.975	-	-	-	-	-	-	-	-	-	-	-	-	-	2	542
RBC	DGLA	0.01	0.034	0.064	0.598	-0.130	0.142	0.456	-	-	-	0.095	0.334	0.021	0.068	0.053	0.052	0.303	4	788
RBC	DGLA	0.1	0.052	0.023	0.021	0.022	0.053	0.690	-	-	-	0.020	0.538	0.229	0.198	0.037	0.028	0.187	14	2375
RBC	DGLA	0.3	0.044	0.014	0.002	0.001	0.034	0.974	-	-	-	0.028	0.185	0.299	0.345	0.028	0.020	0.166	26	5970
Plasma	AA	0.001	-0.022	0.029	0.440	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4616
RBC	AA	0.001	4.31e-04	0.067	0.995	-0.195	0.215	0.532	-	-	-	0.077	0.514	0.285	0.253	-0.002	0.073	0.978	3	268
RBC	AA	0.01	0.005	0.067	0.937	-0.146	0.223	0.630	-	-	-	0.063	0.601	0.275	0.193	0.005	0.068	0.939	3	287
RBC	AA	0.1	-0.099	0.042	0.017	-0.087	0.145	0.574	-	-	-	-0.005	0.935	0.358	0.252	-0.076	0.052	0.144	7	584
RBC	AA	0.3	-0.069	0.028	0.014	0.004	0.086	0.966	-	-	-	-0.030	0.387	0.176	0.172	-0.059	0.034	0.083	14	1440
Plasma	DPA-n3	0.001	-0.089	0.053	0.093	-0.022	0.157	0.913	-	-	-	-0.023	0.717	0.424	0.237	-0.086	0.061	0.158	3	835
Plasma	DPA-n3	0.01	-0.090	0.053	0.089	-0.024	0.157	0.903	-	-	-	-0.022	0.725	0.430	0.238	-0.087	0.059	0.141	3	937
Plasma	DPA-n3	0.1	-0.105	0.039	0.006	0.004	0.086	0.963	-	-	-	-0.034	0.171	0.614	0.716	-0.054	0.057	0.350	14	1506
Plasma	DPA-n3	0.3	-0.101	0.029	0.001	-0.009	0.064	0.894	-	-	-	-0.028	0.120	0.437	0.522	-0.052	0.042	0.218	29	3466
RBC	DPA-n3	0.001	-0.178	0.199	0.370	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.01	-0.178	0.199	0.370	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.1	-0.178	0.199	0.370	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.3	-0.178	0.199	0.370	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DTA	0.001	-	-	-	-	-	-	-0.052	0.108	0.632	-	-	-	-	-	-	-	1	80
RBC	DTA	0.01	-	-	-	-	-	-	-0.052	0.108	0.632	-	-	-	-	-	-	-	1	80
RBC	DTA	0.1	-	-	-	-	-	-	-0.052	0.108	0.632	-	-	-	-	-	-	-	1	80
RBC	DTA	0.3	-0.091	0.068	0.182	-	-	-	-	-	-	-	-	-	-	-	-	-	2	114
Plasma	DHA	0.001	-	-	-	-	-	-	0.491	0.217	0.024	-	-	-	-	-	-	-	1	65
Plasma	DHA	0.01	-	-	-	-	-	-	0.490	0.217	0.024	-	-	-	-	-	-	-	1	64
Plasma	DHA	0.1	-	-	-	-	-	-	0.490	0.217	0.024	-	-	-	-	-	-	-	1	64
Plasma	DHA	0.3	0.401	0.164	0.014	-	-	-	-	-	-	-	-	-	-	-	-	-	2	95

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 11. Forward Mendelian randomization estimates of associations of genetically predicted polyunsaturated fatty acids with COVID-19 severity based on the release 4 HGI B2.

			IVW_MRE			**MR-Egger**			**Wald ratio**			**MR-Egger intercept**		**Heterogeneity test**		**Weighted median**				
Group name	**PUFA**	**R^2**	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	***P***	***P*_IVW**	***P*_Egger**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	0.001	-	-	-	-	-	-	0.105	0.076	0.166	-	-	-	-	-	-	-	1	256
Plasma	ALA	0.01	-	-	-	-	-	-	0.106	0.076	0.166	-	-	-	-	-	-	-	1	312
Plasma	ALA	0.1	0.136	0.082	0.096	-0.040	0.201	0.859	-	-	-	0.050	0.436	0.124	0.141	0.130	0.071	0.067	4	436
Plasma	ALA	0.3	0.150	0.040	1.44e-04	-0.117	0.109	0.309	-	-	-	0.066	0.025	0.340	0.825	0.108	0.050	0.032	13	1107
RBC	ALA	0.001	-	-	-	-	-	-	0.092	0.146	0.526	-	-	-	-	-	-	-	1	31
RBC	ALA	0.01	-	-	-	-	-	-	0.092	0.146	0.526	-	-	-	-	-	-	-	1	31
RBC	ALA	0.1	-	-	-	-	-	-	0.092	0.146	0.526	-	-	-	-	-	-	-	1	31
RBC	ALA	0.3	-	-	-	-	-	-	0.092	0.146	0.526	-	-	-	-	-	-	-	1	31
Plasma	LA	0.001	0.073	0.034	0.032	0.011	0.070	0.900	-	-	-	0.027	0.463	0.531	0.969	0.071	0.043	0.098	3	1329
RBC	LA	0.001	-	-	-	-	-	-	0.118	0.067	0.079	-	-	-	-	-	-	-	1	133
RBC	LA	0.01	-	-	-	-	-	-	0.118	0.067	0.079	-	-	-	-	-	-	-	1	133
RBC	LA	0.1	0.138	0.035	9.47e-05	-	-	-	-	-	-	-	-	-	-	-	-	-	2	175
RBC	LA	0.3	0.123	0.019	1.84e-10	-0.025	0.172	0.888	-	-	-	0.044	0.410	0.950	0.962	0.122	0.041	0.003	9	566
Plasma	GLA	0.001	-0.091	0.113	0.417	-	-	-	-	-	-	-	-	-	-	-	-	-	2	293
RBC	GLA	0.001	-	-	-	-	-	-	-0.074	0.117	0.526	-	-	-	-	-	-	-	1	49
RBC	GLA	0.01	-	-	-	-	-	-	-0.074	0.117	0.526	-	-	-	-	-	-	-	1	49
RBC	GLA	0.1	-	-	-	-	-	-	-0.074	0.117	0.526	-	-	-	-	-	-	-	1	49
RBC	GLA	0.3	-	-	-	-	-	-	-0.074	0.117	0.526	-	-	-	-	-	-	-	1	49
Plasma	DGLA	0.001	0.077	0.010	8.31e-14	-	-	-	-	-	-	-	-	-	-	-	-	-	2	1417
RBC	DGLA	0.001	0.048	0.044	0.271	-	-	-	-	-	-	-	-	-	-	-	-	-	2	542
RBC	DGLA	0.01	0.056	0.026	0.029	-0.039	0.070	0.637	-	-	-	0.055	0.279	0.472	0.837	0.032	0.032	0.316	4	788
RBC	DGLA	0.1	0.043	0.017	0.010	0.036	0.040	0.394	-	-	-	0.005	0.841	0.396	0.324	0.032	0.022	0.138	14	2375
RBC	DGLA	0.3	0.051	0.010	1.07e-07	0.023	0.026	0.388	-	-	-	0.018	0.263	0.736	0.758	0.046	0.016	0.003	26	5970
Plasma	AA	0.001	-0.036	0.030	0.221	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4616
RBC	AA	0.001	-0.080	0.041	0.053	-0.099	0.188	0.692	-	-	-	0.008	0.933	0.481	0.229	-0.054	0.060	0.369	3	268
RBC	AA	0.01	-0.078	0.041	0.058	-0.076	0.176	0.740	-	-	-	-0.001	0.994	0.470	0.219	-0.051	0.056	0.360	3	287
RBC	AA	0.1	-0.116	0.019	1.50e-09	-0.077	0.105	0.497	-	-	-	-0.015	0.711	0.897	0.839	-0.120	0.039	0.002	7	584
RBC	AA	0.3	-0.084	0.013	5.54e-11	0.005	0.060	0.940	-	-	-	-0.037	0.149	0.961	0.994	-0.068	0.026	0.008	14	1440
Plasma	DPA-n3	0.001	-0.082	0.024	0.001	-0.108	0.106	0.495	-	-	-	0.009	0.831	0.769	0.502	-0.086	0.050	0.088	3	835
Plasma	DPA-n3	0.01	-0.082	0.024	0.001	-0.109	0.107	0.492	-	-	-	0.009	0.824	0.775	0.512	-0.086	0.050	0.086	3	937
Plasma	DPA-n3	0.1	-0.120	0.031	1.04e-04	-0.033	0.069	0.642	-	-	-	-0.027	0.169	0.620	0.724	-0.078	0.048	0.100	14	1506
Plasma	DPA-n3	0.3	-0.116	0.021	5.54e-08	-0.029	0.051	0.580	-	-	-	-0.026	0.068	0.661	0.797	-0.085	0.033	0.010	29	3466
RBC	DPA-n3	0.001	-0.162	0.028	1.19e-08	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.01	-0.162	0.028	1.19e-08	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.1	-0.162	0.028	1.19e-08	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.3	-0.162	0.028	1.19e-08	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DTA	0.001	-	-	-	-	-	-	-0.103	0.088	0.244	-	-	-	-	-	-	-	1	80
RBC	DTA	0.01	-	-	-	-	-	-	-0.103	0.088	0.244	-	-	-	-	-	-	-	1	80
RBC	DTA	0.1	-	-	-	-	-	-	-0.103	0.088	0.244	-	-	-	-	-	-	-	1	80
RBC	DTA	0.3	-0.152	0.077	0.048	-	-	-	-	-	-	-	-	-	-	-	-	-	2	114
Plasma	DHA	0.001	-	-	-	-	-	-	0.260	0.185	0.159	-	-	-	-	-	-	-	1	65
Plasma	DHA	0.01	-	-	-	-	-	-	0.260	0.184	0.159	-	-	-	-	-	-	-	1	64
Plasma	DHA	0.1	-	-	-	-	-	-	0.260	0.184	0.159	-	-	-	-	-	-	-	1	64
Plasma	DHA	0.3	0.270	0.018	1.86e-51	-	-	-	-	-	-	-	-	-	-	-	-	-	2	95

