

Supplementary Material

Title: Comparative analysis of SNPs associated with COVID-19 and chronic liver disease identifies *DPP9* as a candidate genetic marker for Long COVID.

Supplementary Table S1 Candidate SNPs included in the study, their associated genes, biological relevance, previously reported associations, and the main literature supporting their selection.

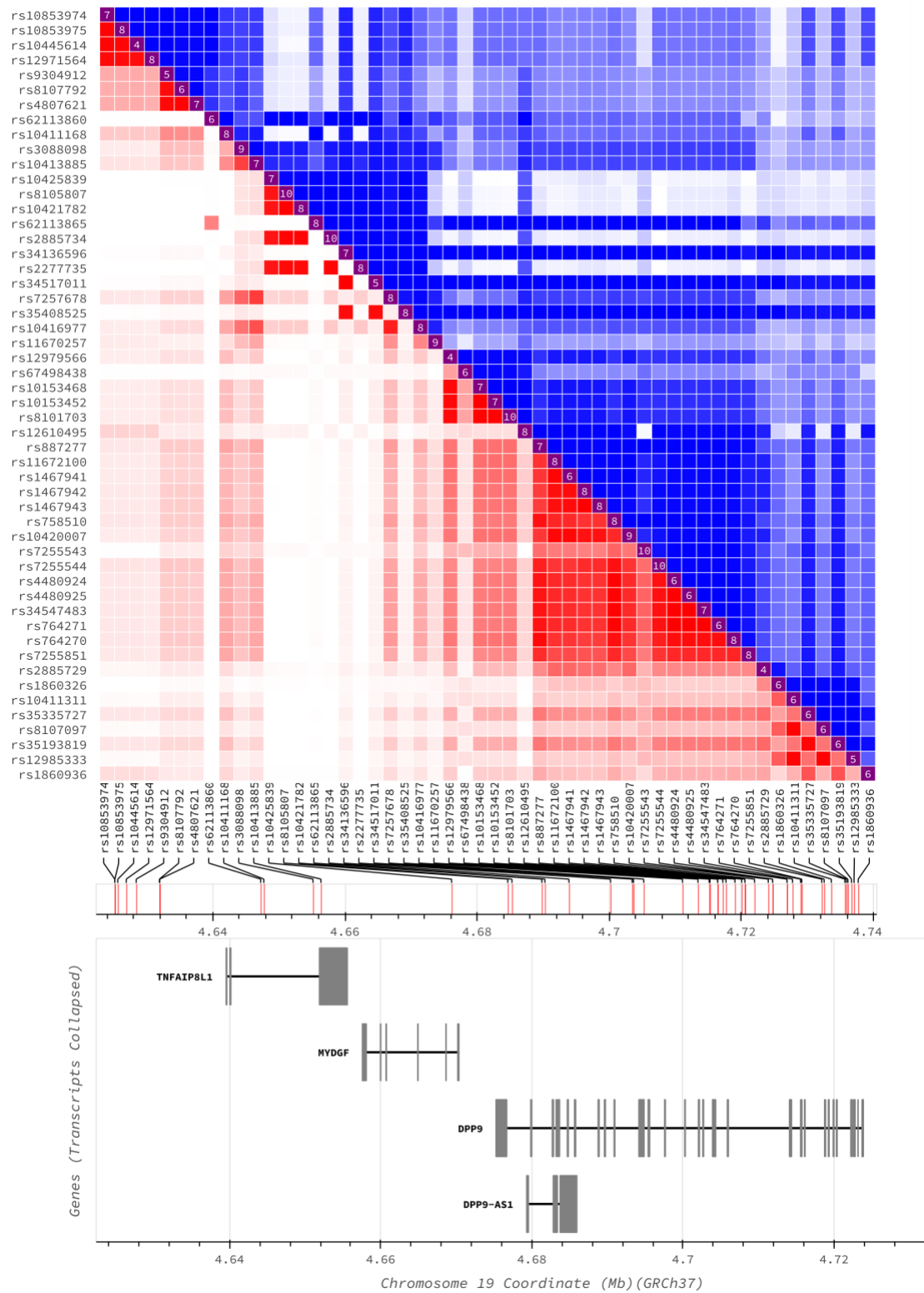
SNP	Gene	Biological relevance	Previously reported association	Main reference
rs1800795	IL6	Inflammatory cytokine	Cytokine production; inflammatory response	Abuelnadar et al. 2024; Sezer et al. 2024
rs10490770	LZTFL1 locus (3p21.31)	COVID-19 susceptibility	Severe COVID-19 and respiratory failure	Udomsinprasert et al. 2023
rs838133	FGF21	Metabolic regulation	MASLD, obesity, eating behaviour	Gallego-Durán et al. 2024; Pirola et al. 2022
rs12660421	FOXP4	Lung development / immune regulation	Long COVID susceptibility locus	Cheng et al. 2026.
rs12785878	DHCR7/NADSYN1	Vitamin D metabolism	Vitamin D deficiency; Long COVID	Mohamed A Abu El Maaty , Sally I Hassanein, Hameis M Sleem, Mohamed Z Gad, 2013
rs1424597	PLXNA4	Immune regulation	Long COVID susceptibility	<u>Wanvisa</u> <u>Udomsinprasert</u> et al, 2023.
rs17713054	LZTFL1	COVID-19 susceptibility	Severe COVID-19; Long COVID	<u>Wanvisa</u> <u>Udomsinprasert</u> et al, 2023.
rs2285666	ACE2	Viral entry	COVID-19 susceptibility; Long COVID	<u>Wanvisa</u> <u>Udomsinprasert</u> et al, 2023.
rs6020298	PEDS1 (TMEM189)	Lipid metabolism	Long COVID susceptibility	<u>Wanvisa</u> <u>Udomsinprasert</u> et al, 2023.

