Plasma proteomic profiles in multiple populations identify biomarkers predicting metabolic dysfunction-associated steatotic liver disease up to 16 years before onset

Contents

Supplementary Methods.

Supplementary Figure 1. Flowchart of Eligible Participants' Selection.

Supplementary Figure 2. Data distribution plots of Normalized Protein eXpression (NPX) values.

Supplementary Figure 3. Trajectories of the top 30 plasma proteins preceding MASLD diagnosis.

Supplementary Figure 4. Trajectories of other plasma proteins preceding MASLD diagnosis (selected by interval).

Supplementary Table 1: Definitions for outcome.

Supplementary Table 2: Associations of plasma proteins with incident MASLD.

Supplementary Table 3: Results of enrichment analyses.

Supplementary Table 4: Results of protein importance ranking.

Supplementary Table 5: Results of ROC analyses.

Supplementary Table 6: Prognostic performance of baseline plasma proteins on the risk of clinical progression.

Supplementary Table 7: Results of trend tests in the total population.

Supplementary Methods

Covariates assessment

Age at baseline was determined from the date of birth recorded during the baseline assessment. Ethnicity was self-reported and categorized as White and non-White in this study. Deprivation (area-based socioeconomic status) was derived from residential postal codes using the Townsend score. Educational level was classified based on whether a university degree was obtained. Smoking status was classified as never smoker, previous smoker, or current smoker. Alcohol consumption frequency was divided into six categories: almost daily, 3-4 times per week, once or twice per week, 1-3 times per month, special occasions only, and never. Hyperglycemia/diabetes was defined as fasting blood glucose > 5.6 mmol/L or self-reported physician-diagnosed diabetes[47]. Hypertension was defined as systolic blood pressure > 130 mmHg and/or diastolic blood pressure > 85 mmHg or self-reported physician-diagnosed hypertension[48,49]. Physical activity was self-reported using the International Physical Activity Questionnaire short form, based on WHO recommendations. A cumulative dietary risk score was calculated based on the intake of seven food categories.

Plasma collection and Olink 3072 Explore platform

Blood samples were collected at baseline (2006-2010) and stored at -80°C[50]. During the baseline assessment visit, 45 mL of blood was collected from each participant using EDTA vacutainers containing anticoagulants, and stored at 4°C, with a lithium-heparin plasma separation tube (LH-PST) and a clot activator serum separation tube (SST) used to prevent changes due to delayed separation[33]. The collected blood samples were immediately centrifuged at 2500g for 10 minutes at 4°C, and after approximately 25 minutes of coagulation at room temperature, they were centrifuged again under the same conditions. The separated plasma samples were then stored at -80°C and sent to the Olink Analysis Service in Sweden for further processing[17]. The Olink technology involves the hybridization of nucleotide probes to proteins in plasma samples, followed by DNA

amplification of the protein signals, and further quantification[51]. The primary focus was on 2,923 independent proteins related to inflammation, oncology, cardiometabolic, and neurological conditions. Protein expression was standardized using Normalized Protein eXpression (NPX) values as relative quantification units on a log2 scale. Finally, the UKB-PPP removed outliers and low-quality samples through quality control (QC) of the Olink data, ensuring that all Olink panel data points passing QC exceeded 97.6%[52].

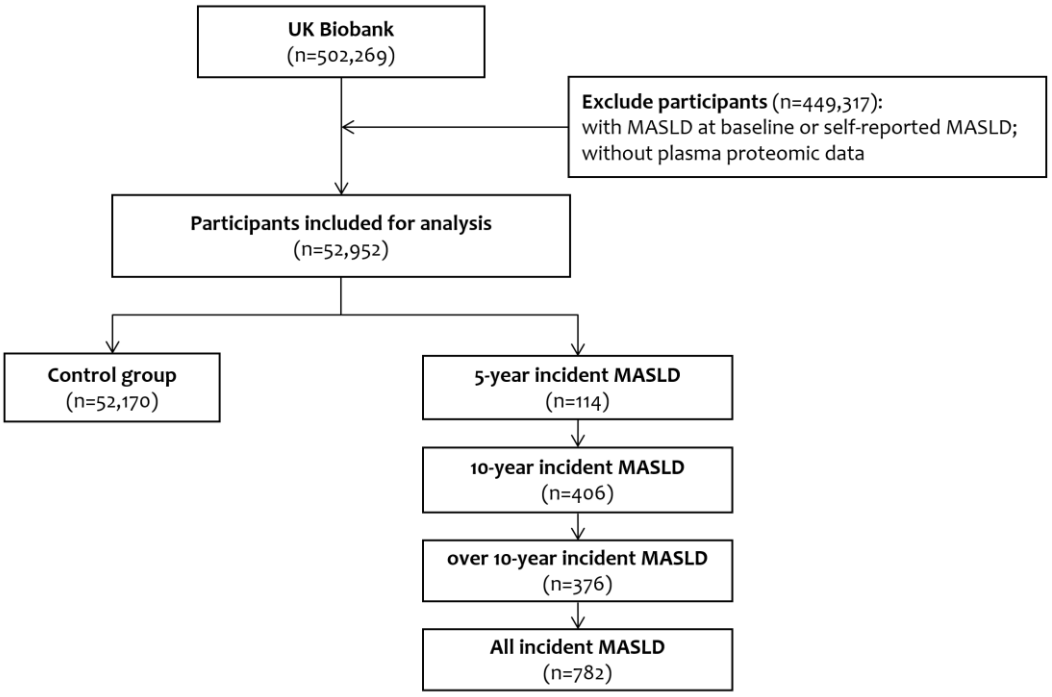
Polygenic risk score (PRS) calculations

Calculating the PRS involves a discovery sample and a target sample. In the discovery sample, genetic variants associated with disease status at a specified *P* value were identified. The target sample included 413,164 individuals, excluded outliers based on heterozygosity, variants with a call rate < 99%, or individuals related up to the third degree (kinship coefficients > 0.044), identified using the ukbtools package in R. The GWAS summary statistics of MASLD was obtained from previously published data (doi: 10.1186/s12916-019-1364-z), with further exclusions for variants with call rates < 99%, minor allele frequencies < 0.01, deviations from Hardy-Weinberg equilibrium ($P < 10^{-6}$), or ambiguous strand assignments. After LD clumping (r2 < 0.1 in 250 kb window) using the same LD reference previously described, 182,790 SNPs exhibiting significant independence were retained for PRS calculation. PRS for MASLD in the target sample was calculated by summing imputed SNP dosages weighted by allele effect (logistic regression coefficients) from the discovery set across *P* value thresholds of 1×10^{-3}, 0.05, 0.1, 0.2, 0.3, 0.4, and 0.5. PLINK (version 1.9) was utilized for PRS profiling, with scores standardized within each target set to adjust for SNP number variations used in PRS calculation. Subsequently, logistic regression analyses were then conducted in R (version 4.2.0). We examined associations from a low *P* value threshold up to 0.5, identifying the optimal threshold with the highest explained variance, encompassing the most significant associations. Adjustments were made for the first six principal components (PCs), in addition to sex, age, BMI, and genotyping platform.

Data analysis and visualization

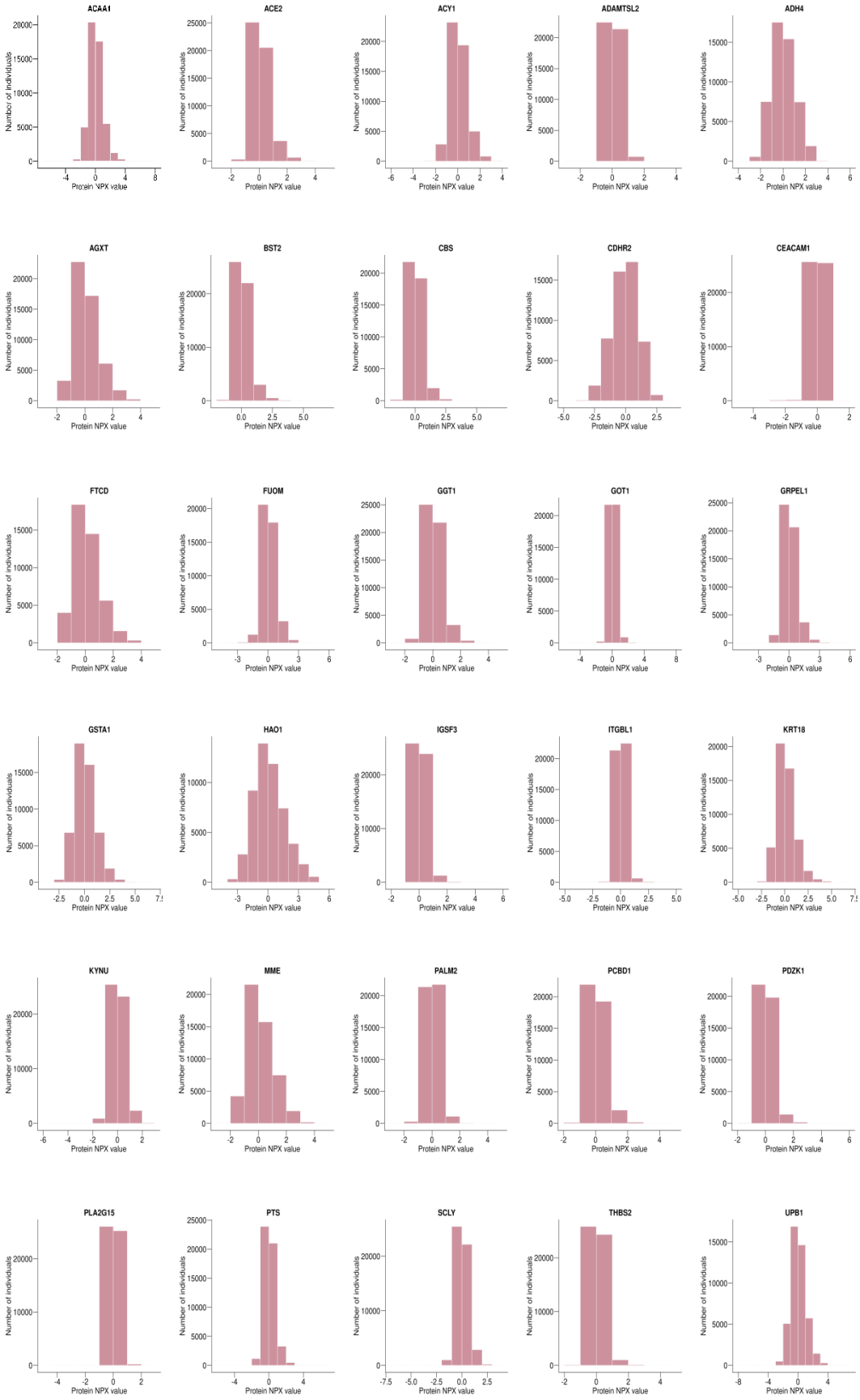
Data analysis and visualization are conducted with libraries of dplyr (v.1.1.4), caTools (v.1.18.2), pROC (v.1.18.5), boot (v.1.3-28.1) and survival (v.3.5-5) under Python (v3.10.12 (2024-03-22), created by Guido van Rossum at Stichting Mathematisch Centrum (CWI, see https://www.cwi.nl) in the Netherlands) and R (v4.3.0 (2023-04-21), R Foundation for Statistical Computing, Vienna, Austria. <https://www.R-project.org/>). We consider a two-tailed $P < 0.05$ to be statistically significant.

Supplementary Figure 1. Flowchart of Eligible Participants' Selection.



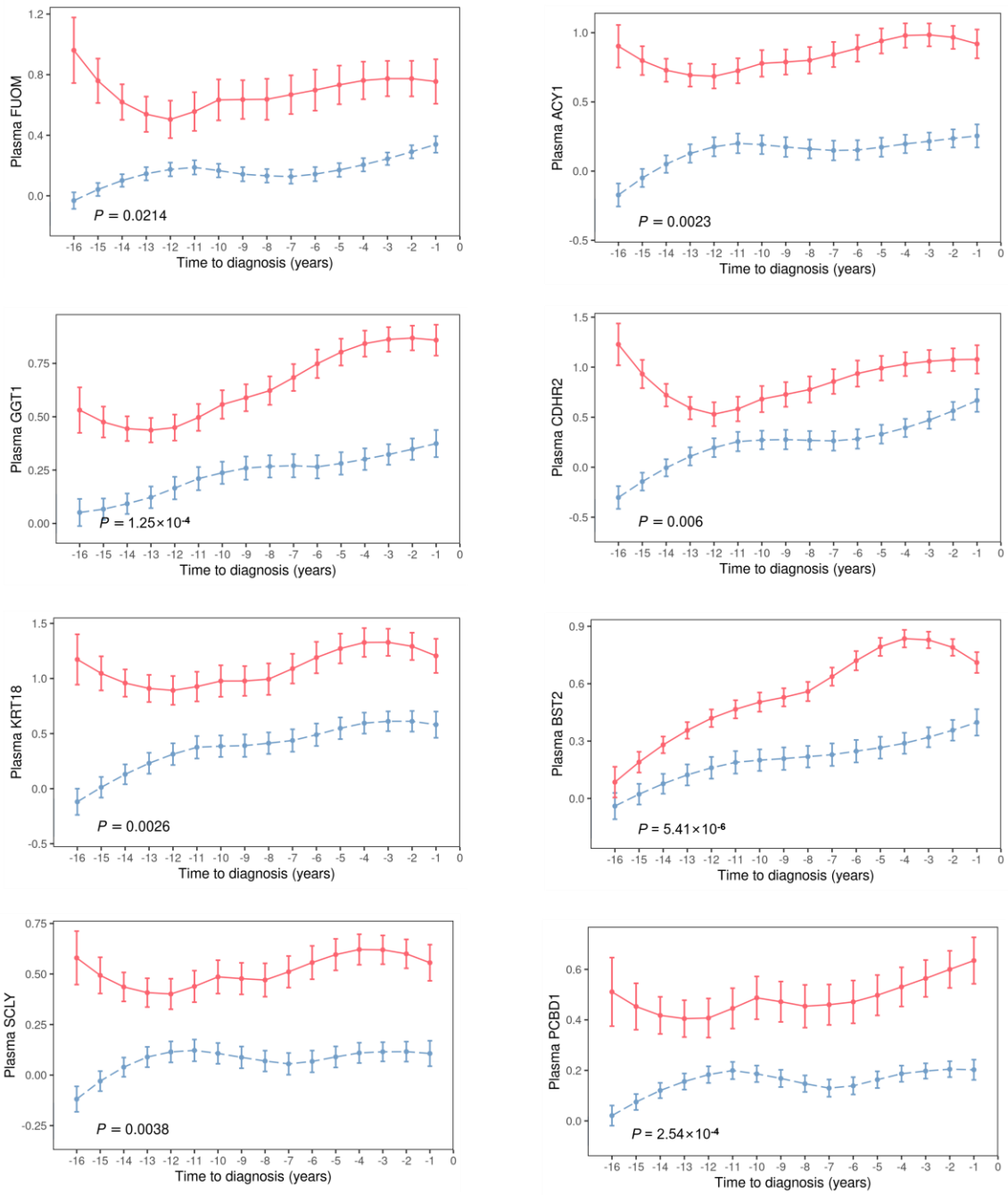
Individuals diagnosed with MASLD at baseline or with self-reported MASLD and those who did not undergo plasma proteomic assay were excluded from the UK Biobank cohort. The rest participants were grouped by the year they initially diagnosed with MASLD post-baseline. Abbreviations: MASLD, metabolic dysfunction-associated steatotic liver disease.

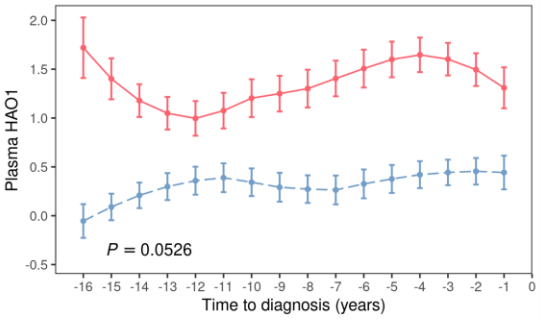
Supplementary Figure 2. Data distribution plots of Normalized Protein eXpression (NPX) values.

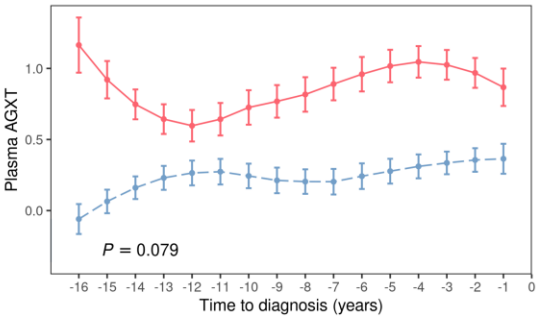


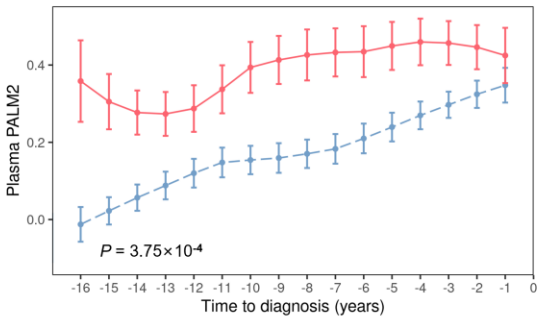
The bar chart shows the distribution of NPX values for the top 30 proteins included in the population. Olink uses a relative quantitative value called Normalized Protein eXexpression (NPX), which is a normalized dimensionless data matrix and has a log2 attribute.

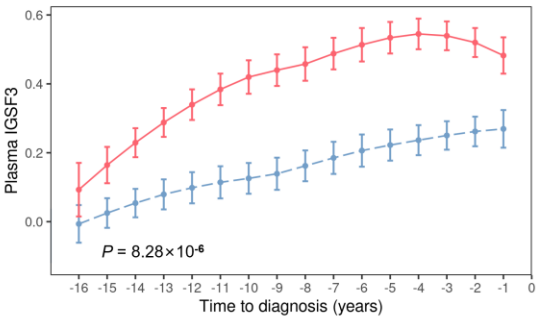
Supplementary Figure 3. Trajectories of the top 30 plasma proteins preceding MASLD diagnosis.