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 12. Forward Mendelian randomization estimates of associations of genetically predicted polyunsaturated fatty acids with COVID-19 severity based on the release 4 HGI B1.

			IVW_MRE			MR-Egger			Wald ratio			MR-Egger intercept		Heterogeneity test		Weighted median				
Group name	**PUFA**	**R^2**	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	***P***	***P*_IVW**	***P*_Egger**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	0.001	-	-	-	-	-	-	0.080	0.137	0.558	-	-	-	-	-	-	-	1	256
Plasma	ALA	0.01	-	-	-	-	-	-	0.081	0.138	0.558	-	-	-	-	-	-	-	1	312
Plasma	ALA	0.1	0.174	0.155	0.261	-0.085	0.408	0.855	-	-	-	0.073	0.558	0.068	0.057	0.124	0.130	0.338	4	436
Plasma	ALA	0.3	0.142	0.072	0.050	-0.119	0.210	0.583	-	-	-	0.064	0.214	0.100	0.140	0.052	0.083	0.531	13	1107
RBC	ALA	0.001	-	-	-	-	-	-	0.125	0.248	0.615	-	-	-	-	-	-	-	1	31
RBC	ALA	0.01	-	-	-	-	-	-	0.125	0.248	0.615	-	-	-	-	-	-	-	1	31
RBC	ALA	0.1	-	-	-	-	-	-	0.125	0.248	0.615	-	-	-	-	-	-	-	1	31
RBC	ALA	0.3	-	-	-	-	-	-	0.125	0.248	0.615	-	-	-	-	-	-	-	1	31
Plasma	LA	0.001	0.036	0.028	0.198	0.085	0.127	0.624	-	-	-	-0.021	0.712	0.877	0.871	0.037	0.080	0.640	3	1329
RBC	LA	0.001	-	-	-	-	-	-	0.051	0.113	0.651	-	-	-	-	-	-	-	1	133
RBC	LA	0.01	-	-	-	-	-	-	0.051	0.113	0.651	-	-	-	-	-	-	-	1	133
RBC	LA	0.1	0.113	0.110	0.306	-	-	-	-	-	-	-	-	-	-	-	-	-	2	175
RBC	LA	0.3	0.146	0.049	0.003	-0.098	0.296	0.750	-	-	-	0.072	0.430	0.598	0.570	0.145	0.076	0.057	9	566
Plasma	GLA	0.001	-0.103	0.017	2.42e-09	-	-	-	-	-	-	-	-	-	-	-	-	-	2	293
RBC	GLA	0.001	-	-	-	-	-	-	-0.100	0.199	0.615	-	-	-	-	-	-	-	1	49
RBC	GLA	0.01	-	-	-	-	-	-	-0.100	0.199	0.615	-	-	-	-	-	-	-	1	49
RBC	GLA	0.1	-	-	-	-	-	-	-0.100	0.199	0.615	-	-	-	-	-	-	-	1	49
RBC	GLA	0.3	-	-	-	-	-	-	-0.100	0.199	0.615	-	-	-	-	-	-	-	1	49
Plasma	DGLA	0.001	0.025	0.048	0.595	-	-	-	-	-	-	-	-	-	-	-	-	-	2	1417
RBC	DGLA	0.001	-0.015	0.013	0.231	-	-	-	-	-	-	-	-	-	-	-	-	-	2	542
RBC	DGLA	0.01	0.005	0.028	0.855	-0.076	0.117	0.582	-	-	-	0.048	0.530	0.754	0.731	-0.008	0.050	0.867	4	788
RBC	DGLA	0.1	0.041	0.032	0.202	0.062	0.081	0.458	-	-	-	-0.013	0.778	0.175	0.134	0.046	0.038	0.224	14	2375
RBC	DGLA	0.3	0.041	0.020	0.034	0.055	0.051	0.293	-	-	-	-0.008	0.780	0.137	0.111	0.038	0.025	0.130	26	5970
Plasma	AA	0.001	-0.031	0.014	0.023	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4616
RBC	AA	0.001	-0.216	0.082	0.008	0.061	0.251	0.848	-	-	-	-0.113	0.454	0.312	0.320	-0.207	0.088	0.019	3	268
RBC	AA	0.01	-0.218	0.080	0.006	0.055	0.235	0.854	-	-	-	-0.114	0.435	0.326	0.393	-0.209	0.088	0.017	3	287
RBC	AA	0.1	-0.112	0.062	0.073	0.079	0.225	0.738	-	-	-	-0.074	0.416	0.172	0.167	-0.039	0.069	0.577	7	584
RBC	AA	0.3	-0.068	0.035	0.051	0.107	0.103	0.322	-	-	-	-0.071	0.101	0.319	0.474	-0.042	0.046	0.361	14	1440
Plasma	DPA-n3	0.001	-0.117	0.071	0.097	-0.018	0.177	0.936	-	-	-	-0.033	0.637	0.495	0.319	-0.087	0.087	0.317	3	835
Plasma	DPA-n3	0.01	-0.118	0.071	0.093	-0.021	0.177	0.926	-	-	-	-0.032	0.643	0.501	0.320	-0.089	0.093	0.340	3	937
Plasma	DPA-n3	0.1	-0.121	0.065	0.061	0.003	0.131	0.980	-	-	-	-0.039	0.296	0.143	0.160	-0.096	0.079	0.226	14	1506
Plasma	DPA-n3	0.3	-0.124	0.042	0.003	0.008	0.094	0.932	-	-	-	-0.040	0.132	0.060	0.092	-0.053	0.055	0.336	29	3466
RBC	DPA-n3	0.001	-0.240	0.048	6.15e-07	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.01	-0.240	0.048	6.15e-07	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.1	-0.240	0.048	6.15e-07	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.3	-0.240	0.048	6.15e-07	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DTA	0.001	-	-	-	-	-	-	-0.089	0.154	0.563	-	-	-	-	-	-	-	1	80
RBC	DTA	0.01	-	-	-	-	-	-	-0.089	0.154	0.563	-	-	-	-	-	-	-	1	80
RBC	DTA	0.1	-	-	-	-	-	-	-0.089	0.154	0.563	-	-	-	-	-	-	-	1	80
RBC	DTA	0.3	-0.232	0.190	0.223	-	-	-	-	-	-	-	-	-	-	-	-	-	2	114
Plasma	DHA	0.001	-	-	-	-	-	-	0.468	0.329	0.155	-	-	-	-	-	-	-	1	65
Plasma	DHA	0.01	-	-	-	-	-	-	0.467	0.328	0.155	-	-	-	-	-	-	-	1	64
Plasma	DHA	0.1	-	-	-	-	-	-	0.467	0.328	0.155	-	-	-	-	-	-	-	1	64
Plasma	DHA	0.3	0.362	0.145	0.013	-	-	-	-	-	-	-	-	-	-	-	-	-	2	95

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 13. Forward Mendelian randomization estimates of associations of genetically predicted polyunsaturated fatty acids with COVID-19 susceptibility based on the release 4 HGI C2.