rs12610495	DPP9	Inflammasome / pulmonary fibrosis	Severe COVID-19; pulmonary fibrosis	Ana Caroline Alves da Costa et al, 2024; Pooja Singh et al, 2024; Alexey Loktionov et al, 2024.
rs1800562	HFE	Iron metabolism	Hemochromatosis; COVID-19 susceptibility	J A Hubacek et al, 2023
rs8099917	IFNL3 (IL28B)	Antiviral response	HCV spontaneous clearance; interferon response	Sanja Matic et al, 2023; Pooneh Rahimi et al, 2021.
rs641738	MBOAT7	Lipid remodeling	MASLD; liver fibrosis; COVID- 19-related liver injury	Deepak Parchwani et al, 2023
rs780094	GCKR	Glucose/lipid metabolism	MASLD; COVID- 19 severity	Bianco C et al. J Clin Med. 2023.
rs1260326	GCKR	Metabolic regulation	Obesity; COVID-19	Jiaying Li et al, 2021; Xiude Fan et al, 2021
rs5743836	TLR9	Innate immunity	COVID-19 susceptibility	Alshaymaa M Alhabibi et al, 2023
rs58542926	TM6SF2	Lipid metabolism	MASLD progression; liver injury; COVID-19 outcomes	Mykhailo Buchynskyi et al, 2023
rs738409	PNPLA3	Hepatic steatosis / fibrosis	MASLD, fibrosis, cirrhosis; COVID- 19 Mortality and Hospitalization	Hamish Innes et al, 2021; Mykhailo Buchynskyi et al, 2023

SNPs were selected based on previous evidence of associations with Long COVID, COVID-19 severity, chronic viral hepatitis, liver disease progression, inflammation, or metabolic pathways potentially involved in both conditions.

Supplementary Table S2. Sociodemographic characteristics of the study population.