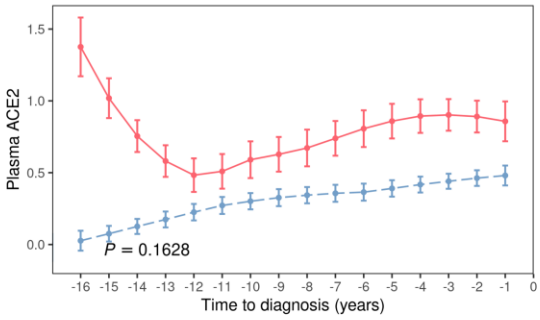


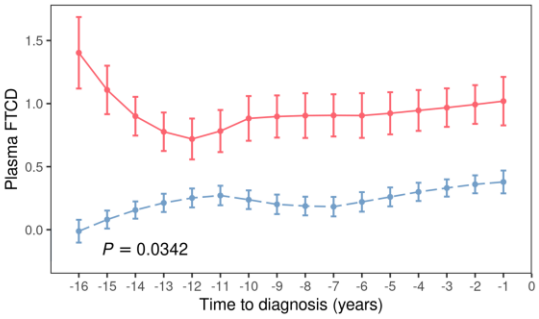

Plasma HAO1
P = 0.0526
Time to diagnosis (years)

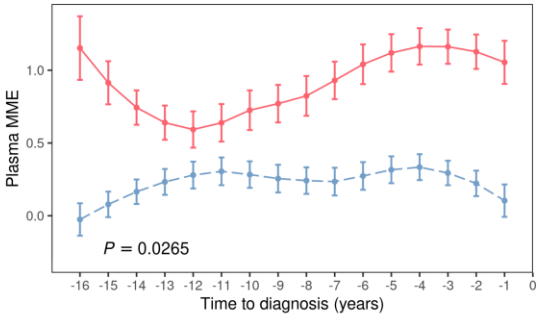

Plasma AGXT
P = 0.079
Time to diagnosis (years)

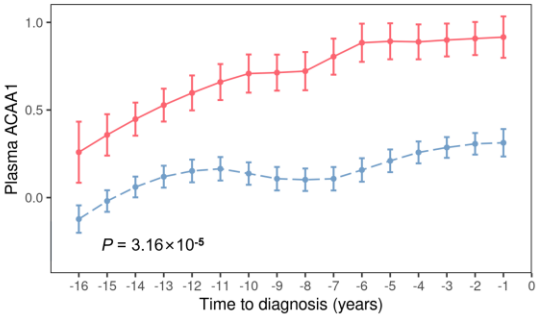

Plasma PALM2
P = 3.75×10-4
Time to diagnosis (years)

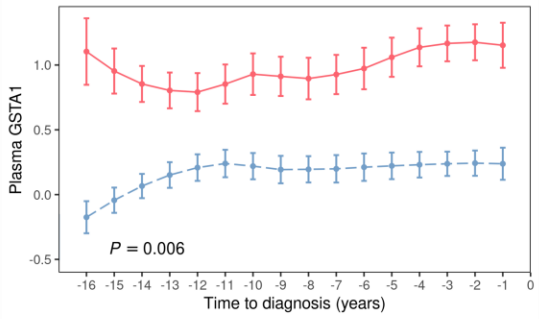

Plasma IGSF3
P = 8.28×10-6
Time to diagnosis (years)

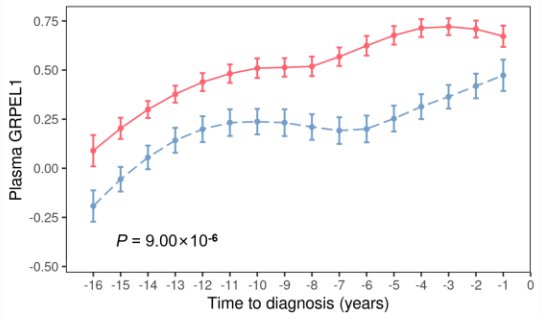

Plasma ACE2
P = 0.1628
Time to diagnosis (years)

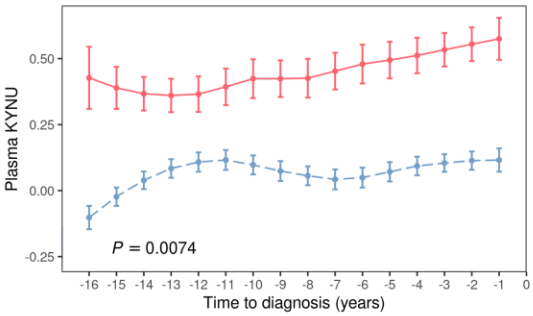

Plasma FTCD
P = 0.0342
Time to diagnosis (years)

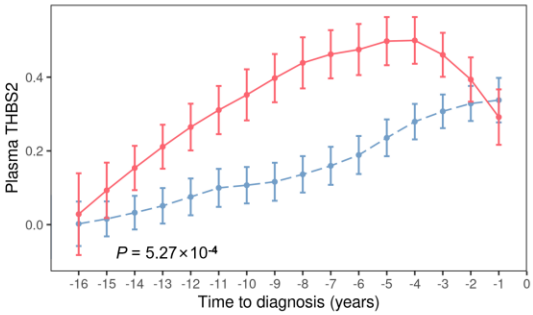

Plasma MME
P = 0.0265
Time to diagnosis (years)

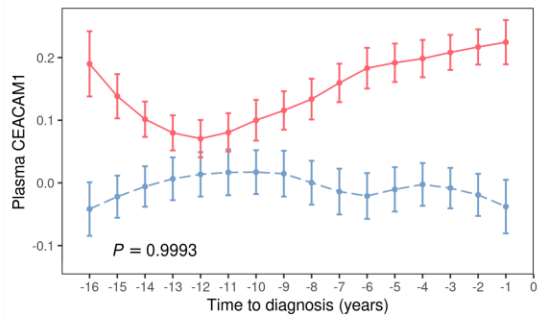

Plasma ACAA1
P = 3.16×10-5
Time to diagnosis (years)

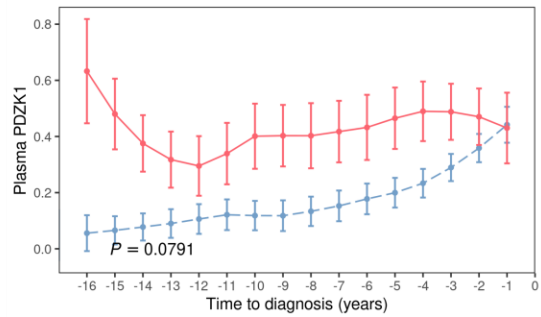

Plasma GSTA1
P = 0.006
Time to diagnosis (years)

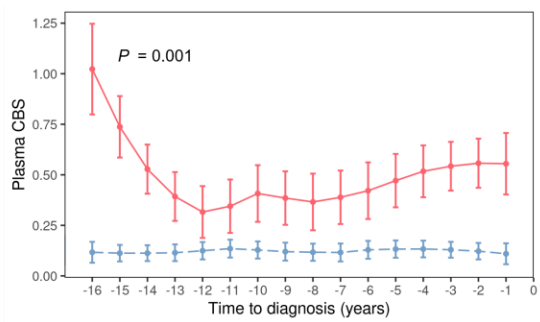

Plasma GRPEL1
P = 9.00×10-6
Time to diagnosis (years)

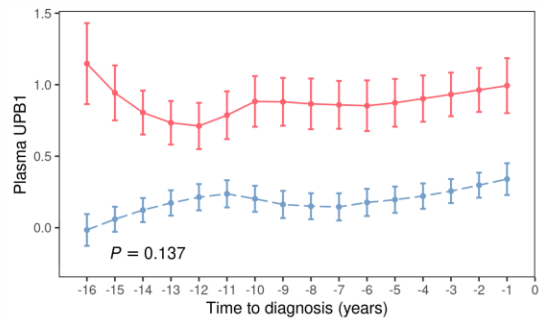

Plasma KYNU
P = 0.0074
Time to diagnosis (years)

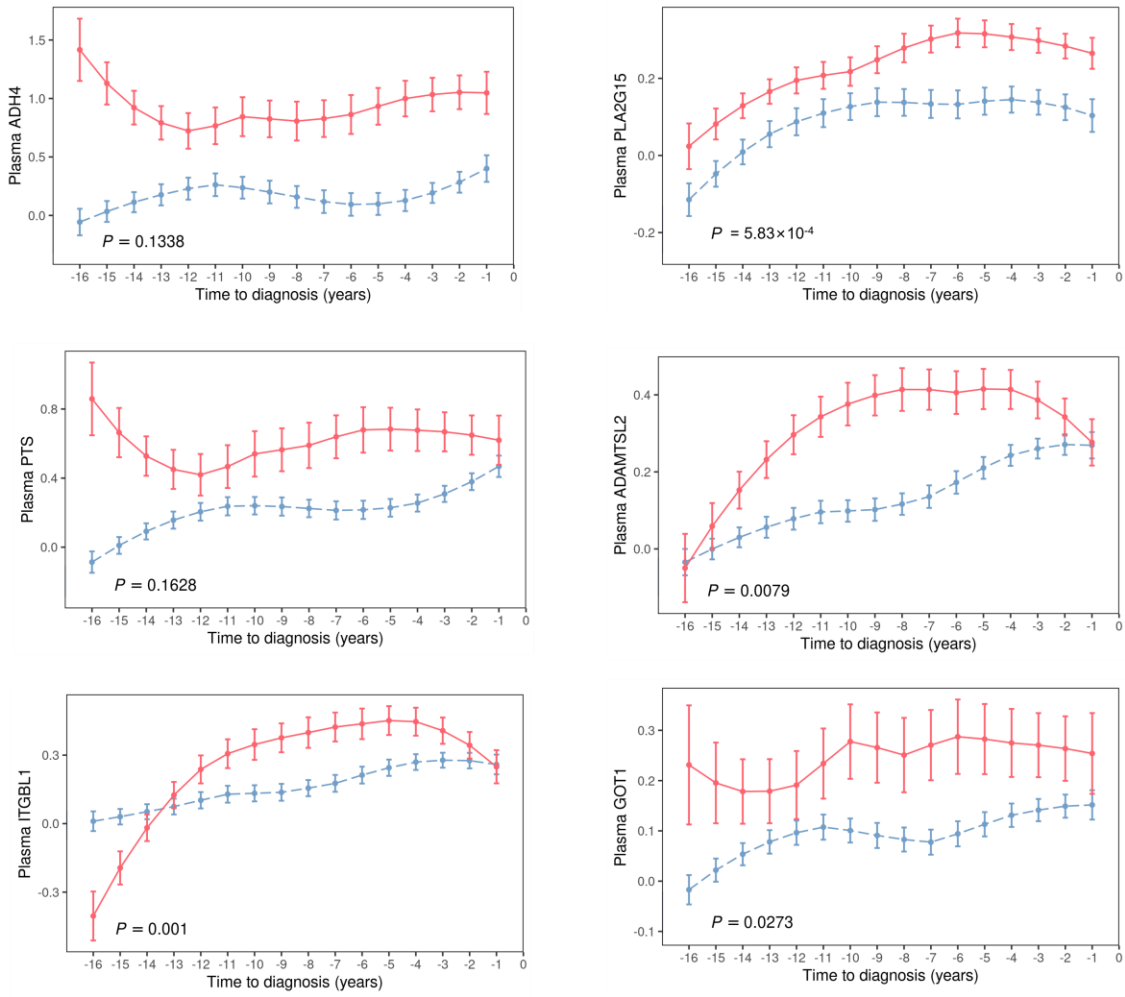

Plasma THBS2
P = 5.27×10-4
Time to diagnosis (years)


Plasma CEACAM1
P = 0.9993
Time to diagnosis (years)


Plasma PDZK1
P = 0.0791
Time to diagnosis (years)

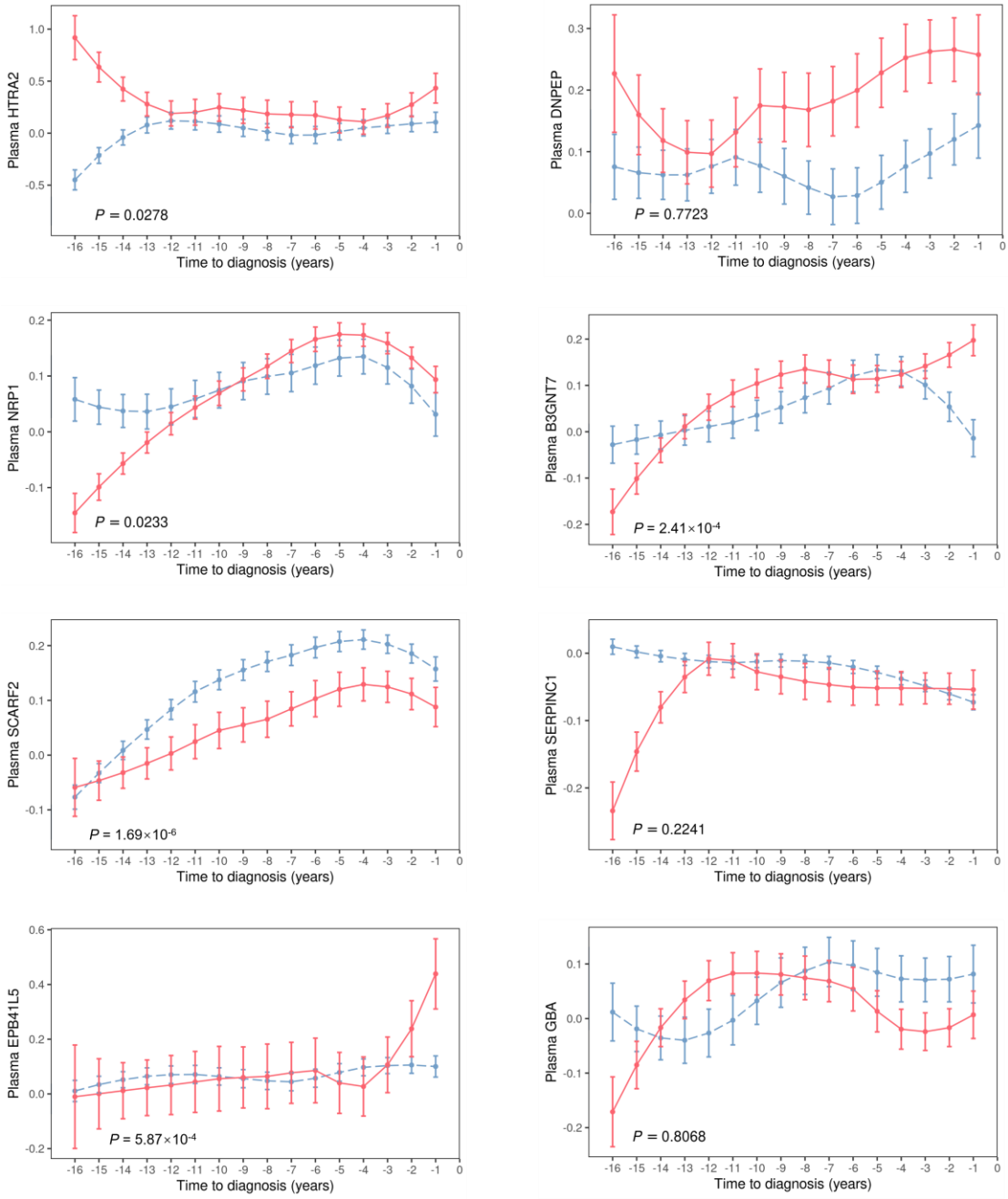

Plasma CBS
P = 0.001
Time to diagnosis (years)

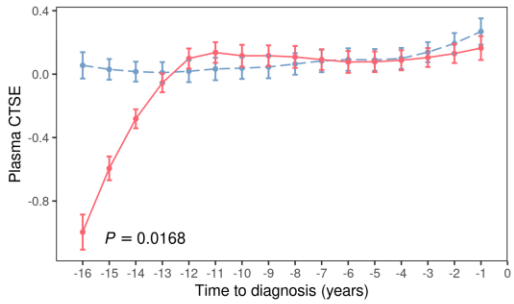

Plasma UPB1
P = 0.137
Time to diagnosis (years)

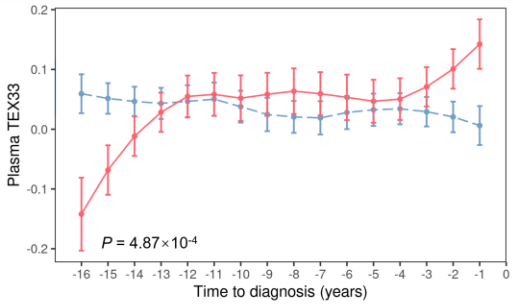


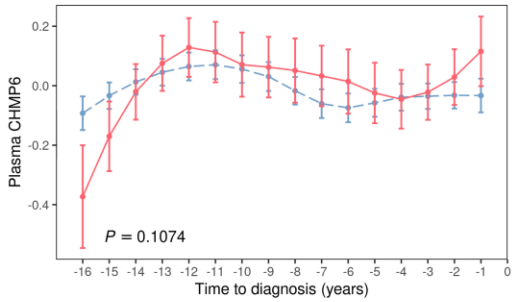
The fluctuations in plasma levels prior to MASLD onset were charted. Based on the Bonferroni corrected *P* value, the top 30 proteins were chosen to plot the protein time trajectory of plasma proteins. Nested case-control studies matched individuals who developed MASLD (over a 16-year observation period) with five healthy controls based on age, sex, and ethnicity, resulting in 782 MASLD cases and 3,910 controls. Red lines represent MASLD patients, while blue lines denote controls. Mean protein concentrations relative to the index date were smoothed using locally weighted regression. Error bars indicate standard errors. The Mann-Kendall trend tests assessed differences in plasma protein level trends over time between those who developed MASLD and those who did not, with *P* values determined by two-sided tests without multiple comparison corrections.

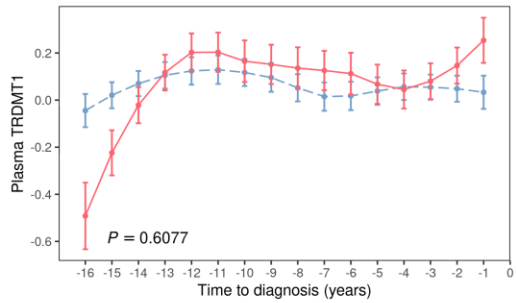
Supplementary Figure 4. Trajectories of other plasma proteins preceding MASLD diagnosis (selected by interval).

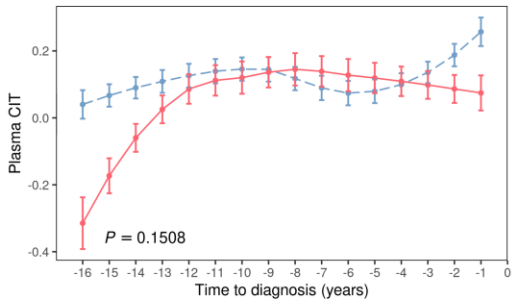


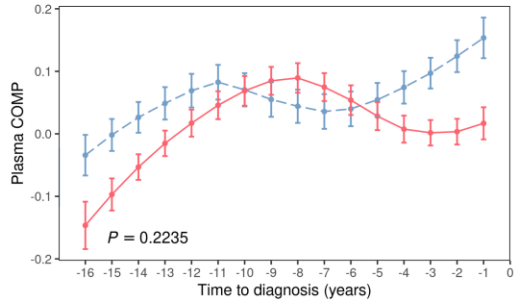

Plasma CTSE
P = 0.0168
Time to diagnosis (years)

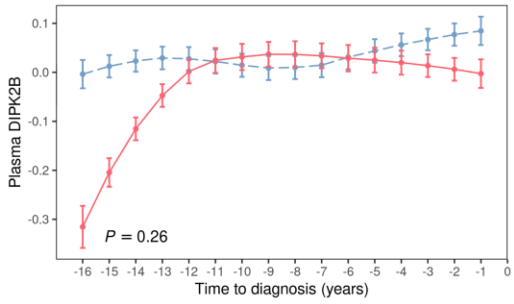

Plasma TEX33
P = 4.87×10-4
Time to diagnosis (years)

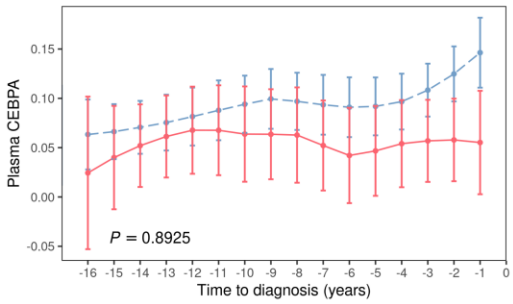

Plasma CHMP6
P = 0.1074
Time to diagnosis (years)

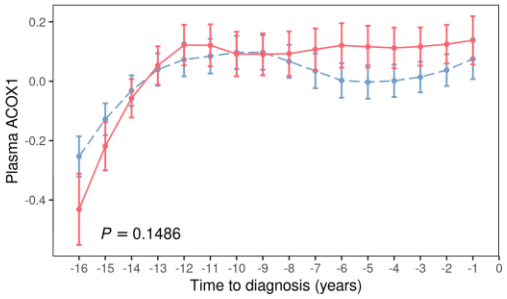

Plasma TRDMT1
P = 0.6077
Time to diagnosis (years)

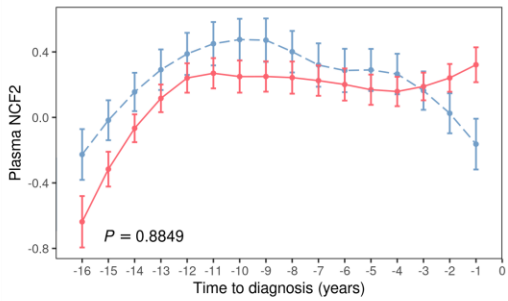

Plasma CIT
P = 0.1508
Time to diagnosis (years)