			IVW_MRE			**MR-Egger**			**Wald ratio**			**MR-Egger intercept**		**Heterogeneity test**		**Weighted median**				
Group name	**PUFA**	**R^2**	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	***P***	***P*_IVW**	***P*_Egger**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	0.001	-	-	-	-	-	-	0.005	0.047	0.908	-	-	-	-	-	-	-	1	256
Plasma	ALA	0.01	-	-	-	-	-	-	0.005	0.048	0.908	-	-	-	-	-	-	-	1	312
Plasma	ALA	0.1	0.003	0.011	0.782	-0.012	0.086	0.904	-	-	-	0.004	0.868	0.957	0.870	0.007	0.039	0.861	4	436
Plasma	ALA	0.3	-0.003	0.015	0.811	-0.019	0.063	0.775	-	-	-	0.004	0.805	0.937	0.905	-0.013	0.028	0.643	13	1107
RBC	ALA	0.001	-	-	-	-	-	-	-0.023	0.090	0.796	-	-	-	-	-	-	-	1	31
RBC	ALA	0.01	-	-	-	-	-	-	-0.023	0.090	0.796	-	-	-	-	-	-	-	1	31
RBC	ALA	0.1	-	-	-	-	-	-	-0.023	0.090	0.796	-	-	-	-	-	-	-	1	31
RBC	ALA	0.3	-	-	-	-	-	-	-0.023	0.090	0.796	-	-	-	-	-	-	-	1	31
Plasma	LA	0.001	0.009	0.028	0.740	-0.029	0.044	0.625	-	-	-	0.017	0.465	0.326	0.318	0.003	0.027	0.900	3	1329
RBC	LA	0.001	-	-	-	-	-	-	-0.003	0.042	0.949	-	-	-	-	-	-	-	1	133
RBC	LA	0.01	-	-	-	-	-	-	-0.003	0.042	0.949	-	-	-	-	-	-	-	1	133
RBC	LA	0.1	-0.002	0.001	0.168	-	-	-	-	-	-	-	-	-	-	-	-	-	2	175
RBC	LA	0.3	-0.009	0.014	0.518	0.016	0.106	0.885	-	-	-	-0.007	0.816	0.835	0.758	-0.016	0.025	0.527	9	566
Plasma	GLA	0.001	-0.005	0.004	0.230	-	-	-	-	-	-	-	-	-	-	-	-	-	2	293
RBC	GLA	0.001	-	-	-	-	-	-	0.019	0.072	0.796	-	-	-	-	-	-	-	1	49
RBC	GLA	0.01	-	-	-	-	-	-	0.019	0.072	0.796	-	-	-	-	-	-	-	1	49
RBC	GLA	0.1	-	-	-	-	-	-	0.019	0.072	0.796	-	-	-	-	-	-	-	1	49
RBC	GLA	0.3	-	-	-	-	-	-	0.019	0.072	0.796	-	-	-	-	-	-	-	1	49
Plasma	DGLA	0.001	0.003	0.001	1.64e-11	-	-	-	-	-	-	-	-	-	-	-	-	-	2	1417
RBC	DGLA	0.001	0.029	0.011	0.008	-	-	-	-	-	-	-	-	-	-	-	-	-	2	542
RBC	DGLA	0.01	0.017	0.015	0.270	0.032	0.046	0.556	-	-	-	-0.009	0.751	0.429	0.273	0.022	0.019	0.240	4	788
RBC	DGLA	0.1	0.003	0.009	0.742	-0.004	0.023	0.853	-	-	-	0.005	0.727	0.507	0.436	-0.015	0.013	0.254	14	2375
RBC	DGLA	0.3	-4.41e-04	0.005	0.936	0.001	0.016	0.965	-	-	-	-0.001	0.938	0.800	0.755	-0.009	0.009	0.306	26	5970
Plasma	AA	0.001	-0.002	0.001	0.047	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4616
RBC	AA	0.001	-0.001	0.015	0.952	0.004	0.096	0.973	-	-	-	-0.002	0.966	0.756	0.455	-0.007	0.031	0.823	3	268
RBC	AA	0.01	-0.007	0.019	0.705	-0.019	0.087	0.865	-	-	-	0.005	0.911	0.634	0.345	-0.010	0.032	0.767	3	287
RBC	AA	0.1	-0.004	0.017	0.796	-0.011	0.064	0.873	-	-	-	0.002	0.921	0.542	0.416	0.013	0.025	0.607	7	584
RBC	AA	0.3	0.003	0.010	0.772	-0.003	0.037	0.941	-	-	-	0.002	0.877	0.792	0.727	0.007	0.016	0.651	14	1440
Plasma	DPA-n3	0.001	-0.001	0.024	0.961	-0.049	0.063	0.580	-	-	-	0.016	0.549	0.509	0.432	-0.007	0.030	0.810	3	835
Plasma	DPA-n3	0.01	-0.001	0.024	0.956	-0.050	0.063	0.575	-	-	-	0.016	0.545	0.509	0.439	-0.007	0.030	0.812	3	937
Plasma	DPA-n3	0.1	-0.005	0.015	0.717	-0.036	0.040	0.384	-	-	-	0.010	0.392	0.902	0.905	-0.006	0.026	0.834	14	1506
Plasma	DPA-n3	0.3	0.001	0.010	0.937	0.010	0.030	0.736	-	-	-	-0.003	0.729	0.955	0.943	0.017	0.018	0.358	29	3466
RBC	DPA-n3	0.001	-0.010	0.004	0.004	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.01	-0.010	0.004	0.004	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.1	-0.010	0.004	0.004	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DPA-n3	0.3	-0.010	0.004	0.004	-	-	-	-	-	-	-	-	-	-	-	-	-	2	62
RBC	DTA	0.001	-	-	-	-	-	-	0.003	0.055	0.963	-	-	-	-	-	-	-	1	80
RBC	DTA	0.01	-	-	-	-	-	-	0.003	0.055	0.963	-	-	-	-	-	-	-	1	80
RBC	DTA	0.1	-	-	-	-	-	-	0.003	0.055	0.963	-	-	-	-	-	-	-	1	80
RBC	DTA	0.3	0.015	0.018	0.391	-	-	-	-	-	-	-	-	-	-	-	-	-	2	114
Plasma	DHA	0.001	-	-	-	-	-	-	0.046	0.114	0.689	-	-	-	-	-	-	-	1	65
Plasma	DHA	0.01	-	-	-	-	-	-	0.045	0.113	0.689	-	-	-	-	-	-	-	1	64
Plasma	DHA	0.1	-	-	-	-	-	-	0.045	0.113	0.689	-	-	-	-	-	-	-	1	64
Plasma	DHA	0.3	0.029	0.025	0.245	-	-	-	-	-	-	-	-	-	-	-	-	-	2	95

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 14. Reverse Mendelian randomization estimates of associations of genetically predicted COVID-19 severity with polyunsaturated fatty acids based on the release 5 HGI A2 (COVID-19 SNP *P* < 5e-8).

		IVW_MRE			**MR-Egger**			**MR-Egger intercept**		**Heterogeneity test**		**Weighted median**				
Group name	**PUFA**	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	***P***	***P*_IVW**	***P*_Egger**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	0.02	0.009	0.019	-	-	-	-	-	-	-	-	-	-	2	119
RBC	ALA	0.008	0.009	0.37	0.019	0.023	0.43	-0.004	0.596	0.544	0.464	0.013	0.012	0.31	8	536
RBC	LA	-0.004	0.003	0.241	-0.014	0.009	0.146	0.003	0.229	0.527	0.634	-0.005	0.004	0.233	8	536
RBC	GLA	-0.006	0.006	0.279	0.015	0.033	0.668	-0.007	0.515	0.991	0.994	-0.008	0.016	0.603	8	536
RBC	DGLA	-0.004	0.004	0.29	-0.01	0.012	0.444	0.002	0.601	0.802	0.744	-0.004	0.006	0.494	8	536
RBC	AA	0.001	0.002	0.595	0.006	0.006	0.335	-0.002	0.373	0.747	0.764	0.001	0.003	0.799	8	536
Plasma	DPA-n3	-0.031	0.053	0.554	-	-	-	-	-	-	-	-	-	-	2	119
RBC	DPA-n3	0.004	0.003	0.165	-0.002	0.009	0.862	0.002	0.539	0.8	0.757	0.003	0.005	0.466	8	536
RBC	DTA	0.007	0.005	0.152	-0.002	0.014	0.906	0.003	0.509	0.58	0.523	-0.001	0.007	0.914	8	536
Plasma	DHA	-0.061	0.164	0.71	-	-	-	-	-	-	-	-	-	-	2	119

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 15. Reverse Mendelian randomization estimates of associations of genetically predicted COVID-19 severity with polyunsaturated fatty acids based on the release 5 HGI B2 (COVID-19 SNP *P* < 5e-8).