Characteristic	Total population (n = 150)	Long COVID (n = 55)	Chronic viral hepatitis (n = 81)
Sex			
Female	90 (60.0%)	42 (76.4%)	47 (58.0%)
Male	60 (40.0%)	13 (23.6%)	34 (42.0%)
Self-declared skin color			
White	66 (44.0%)	18 (32.7%)	27 (33.3%)
Brown	51 (34.0%)	25 (45.5%)	38 (46.9%)
Black	20 (13.3%)	9 (16.4%)	11 (13.6%)
Missing / Not reported	13 (8.7%)	3 (5.5%)	5 (6.2%)
Type of viral hepatitis			
Hepatitis B	—	—	60 (74.1%)
Hepatitis C	—	—	21 (25.9%)



Supplementary Figure S3. Linkage disequilibrium (LD) map of regulatory SNPs across the *DPP9* locus.

Pairwise linkage disequilibrium analysis was performed using regulatory variants identified in the GTEx database. The upper panel shows the LD heatmap across the *DPP9* genomic region, with rs12610495 included among the analyzed variants. The lower panel depicts the genomic organization of the locus, including the neighboring genes TNFAIP8L1, MYDGF, DPP9, and DPP9-AS1 (GRCh37 coordinates).

Supplementary Table S4. Association between candidate SNPs and Long COVID

SNP	Selected genetic comparison	OR (95% CI)	P-value
rs1800795	Dominant	1.06 (0.43-2.63)	0.900
rs10490770	Carrier	0.46 (0.07-3.20)	0.430
rs838133	Dominant	0.73 (0.29-1.81)	0.490
rs12660421	Dominant	0.97 (0.39-2.38)	0.950
rs12785878	Dominant	1.03 (0.40-2.67)	0.950
rs1424597	Dominant	1.24 (0.49-3.15)	0.650
rs17713054	Carrier	0.21 (0.02-2.17)	0.150
rs2285666	Dominant	0.96 (0.39-2.39)	0.940
rs6020298	Dominant	1.81 (0.70-4.65)	0.220
rs12610495	Dominant	2.66 (1.08-6.57)	0.029
rs1800562	Carrier	0.93 (0.41-2.32)	0.092
rs8099917	Dominant	0.62 (0.25-1.52)	0.290
rs641738	Dominant	0.55 (0.22-1.35)	0.190
rs780094	Dominant	0.98 (0.39-2.42)	0.970
rs1260326	Dominant	0.93 (0.37-2.31)	0.880
rs5743836	Dominant	0.83 (0.34-2.04)	0.680
rs58542926	Carrier	4.41 (0.42-46.69)	0.180
rs738409	Dominant	0.24 (0.03-2.18)	0.450

Note. One prespecified comparison is reported per SNP. Carrier indicates that only two genotype categories were observed. The main finding included in the manuscript is highlighted in bold.

Supplementary Table S5. Association between candidate SNPs and chronic viral hepatitis

SNP	Selected genetic comparison	OR (95% CI)	P-value
rs1800795	Dominant	0.53 (0.23-1.21)	0.130
rs10490770	Carrier	0.41 (0.08-2.22)	0.280
rs838133	Dominant	1.21 (0.54-2.72)	0.640
rs12660421	Dominant	0.95 (0.42-2.17)	0.910
rs12785878	Dominant	0.47 (0.21-1.08)	0.072
rs1424597	Dominant	2.36 (1.01-5.49)	0.044
rs17713054	Carrier	0.41 (0.08-2.22)	0.280
rs2285666	Dominant	0.80 (0.35-1.83)	0.600
rs6020298	Dominant	0.80 (0.35-1.87)	0.610
rs12610495	Dominant	0.86 (0.38-1.93)	0.710
rs1800562	Carrier	0.92 (0.06-15.12)	0.950
rs8099917	Dominant	1.25 (0.55-2.85)	0.590
rs641738	Dominant	0.56 (0.25-1.28)	0.170
rs780094	Dominant	0.67 (0.30-1.50)	0.320
rs1260326	Dominant	0.56 (0.25-1.27)	0.160
rs5743836	Dominant	0.89 (0.39-2.01)	0.770
rs58542926	Carrier	1.67 (0.27-10.50)	0.580
rs738409	Dominant	0.45 (0.06-2.18)	0.600

Note. One prespecified comparison is reported per SNP. Carrier indicates that only two genotype categories were observed. The main finding included in the manuscript is highlighted in bold.