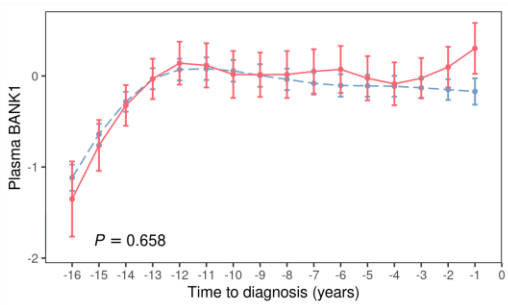

Plasma COMP
P = 0.2235
Time to diagnosis (years)

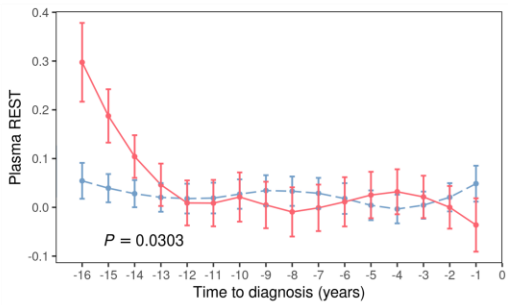

Plasma DIPK2B
P = 0.26
Time to diagnosis (years)

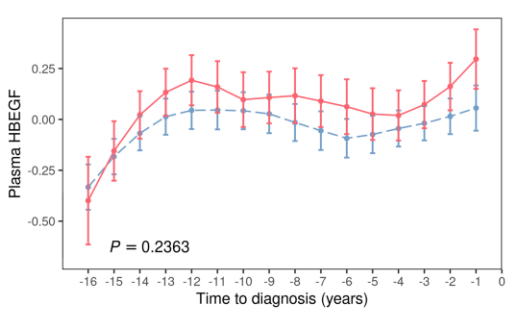

Plasma CEBPA
P = 0.8925
Time to diagnosis (years)

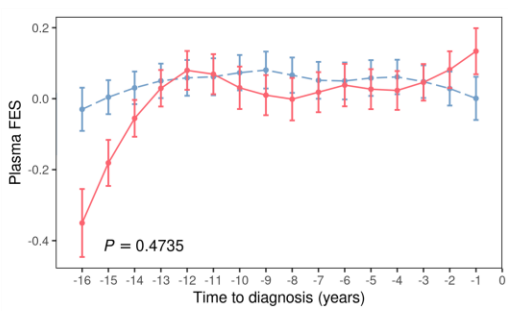

Plasma ACOX1
P = 0.1486
Time to diagnosis (years)

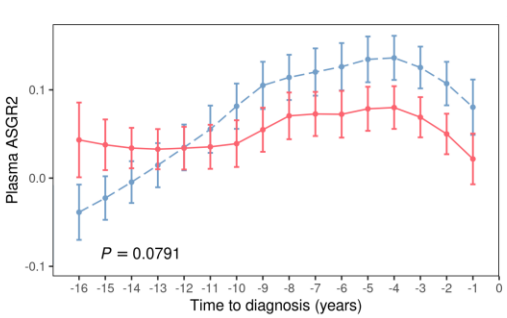

Plasma NCF2
P = 0.8849
Time to diagnosis (years)

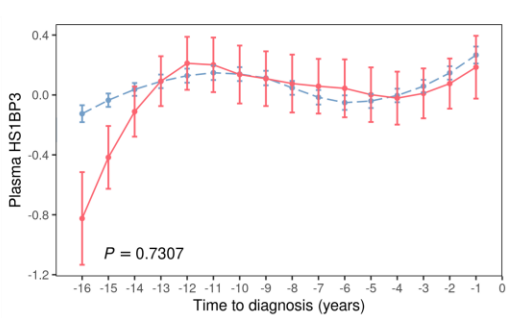

Plasma BANK1
P = 0.658
Time to diagnosis (years)

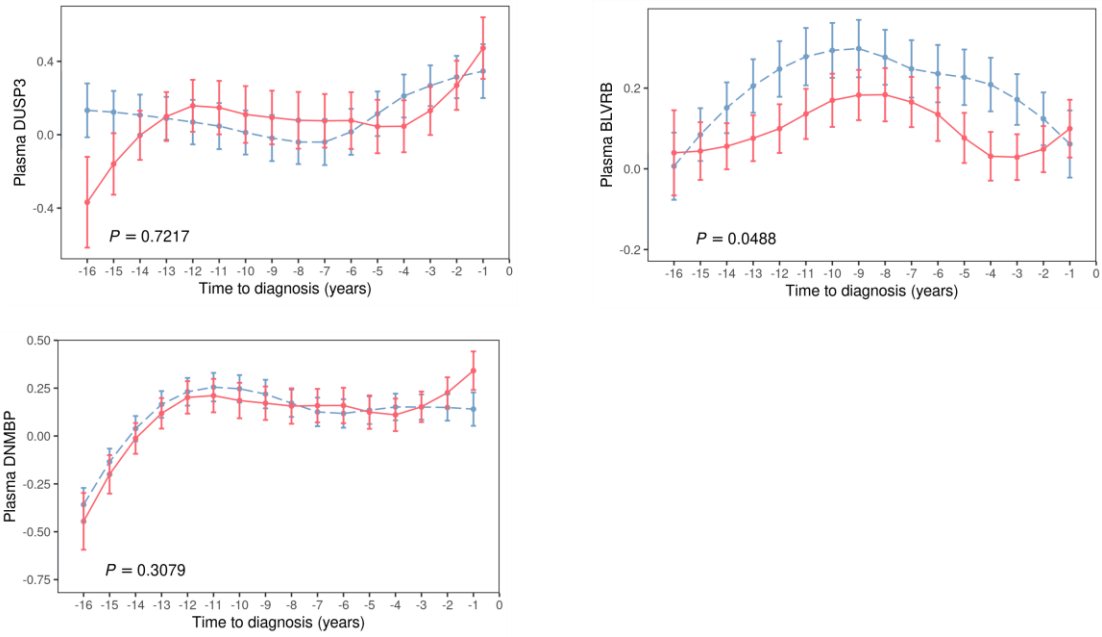

Plasma REST
P = 0.0303
Time to diagnosis (years)


Plasma HBEGF
P = 0.2363
Time to diagnosis (years)


Plasma FES
P = 0.4735
Time to diagnosis (years)


Plasma ASGR2
P = 0.0791
Time to diagnosis (years)


Plasma HS1BP3
P = 0.7307
Time to diagnosis (years)



The fluctuations in plasma levels prior to MASLD onset were charted. Based on the Bonferroni corrected *P* value, three proteins were selected at intervals of 300 to plot the protein time trajectory of plasma proteins. Nested case-control studies matched individuals who developed MASLD (over a 16-year observation period) with five healthy controls based on age, sex, and ethnicity, resulting in 782 MASLD cases and 3,910 controls. Red lines represent MASLD patients, while blue lines denote controls. Mean protein concentrations relative to the index date were smoothed using locally weighted regression. Error bars indicate standard errors. The Mann-Kendall trend tests assessed differences in plasma protein level trends over time between those who developed MASLD and those who did not, with *P* values determined by two-sided tests without multiple comparison corrections.

Supplementary Tables

ST1	Supplementary Table 1: Definitions for outcome.
ST2	Supplementary Table 2: Associations of plasma proteins with incident MASLD.
ST3	Supplementary Table 3: Results of enrichment analyses.
ST4	Supplementary Table 4: Results of protein importance ranking.
ST5	Supplementary Table 5: Results of ROC analyses.
ST6	Supplementary Table 6: Prognostic performance of baseline plasma proteins on the risk of clinical progression.
ST7	Supplementary Table 7: Results of trend tests in the total population.

Supplementary Table 1: Definitions for outcome.

			Description
Metabolic dysfunction-associated steatotic liver disease	**Field ID**	53	Date of attending assessment centre
		40000	Date of death
		41270	Diagnoses - ICD10
		41280	Date of first in-patient diagnosis - ICD10
	ICD-10	K758	Other specified inflammatory liver diseases
		K760	Fatty (change of) liver, not elsewhere classified

Supplementary Table 2: Association of plasma proteins with incident MASLD.
Direction: MASLD

Model 0					Model 1				
Protein	Description of protein	HR	Lower confidence interval of HR	Upper confidence interval of HR	p_value_bonferroni	HR	Lower confidence interval of HR	Upper confidence interval of HR	p_value_bonferroni
ALT1	Aminocarboxy-t	1.34	1.21	1.48	1.34E-05	1.32	1.19	1.47	4.69E-05
ANGPT2	Angiopoietin-2	1.29	1.17	1.42	1.00E-04	1.25	1.13	1.38	1.00E-03
ANXA5	Annexin-5	1.26	1.14	1.4	1.22E-03	1.27	1.15	1.41	1.09E-03
APOC3	Apolipoprotein C-III	1.24	1.12	1.36	1.21E-03	1.24	1.12	1.36	5.89E-03
ASRT1	Aspartate aminotransferase, cytoplasmic 1	1.29	1.16	1.43	9.99E-04	1.27	1.14	1.41	3.70E-03
ATS13	A disintegrin and metalloproteinase with thrombospondin motifs 13	1.27	1.15	1.41	5.00E-04	1.25	1.13	1.39	2.00E-03
BTD	Biotinidase	1.29	1.16	1.43	9.99E-04	1.27	1.14	1.41	3.70E-03
CA060	Cadherin-like protein 26	1.29	1.16	1.44	1.29E-03	1.27	1.14	1.42	4.79E-03
CADH5	Cadherin-5	1.29	1.16	1.44	1.29E-03	1.27	1.14	1.42	4.79E-03
CAH13	Beta-type carbonic anhydrase 13	1.29	1.16	1.44	1.29E-03	1.27	1.14	1.42	4.79E-03
CAMP1	Cathelicidin antimicrobial peptide	1.29	1.16	1.44	1.29E-03	1.27	1.14	1.42	4.79E-03
CBPB2	Carboxypeptidase B2	1.29	1.16	1.44	1.29E-03	1.27	1.14	1.42	4.79E-03
CCL25	C-C motif chemokine 25	1.29	1.16	1.44	1.29E-03	1.27	1.14	1.42	4.79E-03
CCL28	C-C motif chemokine 28	1.29	1.16	1.44	1.29E-03	1.27	1.14	1.42	4.79E-03
CD109	CD109 antigen	1.29	1.16	1.44	1.29E-03	1.27	1.14	1.42	4.79E-03
CD14	Monocyte differentiation antigen CD14	1.29	1.16	1.44	1.29E-03	1.27	1.14	1.42	4.79E-03
CD40L	CD40 ligand	1.29	1.16	1.44	1.29E-03	1.27	1.14	1.42	4.79E-03
CD5L	CD5 antigen-like	1.29	1.16	1.44	1.29E-03	1.27	1.14	1.42	4.79E-03
CEAM5	Carcinoembryonic antigen-related cell adhesion molecule 5	1.29	1.16	1.44	1.29E-03	1.27	1.14	1.42	4.79E-03
CEAM8	Carcinoembryonic antigen-related cell adhesion molecule 8

PKN1	Protogenin	0.35	0.5
TMTC2	Tetratricopeptide repeat domain 2	0.34	0.42
ZNF521	Zinc finger protein 521	0.34	0.47
LRRC4B	Leucine rich repeat containing 4B	0.34	0.47
LGR5	Leucine rich repeat containing G protein coupled receptor 5	0.33	0.46
ATP1B2	ATPase, Na+/K+ transporting, beta 2 polypeptide	0.33	0.46
PCDH9	Protocadherin 9	0.33	0.46
PARP1	Poly (ADP-ribose) polymerase 1	0.33	0.46
MYRIP	Myosin VIIA and Rab interacting protein	0.33	0.46
MYRIP	Myosin VIIA and Rab interacting protein	0.33	0.46
GPC2	Glypican 2 (cerebroglycan, fetal antigen)	0.32	0.47
VSIG2	V-set and immunoglobulin domain containing protein 2	0.33	0.47
CTBP2	C-terminal binding protein 2	0.33	0.47
IGSF11	Immunoglobulin superfamily, member 11	0.33	0.47
ATP1B2	ATPase, Na+/K+ transporting, beta 2 polypeptide	0.33	0.47
CTBP2	C-terminal binding protein 2	0.33	0.47
CDH13	Cadherin 13, H-cadherin (heart)	0.32	0.46
ADRB2	Adrenergic, beta-2-, receptor, surface	0.32	0.46
ANK2	Ankyrin 2, neuronal	0.32	0.46
PTPRD	Protein tyrosine phosphatase, receptor type, D	0.32	0.46
CLSTN2	Calsyntenin 2	0.32	0.46
CLSTN2	Calsyntenin 2	0.32	0.46
CADM1	Cell adhesion molecule 1	0.32	0.46
ANK2	Ankyrin 2, neuronal	0.32	0.46
ADRB2	Adrenergic, beta-2-, receptor, surface

MUC12	Mucin-like protein 12	0.95	0.47	1.52
ARHGEF11	Myosin-binding protein C, slow-type	0.87	0.47	1.45
MYBPC1	Myosin-binding protein C, slow-type	0.16	0.05	2.21
MYH7	Myosin-7	0.16	0.05	2.21
MYOM2	Myomesin-2	0.38	0.19	1.16
MYOM3	Myomesin-3	0.38	0.19	1.16
MYOZ1	Myozenin-1	0.87	0.47	1.45
MYOZ2	Myozenin-2	0.87	0.47	1.45
NAA15	N(Alpha)-acetyltransferase 15, NatA auxiliary subunit	0.95	0.47	1.52
NAA50	N(Alpha)-acetyltransferase 50, NatE catalytic subunit	0.17	0.05	2.21
NAP1L4	Nucleosome assembly protein 1-like 4	0.87	0.47	1.45
NAPSA	Napsin-A	0.87	0.47	1.45
NBEA	Neurobeachin	0.46	0.07	3.13
NFU1	Monothiol iron-sulfur cluster scaffold protein NFU1, mitochondrial	0.87	0.47	1.45

Supplementary Table 3: Results of enrichment analyses.