		IVW_MRE			MR-Egger			MR-Egger intercept		Heterogeneity test		Weighted median				
Group name	**PUFA**	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	***P***	***P*_IVW**	***P*_Egger**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	0.005	0.013	0.706	-	-	-	-	-	-	-	-	-	-	2	94
RBC	ALA	0.010	0.019	0.606	0.035	0.040	0.453	-0.006	0.527	0.132	0.109	0.021	0.016	0.192	5	438
RBC	LA	-0.005	0.005	0.302	-0.016	0.011	0.239	0.002	0.350	0.405	0.426	-0.008	0.006	0.208	5	438
RBC	GLA	-0.017	0.010	0.109	0.019	0.042	0.672	-0.008	0.392	0.901	0.996	-0.019	0.025	0.439	5	438
RBC	DGLA	-0.003	0.006	0.595	-0.004	0.015	0.831	1.08e-04	0.974	0.656	0.487	-0.005	0.009	0.547	5	438
RBC	AA	0.001	0.003	0.806	0.003	0.008	0.752	-4.23e-04	0.800	0.457	0.314	2.77e-05	0.004	0.995	5	438
Plasma	DPA-n3	0.022	0.012	0.062	-	-	-	-	-	-	-	-	-	-	2	94
RBC	DPA-n3	0.006	0.004	0.125	0.004	0.012	0.732	4.95e-04	0.843	0.686	0.528	0.005	0.007	0.423	5	438
RBC	DTA	0.005	0.009	0.551	-0.015	0.017	0.430	0.005	0.257	0.339	0.461	-0.002	0.010	0.805	5	438
Plasma	DHA	-0.107	0.044	0.014	-	-	-	-	-	-	-	-	-	-	2	94

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 16. Reverse Mendelian randomization estimates of associations of genetically predicted COVID-19 severity with polyunsaturated fatty acids based on the release 5 HGI B1 (COVID-19 SNP *P* < 5e-8).

		Wald ratio				
Group name	**PUFA**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	3.68E-04	0.005	0.939	1	34
RBC	ALA	-0.025	0.029	0.402	1	34
RBC	LA	-0.012	0.011	0.289	1	34
RBC	GLA	0.022	0.043	0.604	1	34
RBC	DGLA	-0.003	0.016	0.844	1	34
RBC	AA	0.012	0.007	0.1	1	34
Plasma	DPA-n3	-0.001	0.016	0.946	1	34
RBC	DPA-n3	-0.005	0.012	0.7	1	34
RBC	DTA	0.01	0.018	0.562	1	34
Plasma	DHA	0.104	0.079	0.186	1	34

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 17. Reverse Mendelian randomization estimates of associations of genetically predicted COVID-19 susceptibility with polyunsaturated fatty acids based on the release 5 HGI C2 (COVID-19 SNP *P* < 5e-8).

		IVW_MRE			MR-Egger			MR-Egger intercept		Heterogeneity test		Weighted median				
Group name	**PUFA**	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	***P***	***P*_IVW**	***P*_Egger**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	0.009	0.004	0.017	0.024	0.041	0.660	-0.001	0.770	0.794	0.572	0.008	0.009	0.393	3	139
RBC	ALA	0.038	0.017	0.026	0.133	0.150	0.425	-0.008	0.548	0.952	0.952	0.025	0.045	0.574	6	319
RBC	LA	-0.004	0.013	0.772	0.001	0.062	0.992	-3.71e-04	0.944	0.424	0.295	0.012	0.017	0.495	6	319
RBC	GLA	-0.026	0.057	0.656	-0.347	0.219	0.188	0.026	0.204	0.299	0.437	-0.021	0.068	0.760	6	319
RBC	DGLA	-0.004	0.024	0.870	0.060	0.108	0.606	-0.005	0.573	0.145	0.112	-0.026	0.026	0.322	6	319
RBC	AA	0.003	0.005	0.527	-0.022	0.037	0.577	0.002	0.513	0.876	0.863	0.004	0.011	0.735	6	319
Plasma	DPA-n3	-0.025	0.025	0.328	-0.202	0.137	0.380	0.014	0.414	0.400	0.749	-0.037	0.030	0.226	3	139
RBC	DPA-n3	-0.001	0.010	0.888	0.023	0.060	0.723	-0.002	0.700	0.814	0.722	0.006	0.018	0.756	6	319
RBC	DTA	-0.005	0.018	0.771	-0.122	0.089	0.243	0.009	0.249	0.616	0.785	-0.003	0.026	0.904	6	319
Plasma	DHA	0.149	0.014	6.08e-26	0.250	0.657	0.769	-0.008	0.901	0.988	0.998	0.160	0.141	0.256	3	139

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 18. Reverse Mendelian randomization estimates of associations of genetically predicted COVID-19 severity with polyunsaturated fatty acids based on the release 5 HGI A2 (COVID-19 SNP *P* < 5e-6).

		IVW_MRE			**MR-Egger**			**MR-Egger intercept**		**Heterogeneity test**		**Weighted median**				
Group name	**PUFA**	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	***P***	***P*_IVW**	***P*_Egger**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	0.002	0.003	0.568	-3.09e-04	0.011	0.979	3.44e-04	0.868	0.302	0.216	0.002	0.003	0.583	8	262
RBC	ALA	0.010	0.006	0.099	0.007	0.017	0.696	0.001	0.833	0.653	0.605	0.014	0.010	0.150	31	1078
RBC	LA	-0.004	0.002	0.057	-0.006	0.006	0.360	4.00e-04	0.775	0.722	0.679	-0.005	0.004	0.187	31	1078
RBC	GLA	-0.015	0.007	0.050	0.011	0.025	0.648	-0.006	0.265	0.948	0.957	-0.015	0.014	0.276	31	1078
RBC	DGLA	-0.002	0.003	0.459	-0.004	0.009	0.651	4.09e-04	0.836	0.666	0.618	-0.004	0.005	0.422	31	1078
RBC	AA	0.002	0.001	0.139	0.003	0.004	0.538	-1.56e-04	0.865	0.907	0.883	0.003	0.002	0.292	31	1078
Plasma	DPA-n3	-0.002	0.011	0.822	-0.016	0.045	0.736	0.002	0.768	0.075	0.049	0.008	0.012	0.533	8	262
RBC	DPA-n3	2.17e-04	0.003	0.933	0.002	0.007	0.763	-4.42e-04	0.770	0.479	0.432	0.002	0.004	0.567	31	1078
RBC	DTA	0.004	0.004	0.349	0.011	0.010	0.302	-0.002	0.455	0.521	0.499	0.003	0.006	0.645	31	1078
Plasma	DHA	-0.005	0.029	0.862	0.034	0.141	0.818	-0.007	0.783	0.769	0.675	-0.022	0.049	0.657	8	262

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 19. Reverse Mendelian randomization estimates of associations of genetically predicted COVID-19 severity with polyunsaturated fatty acids based on the release 5 HGI B2 (COVID-19 SNP *P* < 5e-6).

		IVW_MRE			MR-Egger			MR-Egger intercept		Heterogeneity test		Weighted median				
Group name	**PUFA**	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	***P***	***P*_IVW**	***P*_Egger**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	0.002	0.003	0.458	-0.006	0.014	0.688	0.001	0.556	0.190	0.160	0.002	0.004	0.613	13	350
RBC	ALA	0.006	0.008	0.514	0.010	0.022	0.653	-0.001	0.823	0.832	0.794	0.018	0.015	0.215	27	960
RBC	LA	-0.002	0.003	0.560	-0.012	0.008	0.175	0.002	0.193	0.948	0.967	-0.007	0.005	0.194	27	960
RBC	GLA	3.35e-04	0.012	0.977	0.027	0.032	0.399	-0.005	0.352	0.900	0.903	-0.004	0.022	0.867	27	960
RBC	DGLA	0.003	0.006	0.633	-0.002	0.013	0.887	0.001	0.694	0.179	0.152	-0.006	0.008	0.482	27	960
RBC	AA	-0.002	0.003	0.442	0.005	0.006	0.360	-0.001	0.162	0.216	0.266	0.001	0.004	0.813	27	960
Plasma	DPA-n3	-0.002	0.008	0.765	-0.053	0.039	0.201	0.006	0.207	0.777	0.852	-0.002	0.013	0.898	13	350
RBC	DPA-n3	0.004	0.005	0.403	0.001	0.010	0.961	0.001	0.723	0.108	0.089	0.005	0.006	0.456	27	960
RBC	DTA	-0.002	0.006	0.684	2.81e-05	0.013	0.998	-4.08e-04	0.840	0.497	0.443	-0.003	0.009	0.718	27	960
Plasma	DHA	-0.033	0.033	0.314	-0.073	0.193	0.712	0.005	0.836	0.880	0.831	-0.033	0.058	0.573	13	350

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 20. Reverse Mendelian randomization estimates of associations of genetically predicted COVID-19 severity with polyunsaturated fatty acids based on the release 5 HGI B1 (COVID-19 SNP *P* < 5e-6).

		IVW_MRE			**MR-Egger**			**MR-Egger intercept**		**Heterogeneity test**		**Weighted median**				
Group name	**PUFA**	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	***P***	***P*_IVW**	***P*_Egger**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	0.003	0.002	0.162	-0.004	0.014	0.810	0.002	0.679	0.674	0.486	0.003	0.004	0.440	3	81
RBC	ALA	0.009	0.014	0.529	0.046	0.038	0.244	-0.011	0.306	0.068	0.080	1.97e-04	0.016	0.990	13	317
RBC	LA	-0.001	0.004	0.891	-0.010	0.011	0.404	0.003	0.397	0.451	0.431	-0.002	0.006	0.698	13	317
RBC	GLA	0.025	0.015	0.097	0.032	0.043	0.467	-0.002	0.850	0.598	0.516	0.022	0.022	0.299	13	317
RBC	DGLA	-0.010	0.004	0.014	-0.017	0.016	0.293	0.002	0.610	0.947	0.929	-0.006	0.007	0.395	13	317
RBC	AA	-0.001	0.003	0.753	-0.005	0.009	0.629	0.001	0.687	0.091	0.068	-0.001	0.004	0.744	13	317
Plasma	DPA-n3	-0.004	0.007	0.566	-0.015	0.047	0.809	0.002	0.857	0.696	0.412	-0.002	0.014	0.856	3	81
RBC	DPA-n3	0.005	0.003	0.147	-0.001	0.012	0.948	0.002	0.615	0.866	0.831	0.005	0.006	0.388	13	317
RBC	DTA	-0.009	0.009	0.340	0.004	0.025	0.862	-0.004	0.582	0.035	0.028	-2.75e-05	0.010	0.998	13	317
Plasma	DHA	0.048	0.051	0.345	0.210	0.237	0.539	-0.035	0.609	0.482	0.327	0.050	0.066	0.453	3	81

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 21. Reverse Mendelian randomization estimates of associations of genetically predicted COVID-19 susceptibility with polyunsaturated fatty acids based on the release 5 HGI C2 (COVID-19 SNP *P* < 5e-6).

		IVW_MRE			MR-Egger			MR-Egger intercept		Heterogeneity test		Weighted median				
Group name	**PUFA**	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	***P***	***P*_IVW**	***P*_Egger**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	-0.003	0.009	0.759	0.046	0.037	0.262	-0.004	0.227	0.060	0.108	0.004	0.009	0.634	8	268
RBC	ALA	0.059	0.024	0.015	0.084	0.087	0.343	-0.002	0.760	0.304	0.261	0.053	0.032	0.103	26	792
RBC	LA	-0.004	0.007	0.572	-0.041	0.030	0.185	0.003	0.212	0.863	0.894	0.001	0.012	0.952	26	792
RBC	GLA	-0.008	0.034	0.826	-0.116	0.122	0.352	0.008	0.365	0.377	0.370	-0.047	0.048	0.323	26	792
RBC	DGLA	-0.011	0.015	0.451	-0.057	0.053	0.293	0.003	0.378	0.044	0.044	-0.003	0.019	0.868	26	792
RBC	AA	1.24e-04	0.005	0.980	0.001	0.020	0.952	-7.98e-05	0.955	0.761	0.712	0.001	0.008	0.910	26	792
Plasma	DPA-n3	-0.030	0.030	0.310	-0.056	0.144	0.712	0.002	0.862	0.054	0.032	-0.033	0.028	0.236	8	268
RBC	DPA-n3	4.15e-04	0.009	0.963	0.033	0.032	0.316	-0.002	0.303	0.511	0.518	0.004	0.013	0.744	26	792
RBC	DTA	0.011	0.013	0.378	-0.037	0.048	0.446	0.004	0.302	0.573	0.582	0.001	0.019	0.945	26	792
Plasma	DHA	-0.074	0.160	0.645	0.429	0.739	0.583	-0.036	0.511	0.014	0.012	0.132	0.127	0.300	8	268

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 22. Reverse Mendelian randomization estimates of associations of genetically predicted COVID-19 severity with polyunsaturated fatty acids based on the release 4 HGI A2 (COVID-19 SNP *P* < 5e-8).

		IVW_MRE			**MR-Egger**			**MR-Egger intercept**		**Heterogeneity test**		**Weighted median**				
Group name	**PUFA**	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	***P***	***P*_IVW**	***P*_Egger**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	0.001	0.006	0.874	0.125	0.071	0.331	-0.024	0.332	0.134	0.318	-0.002	0.005	0.677	3	135
RBC	ALA	0.008	0.009	0.383	0.014	0.022	0.558	-0.002	0.781	0.449	0.339	0.011	0.012	0.376	7	487
RBC	LA	-0.003	0.003	0.406	-0.011	0.008	0.226	0.003	0.301	0.514	0.564	-0.005	0.004	0.200	7	487
RBC	GLA	-0.006	0.006	0.350	0.014	0.030	0.650	-0.006	0.483	0.976	0.985	-0.009	0.016	0.592	7	487
RBC	DGLA	-0.003	0.004	0.338	-0.009	0.011	0.455	0.002	0.603	0.785	0.719	-0.004	0.006	0.500	7	487
RBC	AA	1.46e-04	0.001	0.918	0.004	0.005	0.479	-0.001	0.446	0.887	0.895	0.001	0.003	0.792	7	487
Plasma	DPA-n3	0.009	0.018	0.626	-0.293	0.296	0.503	0.058	0.493	0.230	0.231	0.012	0.015	0.432	3	135
RBC	DPA-n3	0.005	0.002	0.068	0.001	0.008	0.894	0.001	0.663	0.851	0.785	0.003	0.005	0.462	7	487
RBC	DTA	0.004	0.004	0.340	-0.007	0.012	0.587	0.004	0.346	0.699	0.738	-0.001	0.007	0.847	7	487
Plasma	DHA	-0.091	0.066	0.166	-0.032	1.141	0.982	-0.012	0.967	0.380	0.165	-0.080	0.070	0.254	3	135

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 23. Reverse Mendelian randomization estimates of associations of genetically predicted COVID-19 severity with polyunsaturated fatty acids based on the release 4 HGI B2 (COVID-19 SNP *P* < 5e-8).

		IVW_MRE			MR-Egger			Wald ratio			MR-Egger intercept		Heterogeneity test		Weighted median				
Group name	**PUFA**	**β**	**SE**	**P**	**β**	**SE**	**P**	**β**	**SE**	**P**	**β**	**P**	**P_IVW**	**P_Egger**	**β**	**SE**	**P**	**nsnps**	**F-statistic**
Plasma	ALA	-	-	-	-	-	-	0.03	0.015	0.049	-	-	-	-	-	-	-	1	61
RBC	ALA	0.005	0.013	0.688	0.022	0.03	0.501	-	-	-	-0.005	0.558	0.197	0.155	0.013	0.014	0.333	6	462
RBC	LA	-0.003	0.004	0.366	-0.011	0.009	0.29	-	-	-	0.002	0.402	0.498	0.48	-0.006	0.005	0.224	6	462
RBC	GLA	-0.01	0.009	0.279	0.018	0.034	0.625	-	-	-	-0.008	0.409	0.891	0.934	-0.012	0.019	0.542	6	462
RBC	DGLA	-0.005	0.005	0.349	-0.004	0.012	0.737	-	-	-	-8.21E-05	0.98	0.548	0.405	-0.004	0.007	0.546	6	462
RBC	AA	0.001	0.002	0.818	0.002	0.006	0.734	-	-	-	-4.40E-04	0.774	0.599	0.468	3.89E-04	0.003	0.905	6	462
Plasma	DPA-n3	-	-	-	-	-	-	-0.009	0.055	0.864	-	-	-	-	-	-	-	1	61
RBC	DPA-n3	0.005	0.003	0.079	0.003	0.009	0.792	-	-	-	0.001	0.767	0.786	0.675	0.004	0.005	0.429	6	462
RBC	DTA	0.005	0.006	0.422	-0.013	0.014	0.417	-	-	-	0.005	0.23	0.464	0.624	-0.002	0.008	0.826	6	462
Plasma	DHA	-	-	-	-	-	-	-0.027	0.155	0.862	-	-	-	-	-	-	-	1	61

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 24. Reverse Mendelian randomization estimates of associations of genetically predicted COVID-19 severity with polyunsaturated fatty acids based on the release 4 HGI B1 (COVID-19 SNP *P* < 5e-8).