Ontology	Term	Observed protein count	P value	P value (false discovery rate-corrected)	Matching proteins in the network
GOTERM_BP_DIRECT	GO:0007155~cell adhesion	36	4.10E-13	8.70E-10	DDR1, LGALS3BP, NRP2, THBS2, LY9, PCDH17, ROBO1, ICAM1, DPP4, ADGRE1, CD86, LGALS4, ADGRE2, ADGRG1, ALCAM, ADGRE5, CD82, IGFBP7, IL32, CD72, VCAM1, TNFRSF12A, SELE, NELL2, MFAP4, CD4, BCAM, KITLG, CEACAM1, COL5A1, ITGBL1, CNTN3, TGFBI, ITGA5, CD22, ENG
GOTERM_BP_DIRECT	GO:0006954~inflammatory response	29	1.65E-10	1.75E-07	CSF1R, CALCA, SEMA7A, CXCL8, CSF1, IL1RAP, IL1RL1, ADGRE2, CRHBP, ADGRE5, LGALS9, HAVCR2, GGT5, TGFBI, VCAM1, IL10RB, CCL20, IL18, NFATC3, TNFRSF1B, SELE, TNFRSF1A, ATRN, CXCL10, IL6, VNN1, CHI3L1, IL18R1, TLR3
GOTERM_BP_DIRECT	GO:0046718~symbiont entry into host cell	15	8.50E-10	6.01E-07	SCARB2, NRP1, CR1, CXADR, CD80, PVR, ICAM1, DPP4, ACE2, CD4, ANPEP, BSG, ITGA5, HAVCR1, GAS6
GOTERM_BP_DIRECT	GO:0006955~immune response	30	2.22E-09	1.17E-06	CD274, SEMA7A, IL1RN, CXCL8, CD80, IL1RAP, FCAR, TNFSF13B, IL1RL1, ADGRE5, ENPP2, CTSC, IL10, IL32, IL4R, IL10RB, CCL20, TNFSF12, IL1R2, GZMA, IL18, LILRB2, TNFRSF1B, CD4, FAS, HLA-DRA, TNFSF8, LTBR, CD22, IL18R1
GOTERM_BP_DIRECT	GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	13	7.79E-09	3.30E-06	CD74, NRP1, TGFB1, CD80, TREM2, GFRA1, AREG, IL6, CD4, KITLG, CLEC6A, ENPP2, ITGA5
GOTERM_BP_DIRECT	GO:0007165~signal transduction	48	1.91E-08	6.73E-06	LGALS3BP, CD274, CSF1R, NRP1, IL1RN, CD83, CXCL8, OXT, TNFRSF11B, LILRA2, IQGAP2, TNFSF13B, IL1RL1, CRHBP, ALCAM, PLAU, ERBB2, TIMP1, INSL5, FGF21, IL32, IL4R, IL10RB, CCL20, GDF15, TNFSF12, CLEC11A, PLAUR, TNFRSF10A, ADA2, LILRB1, PILRA, LILRB2, INHBC, GFER, IGF2R, PGF, CXCL10, CD4, BCAM, CEACAM1, FAS, TNFSF8, LTBR, AGRN, GAS6, IL18R1, TLR3
GOTERM_BP_DIRECT	GO:0042102~positive regulation of T cell proliferation	11	3.62E-08	1.10E-05	CD274, IL6, KITLG, VCAM1, LEP, CD80, CD28, LILRB2, IL6ST, TNFSF13B, HAVCR2
GOTERM_BP_DIRECT	GO:0006508~proteolysis	29	6.52E-08	1.73E-05	DPP10, CPB1, CPQ, CTSZ, HTRA2, PLAT, PRCP, DPP4, ADAMTS15, CTSO, DPP7, DNPEP, PLAU, ANPEP, ADAMTSL2, PRSS8, GGT1, PRSS2, PAMR1, CTSD, CTSC, GGT5, MMP7, MME, HGF, ACE2, PRTN3, TPP1, THOP1
GOTERM_BP_DIRECT	GO:0070374~positive regulation of ERK1 and ERK2 cascade	18	1.37E-07	3.23E-05	CD74, CSF1R, NRP1, SEMA7A, TGFB1, CCL20, TREM2, ICAM1, MARCO, CD4, BMPER, CHI3L1, TEK, LGALS9, GAS6, FGFR2, HAVCR2, FGF21
GOTERM_BP_DIRECT	GO:0001934~positive regulation of protein phosphorylation	17	1.84E-07	3.90E-05	CD74, CSF1R, SEMA7A, HGF, PLAUR, TREM2, PGF, MARCO, CD4, LEP, ERBB2, FAS, TEK, FAM20A, GAS6, ENG, FGF21
GOTERM_BP_DIRECT	GO:0032722~positive regulation of chemokine production	9	3.12E-07	6.01E-05	IL1RL1, CSF1R, CD74, IL6, IL4R, IL18, HMOX1, TLR3, HAVCR2
GOTERM_BP_DIRECT	GO:0001525~angiogenesis	18	7.46E-07	1.24E-04	NRP1, NRP2, CXCL8, TNFRSF12A, TNFSF12, IL18, AMOT, NELL2, ADGRG1, CEACAM1, ANPEP, LEP, BSG, HMOX1, TEK, TGFBI, ITGA5, FGFR2
GOTERM_BP_DIRECT	GO:0042130~negative regulation of T cell proliferation	9	7.59E-07	1.24E-04	IL10, CD274, TGFB1, CR1, CD80, LILRB1, LILRB2, VSIG4, HAVCR2
GOTERM_BP_DIRECT	GO:0007267~cell-cell signaling	17	1.02E-06	1.55E-04	NRP1, CALCA, GDF15, CCL20, IL18, LILRB2, AREG, EFNA4, PGF, CXCL10, ADGRG1, ADGRE5, ANGPTL2, TNFSF8, TEK, FGFR2, FGF21
GOTERM_BP_DIRECT	GO:0006520~amino acid metabolic process	7	1.55E-06	2.19E-04	QDPR, GGT5, DDC, ACY1, SCLY, GGT1, PTS
GOTERM_BP_DIRECT	GO:0097490~sympathetic neuron projection extension	5	2.04E-06	2.70E-04	NELL2, NRP1, NRP2, CLSTN3, SEMA3F
GOTERM_BP_DIRECT	GO:0019221~cytokine-mediated signaling pathway	13	6.61E-06	8.24E-04	CSF1R, IL4R, IL10RB, IFNGR2, IL1R2, IL18, LILRB1, LILRB2, LILRA2, TNFRSF1A, IL6, IL6ST, CRLF1
GOTERM_BP_DIRECT	GO:0032689~negative regulation of type II interferon production	8	8.27E-06	9.73E-04	IL10, IL1RL1, CD274, CR1, LILRB1, LGALS9, GAS6, HAVCR2
GOTERM_BP_DIRECT	GO:0071356~cellular response to tumor necrosis factor	12	1.06E-05	1.18E-03	CRHBP, CALCA, VCAM1, FABP4, CXCL8, CCL20, GPD1, CHI3L1, GFER, FCAR, ASS1, IL18BP
GOTERM_BP_DIRECT	GO:0071222~cellular response to lipopolysaccharide	14	1.12E-05	1.18E-03	IL10, CD274, CXCL8, CD80, IL18, LILRB1, LILRB2, TNFRSF1B, GFER, FCAR, ASS1, CXCL10, IL6, HAVCR2
GOTERM_BP_DIRECT	GO:0051897~positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	14	1.18E-05	1.19E-03	DDR1, CSF1R, TGFB1, GDF15, HGF, IL6, CD4, C1QTNF1, CD72, LEP, CD28, CHI3L1, TEK, GAS6, ENG
GOTERM_BP_DIRECT	GO:0007166~cell surface receptor signaling pathway	18	1.48E-05	1.41E-03	RTN4R, CD274, IFNGR2, CD80, GFRA1, LILRB2, ADGRE1, ADGRE2, CXCL10, MARCO, ADGRD1, ADGRG1, CD4, ADGRE5, BSG, ERBB2, CD28, GAS6
GOTERM_BP_DIRECT	GO:0036486~ventral trunk neural crest cell migration	4	1.53E-05	1.41E-03	NELL2, NRP1, NRP2, SEMA3F
GOTERM_BP_DIRECT	GO:0097191~extrinsic apoptotic signaling pathway	8	1.87E-05	1.65E-03	TGFB1, KRT18, TNFSF12, KRT8, FAS, TNFRSF10A, TNFRSF1B, TLR3
GOTERM_BP_DIRECT	GO:0033674~positive regulation of kinase activity	8	2.39E-05	2.03E-03	DDR1, CSF1R, CD74, CD4, ERBB2, TREM2, TEK, FGFR2
GOTERM_BP_DIRECT	GO:0140105~interleukin-10-mediated signaling pathway	5	2.71E-05	2.13E-03	IL10, IL10RB, LILRB1, LILRB2, LILRA2
GOTERM_BP_DIRECT	GO:0048846~axon extension involved in axon guidance	5	2.71E-05	2.13E-03	NELL2, NRP1, NRP2, ALCAM, SEMA3F
GOTERM_BP_DIRECT	GO:0032755~positive regulation of interleukin-6 production	10	3.66E-05	2.73E-03	CD74, IL6, TGFB1, LEP, BSG, LILRB2, IL1RAP, LGALS9, LILRA2, TLR3
GOTERM_BP_DIRECT	GO:0097491~sympathetic neuron projection guidance	4	3.79E-05	2.73E-03	NELL2, NRP1, NRP2, SEMA3F
GOTERM_BP_DIRECT	GO:0003148~outflow tract septum morphogenesis	6	3.86E-05	2.73E-03	NELL2, NRP1, NRP2, FGFR2, ENG, ROBO1
GOTERM_BP_DIRECT	GO:0007275~multicellular organism development	9	4.12E-05	2.82E-03	DDR1, CD86, CSF1R, CDH2, ERBB2, TEK, FSTL1, FGFR2, FSTL3
GOTERM_BP_DIRECT	GO:0043410~positive regulation of MAPK cascade	13	4.57E-05	3.03E-03	CD74, TGFB1, GDF15, HGF, IL6, CD4, C1QTNF1, CDH2, LEP, ERBB2, TEK, FGFR2, FGF21
GOTERM_BP_DIRECT	GO:0032733~positive regulation of interleukin-10 production	7	4.75E-05	3.05E-03	CD274, IL6, CD83, HGF, CD28, TREM2, LGALS9
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptotic process	22	5.96E-05	3.71E-03	IL10, CD74, CSF1R, TNFRSF6B, HGF, HIP1R, PLAUR, PRAP1, GFER, FSTL1, FABP1, IL6, KRT18, CBS, LEP, ERBB2, CD28, FAS, TEK, TIMP1, IL6ST, GAS6
GOTERM_BP_DIRECT	GO:0032757~positive regulation of interleukin-8 production	8	6.50E-05	3.93E-03	CD74, IL6, CALCA, LEP, CHI3L1, LGALS9, LILRA2, TLR3
GOTERM_BP_DIRECT	GO:0046596~positive regulation of viral entry into host cell	5	7.20E-05	4.24E-03	CD74, CD4, BSG, FURIN, LGALS9
GOTERM_BP_DIRECT	GO:0051384~response to glucocorticoid	7	1.29E-04	6.86E-03	IL10, IL6, IL1RN, GOT1, SDC1, OXT, AREG
GOTERM_BP_DIRECT	GO:1901166~neural crest cell migration involved in autonomic nervous system development	4	1.29E-04	6.86E-03	NELL2, NRP1, NRP2, SEMA3F
GOTERM_BP_DIRECT	GO:0021637~trigeminal nerve structural organization	4	1.29E-04	6.86E-03	NELL2, NRP1, NRP2, SEMA3F
GOTERM_BP_DIRECT	GO:0046813~receptor-mediated virion attachment to host cell	4	1.29E-04	6.86E-03	DPP4, ACE2, GAS6, ICAM1
GOTERM_BP_DIRECT	GO:0007159~leukocyte cell-cell adhesion	6	1.34E-04	6.91E-03	NT5E, CALCA, VCAM1, ITGA5, SELE, ICAM1
GOTERM_BP_DIRECT	GO:0007157~heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	8	1.38E-04	6.98E-03	VCAM1, CXADR, ALCAM, CDH2, ITGA5, SELE, PVR, ICAM1
GOTERM_BP_DIRECT	GO:0098609~cell-cell adhesion	13	1.64E-04	8.10E-03	VCAM1, BAIAP2, ROBO1, ICAM1, NFASC, BCAM, KRT18, VNN1, CDH2, CDHR2, ITGBL1, ITGA5, FGFR2
GOTERM_BP_DIRECT	GO:0021785~branchiomotor neuron axon guidance	4	2.05E-04	9.86E-03	NELL2, NRP1, NRP2, SEMA3F
GOTERM_BP_DIRECT	GO:0006693~prostaglandin metabolic process	5	3.54E-04	1.67E-02	GSTA1, AKR1C4, PTGR1, CES2, TNFRSF1A
GOTERM_BP_DIRECT	GO:0061549~sympathetic ganglion development	4	4.29E-04	1.93E-02	NELL2, NRP1, NRP2, SEMA3F
GOTERM_BP_DIRECT	GO:0021612~facial nerve structural organization	4	4.29E-04	1.93E-02	NELL2, NRP1, NRP2, SEMA3F
GOTERM_BP_DIRECT	GO:0007411~axon guidance	12	4.82E-04	2.13E-02	NELL2, CSF1R, NRP1, SEMA7A, NFASC, NRP2, BSG, CNTN3, SEMA3F, EFNA4, FGFR2, IGSF9
GOTERM_BP_DIRECT	GO:0071526~semaphorin-plexin signaling pathway	6	4.97E-04	2.15E-02	NELL2, NRP1, SEMA7A, NRP2, ERBB2, SEMA3F
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	15	6.31E-04	2.65E-02	TGFB1, TNFRSF12A, GZMA, HIP1R, NFATC3, HTRA2, LILRB1, TNFRSF10A, IGF2R, IL6, AIFM1, TCTN3, FAS, CTSD, TLR3
GOTERM_BP_DIRECT	GO:0042531~positive regulation of tyrosine phosphorylation of STAT protein	7	6.50E-04	2.65E-02	CSF1R, IL6, LEP, IL18, IL6ST, CRLF1, TNFRSF1A
GOTERM_BP_DIRECT	GO:1901224~positive regulation of non-canonical NF-kappaB signal transduction	7	6.50E-04	2.65E-02	PTPA43, IL18, TREM2, LGALS9, IL18R1, TLR3, HAVCR2
GOTERM_BP_DIRECT	GO:1903375~facioacoustic ganglion development	3	7.35E-04	2.78E-02	NELL2, NRP1, NRP2
GOTERM_BP_DIRECT	GO:0002859~negative regulation of natural killer cell mediated cytotoxicity directed against tumor cell target	3	7.35E-04	2.78E-02	CEACAM1, TGFB1, HAVCR2
GOTERM_BP_DIRECT	GO:1904835~dorsal root ganglion morphogenesis	3	7.35E-04	2.78E-02	NELL2, NRP1, NRP2
GOTERM_BP_DIRECT	GO:0021649~vestibulocochlear nerve structural organization	3	7.35E-04	2.78E-02	NELL2, NRP1, NRP2
GOTERM_BP_DIRECT	GO:0007156~homophilic cell adhesion via plasma membrane adhesion molecules	11	7.94E-04	2.95E-02	CDH6, CEACAM1, CLSTN2, CDH2, CLSTN3, CDHR2, BSG, PVR, PCDH17, IGSF9, ROBO1
GOTERM_BP_DIRECT	GO:0006898~receptor-mediated endocytosis	7	8.85E-04	3.23E-02	SCARB2, MSR1, MARCO, HIP1R, SDC1, ASGR1, IGF2R
GOTERM_BP_DIRECT	GO:0001523~retinoid metabolic process	5	9.19E-04	3.30E-02	ADH4, AKR1B10, ADH1B, ALDH1A1, AKR1C4
GOTERM_BP_DIRECT	GO:0001935~positive regulation of endothelial cell proliferation	7	9.53E-04	3.37E-02	NELL2, IL10, NRP1, NRP2, TNFSF12, TEK, PGF
GOTERM_BP_DIRECT	GO:0045766~positive regulation of angiogenesis	10	1.15E-03	3.99E-02	NRP1, CXCL8, DDAH1, TNFSF12, HMOX1, CHI3L1, TEK, TLR3, PGF, ENG
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell population proliferation	19	1.19E-03	4.06E-02	CSF1R, TGFB1, CR1, CSF1, CLEC11A, AREG, PGF, DPP4, CXCL10, IL6, KITLG, LEP, ERBB2, PRTN3, TIMP1, IL6ST, FGFR2, CRLF1, FGF21
GOTERM_BP_DIRECT	GO:0071260~cellular response to mechanical stimulus	7	1.35E-03	4.56E-02	TGFB1, FAS, TNFRSF10A, LTBR, TLR3, ENG, TNFRSF1A
GOTERM_BP_DIRECT	GO:0097374~sensory neuron axon guidance	3	1.45E-03	4.82E-02	NELL2, NRP1, NRP2
GOTERM_BP_DIRECT	GO:0032720~negative regulation of tumor necrosis factor production	7	1.55E-03	5.04E-02	IL10, ACP5, TREM2, LILRB1, LGALS9, GAS6, HAVCR2
GOTERM_BP_DIRECT	GO:0030198~extracellular matrix organization	10	1.74E-03	5.58E-02	ADAMTS15, MARCO, MMP7, COL5A1, COL4A1, ADAMTSL2, VWA1, FURIN, TNFRSF11B, TGFBI
GOTERM_BP_DIRECT	GO:0006518~peptide metabolic process	4	1.86E-03	5.90E-02	CPM, DNPEP, MME, THOP1
GOTERM_BP_DIRECT	GO:0007169~cell surface receptor protein tyrosine kinase signaling pathway	8	1.90E-03	5.91E-02	DDR1, CSF1R, CD4, CSF1, ERBB2, TEK, FGFR2, ANGPTL1
GOTERM_BP_DIRECT	GO:0001666~response to hypoxia	10	2.03E-03	6.24E-02	DPP4, TGFB1, VCAM1, PLAU, LEP, PLAT, TEK, HMOX2, PGF, ENG
GOTERM_BP_DIRECT	GO:0045765~regulation of angiogenesis	5	2.40E-03	7.06E-02	IL6, BMPER, LEP, ERBB2, HMOX1
GOTERM_BP_DIRECT	GO:0043542~endothelial cell migration	5	2.40E-03	7.06E-02	DPP4, PTPA43, CALCA, TNFSF12, FSTL1
GOTERM_BP_DIRECT	GO:0061551~trigeminal ganglion development	3	2.40E-03	7.06E-02	NELL2, NRP1, NRP2
GOTERM_BP_DIRECT	GO:0001657~ureteric bud development	5	2.65E-03	7.60E-02	TGFB1, BMPER, SDC1, FGFR2, CRLF1
GOTERM_BP_DIRECT	GO:0060135~maternal process involved in female pregnancy	4	2.65E-03	7.60E-02	ACE2, CBS, LGALS9, HAVCR2
GOTERM_BP_DIRECT	GO:0033209~tumor necrosis factor-mediated signaling pathway	6	2.72E-03	7.69E-02	KRT18, KRT8, FAS, TNFRSF1B, TNFSF13B, TNFRSF1A
GOTERM_BP_DIRECT	GO:2000352~negative regulation of endothelial cell apoptotic process	5	2.93E-03	8.06E-02	IL10, TEK, GAS6, FGF21, ICAM1
GOTERM_BP_DIRECT	GO:0051591~response to cAMP	5	2.93E-03	8.06E-02	BSG, SDC1, OXT, TEK, AREG
GOTERM_BP_DIRECT	GO:0006935~chemotaxis	8	3.09E-03	8.31E-02	CXCL10, CXCL8, PLAU, CCL20, ENPP2, PLAUR, LGALS9, AMOT
GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression	18	3.10E-03	8.31E-02	IL32, CD74, TGFB1, CXCL8, CSF1, TREM2, LILRB1, ROBO1, IL6, OCLN, C1QTNF1, ERBB2, CD28, LGALS9, GAS6, TLR3, ENG, FGF21
GOTERM_BP_DIRECT	GO:0043123~positive regulation of canonical NF-kappaB signal transduction	11	3.33E-03	8.83E-02	BST2, CD74, CD4, TGFB1, CANT1, CLEC6A, HMOX1, LTBR, LGALS9, TLR3, TNFRSF1A
GOTERM_BP_DIRECT	GO:0032692~negative regulation of interleukin-1 production	3	3.56E-03	9.20E-02	IL10, CEACAM1, GAS6
GOTERM_BP_DIRECT	GO:2001209~positive regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	3	3.56E-03	9.20E-02	FAS, HTRA2, LGALS9
GOTERM_BP_DIRECT	GO:0043032~positive regulation of macrophage activation	4	3.62E-03	9.25E-02	IL10, IL1RL1, IL4R, HAVCR2
GOTERM_BP_DIRECT	GO:0098586~cellular response to virus	7	3.73E-03	9.40E-02	CXCL10, IL6, TGFB1, IL10RB, IFNGR2, LGALS9, TLR3
GOTERM_BP_DIRECT	GO:0035025~positive regulation of Rho protein signal transduction	5	4.23E-03	1.05E-01	RTN4R, ADGRG1, ERBB2, TEK, ROBO1
GOTERM_BP_DIRECT	GO:0031295~T cell costimulation	5	4.60E-03	1.13E-01	DPP4, CD274, CD80, CD28, TNFSF13B
GOTERM_BP_DIRECT	GO:0021828~gonadotrophin-releasing hormone neuronal migration to the hypothalamus	3	4.93E-03	1.20E-01	NELL2, NRP1, NRP2
GOTERM_BP_DIRECT	GO:0050919~negative chemotaxis	5	5.00E-03	1.20E-01	NELL2, DPP4, SEMA7A, NRP2, SEMA3F
GOTERM_BP_DIRECT	GO:0043434~response to peptide hormone	5	5.87E-03	1.37E-01	BSG, OXT, TEK, TIMP1, AREG
GOTERM_BP_DIRECT	GO:0034097~response to cytokine	5	5.87E-03	1.37E-01	CD274, ACP5, TIMP1, IL6ST, SELE
GOTERM_BP_DIRECT	GO:0022617~extracellular matrix disassembly	5	5.87E-03	1.37E-01	ADAMTS15, MMP7, FURIN, PRSS2, ENG
GOTERM_BP_DIRECT	GO:0006911~phagocytosis, engulfment	4	6.14E-03	1.41E-01	MSR1, MARCO, TREM2, HAVCR1
GOTERM_BP_DIRECT	GO:2000660~negative regulation of interleukin-1-mediated signaling pathway	3	6.51E-03	1.45E-01	IL6, IL1RN, IL1R2
GOTERM_BP_DIRECT	GO:0006729~tetrahydrobiopterin biosynthetic process	3	6.51E-03	1.45E-01	QDPR, PCBD1, PTS
GOTERM_BP_DIRECT	GO:0010757~negative regulation of plasminogen activation	3	6.51E-03	1.45E-01	PLAU, CTSZ, PLAT
GOTERM_BP_DIRECT	GO:0060907~positive regulation of macrophage cytokine production	4	6.90E-03	1.52E-01	CD74, SEMA7A, LILRB1, TLR3
GOTERM_BP_DIRECT	GO:0001558~regulation of cell growth	6	6.99E-03	1.53E-01	DDR1, CEACAM1, IGFBPL1, CLSTN3, CRIM1, IGFBP7
GOTERM_BP_DIRECT	GO:0009636~response to toxic substance	6	7.79E-03	1.67E-01	PON3, DDC, ABCC1, PON2, SDC1, CES1
GOTERM_BP_DIRECT	GO:0032729~positive regulation of type II interferon production	6	7.79E-03	1.67E-01	IL18, LILRB1, LGALS9, IL18R1, TLR3, HAVCR2
GOTERM_BP_DIRECT	GO:0014823~response to activity	5	7.89E-03	1.67E-01	IL10, IL6, LEP, OXT, FGF21
GOTERM_BP_DIRECT	GO:0061518~microglial cell proliferation	3	8.28E-03	1.69E-01	CSF1R, CSF1, TREM2
GOTERM_BP_DIRECT	GO:0030200~heparan sulfate proteoglycan catabolic process	3	8.28E-03	1.69E-01	GLB1, IDUA, GUSB
GOTERM_BP_DIRECT	GO:0014909~smooth muscle cell migration	3	8.28E-03	1.69E-01	DDR1, PLAU, PLAT
GOTERM_BP_DIRECT	GO:1905146~lysosomal protein catabolic process	3	8.28E-03	1.69E-01	DPP7, LAMP2, TPP1
GOTERM_BP_DIRECT	GO:0032740~positive regulation of interleukin-17 production	4	8.57E-03	1.70E-01	IL6, TGFB1, IL18, LY9
GOTERM_BP_DIRECT	GO:0032753~positive regulation of interleukin-4 production	4	8.57E-03	1.70E-01	CD28, IL18AP, LGALS9, HAVCR2
GOTERM_BP_DIRECT	GO:0007565~female pregnancy	6	8.64E-03	1.70E-01	CRHBP, TGFB1, LEP, OXT, LGALS9, ITGA5
GOTERM_BP_DIRECT	GO:0032760~positive regulation of tumor necrosis factor production	7	8.67E-03	1.70E-01	IL6, TGFB1, LEP, LGALS9, LILRA2, TLR3, HAVCR2
GOTERM_BP_DIRECT	GO:0005975~carbohydrate metabolic process	8	1.01E-02	1.94E-01	GLB1, IDUA, MAN1A2, GPD1, CHI3L1, NPL, NAGPA, GUSB
GOTERM_BP_DIRECT	GO:0072540~T-helper 17 cell lineage commitment	3	1.02E-02	1.94E-01	IL6, IL6ST, LY9
GOTERM_BP_DIRECT	GO:0010888~negative regulation of lipid storage	3	1.02E-02	1.94E-01	IL6, CLSTN3, LEP
GOTERM_BP_DIRECT	GO:0045657~positive regulation of monocyte differentiation	3	1.02E-02	1.94E-01	CD74, CD4, CSF1
GOTERM_BP_DIRECT	GO:0045216~cell-cell junction organization	4	1.15E-02	2.15E-01	OCLN, TGFB1, CXADR, HEG1
GOTERM_BP_DIRECT	GO:0006081~cellular aldehyde metabolic process	3	1.24E-02	2.30E-01	ALDH3A1, ADH4, ALDH1A1
GOTERM_BP_DIRECT	GO:0097421~liver regeneration	4	1.26E-02	2.30E-01	IL10, IL6, TGFB1, GFER
GOTERM_BP_DIRECT	GO:0019886~antigen processing and presentation of exogenous peptide antigen via MHC class II	4	1.26E-02	2.30E-01	CD74, HLA-DRA, IFI30, CTSD
GOTERM_BP_DIRECT	GO:0006915~apoptotic process	18	1.36E-02	2.46E-01	TNFRSF6B, TNFRSF12A, TNFSF12, GZMA, PRUNE2, TNFRSF11B, TNFRSF10A, PTPRH, TNFRSF1A, AIFM1, TCTN3, GAS2, FAS, CHI3L1, C19ORF12, LTBR, CTSC, FGFR2
GOTERM_BP_DIRECT	GO:0010575~positive regulation of vascular endothelial growth factor production	4	1.37E-02	2.46E-01	IL6, TGFB1, BSG, IL6ST
GOTERM_BP_DIRECT	GO:0030155~regulation of cell adhesion	5	1.40E-02	2.49E-01	CXCL8, PLAU, PLAUR, IL18, ENG
GOTERM_BP_DIRECT	GO:0046479~glycosphingolipid catabolic process	3	1.47E-02	2.55E-01	GLB1, GLA, ENPP7
GOTERM_BP_DIRECT	GO:0007167~enzyme-linked receptor protein signaling pathway	3	1.47E-02	2.55E-01	CD4, ERBB2, GAS6
GOTERM_BP_DIRECT	GO:0042110~T cell activation	5	1.48E-02	2.55E-01	DPP4, CD4, CD80, CD28, LY9
GOTERM_BP_DIRECT	GO:0045671~negative regulation of osteoclast differentiation	4	1.49E-02	2.55E-01	CALCA, TNFRSF11B, TLR3, FSTL3
GOTERM_BP_DIRECT	GO:0030225~macrophage differentiation	4	1.49E-02	2.55E-01	IL1RL1, CSF1R, CD4, CSF1
GOTERM_BP_DIRECT	GO:0051965~positive regulation of synapse assembly	5	1.56E-02	2.65E-01	CLSTN2, CLSTN3, OXT, IL1RAP, THBS2
GOTERM_BP_DIRECT	GO:0030335~positive regulation of cell migration	11	1.62E-02	2.72E-01	CD274, CSF1R, SEMA7A, TGFB1, MMP7, CSF1, PLAU, CCL20, HGF, SEMA3F, ITGA5
GOTERM_BP_DIRECT	GO:0097242~amyloid-beta clearance	3	1.72E-02	2.85E-01	MSR1, MARCO, MME
GOTERM_BP_DIRECT	GO:0097028~dendritic cell differentiation	3	1.72E-02	2.85E-01	TREM2, LILRB1, GAS6
GOTERM_BP_DIRECT	GO:0032743~positive regulation of interleukin-2 production	4	1.75E-02	2.87E-01	CD4, CD83, CD80, CD28
GOTERM_BP_DIRECT	GO:0032956~regulation of actin cytoskeleton organization	6	1.80E-02	2.93E-01	BST2, CSF1R, TGFB1, HIP1R, IQGAP2, BAIAP2