		Wald ratio				
Group name	**PUFA**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
RBC	ALA	0.004	0.023	0.874	1	31
RBC	LA	-0.008	0.009	0.347	1	31
RBC	GLA	0.02	0.033	0.545	1	31
RBC	DGLA	0.001	0.012	0.91	1	31
RBC	AA	0.006	0.006	0.299	1	31
RBC	DPA-n3	-0.003	0.009	0.771	1	31
RBC	DTA	0.006	0.014	0.635	1	31

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 25. Reverse Mendelian randomization estimates of associations of genetically predicted COVID-19 susceptibility with polyunsaturated fatty acids based on the release 4 HGI C2 (COVID-19 SNP *P* < 5e-8).

		IVW_MRE			MR-Egger			Wald ratio			MR-Egger intercept		Heterogeneity test		Weighted median				
Group name	**PUFA**	**β**	**SE**	**P**	**β**	**SE**	**P**	**β**	**SE**	**P**	**β**	**P**	**P_IVW**	**P_Egger**	**β**	**SE**	**P**	**nsnps**	**F-statistic**
Plasma	ALA	-	-	-	-	-	-	0.066	0.034	0.049	-	-	-	-	-	-	-	1	31
RBC	ALA	0.034	0.018	0.057	-0.005	0.059	0.942	-	-	-	0.008	0.583	0.686	0.686	0.034	0.032	0.292	3	183
RBC	LA	-0.014	0.013	0.289	-0.020	0.037	0.687	-	-	-	0.001	0.885	0.238	0.096	-0.018	0.012	0.129	3	183
RBC	GLA	-0.022	0.024	0.352	0.001	0.087	0.995	-	-	-	-0.004	0.810	0.727	0.461	-0.017	0.046	0.709	3	183
RBC	DGLA	-0.011	0.026	0.666	-0.039	0.066	0.660	-	-	-	0.005	0.712	0.066	0.036	-0.005	0.016	0.757	3	183
RBC	AA	0.001	0.007	0.881	0.010	0.018	0.682	-	-	-	-0.002	0.675	0.388	0.230	0.002	0.008	0.756	3	183
Plasma	DPA-n3	-	-	-	-	-	-	-0.021	0.121	0.864	-	-	-	-	-	-	-	1	31
RBC	DPA-n3	0.012	0.009	0.176	-0.002	0.024	0.941	-	-	-	0.003	0.623	0.582	0.427	0.011	0.012	0.380	3	183
RBC	DTA	-0.005	0.039	0.891	-0.055	0.096	0.670	-	-	-	0.009	0.660	0.007	0.007	0.002	0.018	0.901	3	183
Plasma	DHA	-	-	-	-	-	-	-0.059	0.337	0.862	-	-	-	-	-	-	-	1	31

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 26. Reverse Mendelian randomization estimates of associations of genetically predicted COVID-19 severity with polyunsaturated fatty acids based on the release 4 HGI A2 (COVID-19 SNP *P* < 5e-6).

		IVW_MRE			MR-Egger			MR-Egger intercept		Heterogeneity test		Weighted median				
Group name	**PUFA**	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	***P***	***P*_IVW**	***P*_Egger**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	4.31e-04	0.004	0.909	0.019	0.024	0.464	-0.003	0.468	0.120	0.110	-0.001	0.004	0.685	6	202
RBC	ALA	0.012	0.007	0.080	-0.007	0.014	0.634	0.005	0.153	0.431	0.498	0.014	0.011	0.184	25	905
RBC	LA	-0.004	0.003	0.085	-0.006	0.005	0.279	4.86e-04	0.721	0.471	0.420	-0.006	0.004	0.126	25	905
RBC	GLA	-0.016	0.010	0.100	-0.011	0.021	0.609	-0.001	0.794	0.470	0.416	-0.006	0.014	0.692	25	905
RBC	DGLA	-0.001	0.004	0.809	1.97e-04	0.008	0.981	-3.03e-04	0.880	0.346	0.296	-0.004	0.006	0.456	25	905
RBC	AA	0.001	0.001	0.419	0.001	0.004	0.848	1.20e-04	0.891	0.849	0.810	0.002	0.002	0.454	25	905
Plasma	DPA-n3	0.007	0.009	0.446	-0.016	0.064	0.816	0.004	0.732	0.404	0.294	0.008	0.011	0.467	6	202
RBC	DPA-n3	0.004	0.003	0.155	0.005	0.006	0.367	-4.37e-04	0.763	0.486	0.433	0.003	0.004	0.404	25	905
RBC	DTA	0.004	0.004	0.366	-0.005	0.009	0.604	0.002	0.294	0.257	0.268	0.003	0.006	0.623	25	905
Plasma	DHA	-0.081	0.064	0.204	-0.155	0.403	0.720	0.012	0.860	0.067	0.037	-0.087	0.060	0.146	6	202

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 27. Reverse Mendelian randomization estimates of associations of genetically predicted COVID-19 severity with polyunsaturated fatty acids based on the release 4 HGI B2 (COVID-19 SNP *P* < 5e-6).

		IVW_MRE			**MR-Egger**			**MR-Egger intercept**		**Heterogeneity test**		**Weighted median**				
Group name	**PUFA**	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	***P***	***P*_IVW**	***P*_Egger**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	1.44e-04	0.005	0.975	-0.005	0.019	0.794	0.001	0.781	0.173	0.110	-0.001	0.005	0.889	6	180
RBC	ALA	0.005	0.005	0.357	0.005	0.015	0.761	-1.07e-05	0.997	0.990	0.985	0.014	0.011	0.197	32	1076
RBC	LA	-4.20e-04	0.003	0.874	-0.009	0.006	0.149	0.002	0.122	0.543	0.626	-0.005	0.004	0.219	32	1076
RBC	GLA	-0.016	0.008	0.043	0.014	0.023	0.529	-0.007	0.135	0.965	0.983	-0.019	0.015	0.208	32	1076
RBC	DGLA	-1.03e-04	0.004	0.977	0.004	0.008	0.640	-0.001	0.588	0.648	0.614	-0.003	0.006	0.569	32	1076
RBC	AA	3.42e-04	0.002	0.840	0.003	0.004	0.393	-0.001	0.387	0.605	0.595	-0.002	0.003	0.406	32	1076
Plasma	DPA-n3	0.005	0.013	0.726	0.019	0.056	0.757	-0.002	0.810	0.275	0.183	-0.011	0.015	0.482	6	180
RBC	DPA-n3	0.002	0.003	0.501	-2.94e-04	0.006	0.963	5.00e-04	0.696	0.585	0.542	0.002	0.004	0.571	32	1076
RBC	DTA	-2.57e-04	0.004	0.952	0.002	0.009	0.814	-0.001	0.767	0.477	0.430	-0.002	0.006	0.701	32	1076
Plasma	DHA	-0.058	0.037	0.120	-0.098	0.200	0.648	0.006	0.842	0.807	0.690	-0.046	0.065	0.480	6	180

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 28. Reverse Mendelian randomization estimates of associations of genetically predicted COVID-19 severity with polyunsaturated fatty acids based on the release 4 HGI B1 (COVID-19 SNP *P* < 5e-6).

		IVW_MRE			MR-Egger			Wald ratio			MR-Egger intercept		Heterogeneity test		Weighted median				
Group name	**PUFA**	**β**	**SE**	**P**	**β**	**SE**	**P**	**β**	**SE**	**P**	**β**	**P**	**P_IVW**	**P_Egger**	**β**	**SE**	**P**	**nsnps**	**F-statistic**
Plasma	ALA	-	-	-	-	-	-	0.006	0.006	0.317	-	-	-	-	-	-	-	1	22
RBC	ALA	0.002	0.009	0.834	-0.008	0.021	0.696	-	-	-	0.004	0.588	0.471	0.408	0.004	0.013	0.778	11	262
RBC	LA	0.001	0.003	0.807	-0.001	0.008	0.886	-	-	-	0.001	0.784	0.632	0.546	-0.001	0.005	0.771	11	262
RBC	GLA	0.011	0.014	0.420	0.072	0.030	0.037	-	-	-	-0.026	0.045	0.406	0.837	0.031	0.019	0.099	11	262
RBC	DGLA	0.004	0.006	0.492	0.001	0.013	0.960	-	-	-	0.001	0.778	0.180	0.133	0.001	0.006	0.842	11	262
RBC	AA	0.001	0.002	0.470	0.004	0.005	0.428	-	-	-	-0.001	0.528	0.863	0.837	0.003	0.003	0.359	11	262
Plasma	DPA-n3	-	-	-	-	-	-	0.001	0.021	0.976	-	-	-	-	-	-	-	1	22
RBC	DPA-n3	-0.003	0.004	0.409	-0.007	0.008	0.408	-	-	-	0.002	0.588	0.510	0.445	-0.002	0.005	0.716	11	262
RBC	DTA	0.009	0.004	0.016	0.019	0.012	0.152	-	-	-	-0.004	0.378	0.929	0.941	0.004	0.007	0.589	11	262
Plasma	DHA	-	-	-	-	-	-	0.109	0.095	0.249	-	-	-	-	-	-	-	1	22

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Supplementary Table 29. Reverse Mendelian randomization estimates of associations of genetically predicted COVID-19 susceptibility with polyunsaturated fatty acids based on the release 4 HGI C2 (COVID-19 SNP *P* < 5e-6).

		IVW_MRE			MR-Egger			MR-Egger intercept		Heterogeneity test		Weighted median				
Group name	**PUFA**	**β**	**SE**	***P***	**β**	**SE**	***P***	**β**	***P***	***P*_IVW**	***P*_Egger**	**β**	**SE**	***P***	**nsnps**	***F*-statistic**
Plasma	ALA	-0.001	0.006	0.891	0.021	0.053	0.705	-0.002	0.693	0.349	0.262	-0.002	0.007	0.756	7	172
RBC	ALA	0.013	0.011	0.206	-0.004	0.037	0.909	0.002	0.607	0.982	0.977	0.018	0.022	0.412	19	556
RBC	LA	0.001	0.006	0.881	-0.014	0.014	0.328	0.002	0.252	0.476	0.504	-1.91e-04	0.009	0.983	19	556
RBC	GLA	-0.030	0.015	0.043	-0.015	0.055	0.781	-0.002	0.776	0.990	0.985	-0.015	0.032	0.638	19	556
RBC	DGLA	-0.013	0.010	0.171	-0.020	0.023	0.401	0.001	0.754	0.166	0.133	-0.008	0.013	0.543	19	556
RBC	AA	-0.003	0.005	0.518	0.001	0.011	0.894	-0.001	0.658	0.183	0.152	-0.002	0.006	0.733	19	556
Plasma	DPA-n3	0.006	0.018	0.732	-0.178	0.151	0.293	0.014	0.275	0.341	0.390	0.019	0.023	0.417	7	172
RBC	DPA-n3	0.008	0.007	0.286	0.005	0.017	0.759	2.77e-04	0.883	0.212	0.168	0.005	0.010	0.587	19	556
RBC	DTA	-0.003	0.012	0.818	-0.019	0.029	0.515	0.002	0.538	0.050	0.043	-0.004	0.014	0.769	19	556
Plasma	DHA	-0.137	0.082	0.095	-0.840	0.710	0.290	0.055	0.364	0.467	0.463	-0.120	0.116	0.301	7	172

PUFA, polyunsaturated fatty acid; RBC, red blood cell; ALA, α-Linolenic acid; LA: linoleic acid; GLA, γ-Linoleic acid; DGLA, dihomo-γ-linoleic acid; AA, arachidonic acid; DPA-n3, docosapentaenoic acid; DTA, docosatetraenoic acid; DHA, docosahexaenoic acid; β, causal effect size; SE, standard error; IVW_MRE, inverse-variance weighted random-effects model; Egger, MR-Egger; nsnps, number of SNPs retained for this analysis.

Reference

1. Zhao JV, Schooling CM. Effect of linoleic acid on ischemic heart disease and its risk factors: a Mendelian randomization study. BMC Med 2019;17(1):61. doi: 10.1186/s12916-019-1293-x.
2. Zhang T, Au Yeung SL, Schooling CM. Associations of Arachidonic Acid Synthesis with Cardiovascular Risk Factors and Relation to Ischemic Heart Disease and Stroke: A Univariable and Multivariable Mendelian Randomization Study. Nutrients 2021;13(5). doi: 10.3390/nu13051489.
3. Yuan S, Back M, Bruzelius M, Mason AM, Burgess S, Larsson S. Plasma Phospholipid Fatty Acids, FADS1 and Risk of 15 Cardiovascular Diseases: A Mendelian Randomisation Study. Nutrients 2019;11(12). doi: 10.3390/nu11123001.
4. Yuan T, Si S, Li Y, Li W, Chen X, Liu C, Li J, Wang B, Hou L, Liu Y, et al. Roles for circulating polyunsaturated fatty acids in ischemic stroke and modifiable factors: a Mendelian randomization study. Nutr J 2020;19(1):70. doi: 10.1186/s12937-020-00582-4.
5. Liao LZ, Li WD, Liu Y, Li JP, Zhuang XD, Liao XX. Exploring the causal pathway from omega-6 levels to coronary heart disease: A network Mendelian randomization study. Nutr Metab Cardiovasc Dis 2020;30(2):233-40. doi: 10.1016/j.numecd.2019.09.013.
6. Mazidi M, Katsiki N, Shekoohi N, Banach M. Monounsaturated Fatty Acid Levels May Not Affect Cardiovascular Events: Results From a Mendelian Randomization Analysis. Front Nutr 2020;7:123. doi: 10.3389/fnut.2020.00123.
7. Zhang T, Zhao JV, Schooling CM. The associations of plasma phospholipid arachidonic acid with cardiovascular diseases: A Mendelian randomization study. EBioMedicine 2021;63:103189. doi: 10.1016/j.ebiom.2020.103189.
8. Yuan S, Larsson SC. Plasma Phospholipid Fatty Acids and Risk of Atrial Fibrillation: A Mendelian Randomization Study. Nutrients 2019;11(7). doi: 10.3390/nu11071651.
9. Park S, Lee S, Kim Y, Lee Y, Kang M, Kim K, Kim Y, Han S, Lee H, Lee J, et al. Causal Effects of Serum Levels of n-3 or n-6 Polyunsaturated Fatty Acids on Coronary Artery Disease: Mendelian Randomization Study. Nutrients 2021;13(5). doi: 10.3390/nu13051490.
10. Wang W, Wang J, Zhuang Z, Gao M, Yang R, Liu Z, Huang T. Assessment of causality between modifiable factors and heart failure: A Mendelian randomization analysis. Asia Pac J Clin Nutr 2021;30(2):340-7. doi: 10.6133/apjcn.202106_30(2).0019.
11. Chen HY, Cairns BJ, Small AM, Burr HA, Ambikkumar A, Martinsson A, Theriault S, Munter HM, Steffen B, Zhang R, et al. Association of FADS1/2 Locus Variants and Polyunsaturated Fatty Acids With Aortic Stenosis. JAMA Cardiol 2020;5(6):694-702. doi: 10.1001/jamacardio.2020.0246.
12. Yuan S, Larsson SC. Association of genetic variants related to plasma fatty acids with type 2 diabetes mellitus and glycaemic traits: a Mendelian randomisation study. Diabetologia 2020;63(1):116-23. doi: 10.1007/s00125-019-05019-0.
13. Jager S, Cuadrat R, Hoffmann P, Wittenbecher C, Schulze MB. Desaturase Activity and the Risk of Type 2 Diabetes and Coronary Artery Disease: A Mendelian Randomization Study. Nutrients 2020;12(8). doi: 10.3390/nu12082261.