GOTERM_BP_DIRECT	GO:0006629~lipid metabolic process	9	1.81E-02	2.93E-01	ALDH1A1, ARSA, IL1RN, RIDA, GSTA3, LEP, APOF, TPP1, GLA
GOTERM_BP_DIRECT	GO:0002040~sprouting angiogenesis	4	1.89E-02	3.03E-01	NRP1, TGFB1, TEK, PGF
GOTERM_BP_DIRECT	GO:0001570~vasculogenesis	5	1.93E-02	3.08E-01	NRP1, TGFB1, HEG1, ENG, AMOT
GOTERM_BP_DIRECT	GO:0030855~epithelial cell differentiation	6	1.95E-02	3.08E-01	COL4A1, CDH2, CDR2, GSTA1, TPP1, FGFR2, CES1
GOTERM_BP_DIRECT	GO:0007250~activation of NF-kappaB-inducing kinase activity	3	1.99E-02	3.12E-01	CHI3L1, TNFRSF10A, TLR3
GOTERM_BP_DIRECT	GO:0010595~positive regulation of endothelial cell migration	5	2.03E-02	3.16E-01	NELL2, NRP1, NRP2, BSG, TEK
GOTERM_BP_DIRECT	GO:0007179~transforming growth factor beta receptor signaling pathway	6	2.10E-02	3.26E-01	TGFB1, GDF15, FURIN, LTBP2, LTBP3, ENG
GOTERM_BP_DIRECT	GO:0002764~immune response-regulating signaling pathway	4	2.18E-02	3.32E-01	LILRB1, LILRB2, LILRA2, FCAR
GOTERM_BP_DIRECT	GO:0120162~positive regulation of cold-induced thermogenesis	6	2.19E-02	3.32E-01	FABP4, IL4R, LEP, IL18, OXT, FGF21
GOTERM_BP_DIRECT	GO:0071466~cellular response to xenobiotic stimulus	5	2.24E-02	3.32E-01	CRHBP, GAS6, FBP1, TLR3, FGF21
GOTERM_BP_DIRECT	GO:0045953~negative regulation of natural killer cell mediated cytotoxicity	3	2.27E-02	3.32E-01	LILRB1, LGALS9, GFER
GOTERM_BP_DIRECT	GO:0032736~positive regulation of interleukin-13 production	3	2.27E-02	3.32E-01	IL18, IL1RAP, LGALS9
GOTERM_BP_DIRECT	GO:0085029~extracellular matrix assembly	3	2.27E-02	3.32E-01	TGFB1, QSOX1, GAS6
GOTERM_BP_DIRECT	GO:0032725~positive regulation of granulocyte macrophage colony-stimulating factor production	3	2.27E-02	3.32E-01	CD80, IL18, LILRA2
GOTERM_BP_DIRECT	GO:0035729~cellular response to hepatocyte growth factor stimulus	3	2.27E-02	3.32E-01	IL10, NRP1, HGF
GOTERM_BP_DIRECT	GO:0007189~adenylate cyclase-activating G protein-coupled receptor signaling pathway	7	2.30E-02	3.33E-01	ADGRE1, ADGRE2, ADGRD1, CXCL10, ADGRG1, CALCA, ADGRE5
GOTERM_BP_DIRECT	GO:0006953~acute-phase response	4	2.49E-02	3.59E-01	IL6, CD163, IL1RN, ASS1
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia	7	2.52E-02	3.61E-01	FABP1, TGFB1, AIFM1, CBS, HMOX1, TREM2, FGFR2
GOTERM_BP_DIRECT	GO:0006957~complement activation, alternative pathway	3	2.57E-02	3.65E-01	CR1, C7, VSIG4
GOTERM_BP_DIRECT	GO:0030574~collagen catabolic process	4	2.66E-02	3.76E-01	MMP7, FURIN, PRTN3, PRSS2
GOTERM_BP_DIRECT	GO:0043116~negative regulation of vascular permeability	3	2.88E-02	4.02E-01	CEACAM1, DDAH1, AMOT
GOTERM_BP_DIRECT	GO:0006536~glutamate metabolic process	3	2.88E-02	4.02E-01	ALDH5A1, GOT1, GGT1
GOTERM_BP_DIRECT	GO:0050728~negative regulation of inflammatory response	7	2.92E-02	4.04E-01	IL10, NT5E, MVK, HGF, ACP5, TEK, TNFRSF1A
GOTERM_BP_DIRECT	GO:0046427~positive regulation of receptor signaling pathway via JAK-STAT	4	3.01E-02	4.09E-01	IL10, IL6, IL10RB, LEP
GOTERM_BP_DIRECT	GO:0050729~positive regulation of inflammatory response	6	3.02E-02	4.09E-01	IL1RL1, TGFB1, FABP4, IL18, TLR3, TNFRSF1A
GOTERM_BP_DIRECT	GO:0006788~heme oxidation	2	3.13E-02	4.09E-01	HMOX1, HMOX2
GOTERM_BP_DIRECT	GO:0002780~antibacterial peptide biosynthetic process	2	3.13E-02	4.09E-01	LGALS4, MMP7
GOTERM_BP_DIRECT	GO:0034346~positive regulation of type III interferon production	2	3.13E-02	4.09E-01	IL32, TLR3
GOTERM_BP_DIRECT	GO:0009966~regulation of signal transduction	4	3.19E-02	4.09E-01	IGFBPL1, CRIM1, IGFBP7, FURIN
GOTERM_BP_DIRECT	GO:0030277~maintenance of gastrointestinal epithelium	3	3.21E-02	4.09E-01	TFF2, MUC13, PBLD
GOTERM_BP_DIRECT	GO:0042119~neutrophil activation	3	3.21E-02	4.09E-01	CXCL8, IL18, FCAR
GOTERM_BP_DIRECT	GO:0045019~negative regulation of nitric oxide biosynthetic process	3	3.21E-02	4.09E-01	IL10, ACP5, GLA
GOTERM_BP_DIRECT	GO:0043171~peptide catabolic process	3	3.21E-02	4.09E-01	CPQ, ANPEP, TPP1
GOTERM_BP_DIRECT	GO:0097435~supramolecular fiber organization	3	3.21E-02	4.09E-01	MFAP4, COL5A1, LTBP2
GOTERM_BP_DIRECT	GO:0045591~positive regulation of regulatory T cell differentiation	3	3.21E-02	4.09E-01	TGFB1, CR1, LILRB2
GOTERM_BP_DIRECT	GO:0045779~negative regulation of bone resorption	3	3.21E-02	4.09E-01	IL6, CALCA, TNFRSF11B
GOTERM_BP_DIRECT	GO:0007566~embryo implantation	4	3.38E-02	4.22E-01	DDR1, CALCA, BSG, IGFBP7
GOTERM_BP_DIRECT	GO:0001755~neural crest cell migration	4	3.38E-02	4.22E-01	NRP1, SEMA7A, KITLG, SEMA3F
GOTERM_BP_DIRECT	GO:0051603~proteolysis involved in protein catabolic process	4	3.38E-02	4.22E-01	CTSO, GZMA, CTSZ, CTSC
GOTERM_BP_DIRECT	GO:0030316~osteoclast differentiation	4	3.38E-02	4.22E-01	CSF1R, TGFB1, CSF1, TREM2
GOTERM_BP_DIRECT	GO:0016477~cell migration	10	3.47E-02	4.30E-01	CDH6, ADGRE2, ADGRG1, CEACAM1, CDH2, COL5A1, ITGBL1, SDC1, GFRA1, ENG
GOTERM_BP_DIRECT	GO:0043277~apoptotic cell clearance	3	3.55E-02	4.32E-01	MARCO, TREM2, GAS6
GOTERM_BP_DIRECT	GO:0032695~negative regulation of interleukin-12 production	3	3.55E-02	4.32E-01	IL10, ACP5, LILRB1
GOTERM_BP_DIRECT	GO:0050806~positive regulation of synaptic transmission	3	3.55E-02	4.32E-01	CLSTN2, CLSTN3, OXT
GOTERM_BP_DIRECT	GO:0071333~cellular response to glucose stimulus	5	3.62E-02	4.38E-01	TGFB1, TREM2, GAS6, FGF21, ICAM1
GOTERM_BP_DIRECT	GO:0021675~nerve development	3	3.90E-02	4.65E-01	NELL2, NRP2, SEMA3F
GOTERM_BP_DIRECT	GO:0050901~leukocyte tethering or rolling	3	3.90E-02	4.65E-01	VCAM1, LEP, SELE
GOTERM_BP_DIRECT	GO:0010744~positive regulation of macrophage derived foam cell differentiation	3	3.90E-02	4.65E-01	MSR1, CSF1, IL18
GOTERM_BP_DIRECT	GO:0030593~neutrophil chemotaxis	5	4.22E-02	4.99E-01	CXCL10, CXADR, CXCL8, CCL20, BSG
GOTERM_BP_DIRECT	GO:0001889~liver development	5	4.38E-02	5.06E-01	HGF, UPB1, GFER, IGF2R, ASS1
GOTERM_BP_DIRECT	GO:0006094~gluconeogenesis	4	4.41E-02	5.06E-01	GOT1, GPD1, FBP1, ENO3
GOTERM_BP_DIRECT	GO:0050918~positive chemotaxis	4	4.41E-02	5.06E-01	CXCL10, NRP1, HGF, PGF
GOTERM_BP_DIRECT	GO:0006979~response to oxidative stress	6	4.53E-02	5.06E-01	VNN1, ANGPTL7, HMOX1, C19ORF12, HAO1, HMOX2
GOTERM_BP_DIRECT	GO:0030886~negative regulation of myeloid dendritic cell activation	2	4.65E-02	5.06E-01	IL10, HAVCR2
GOTERM_BP_DIRECT	GO:0045957~negative regulation of complement activation, alternative pathway	2	4.65E-02	5.06E-01	CR1, VSIG4
GOTERM_BP_DIRECT	GO:0002767~immune response-inhibiting cell surface receptor signaling pathway	2	4.65E-02	5.06E-01	LILRB1, LILRB2
GOTERM_BP_DIRECT	GO:1902339~positive regulation of apoptotic process involved in morphogenesis	2	4.65E-02	5.06E-01	TNFRSF1B, TNFRSF1A
GOTERM_BP_DIRECT	GO:0002519~natural killer cell tolerance induction	2	4.65E-02	5.06E-01	LGALS9, HAVCR2
GOTERM_BP_DIRECT	GO:0045058~T cell selection	2	4.65E-02	5.06E-01	CD74, CD4
GOTERM_BP_DIRECT	GO:0000052~citrulline metabolic process	2	4.65E-02	5.06E-01	DDAH1, ASS1
GOTERM_BP_DIRECT	GO:1901335~lactone catabolic process	2	4.65E-02	5.06E-01	PON3, PON2
GOTERM_BP_DIRECT	GO:0032929~negative regulation of superoxide anion generation	2	4.65E-02	5.06E-01	PON3, ACP5
GOTERM_BP_DIRECT	GO:2001189~negative regulation of T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell	2	4.65E-02	5.06E-01	LILRB1, HAVCR2
GOTERM_BP_DIRECT	GO:0038195~urokinase plasminogen activator signaling pathway	2	4.65E-02	5.06E-01	PLAU, PLAUR
GOTERM_BP_DIRECT	GO:0010755~regulation of plasminogen activation	2	4.65E-02	5.06E-01	PLAU, PLAUR
GOTERM_BP_DIRECT	GO:0032355~response to estradiol	5	4.70E-02	5.09E-01	TGFB1, LEP, OXT, AREG, ASS1
GOTERM_BP_DIRECT	GO:0071404~cellular response to low-density lipoprotein particle stimulus	3	5.04E-02	5.42E-01	TGFB1, FGF21, CES1
GOTERM_BP_DIRECT	GO:0048661~positive regulation of smooth muscle cell proliferation	4	5.34E-02	5.63E-01	IL6, TGFB1, IL18, HMOX1
GOTERM_BP_DIRECT	GO:0042572~retinol metabolic process	4	5.34E-02	5.63E-01	ADH4, AKR1B10, ADH1B, ALDH1A1
GOTERM_BP_DIRECT	GO:0071320~cellular response to cAMP	4	5.34E-02	5.63E-01	CRHBP, GPD1, FBP1, ASS1
GOTERM_BP_DIRECT	GO:0001837~epithelial to mesenchymal transition	4	5.34E-02	5.63E-01	TGFB1, HGF, FGFR2, ENG
GOTERM_BP_DIRECT	GO:0050830~defense response to Gram-positive bacterium	6	5.66E-02	5.93E-01	IL6, MMP7, IL18, ACP5, TNFSF8, HAVCR2
GOTERM_BP_DIRECT	GO:0043627~response to estrogen	4	5.83E-02	6.07E-01	ARSA, MME, TNFRSF11B, TEK
GOTERM_BP_DIRECT	GO:0038145~macrophage colony-stimulating factor signaling pathway	2	6.16E-02	6.07E-01	CSF1R, CSF1
GOTERM_BP_DIRECT	GO:0019058~viral life cycle	2	6.16E-02	6.07E-01	ACE2, FURIN
GOTERM_BP_DIRECT	GO:0051917~regulation of fibrinolysis	2	6.16E-02	6.07E-01	PLAU, PLAUR
GOTERM_BP_DIRECT	GO:0006114~glycerol biosynthetic process	2	6.16E-02	6.07E-01	GOT1, LEP
GOTERM_BP_DIRECT	GO:0003177~pulmonary valve development	2	6.16E-02	6.07E-01	TNFRSF1B, TNFRSF1A
GOTERM_BP_DIRECT	GO:0045066~regulatory T cell differentiation	2	6.16E-02	6.07E-01	TGFB1, CD28
GOTERM_BP_DIRECT	GO:0060312~regulation of blood vessel remodeling	2	6.16E-02	6.07E-01	CEACAM1, TGFB1
GOTERM_BP_DIRECT	GO:0001332~negative regulation of extracellular matrix constituent secretion	2	6.16E-02	6.07E-01	TNFRSF1B, TNFRSF1A
GOTERM_BP_DIRECT	GO:0019448~L-cysteine catabolic process	2	6.16E-02	6.07E-01	CBS, AGXT
GOTERM_BP_DIRECT	GO:2001186~negative regulation of CD8-positive, alpha-beta T cell activation	2	6.16E-02	6.07E-01	CD274, LILRB1
GOTERM_BP_DIRECT	GO:1901143~insulin catabolic process	2	6.16E-02	6.07E-01	CEACAM1, CTSD
GOTERM_BP_DIRECT	GO:0002826~negative regulation of T-helper 1 type immune response	2	6.16E-02	6.07E-01	IL1RL1, HAVCR2
GOTERM_BP_DIRECT	GO:0008045~motor neuron axon guidance	3	6.28E-02	6.16E-01	NRP1, ALCAM, ERBB2
GOTERM_BP_DIRECT	GO:0071363~cellular response to growth factor stimulus	4	6.35E-02	6.20E-01	ERBB2, HTRA2, GAS6, TNFRSF1B
GOTERM_BP_DIRECT	GO:0002639~positive regulation of immunoglobulin production	3	6.71E-02	6.52E-01	IL10, IL6, IL4R
GOTERM_BP_DIRECT	GO:0007584~response to nutrient	4	6.88E-02	6.66E-01	ARSA, VCAM1, TNFRSF11B, ASS1
GOTERM_BP_DIRECT	GO:0032496~response to lipopolysaccharide	6	6.93E-02	6.67E-01	VCAM1, ACP5, LGALS9, SELE, FGFR2, IL18BP
GOTERM_BP_DIRECT	GO:0034341~response to type II interferon	3	7.16E-02	6.77E-01	BST2, CD74, KYNU
GOTERM_BP_DIRECT	GO:0045662~negative regulation of myoblast differentiation	3	7.16E-02	6.77E-01	CXCL10, TGFB1, IL18
GOTERM_BP_DIRECT	GO:0048843~negative regulation of axon extension involved in axon guidance	3	7.16E-02	6.77E-01	NRP1, SEMA7A, SEMA3F
GOTERM_BP_DIRECT	GO:0010507~negative regulation of autophagy	4	7.16E-02	6.77E-01	IL10, LEP, HGF, TREM2
GOTERM_BP_DIRECT	GO:0045742~positive regulation of epidermal growth factor receptor signaling pathway	3	7.61E-02	6.80E-01	TGFB1, PLAUR, HIP1R
GOTERM_BP_DIRECT	GO:0060349~bone morphogenesis	3	7.61E-02	6.80E-01	ACP5, LTBP3, FGFR2
GOTERM_BP_DIRECT	GO:0001774~microglial cell activation	3	7.61E-02	6.80E-01	IFNGR2, TREM2, TLR3
GOTERM_BP_DIRECT	GO:0010043~response to zinc ion	3	7.61E-02	6.80E-01	VCAM1, ASS1, KHK
GOTERM_BP_DIRECT	GO:0019064~fusion of virus membrane with host plasma membrane	2	7.64E-02	6.80E-01	GAS6, PVR
GOTERM_BP_DIRECT	GO:0060744~mammary gland branching involved in thelarche	2	7.64E-02	6.80E-01	TGFB1, AREG
GOTERM_BP_DIRECT	GO:0022614~membrane to membrane docking	2	7.64E-02	6.80E-01	VCAM1, ICAM1
GOTERM_BP_DIRECT	GO:0019344~cysteine biosynthetic process	2	7.64E-02	6.80E-01	CBS, GGT1
GOTERM_BP_DIRECT	GO:0002774~Fc receptor mediated inhibitory signaling pathway	2	7.64E-02	6.80E-01	LILRB1, LILRB2
GOTERM_BP_DIRECT	GO:0061041~regulation of wound healing	2	7.64E-02	6.80E-01	TNFRSF12A, PLAU
GOTERM_BP_DIRECT	GO:0038093~Fc receptor signaling pathway	2	7.64E-02	6.80E-01	PIGR, FCAR
GOTERM_BP_DIRECT	GO:0003209~cardiac atrium morphogenesis	2	7.64E-02	6.80E-01	HEG1, ENG
GOTERM_BP_DIRECT	GO:0002248~connective tissue replacement involved in inflammatory response wound healing	2	7.64E-02	6.80E-01	TGFB1, TIMP1
GOTERM_BP_DIRECT	GO:0003176~aortic valve development	2	7.64E-02	6.80E-01	TNFRSF1B, TNFRSF1A
GOTERM_BP_DIRECT	GO:0006959~humoral immune response	4	7.72E-02	6.85E-01	IL6, CD83, CD28, TREM2
GOTERM_BP_DIRECT	GO:0071346~cellular response to type II interferon	5	8.00E-02	6.92E-01	CCL20, LGALS9, TLR3, FCAR, ASS1
GOTERM_BP_DIRECT	GO:0042552~myelination	4	8.01E-02	6.92E-01	ATRN, NFASC, TGFB1, ERBB2
GOTERM_BP_DIRECT	GO:0015908~fatty acid transport	3	8.07E-02	6.92E-01	FABP1, FABP4, RBP5
GOTERM_BP_DIRECT	GO:1902042~negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	3	8.07E-02	6.92E-01	HGF, HMOX1, ICAM1
GOTERM_BP_DIRECT	GO:0099560~synaptic membrane adhesion	3	8.07E-02	6.92E-01	CDH6, IL1RAP, PCDH17
GOTERM_BP_DIRECT	GO:2001238~positive regulation of extrinsic apoptotic signaling pathway	3	8.07E-02	6.92E-01	TNFRSF12A, TNFSF12, LTBR
GOTERM_BP_DIRECT	GO:0032703~negative regulation of interleukin-2 production	3	8.07E-02	6.92E-01	CR1, VSIG4, HAVCR2
GOTERM_BP_DIRECT	GO:1903672~negative regulation of sprouting angiogenesis	3	8.07E-02	6.92E-01	IL10, BMPER, ITGA5
GOTERM_BP_DIRECT	GO:0042127~regulation of cell population proliferation	6	8.34E-02	7.12E-01	ACE2, CXCL10, TGFB1, MMP7, PLAU, ENG
GOTERM_BP_DIRECT	GO:0001935~endothelial cell proliferation	3	8.54E-02	7.24E-01	CALCA, HMOX1, TEK
GOTERM_BP_DIRECT	GO:0034113~heterotypic cell-cell adhesion	3	8.54E-02	7.24E-01	VCAM1, LILRB2, ITGA5
GOTERM_BP_DIRECT	GO:0001569~branching involved in blood vessel morphogenesis	3	9.02E-02	7.34E-01	NRP1, COL4A1, ENG
GOTERM_BP_DIRECT	GO:0070050~neuron cellular homeostasis	3	9.02E-02	7.34E-01	NELL2, IL6, IMMT
GOTERM_BP_DIRECT	GO:0010716~negative regulation of extracellular matrix disassembly	2	9.09E-02	7.34E-01	DPP4, TGFB1
GOTERM_BP_DIRECT	GO:0033005~positive regulation of mast cell activation	2	9.09E-02	7.34E-01	HAVCR1, PVR
GOTERM_BP_DIRECT	GO:0032687~negative regulation of interferon-alpha production	2	9.09E-02	7.34E-01	IL10, HAVCR2
GOTERM_BP_DIRECT	GO:0110095~cellular detoxification of aldehyde	2	9.09E-02	7.34E-01	AKR1B10, ALDH1A1
GOTERM_BP_DIRECT	GO:0035655~interleukin-18-mediated signaling pathway	2	9.09E-02	7.34E-01	IL18, IL18R1
GOTERM_BP_DIRECT	GO:0048845~venous blood vessel morphogenesis	2	9.09E-02	7.34E-01	HEG1, ENG
GOTERM_BP_DIRECT	GO:0006196~AMP catabolic process	2	9.09E-02	7.34E-01	NT5E, NT5C1A
GOTERM_BP_DIRECT	GO:0009134~nucleoside diphosphate catabolic process	2	9.09E-02	7.34E-01	ENTPD2, ENTPD6
GOTERM_BP_DIRECT	GO:0006531~aspartate metabolic process	2	9.09E-02	7.34E-01	GOT1, ASS1
GOTERM_BP_DIRECT	GO:0009744~response to sucrose	2	9.09E-02	7.34E-01	OXT, KHK
GOTERM_BP_DIRECT	GO:0070301~cellular response to hydrogen peroxide	4	9.22E-02	7.34E-01	FABP1, IL6, AIFM1, IL18BP
GOTERM_BP_DIRECT	GO:0002931~response to ischemia	4	9.22E-02	7.34E-01	CSF1R, CSF1, AIFM1, TREM2
GOTERM_BP_DIRECT	GO:0001819~positive regulation of cytokine production	4	9.22E-02	7.34E-01	IL10, CLEC6A, IL18, CD28
GOTERM_BP_DIRECT	GO:0032715~negative regulation of interleukin-6 production	4	9.22E-02	7.34E-01	IL10, HGF, GAS6, HAVCR2
GOTERM_BP_DIRECT	GO:0031638~zymogen activation	3	9.50E-02	7.54E-01	CD163, FURIN, GGT1
GOTERM_BP_DIRECT	GO:0007229~integrin-mediated signaling pathway	5	9.62E-02	7.60E-01	NRP1, SEMA7A, CEACAM1, ITGBL1, ITGA5
GOTERM_BP_DIRECT	GO:0070098~chemokine-mediated signaling pathway	4	9.84E-02	7.76E-01	CXCL10, CXCL8, CCL20, TFF2
GOTERM_BP_DIRECT	GO:2000379~positive regulation of reactive oxygen species metabolic process	3	1.00E-01	7.84E-01	ACE2, LEP, DCXR
GOTERM_MF_DIRECT	GO:0038023~signaling receptor activity	24	2.56E-12	1.38E-09	RTN4R, NRP2, TNFRSF6B, IL10RB, PLAUR, TREM2, GFRA1, TNFRSF11B, TNFRSF10A, LILRA2, PVR, ASGR1, IGF2R, AMOT, ICAM1, NELL2, ATRN, CD4, ANPEP, BSG, FAS, TEK, IL18R1, TLR3
GOTERM_MF_DIRECT	GO:0001618~virus receptor activity	13	6.24E-09	1.17E-06	SCARB2, CR1, CXADR, CD80, PVR, ICAM1, DPP4, ACE2, CD4, ANPEP, BSG, ITGA5, HAVCR1
GOTERM_MF_DIRECT	GO:0042802~identical protein binding	62	6.47E-09	1.17E-06	ACY3, NRP2, CSF1, ACY1, DPY30, ASGR1, LMNB2, AMOT, ROBO1, C1QTNF1, ALCAM, CDH2, CTSC, CXADR, PHYKPL, HGF, DCXR, KCTD5, ACE2, CEACAM1, ALDH5A1, ANGPTL7, AGXT, IL6ST, FBP1, TLR3, RNKS, ENG, CALCA, MVK, PON2, HTRA2, HSD17B14, NPL, PTS, PBLD, DPP4, NT5E, DNPEP, GRPEL1, CBS, ERBB2, HMOX1, PCBD1, CD74, TGFB1, HIP1R, TNFRSF10A, BAIAP2, IGF2R, ASS1, NELL2, BST2, CD4, GIPC2, CD28, FAS, SDC1, TGFBI, LTBR, TEK, FGFR2
GOTERM_MF_DIRECT	GO:0005102~signaling receptor binding	24	4.33E-08	5.85E-06	CALCA, CD72, CXADR, IDUA, TNFSF12, HGF, PLAUR, PLAT, GFRA1, PDZK1, TNFSF13B, DPP4, CXCL10, ALCAM, ERBB2, APOF, ANGPTL2, TNFSF8, PRTN3, GUSB, GAS6, GLA, CD22, ANGPTL1