14. Adams CD, Neuhausen SL. Evaluating causal associations between chronotype and fatty acids and between fatty acids and type 2 diabetes: A Mendelian randomization study. Nutr Metab Cardiovasc Dis 2019;29(11):1176-84. doi: 10.1016/j.numecd.2019.06.020.
15. Zulyniak MA, Fuller H, Iles MM. Investigation of the Causal Association between Long-Chain n-6 Polyunsaturated Fatty Acid Synthesis and the Risk of Type 2 Diabetes: A Mendelian Randomization Analysis. Lifestyle Genom 2020;13(5):146-53. doi: 10.1159/000509663.
16. Ma M, Yang F, Wang Z, Bao Q, Shen J, Xie X. Association of plasma polyunsaturated fatty acids with arterial blood pressure: A Mendelian randomization study. Medicine (Baltimore) 2021;100(3):e24359. doi: 10.1097/MD.0000000000024359.
17. Zhao JV, Schooling CM. The role of linoleic acid in asthma and inflammatory markers: a Mendelian randomization study. Am J Clin Nutr 2019;110(3):685-90. doi: 10.1093/ajcn/nqz130.
18. Liyanage UE, Ong JS, An J, Gharahkhani P, Law MH, MacGregor S. Mendelian Randomization Study for Genetically Predicted Polyunsaturated Fatty Acids Levels on Overall Cancer Risk and Mortality. Cancer Epidemiol Biomarkers Prev 2019;28(6):1015-23. doi: 10.1158/1055-9965.EPI-18-0940.
19. Larsson SC, Carter P, Vithayathil M, Mason AM, Michaelsson K, Baron JA, Burgess S. Genetically predicted plasma phospholipid arachidonic acid concentrations and 10 site-specific cancers in UK biobank and genetic consortia participants: A mendelian randomization study. Clin Nutr 2021;40(5):3332-7. doi: 10.1016/j.clnu.2020.11.004.
20. Liu J, Zhou H, Zhang Y, Huang Y, Fang W, Yang Y, Hong S, Chen G, Zhao S, Chen X, et al. Docosapentaenoic acid and lung cancer risk: A Mendelian randomization study. Cancer Med 2019;8(4):1817-25. doi: 10.1002/cam4.2018.
21. Shen J, Zhou H, Liu J, Zhang Y, Zhou T, Yang Y, Fang W, Huang Y, Zhang L. A modifiable risk factors atlas of lung cancer: A Mendelian randomization study. Cancer Med 2021;10(13):4587-603. doi: 10.1002/cam4.4015.
22. Yang Z, Li J, Sun Y, Qu Z, Lin Y, Zhang L, He Q, Jia X, Ahmad M, Zhang X, et al. Using Genetic Variants to Evaluate the Causal Effect of Plasma Phospholipid Fatty Acids on Breast Cancer and Prostate Cancer: A Mendelian Randomization Study. Front Genet 2021;12:664498. doi: 10.3389/fgene.2021.664498.
23. Guo F, Wang M, Guo X, Pu L, Sun M, Li S, Feng T, Tong L, Zhao S, Gao W, et al. The association between fatty acid intake and breast cancer based on the NHANES and Mendelian randomization study. Cancer Epidemiol 2021;73:101966. doi: 10.1016/j.canep.2021.101966.
24. Khankari NK, Murff HJ, Zeng C, Wen W, Eeles RA, Easton DF, Kote-Jarai Z, Al Olama AA, Benlloch S, Muir K, et al. Polyunsaturated fatty acids and prostate cancer risk: a Mendelian randomisation analysis from the PRACTICAL consortium. Br J Cancer 2016;115(5):624-31. doi: 10.1038/bjc.2016.228.
25. Ghoneim DH, Zhu J, Zheng W, Long J, Murff HJ, Ye F, Setiawan VW, Wilkens LR, Khankari NK, Haycock P, et al. Mendelian Randomization Analysis of n-6 Polyunsaturated Fatty Acid Levels and Pancreatic Cancer Risk. Cancer Epidemiol Biomarkers Prev 2020;29(12):2735-9. doi: 10.1158/1055-9965.EPI-20-0651.

26. Seviiri M, Law MH, Ong JS, Gharahkhani P, Nyholt DR, Olsen CM, Whiteman DC, MacGregor S. Polyunsaturated Fatty Acid Levels and the Risk of Keratinocyte Cancer: A Mendelian Randomization Analysis. Cancer Epidemiol Biomarkers Prev 2021;30(8):1591-8. doi: 10.1158/1055-9965.EPI-20-1765.
27. Khankari NK, Banbury BL, Borges MC, Haycock P, Albanes D, Arndt V, Berndt SI, Bezieau S, Brenner H, Campbell PT, et al. Mendelian Randomization of Circulating Polyunsaturated Fatty Acids and Colorectal Cancer Risk. Cancer Epidemiol Biomarkers Prev 2020;29(4):860-70. doi: 10.1158/1055-9965.EPI-19-0891.
28. May-Wilson S, Sud A, Law PJ, Palin K, Tuupanen S, Gylfe A, Hanninen UA, Cajuso T, Tanskanen T, Kondelin J, et al. Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. Eur J Cancer 2017;84:228-38. doi: 10.1016/j.ejca.2017.07.034.
29. Isom CA, Shrubsole MJ, Cai Q, Smalley WE, Ness RM, Zheng W, Murff HJ. Arachidonic acid and colorectal adenoma risk: a Mendelian randomization study. Clin Epidemiol 2019;11:17-22. doi: 10.2147/CLEP.S186883.
30. Liyanage UE, Law MH, Ong JS, Cust AE, Mann GJ, Ward SV, Melanoma Meta-Analysis C, Gharahkhani P, Iles MM, MacGregor S. Polyunsaturated fatty acids and risk of melanoma: A Mendelian randomisation analysis. Int J Cancer 2018;143(3):508-14. doi: 10.1002/ijc.31334.
31. Saunders CN, Cornish AJ, Kinnersley B, Law PJ, Claus EB, Il'yasova D, Schildkraut J, Barnholtz-Sloan JS, Olson SH, Bernstein JL, et al. Lack of association between modifiable exposures and glioma risk: a Mendelian randomization analysis. Neuro Oncol 2020;22(2):207-15. doi: 10.1093/neuonc/noz209.
32. Yuan S, Lemming EW, Michaelsson K, Larsson SC. Plasma phospholipid fatty acids, bone mineral density and fracture risk: Evidence from a Mendelian randomization study. Clin Nutr 2020;39(7):2180-6. doi: 10.1016/j.clnu.2019.09.005.
33. Zhao JV, Schooling CM. Role of linoleic acid in autoimmune disorders: a Mendelian randomisation study. Ann Rheum Dis 2019;78(5):711-3. doi: 10.1136/annrheumdis-2018-214519.
34. Sun L, Zhu J, Mi S, Li Y, Wang T, Li Y. Causal association of monounsaturated fatty acids with rheumatoid arthritis but not osteoarthritis: A two-sample Mendelian randomization study. Nutrition 2021;91-92:111363. doi: 10.1016/j.nut.2021.111363.
35. Wang K, Zhong Y, Yang F, Hu C, Liu X, Zhu Y, Yao K. Causal Effects of N-6 Polyunsaturated Fatty Acids on Age-related Macular Degeneration: A Mendelian Randomization Study. J Clin Endocrinol Metab 2021;106(9):e3565-e72. doi: 10.1210/clinem/dgab338.
36. Carreras-Torres R, Ibanez-Sanz G, Obon-Santacana M, Duell EJ, Moreno V. Identifying environmental risk factors for inflammatory bowel diseases: a Mendelian randomization study. Sci Rep 2020;10(1):19273. doi: 10.1038/s41598-020-76361-2.
37. Cheng TS, Day FR, Perry JRB, Luan J, Langenberg C, Forouhi NG, Wareham NJ, Ong KK. Prepubertal Dietary and Plasma Phospholipid Fatty Acids Related to Puberty Timing: Longitudinal Cohort and Mendelian Randomization Analyses. Nutrients 2021;13(6). doi: 10.3390/nu13061868.

38. Milaneschi Y, Peyrot WJ, Nivard MG, Mbarek H, Boomsma DI, B WJHP. A role for vitamin D and omega-3 fatty acids in major depression? An exploration using genomics. Transl Psychiatry 2019;9(1):219. doi: 10.1038/s41398-019-0554-y.
39. Tomata Y, Larsson SC, Hagg S. Polyunsaturated fatty acids and risk of Alzheimer's disease: a Mendelian randomization study. Eur J Nutr 2020;59(4):1763-6. doi: 10.1007/s00394-019-02126-x.
40. Wang Z, Meng L, Shen L, Ji HF. Impact of modifiable risk factors on Alzheimer's disease: A two-sample Mendelian randomization study. Neurobiol Aging 2020;91:167 e11- e19. doi: 10.1016/j.neurobiolaging.2020.02.018.
41. Jones HJ, Borges MC, Carnegie R, Mongan D, Rogers PJ, Lewis SJ, Thompson AD, Zammit S. Associations between plasma fatty acid concentrations and schizophrenia: a two-sample Mendelian randomisation study. Lancet Psychiatry 2021. doi: 10.1016/S2215-0366(21)00286-8.
42. Sallis H, Steer C, Paternoster L, Davey Smith G, Evans J. Perinatal depression and omega-3 fatty acids: a Mendelian randomisation study. J Affect Disord 2014;166:124-31. doi: 10.1016/j.jad.2014.04.077.
43. Thompson AD, Jones HJ, Heron J, Hibbeln J, Sullivan S, Zammit S. Omega-3 and Omega-6 fatty acids and risk of psychotic outcomes in the ALSPAC birth cohort. Schizophr Res 2020;224:108-15. doi: 10.1016/j.schres.2020.09.018.