GOTERM_MF_DIRECT	GO:0042803~protein homodimerization activity	35	7.33E-08	7.94E-06	SCARB2, PON3, CSF1R, CANT1, CSF1, CPQ, PON2, CPOX, DPY30, DPP4, GRPEL1, CBS, KYNU, HMOX1, MUC13, RRM2, MME, GDF15, GZMA, HIP1R, ADA2, LILRB1, LILRB2, UPB1, BST2, CD4, CEACAM1, GLB1, GPD1, VWA1, SCLY, AGXT, GLA, FGFR2, ENG
GOTERM_MF_DIRECT	GO:0005125~cytokine activity	17	1.32E-07	1.19E-05	IL10, IL32, IL1RN, TGFB1, CSF1, GDF15, TNFSF12, IL18, TNFRSF11B, INHBC, AREG, TNFSF13B, IL6, KITLG, TNFSF8, TIMP1, CRLF1
GOTERM_MF_DIRECT	GO:0008201~heparin binding	16	4.70E-07	3.64E-05	RTN4R, NRP1, NRP2, CXCL8, ADA2, FURIN, LTBP2, THBS2, FSTL1, PGF, NELL2, ADAMTS15, CXCL10, ADGRG1, COL5A1, FGFR2
GOTERM_MF_DIRECT	GO:0008083~growth factor activity	15	5.41E-07	3.66E-05	IL10, TGFB1, CSF1, GDF15, HGF, CLEC11A, ADA2, INHBC, GFER, AREG, PGF, IL6, KITLG, TIMP1, FGF21
GOTERM_MF_DIRECT	GO:0004888~transmembrane signaling receptor activity	15	1.76E-06	1.06E-04	SCARB2, PIGR, CD72, TREM2, SELE, ICAM1, FCAMR, MARCO, CD4, BCAM, ADGRE5, ERBB2, CD300C, TLR3, ENG
GOTERM_MF_DIRECT	GO:0019838~growth factor binding	8	2.77E-06	1.50E-04	NELL2, CSF1R, NRP1, NRP2, ERBB2, LTBP2, TEK, IL6ST
GOTERM_MF_DIRECT	GO:0005201~extracellular matrix structural constituent	12	3.32E-06	1.63E-04	MFAP4, CD4, COL4A1, VWA1, CHI3L1, IGFBP7, LTBP2, TGFBI, LTBP3, CRELD1, THBS2, AGRN
GOTERM_MF_DIRECT	GO:0004252~serine-type endopeptidase activity	15	4.75E-06	2.01E-04	CD163, MMP7, IGJ, GZMA, HTRA2, PLAT, FURIN, DPP4, PLAU, TPP1, PRTN3, PRSS8, PAMR1, PRSS2, CTSC
GOTERM_MF_DIRECT	GO:0015026~coreceptor activity	9	4.83E-06	2.01E-04	NRP1, CD4, IL10RB, CD80, ERBB2, CD28, IL1RAP, IL6ST, ENG
GOTERM_MF_DIRECT	GO:0008236~serine-type peptidase activity	9	6.24E-06	2.41E-04	DPP4, DPP10, DPP7, HTRA2, TPP1, FURIN, PRTN3, PRSS8, PRSS2
GOTERM_MF_DIRECT	GO:0004180~carboxypeptidase activity	6	2.31E-05	8.35E-04	CPM, ACE2, CPB1, CPQ, CTSZ, PRCP
GOTERM_MF_DIRECT	GO:0030246~carbohydrate binding	14	3.14E-05	1.06E-03	CD72, CLEC11A, SELE, GALNT10, ASGR1, LGALS4, ATRN, MAN2B2, CLEC6A, CHI3L1, LGALS9, GUSB, CD22, NOMO1
GOTERM_MF_DIRECT	GO:0019955~cytokine binding	7	9.56E-05	3.04E-03	NELL2, CSF1R, CD74, NRP1, NRP2, IL6ST, CRLF1
GOTERM_MF_DIRECT	GO:0004908~interleukin-1 receptor activity	4	1.42E-04	4.27E-03	IL1RL1, IL1R2, IL1RAP, IL18R1
GOTERM_MF_DIRECT	GO:0005509~calcium ion binding	27	2.31E-04	6.58E-03	CANT1, CLSTN2, CLSTN3, LTBP2, LTBP3, THBS2, FSTL1, PCDH17, ADGRE1, CDH6, ADGRE2, ADGRE5, CDH2, MANBA, MANEA, ENPP2, PRSS2, PAMR1, ARSA, HEG1, NELL2, VSNL1, CLEC6A, CDHR2, CRELD1, ITGA5, AGRN, GAS6
GOTERM_MF_DIRECT	GO:0016936~galactoside binding	4	4.70E-04	1.16E-02	LGALS4, GLB1, LGALS9, GLA
GOTERM_MF_DIRECT	GO:0008239~dipeptidyl-peptidase activity	4	4.70E-04	1.16E-02	DPP4, DPP7, PRCP, CTSC
GOTERM_MF_DIRECT	GO:0005520~insulin-like growth factor binding	4	4.70E-04	1.16E-02	IGFBPL1, CRIM1, IGFBP7, IGF2R
GOTERM_MF_DIRECT	GO:0004896~cytokine receptor activity	6	7.91E-04	1.86E-02	IL1RL1, CD74, IL4R, IFNGR2, IL6ST, CRLF1
GOTERM_MF_DIRECT	GO:0050839~cell adhesion molecule binding	7	9.66E-04	2.09E-02	BCAM, VCAM1, CXADR, CDHR2, LILRB2, TGFBI, PVR
GOTERM_MF_DIRECT	GO:0097110~scaffold protein binding	7	9.66E-04	2.09E-02	CD163, KRT18, TCOF1, KRT8, TREM2, IL6ST, BAIAP2
GOTERM_MF_DIRECT	GO:0005044~scavenger receptor activity	5	1.03E-03	2.15E-02	SCARB2, LGALS3BP, MSR1, CD163, ENPP2
GOTERM_MF_DIRECT	GO:0005178~integrin binding	10	1.37E-03	2.74E-02	SEMA7A, VCAM1, CXADR, COL5A1, TSPAN8, ITGBL1, GPRA1, TGFBI, ITGA5, ICAM1
GOTERM_MF_DIRECT	GO:0016597~amino acid binding	4	1.68E-03	3.24E-02	DDAH1, SCLY, AGXT, ASS1
GOTERM_MF_DIRECT	GO:0030170~pyridoxal phosphate binding	6	2.50E-03	4.66E-02	DDC, GOT1, CBS, PHYKPL, KYNU, AGXT
GOTERM_MF_DIRECT	GO:0001540~amyloid-beta binding	7	2.96E-03	5.34E-02	MSR1, CD74, MARCO, CLSTN2, CLSTN3, TREM2, LILRB2
GOTERM_MF_DIRECT	GO:0005515~protein binding	231	3.54E-03	6.18E-02	IL1RN, TNFRSF6B, IFI30, ICAM1, LGALS4, CRHBP, ALCAM, BSG, PRSS8, VSIG4, PRSS2, ARSA, ENTPD2, CXADR, PHYKPL, IL1R2, CLEC11A, ARSB, PDZK1, PRAP1, ACE2, BCAM, RBP5, PPL, PCDH17, ADIH4, GRPEL1, TSPAN8, HMOX1, HMOX2, MSR1, DTNB, TNFSF12, NFATC3, PILRA, BST2, OCLN, AKR1B10, GIPC2, CD28, SDC1, TNFSF8, CD22, DDR1, NRP1, ACY3, NRP2, ACY1, CTSZ, PTPRH, AREG, ASGR1, KHK, ROBO1, CTSO, C1QTNF1, AIFM1, TCTN3, ADAMTSL2, TIMP1, HAVCR1, CTSD, CTSC, HAVCR2, IL10, TNFRSF12A, MME, HEG1, IFNGR2, IL18, PTGR1, GCHFR, CEACAM1, CDCP1, VSNL1, ANGPTL7, TFF2, ANGPTL2, CRELD1, FAM20A, GAS6, VAMP5, TLR3, ENG, ECHS1, PRUNE2, AFM, NPL, FSTL1, PTS, FSTL3, PBLD, RIDA, NT5E, TCOF1, IL32, LBR, CLEC12B, CD74, CD72, IL1OBL, CCL20, GDF15, LILRB1, HLA-DRA, CLEC11A, ARSB, KRT18, FAS, AGRN, CRLF1, IL18R1, SCARB2, CD83, CSF1, CLSTN3, CD80, PLAT, PVR, AMOT, CDH2, PLAU, CHCHD6, LAMP2, ACAA1, GGT1, NOMO1, ENPP7, IL4R, HGF, KCTD5, SDHB, PGF, ALDH3A1, COL4A1, GPD1, PRTN3, CD300C, IL6ST, RTN4R, CSF1R, CD274, CALCA, SEMA7A, CPB1, HTRA2, TNFRSF11B, LTBP2, LTBP3, EFNA4, DPP4, ADGRG1, IGFBP7, FGF21, CD163, TGFB1, CHCHD10, GGH, TNFRSF10A, SELE, COQ7, IGF2R, CXCL10, IL6, COL5A1, MAN2B2, CLEC6A, HLA-DRA, TPP1, TGFBI, FGFR2, LGALS3BP, CXCL8, DPY30, OXT, TREM2, NAGPA, FTCD, LMNB2, TNFSF13B, ADGRE2, ADGRE5, INSL5, MMP7, CR1, DCXR, PLAUR, TNFRSF1B, CKAP4, TNFRSF1A, PTP4A3, CDHR2, ADLH1A1, CHI3L1, ITGA5, AGXT, FBP1, THOP1, RBKS, DDC, CANT1, MVK, HSD17B14, PRCP, FURIN, THBS2, IL1RL1, DNPEP, CBS, ERBB2, EPSIL2, PCBD1, ENTR1, RRM2, GZMA, HIP1R, IMMT, BAIAP2, GFER, ASS1, NELL2, MFAP4, ADGRD1, NFASC, CD4, GLB1, NT5C1A, LEP, SCLY, TEK, LTBR, GLA
GOTERM_MF_DIRECT	GO:0050436~microfibril binding	3	3.79E-03	6.41E-02	ADAMTSL2, VWA1, LTBP2
GOTERM_MF_DIRECT	GO:0048018~receptor ligand activity	6	5.98E-03	9.64E-02	CD274, TNFSF12, CD80, GAS6, AREG, TNFSF13B
GOTERM_MF_DIRECT	GO:0098632~cell-cell adhesion mediator activity	5	6.06E-03	9.64E-02	NFASC, CLSTN3, BSG, CNTN3, IGSF9
GOTERM_MF_DIRECT	GO:0005021~vascular endothelial growth factor receptor activity	3	6.92E-03	1.07E-01	NELL2, NRP1, NRP2
GOTERM_MF_DIRECT	GO:0004175~endopeptidase activity	6	7.53E-03	1.13E-01	ADAMTS15, ACE2, MMP7, MME, TPP1, FURIN
GOTERM_MF_DIRECT	GO:0005537~D-mannose binding	4	8.40E-03	1.22E-01	CLEC6A, BSG, ASGR1, IGF2R
GOTERM_MF_DIRECT	GO:0001758~retinal dehydrogenase activity	3	8.80E-03	1.22E-01	AKR1B10, ALDH1A1, AKR1C4
GOTERM_MF_DIRECT	GO:0045134~UDP phosphatase activity	3	8.80E-03	1.22E-01	CANT1, ENTPD2, ENTPD6
GOTERM_MF_DIRECT	GO:0005031~tumor necrosis factor receptor activity	3	1.09E-02	1.44E-01	FAS, TNFRSF1B, TNFRSF1A
GOTERM_MF_DIRECT	GO:0004382~GDP phosphatase activity	3	1.09E-02	1.44E-01	CANT1, ENTPD2, ENTPD6
GOTERM_MF_DIRECT	GO:0004177~aminopeptidase activity	4	1.14E-02	1.47E-01	DPP4, DPP7, DNPEP, ANPEP
GOTERM_MF_DIRECT	GO:0042277~peptide binding	5	1.22E-02	1.54E-01	CRHBP, MME, ANPEP, TPP1, FURIN
GOTERM_MF_DIRECT	GO:0003953~NAD+ nucleosidase activity	3	1.32E-02	1.58E-01	IL1RL1, IL1RAP, IL18R1
GOTERM_MF_DIRECT	GO:0035374~chondroitin sulfate binding	3	1.32E-02	1.58E-01	RTN4R, ADGRE2, AGRN
GOTERM_MF_DIRECT	GO:0004504~fatty acid binding	4	1.49E-02	1.75E-01	FABP1, FABP4, RBP5, GSTA1
GOTERM_MF_DIRECT	GO:0038024~cargo receptor activity	4	1.62E-02	1.87E-01	SCARB2, MSR1, MARCO, SDC1
GOTERM_MF_DIRECT	GO:0032396~inhibitory MHC class I receptor activity	3	2.11E-02	2.28E-01	LILRB1, LILRB2, LILRA2
GOTERM_MF_DIRECT	GO:0004033~aldo-keto reductase (NADPH) activity	3	2.11E-02	2.28E-01	AKR1B10, AKR7L, AKR1C4
GOTERM_MF_DIRECT	GO:0004032~aldose reductase (NADPH) activity	3	2.11E-02	2.28E-01	ADH4, AKR1B10, AKR1C4
GOTERM_MF_DIRECT	GO:0017154~semaphorin receptor activity	3	2.41E-02	2.55E-01	NELL2, NRP1, NRP2
GOTERM_MF_DIRECT	GO:0004714~transmembrane receptor protein tyrosine kinase activity	4	2.53E-02	2.63E-01	DDR1, CSF1R, ERBB2, TEK
GOTERM_MF_DIRECT	GO:0061809~NAD+ nucleotidase, cyclic ADP-ribose generating	3	2.72E-02	2.78E-01	IL1RL1, IL1RAP, IL18R1
GOTERM_MF_DIRECT	GO:0001786~phosphatidylserine binding	5	2.85E-02	2.86E-01	SCARB2, MME, TREM2, HAVCR1, GAS6
GOTERM_MF_DIRECT	GO:0004392~heme oxygenase (decyclizing) activity	2	3.23E-02	3.01E-01	HMOX1, HMOX2
GOTERM_MF_DIRECT	GO:0042007~interleukin-18 binding	2	3.23E-02	3.01E-01	IL18R1, IL18BP
GOTERM_MF_DIRECT	GO:0023025~MHC class Ib protein complex binding	2	3.23E-02	3.01E-01	LILRB1, LILRB2
GOTERM_MF_DIRECT	GO:0002114~interleukin-33 receptor activity	2	3.23E-02	3.01E-01	IL1RL1, IL1RAP
GOTERM_MF_DIRECT	GO:0004222~metalloendopeptidase activity	6	3.99E-02	3.66E-01	ADAMTS15, MMP7, MME, ADAMTSL2, THOP1, PRSS2
GOTERM_MF_DIRECT	GO:0042288~MHC class I protein binding	3	4.52E-02	3.71E-01	LILRB1, LILRB2, PILRA
GOTERM_MF_DIRECT	GO:0008106~alcohol dehydrogenase (NADP+) activity	3	4.80E-02	3.71E-01	ALDH3A1, AKR1B10
GOTERM_MF_DIRECT	GO:0002951~leukotriene-C(4) hydrolase	2	4.80E-02	3.71E-01	GGT5, GGT1
GOTERM_MF_DIRECT	GO:0016971~flavin-dependent sulfhydryl oxidase activity	2	4.80E-02	3.71E-01	QSOX1, GFER
GOTERM_MF_DIRECT	GO:0042988~X11-like protein binding	2	4.80E-02	3.71E-01	CLSTN2, CLSTN3
GOTERM_MF_DIRECT	GO:0018479~benzaldehyde dehydrogenase (NAD+) activity	2	4.80E-02	3.71E-01	ALDH3A1, ALDH1A1
GOTERM_MF_DIRECT	GO:0047374~methylumbelliferyl-acetate deacetylase activity	2	4.80E-02	3.71E-01	CES2, CES1
GOTERM_MF_DIRECT	GO:0005010~insulin-like growth factor receptor activity	2	4.80E-02	3.71E-01	CRIM1, IGF2R
GOTERM_MF_DIRECT	GO:0102007~acyl-L-homoserine-lactone lactonohydrolase activity	2	4.80E-02	3.71E-01	PON3, PON2
GOTERM_MF_DIRECT	GO:0001791~IgM binding	2	4.80E-02	3.71E-01	LILRA2, CD22
GOTERM_MF_DIRECT	GO:0000048~peptidyltransferase activity	2	4.80E-02	3.71E-01	GGT5, GGT1
GOTERM_MF_DIRECT	GO:0033691~sialic acid binding	3	5.33E-02	4.06E-01	AGRN, SELE, CD22
GOTERM_MF_DIRECT	GO:0038187~pattern recognition receptor activity	3	6.19E-02	4.52E-01	MARCO, CLEC6A, TLR3
GOTERM_MF_DIRECT	GO:0050483~IMP 5'-nucleotidase activity	2	6.35E-02	4.52E-01	NT5E, NT5C1A
GOTERM_MF_DIRECT	GO:0008238~exopeptidase activity	2	6.35E-02	4.52E-01	MME, GGH
GOTERM_MF_DIRECT	GO:0070008~serine-type exopeptidase activity	2	6.35E-02	4.52E-01	DPP7, PRCP
GOTERM_MF_DIRECT	GO:0005534~galactose binding	2	6.35E-02	4.52E-01	LGALS9, ENG
GOTERM_MF_DIRECT	GO:0023026~MHC class II protein complex binding	3	7.09E-02	4.98E-01	CD74, CD4, HLA-DRA
GOTERM_MF_DIRECT	GO:0045499~chemorepellent activity	3	7.56E-02	5.24E-01	DPP4, SEMA7A, SEMA3F
GOTERM_MF_DIRECT	GO:0009055~electron transfer activity	4	7.71E-02	5.28E-01	QDPR, GSR, AKR1C4, SDHB
GOTERM_MF_DIRECT	GO:0008237~metallopeptidase activity	4	8.01E-02	5.41E-01	ACE2, MMP7, DNPEP, ANPEP
GOTERM_MF_DIRECT	GO:0019899~enzyme binding	11	8.34E-02	5.57E-01	SCARB2, CD4, DDC, TGFB1, CBS, LAMP2, PLAUR, HMOX1, PRTN3, LGALS9, IGF2R
GOTERM_MF_DIRECT	GO:0004197~cysteine-type endopeptidase activity	4	8.62E-02	5.69E-01	CTSO, CTSZ, CTSD, CTSC
GOTERM_MF_DIRECT	GO:0004181~metallocarboxypeptidase activity	3	9.01E-02	5.76E-01	CPM, ACE2, CPB1
GOTERM_MF_DIRECT	GO:0120146~sulfatide binding	2	9.37E-02	5.76E-01	TPP1, TREM2
GOTERM_MF_DIRECT	GO:0106435~carboxylesterase activity	2	9.37E-02	5.76E-01	CES2, CES1
GOTERM_MF_DIRECT	GO:0005127~ciliary neurotrophic factor receptor binding	2	9.37E-02	5.76E-01	IL6ST, CRLF1
GOTERM_MF_DIRECT	GO:0004046~aminoacylase activity	2	9.37E-02	5.76E-01	ACY3, ACY1
GOTERM_MF_DIRECT	GO:0004064~arylesterase activity	2	9.37E-02	5.76E-01	PON3, PON2
GOTERM_MF_DIRECT	GO:0005164~tumor necrosis factor receptor binding	3	9.51E-02	5.78E-01	TNFSF12, TNFSF8, TNFSF13B
GOTERM_MF_DIRECT	GO:0005179~hormone activity	5	9.97E-02	5.96E-01	CALCA, GDF15, LEP, INHBC, INSL5
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	125	0.00E+00	0.00E+00	SCARB2, IL1RN, PLAT, HNMT, PVR, ENO3, ICAM1, ALCAM, PLAU, ANPEP, LAMP2, BSG, PRSS8, GGT1, ARSA, ENTPD2, KRT8, PDZK1, UPB1, PLAG15, ACE2, BCAM, RBP5, GPD1, PRTN3, IL6ST, CES2, RTN4R, CD274, LTBP2, LTBP3, IQGAP2, PPL, DPP4, ADGRG1, DPP7, TSPAN8, C7, IGFBP7, VCAM1, GOT1, GGH, PILRA, IGF2R, BST2, QDPR, BPIFB2, MAN2B2, GIPC2, HLA-DRA, SDC1, TPP1, TGFBI, NIT2, CD22, DDR1, LGALS3BP, CPM, PIGR, ACY3, ACY1, CPQ, TREH, CTSZ, FTCD, IL18BP, KHK, ADGRE5, MAN1A2, QSOX1, TIMP1, GUSB, CTSD, CTSC, CR1, MMP7, MME, DCXR, GFRA1, PTGR1, CKAP4, ATRN, CEACAM1, DDAH1, CDHR2, ALDH1A1, VWA1, CHI3L1, ANGPTL2, FAM20A, GAS6, VAMP5, GPRC5C, FBP1, ANGPTL1, PON3, DDC, CANT1, IDUA, AFM, PRCP, FURIN, FSTL1, PBLD, RIDA, NT5E, CREG1, EPSIL2, PCBD1, CD74, GDF15, GSR, AKR7L, AKR1C4, BAIAP2, ASS1, FABP1, KRT18, FABP4, GSTA3, GLB1, GSTA1, FAS, AGRN, GLA
GOTERM_CC_DIRECT	GO:0005615~extracellular space	111	0.00E+00	0.00E+00	IL1RN, TNFRSF6B, CSF1, PLAT, PVR, ENO3, ICAM1, LGALS4, CRHBP, BMPER, PLAU, ANPEP, LAMP2, ENPP2, PRSS8, LGALS9, GGT1, PRSS2, ARSA, CXADR, HGF, CLEC11A, ENTPD6, KRT8, MTUS1, PGF, PLA2G15, ACE2, ALDH3A1, COL4A1, PRTN3, IL6ST, CALCA, CPB1, TNFRSF11B, LTBP2, ADAMTS15, C7, APOF, HMOX1, IGFBP7, FGF21, CD163, TGFB1, VCAM1, TNFSF12, GGH, ADA2, SELE, INHBC, CXCL10, MARCO, IL6, COL5A1, TNFSF8, TGFBI, DDR1, LGALS3BP, CPM, NRP1, PIGR, CXCL8, CPQ, CTSZ, OXT, SERPINA9, AREG, IL18BP, TNFSF13B, CTSO, C1QTNF1, MUC13, QSOX1, TIMP1, GUSB, CTSD, CTSC, IL10, CR1, MMP7, IL18, TNFRSF1A, ATRN, ANGPTL7, VWA1, CHI3L1, TFF2, ANGPTL2, FAM20A, GAS6, ANGPTL1, TLR3, ENG, PON3, PON2, AFM, SEMA3F, FSTL1, FSTL3, IGFBPL1, CREG1, IL32, GDF15, CCL20, GZMA, LILRB2, GFER, NELL2, MFAP4, KITLG, LEP, CRLF1
GOTERM_CC_DIRECT	GO:0005576~extracellular region	112	0.00E+00	0.00E+00	TNFRSF6B, CSF1, PLAT, IL1RAP, IFI30, CRHBP, BMPER, PLAU, PRSS8, ACAA1, PRSS2, PAMR1, ARSA, IL4R, CXADR, NHLRC3, HGF, IL1R2, CLEC11A, ENTPD6, PRAP1, PGF, PLA2G15, ACE2, BCAM, COL4A1, PRTN3, IL6ST, CALCA, TNFRSF11B, LTBP2, LTBP3, EFNA4, DPP4, ADGRG1, DPP7, APOM, C7, IGFBP7, FGF21, CD163, TGFB1, TNFSF12, CRIM1, GGH, ADA2, INHBC, CXCL10, BPIFB2, IL6, VNN1, AKR1B10, COL5A1, ITGBL1, CNTN3, TGFBI, NIT2, FGFR2, LGALS3BP, CPM, NRP2, CXCL8, CTSZ, OXT, TREM2, AREG, FCAR, CXCR, ASGR1, IL18BP, TNFSF13B, C1QTNF1, ADAMTSL2, QSOX1, TIMP1, GUSB, CTSD, INSL5, CTSC, IL10, MMP7, HEG1, IL18, PLAUR, TNFRSF1B, TNFRSF1A, CDCP1, ANGPTL7, CHI3L1, GAS6, PON3, CANT1, PON2, AFM, FURIN, LILRA2, THBS2, FSTL1, FSTL3, IL1RL1, CREG1, GDF15, CCL20, LILRB1, NELL2, MFAP4, KITLG, GLB1, LEP, TEK, AGRN, GLA, CRLF1
GOTERM_CC_DIRECT	GO:0009986~cell surface	49	0.00E+00	0.00E+00	CPM, CLSTN2, CLSTN3, CD80, TREM2, PLAT, PVR, AREG, AMOT, ICAM1, ROBO1, CDH2, PLAU, HAVCR1, HAVCR2, CR1, MME, ENTPD6, PLAUR, TNFRSF1A, ACE2, CEACAM1, ITGA5, VAMP5, ENG, RTN4R, CSF1R, IGSF3, FURIN, IQGAP2, DPP4, ADAMTS15, NT5E, TSPAN8, CD74, TGFB1, VCAM1, TNFRSF10A, LILRB2, IGF2R, BST2, CD28, ITGBL1, HLA-DRA, FAS, SDC1, TEK, CD22, FGFR2
GOTERM_CC_DIRECT	GO:0005887~external side of plasma membrane	37	0.00E+00	4.00E-15	RTN4R, CD274, SEMA7A, CD63, CD80, LY9, ASGR1, AMOT, ICAM1, ADGRE1, IL1RL1, NT5E, ALCAM, PLAU, ANPEP, CD74, CD163, IL4R, VCAM1, HEG1, GSR, PLAUR, LILRB1, GFRA1, SELE, CXCL10, CD4, BCAM, CLEC6A, CD28, FAS, SDC1, ITGA5, IL6ST, CRLF1, CD22, ENG
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	148	5.50E-14	2.55E-12	SCARB2, IL1RN, CD63, CSF1, CD80, IL1RAP, PVR, ENO3, ICAM1, AMOT, LGALS4, CD86, ALCAM, CDH2, PLAU, ANPEP, LAMP2, BSG, ENPP2, PRSS8, GGT1, ENPP7, ENTPD2, IL4R, CXADR, IL1R2, ENTPD6, MTUS1, PDZK1, SDHB, FCAMR, ACE2, ALDH3A1, BCAM, PRTN3, CD300C, IL6ST, RTN4R, CSF1R, CD274, SEMA7A, TNFRSF11B, IQGAP2, PPL, EFNA4, Y9, PCDH17, IGSF9, DPP4, ADGRG1, TSPAN8, C7, HMOX2, GDT5, MSR1, CD163, TGFB1, VCAM1, DTNB, TNFSF12, CRIM1, TNFRSF10A, PILRA, SELE, IGF2R, BST2, MARCO, OCLN, VNN1, CLEC6A, CD83, HLA-DRA, TGFBI, SDC1, TNFSF8, CNTN3, TGFBI, CD22, FGFR2, DDR1, DPP10, CPM, NRP1, PIGR, NRP2, TREH, TREM2, SERPINA9, NAGPA, AREG, ASGR1, IL18BP, TNFSF13B, ADGRE2, AIFM1, ADGRE5, TCTN3, MAN1A2, ACP5, GUSB, CTSC, HAVCR2, MAMDC4, CR1, MME, IFNGR2, HEG1, DCXR, PLAUR, TNFRSF1B, CKAP4, TNFRSF1A, ATRN, CEACAM1, VSNL1, GAS2, CRELD1, TLR3, ENG, CANT1, PON2, PRUNE2, FURIN, NT5E, ERBB2, IL32, LILRB2, CD74, GOLM2, IL10RB, IMMT, LILRB2, BAIAP2, NELL2, ADGRD1, KITLG, AGRN, IL18R1, MEGF9
GOTERM_CC_DIRECT	GO:0062023~collagen-containing extracellular matrix	31	1.18E-12	4.65E-11	LGALS3BP, SEMA7A, CTSZ, LTBP2, LTBP3, THBS2, ICAM1, LGALS4, ADAMTS15, IGFBPL1, CDH2, IGFBP7, LGALS9, CTSD, CTSC, TGFBI, GDF15, MFAP4, MARCO, BCAM, COL5A1, ANGPTL7, COL4A1, VWA1, ANGPTL2, PRTN3, TGFBI, CRELD1, AGRN, FGFR2, ANGPTL1
GOTERM_CC_DIRECT	GO:0043202~lysosomal lumen	14	3.12E-09	1.07E-07	SCARB2, CD74, ARSA, IDUA, IFI30, GLB1, MAN2B2, LAMP2, SDC1, TPP1, AGRN, GUSB, CTSD, GLA
GOTERM_CC_DIRECT	GO:0045121~membrane raft	19	4.30E-09	1.32E-07	RTN4R, CXADR, MME, FURIN, TNFRSF10A, TNFRSF1B, SELE, ICAM1, TNFRSF1A, DPP4, BST2, ACE2, ADGRG1, CD4, FAS, TPP1, TEK, IL6ST, CTSD
GOTERM_CC_DIRECT	GO:0005788~endoplasmic reticulum lumen	22	1.44E-08	3.97E-07	ARSA, CSF1, CTSZ, PLAUR, FSTL1, CKAP4, FSTL3, ACE2, IL6, BPIFB2, CD4, CDH2, COL5A1, COL4A1, VWA1, IGFBP7, QSOX1, TIMP1, GAS6, CTSC, CES2, CES1
GOTERM_CC_DIRECT	GO:0035578~azurophil granule lumen	12	1.37E-07	3.45E-06	ARSA, DPP7, NHLRC3, GLB1, CREG1, GGH, ADA2, PRTN3, GUSB, PRSS2, GLA, CTSC
GOTERM_CC_DIRECT	GO:0016020~membrane	117	5.21E-07	1.20E-05	SCARB2, CD63, CSF1, CPOX, IL1RAP, PVR, ENO3, ICAM1, AMOT, LAMP2, BSG, ENPP2, VSIG4, ACAA1, GGT1, NOMO1, ENPP7, IL4R, HGF, IL1R2, ENTPD6, PGF, PLA2G15, ACE2, BCAM, COL4A1, IL6ST, CSF1R, SEMA7A, IGSF3, HTRA2, LTBP2, LTBP3, IQGAP2, PPL, PCDH17, DPP4, ADGRG1, TSPAN8, HMOX1, HMOX2, MSR1, VCAM1, TNFSF12, CRIM1, TNFRSF10A, PILRA, IGF2R, IST2, MARCO, OCLN, VNN1, HLA-DRA, SDC1, TNFSF8, CD22, FGFR2, DDR1, DPP10, LGALS3BP, CPM, NRP1, NRP2, TREH, TREM2, SERPINA9, NAGPA, AREG, ASGR1, IL18BP, TNFSF13B, ADGRE2, AIFM1, ADGRE5, TCTN3, MAN1A2, ACP5, GUSB, CTSC, HAVCR2, MAMDC4, CR1, MME, IFNGR2, HEG1, DCXR, PLAUR, TNFRSF1B, CKAP4, TNFRSF1A, ATRN, CEACAM1, VSNL1, GAS2, CRELD1, TLR3, ENG, CANT1, PON2, PRUNE2, FURIN, NT5E, ERBB2, IL32, LILRB2, CD74, GOLM2, IL10RB, IMMT, LILRB2, BAIAP2, NELL2, ADGRD1, KITLG, AGRN, IL18R1, MEGF9
GOTERM_CC_DIRECT	GO:0043235~receptor complex	16	2.02E-06	4.30E-05	DDR1, PIGR, CSF1R, NRP1, IL4R, GFRA1, TNFRSF11B, PTPRH, TNFRSF1A, ERBB2, TEK, IL6ST, GPRC5C, FGFR2, CRLF1, ENG
GOTERM_CC_DIRECT	GO:0005764~lysosome	18	6.30E-06	1.24E-04	SCARB2, CD74, ARSA, CPQ, CTSZ, IFI30, PLA2G15, CTSO, AKR1B10, MAN2B2, LAMP2, HLA-DRA, ACP5, TPP1, GUSB, CTSD, GLA, CTSC
GOTERM_CC_DIRECT	GO:0005925~focal adhesion	20	4.26E-05	7.83E-04	SCARB2, NRP1, MME, PLAUR, PVR, IGF2R, TNFSF13B, ICAM1, DPP4, IL1RL1, NFASC, ALCAM, CDH2, ADGRE5, PLAU, BSG, ITGB1, TEK, ITGA5, ENG
GOTERM_CC_DIRECT	GO:0035580~specific granule lumen	8	4.73E-05	8.16E-04	CANT1, CTSZ, GGH, CHI3L1, QSOX1, ACAA1, CTSD, NIT2

GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	14	8.53E-05	1.39E-03
GOTERM_CC_DIRECT	GO:0005604~basement membrane	9	1.18E-04	1.81E-03
GOTERM_CC_DIRECT	GO:0001772~immunological synapse	6	6.51E-04	9.46E-03
GOTERM_CC_DIRECT	GO:0005902~microvillus	7	9.23E-04	1.21E-02
GOTERM_CC_DIRECT	GO:0030666~endocytic vesicle membrane	7	9.23E-04	1.21E-02
GOTERM_CC_DIRECT	GO:0005773~vacuole	4	1.39E-03	1.74E-02
GOTERM_CC_DIRECT	GO:0098552~side of membrane	8	2.01E-03	2.24E-02
GOTERM_CC_DIRECT	GO:0035577~azurophil granule membrane	6	2.03E-03	2.24E-02
GOTERM_CC_DIRECT	GO:0002116~semaphorin receptor complex	4	2.03E-03	2.24E-02
GOTERM_CC_DIRECT	GO:0005758~mitochondrial intermembrane space	7	2.13E-03	2.27E-02
GOTERM_CC_DIRECT	GO:0101003~ficolin-1-rich granule membrane	6	2.35E-03	2.40E-02
GOTERM_CC_DIRECT	GO:0035579~specific granule membrane	7	2.68E-03	2.64E-02
GOTERM_CC_DIRECT	GO:0030669~clathrin-coated endocytic vesicle membrane	6	4.55E-03	4.33E-02
GOTERM_CC_DIRECT	GO:0005794~Golgi apparatus	29	5.58E-03	4.97E-02
GOTERM_CC_DIRECT	GO:0016327~apicolateral plasma membrane	4	5.58E-03	4.97E-02
GOTERM_CC_DIRECT	GO:0061617~MICOS complex	3	9.59E-03	8.04E-02
GOTERM_CC_DIRECT	GO:0005911~cell-cell junction	9	9.62E-03	8.04E-02
GOTERM_CC_DIRECT	GO:1904724~tertiary granule lumen	5	1.04E-02	8.30E-02
GOTERM_CC_DIRECT	GO:0016324~apical plasma membrane	14	1.05E-02	8.30E-02
GOTERM_CC_DIRECT	GO:1905370~serine-type endopeptidase complex	3	1.16E-02	8.90E-02
GOTERM_CC_DIRECT	GO:0030424~axon	13	1.40E-02	1.05E-01
GOTERM_CC_DIRECT	GO:0031528~microvillus membrane	4	1.48E-02	1.07E-01
GOTERM_CC_DIRECT	GO:0098978~glutamatergic synapse	14	1.56E-02	1.10E-01
GOTERM_CC_DIRECT	GO:0044853~plasma membrane raft	4	1.60E-02	1.10E-01
GOTERM_CC_DIRECT	GO:0005581~collagen trimer	6	1.85E-02	1.24E-01
GOTERM_CC_DIRECT	GO:0030667~secretory granule membrane	6	1.99E-02	1.29E-01
GOTERM_CC_DIRECT	GO:0031093~platelet alpha granule lumen	5	2.00E-02	1.29E-01
GOTERM_CC_DIRECT	GO:0034362~low-density lipoprotein particle	3	2.13E-02	1.34E-01
GOTERM_CC_DIRECT	GO:0005769~early endosome	11	2.30E-02	1.41E-01
GOTERM_CC_DIRECT	GO:0005796~Golgi lumen	6	2.39E-02	1.44E-01
GOTERM_CC_DIRECT	GO:1990682~CSF1-CSF1R complex	2	3.02E-02	1.77E-01
GOTERM_CC_DIRECT	GO:0005771~multivesicular body	4	3.28E-02	1.89E-01
GOTERM_CC_DIRECT	GO:0030175~filopodium	5	3.52E-02	1.96E-01
GOTERM_CC_DIRECT	GO:0005802~trans-Golgi network	8	3.55E-02	1.96E-01
GOTERM_CC_DIRECT	GO:0043231~intracellular membrane-bounded organelle	22	4.13E-02	2.23E-01
GOTERM_CC_DIRECT	GO:0005782~peroxisomal matrix	4	4.47E-02	2.34E-01
GOTERM_CC_DIRECT	GO:0005896~interleukin-6 receptor complex	2	4.50E-02	2.34E-01
GOTERM_CC_DIRECT	GO:0005903~brush border	4	5.85E-02	2.93E-01
GOTERM_CC_DIRECT	GO:0030141~secretory granule	5	5.91E-02	2.93E-01
GOTERM_CC_DIRECT	GO:0002947~tumor necrosis factor receptor superfamily complex	2	5.95E-02	2.93E-01
GOTERM_CC_DIRECT	GO:0043025~neuronal cell body	11	6.50E-02	3.15E-01
GOTERM_CC_DIRECT	GO:0030054~cell junction	7	6.65E-02	3.16E-01
GOTERM_CC_DIRECT	GO:0032587~ruffle membrane	3	7.05E-02	3.30E-01
GOTERM_CC_DIRECT	GO:0098636~protein complex involved in cell adhesion	2	7.38E-02	3.32E-01
GOTERM_CC_DIRECT	GO:0097180~serine protease inhibitor complex	2	7.38E-02	3.32E-01
GOTERM_CC_DIRECT	GO:0042470~melanosome	5	7.46E-02	3.32E-01
GOTERM_CC_DIRECT	GO:0005912~adherens junction	7	8.44E-02	3.67E-01
GOTERM_CC_DIRECT	GO:0030139~endocytic vesicle	4	8.52E-02	3.67E-01
GOTERM_CC_DIRECT	GO:0045211~postsynaptic membrane	7	8.75E-02	3.72E-01
GOTERM_CC_DIRECT	GO:0005777~peroxisome	5	8.97E-02	3.75E-01
GOTERM_CC_DIRECT	GO:0031410~cytoplasmic vesicle	9	9.44E-02	3.89E-01
GOTERM_CC_DIRECT	GO:0009925~basal plasma membrane	4	9.71E-02	3.94E-01
KEGG_PATHWAY	hsa04060~Cytokine-cytokine receptor interaction	34	2.80E-14	6.61E-12
KEGG_PATHWAY	hsa05144~Malaria	12	1.22E-08	1.42E-06
KEGG_PATHWAY	hsa04061~Viral protein interaction with cytokine and cytokine receptor	15	5.64E-08	4.38E-06
KEGG_PATHWAY	hsa04142~Lysosome	16	3.15E-07	1.83E-05
KEGG_PATHWAY	hsa05323~Rheumatoid arthritis	13	1.42E-06	6.63E-05
KEGG_PATHWAY	hsa01100~Metabolic pathways	64	1.87E-06	7.25E-05
KEGG_PATHWAY	hsa04640~Hematopoietic cell lineage	13	2.49E-06	8.29E-05
KEGG_PATHWAY	hsa04672~Intestinal immune network for IgA production	9	1.35E-05	3.65E-04
KEGG_PATHWAY	hsa04514~Cell adhesion molecules	15	1.41E-05	3.65E-04
KEGG_PATHWAY	hsa05143~African trypanosomiasis	8	1.74E-05	4.06E-04
KEGG_PATHWAY	hsa04668~TNF signaling pathway	11	3.95E-04	8.36E-03
KEGG_PATHWAY	hsa05321~Inflammatory bowel disease	8	6.84E-04	1.33E-02
KEGG_PATHWAY	hsa05418~Fluid shear stress and atherosclerosis	11	1.48E-03	2.60E-02
KEGG_PATHWAY	hsa04380~Osteoclast differentiation	11	1.56E-03	2.60E-02
KEGG_PATHWAY	hsa04614~Renin-angiotensin system	5	1.70E-03	2.64E-02
KEGG_PATHWAY	hsa05164~Influenza A	12	2.00E-03	2.80E-02
KEGG_PATHWAY	hsa00480~Glutathione metabolism	7	2.04E-03	2.80E-02
KEGG_PATHWAY	hsa05152~Tuberculosis	12	2.86E-03	3.70E-02
KEGG_PATHWAY	hsa00790~Folate biosynthesis	5	3.13E-03	3.84E-02
KEGG_PATHWAY	hsa04659~Th17 cell differentiation	9	3.33E-03	3.88E-02
KEGG_PATHWAY	hsa04010~MAPK signaling pathway	16	3.83E-03	4.25E-02
KEGG_PATHWAY	hsa04210~Apoptosis	10	4.03E-03	4.27E-02
KEGG_PATHWAY	hsa00350~Tyrosine metabolism	5	8.95E-03	9.01E-02
KEGG_PATHWAY	hsa00250~Alanine, aspartate and glutamate metabolism	5	9.86E-03	9.01E-02
KEGG_PATHWAY	hsa04974~Protein digestion and absorption	8	1.04E-02	9.01E-02
KEGG_PATHWAY	hsa00240~Pyrimidine metabolism	6	1.04E-02	9.01E-02
KEGG_PATHWAY	hsa00983~Drug metabolism - other enzymes	7	1.06E-02	9.01E-02
KEGG_PATHWAY	hsa05330~Allograft rejection	5	1.08E-02	9.01E-02
KEGG_PATHWAY	hsa04066~HIF-1 signaling pathway	8	1.26E-02	1.01E-01
KEGG_PATHWAY	hsa01232~Nucleotide metabolism	7	1.33E-02	1.03E-01
KEGG_PATHWAY	hsa05166~Human papillomavirus infection	13	1.70E-02	1.28E-01
KEGG_PATHWAY	hsa05332~Graft-versus-host disease	5	1.79E-02	1.30E-01
KEGG_PATHWAY	hsa04151~PI3K-Akt signaling pathway	16	1.95E-02	1.37E-01
KEGG_PATHWAY	hsa04933~AGE-RAGE signaling pathway in diabetic complications	7	2.85E-02	1.95E-01
KEGG_PATHWAY	hsa05142~Chagas disease	7	3.10E-02	2.06E-01
KEGG_PATHWAY	hsa05166~Human T-cell leukemia virus 1 infection	11	3.27E-02	2.06E-01
KEGG_PATHWAY	hsa05320~Autoimmune thyroid disease	5	3.30E-02	2.06E-01
KEGG_PATHWAY	hsa04064~NF-kappa B signaling pathway	7	3.36E-02	2.06E-01
KEGG_PATHWAY	hsa00980~Metabolism of xenobiotics by cytochrome P450	6	3.49E-02	2.08E-01
KEGG_PATHWAY	hsa05135~Yersinia infection	8	3.95E-02	2.30E-01
KEGG_PATHWAY	hsa01200~Carbon metabolism	7	5.06E-02	2.79E-01
KEGG_PATHWAY	hsa00360~Phenylalanine metabolism	3	5.10E-02	2.79E-01
KEGG_PATHWAY	hsa04610~Complement and coagulation cascades	6	5.15E-02	2.79E-01
KEGG_PATHWAY	hsa04662~B cell receptor signaling pathway	6	5.80E-02	3.07E-01
KEGG_PATHWAY	hsa05417~Lipid and atherosclerosis	10	6.09E-02	3.15E-01
KEGG_PATHWAY	hsa00010~Glycolysis / Gluconeogenesis	5	6.76E-02	3.36E-01
KEGG_PATHWAY	hsa04148~Efferocytosis	8	6.78E-02	3.36E-01
KEGG_PATHWAY	hsa00531~Glycosaminoglycan degradation	3	6.95E-02	3.37E-01
KEGG_PATHWAY	hsa05416~Viral myocarditis	5	7.37E-02	3.38E-01
KEGG_PATHWAY	hsa00230~Purine metabolism	7	7.42E-02	3.38E-01
KEGG_PATHWAY	hsa04940~Type 1 diabetes mellitus	4	7.54E-02	3.38E-01
KEGG_PATHWAY	hsa00071~Fatty acid degradation	4	7.54E-02	3.38E-01
KEGG_PATHWAY	hsa00982~Drug metabolism - cytochrome P450	5	8.66E-02	3.67E-01
KEGG_PATHWAY	hsa05146~Amoebiasis	6	8.80E-02	3.67E-01
KEGG_PATHWAY	hsa00860~Porphyrin metabolism	4	8.83E-02	3.67E-01
KEGG_PATHWAY	hsa03267~Virion - Adenovirus	2	8.88E-02	3.67E-01
KEGG_PATHWAY	hsa00340~Histidine metabolism	3	8.98E-02	3.67E-01
KEGG_PATHWAY	hsa01230~Biosynthesis of amino acids	5	9.34E-02	3.75E-01
KEGG_PATHWAY	hsa00220~Arginine biosynthesis	3	9.69E-02	3.83E-01
REACTOME_PATHWAY	R-HSA-168256~Immune System	101	5.00E-15	3.16E-12
REACTOME_PATHWAY	R-HSA-6783783~Interleukin-10 signaling	15	1.40E-12	4.79E-10
REACTOME_PATHWAY	R-HSA-6798695~Neutrophil degranulation	39	1.80E-11	4.10E-09
REACTOME_PATHWAY	R-HSA-449147~Signaling by Interleukins	33	3.84E-08	6.56E-06
REACTOME_PATHWAY	R-HSA-1280215~Cytokine Signaling in Immune system	44	7.55E-08	1.03E-05
REACTOME_PATHWAY	R-HSA-2022377~Metabolism of Angiotensinogen to Angiotensins	7	1.39E-06	1.59E-04
REACTOME_PATHWAY	R-HSA-168249~Innate Immune System	49	4.13E-06	4.03E-04
REACTOME_PATHWAY	R-HSA-912694~Regulation of IFNA/JAK/STAT signaling	13	6.64E-06	5.67E-04
REACTOME_PATHWAY	R-HSA-449836~Other interleukin signaling	12	1.32E-05	1.00E-03
REACTOME_PATHWAY	R-HSA-381426~Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	13	2.97E-05	2.03E-03
REACTOME_PATHWAY	R-HSA-6785807~Interleukin-4 and Interleukin-13 signaling	12	3.68E-05	2.29E-03
REACTOME_PATHWAY	R-HSA-9694614~Attachment and Entry	6	5.52E-05	3.14E-03
REACTOME_PATHWAY	R-HSA-1474244~Extracellular matrix organization	20	6.32E-05	3.32E-03
REACTOME_PATHWAY	R-HSA-2980736~Peptide hormone metabolism	10	1.83E-04	8.60E-03
REACTOME_PATHWAY	R-HSA-1430728~Metabolism	74	1.89E-04	8.60E-03
REACTOME_PATHWAY	R-HSA-202733~Cell surface interactions at the vascular wall	12	3.15E-04	1.34E-02
REACTOME_PATHWAY	R-HSA-5669034~TNFs bind their physiological receptors	6	4.67E-04	1.88E-02
REACTOME_PATHWAY	R-HSA-5423646~Aflatoxin activation and detoxification	5	8.06E-04	3.06E-02
REACTOME_PATHWAY	R-HSA-9662834~CD163 mediating an anti-inflammatory response	4	9.11E-04	3.27E-02
REACTOME_PATHWAY	R-HSA-198933~Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	11	9.79E-04	3.34E-02
REACTOME_PATHWAY	R-HSA-9772572~Early SARS-CoV-2 Infection Events	6	1.67E-03	5.42E-02
REACTOME_PATHWAY	R-HSA-2024096~HS-GAG degradation	5	2.02E-03	6.27E-02
REACTOME_PATHWAY	R-HSA-5668541~TNFR2 non-canonical NF-kB pathway	9	2.38E-03	7.08E-02
REACTOME_PATHWAY	R-HSA-6811558~PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling	9	3.03E-03	8.47E-02
REACTOME_PATHWAY	R-HSA-189445~Metabolism of porphyrins	5	3.16E-03	8.47E-02
REACTOME_PATHWAY	R-HSA-1566948~Elastic fibre formation	6	3.23E-03	8.47E-02
REACTOME_PATHWAY	R-HSA-1442490~Collagen degradation	7	3.42E-03	8.66E-02
REACTOME_PATHWAY	R-HSA-189483~Heme degradation	4	3.45E-03	1.06E-01
REACTOME_PATHWAY	R-HSA-199418~Negative regulation of the PI3K/AKT network	9	4.49E-03	1.06E-01
REACTOME_PATHWAY	R-HSA-211859~Biological oxidations	13	5.25E-03	1.20E-01
REACTOME_PATHWAY	R-HSA-196854~Metabolism of vitamins and cofactors	12	6.06E-03	1.34E-01

GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	14	8.53E-05	1.39E-03	LGALS3BP, TGFBI, MMP7, LTBP2, TNFRSF11B, LTBP3, ADAMTS15, BMPER, ADAMTSL2, CHI3L1, TIMP1, TGFBI, PRSS2, TLR3
GOTERM_CC_DIRECT	GO:0005604~basement membrane	9	1.18E-04	1.81E-03	ENTPD2, COL5A1, COL4A1, VWA1, TIMP1, TGFBI, THBS2, AGRN, MEGF9
GOTERM_CC_DIRECT	GO:0001772~immunological synapse	6	6.51E-04	9.46E-03	ALCAM, GZMA, CD28, HLA-DRA, HAVCR2, ICAM1
GOTERM_CC_DIRECT	GO:0005902~microvillus	7	9.23E-04	1.21E-02	TGFBI, VCAM1, DCSIR, CDHR2, TEK, IQGAP2, ENPP7
GOTERM_CC_DIRECT	GO:0030666~endocytic vesicle membrane	7	9.23E-04	1.21E-02	SCARB2, MSR1, ACE2, CD74, MARCO, CD163, HLA-DRA
GOTERM_CC_DIRECT	GO:0005773~vacuole	4	1.39E-03	1.74E-02	CD74, GLB1, GGH, PRCP
GOTERM_CC_DIRECT	GO:0098552~side of membrane	8	2.01E-03	2.24E-02	BST2, CPM, NT5E, VNN1, TREH, PLAUR, CNTN3, EFNA4
GOTERM_CC_DIRECT	GO:0035577~azurophil granule membrane	6	2.03E-03	2.24E-02	BST2, PIGR, VNN1, LAMP2, PRCP, CKAP4
GOTERM_CC_DIRECT	GO:0002116~semaphorin receptor complex	4	2.03E-03	2.24E-02	NELL2, NRP1, NRP2, ERBB2
GOTERM_CC_DIRECT	GO:0005758~mitochondrial intermembrane space	7	2.13E-03	2.27E-02	AIFM1, CHCHD10, HTRA2, CPOX, IMMT, THOP1, ERAL1
GOTERM_CC_DIRECT	GO:0101003~ficolin-1-rich granule membrane	6	2.35E-03	2.40E-02	NFASC, CR1, LAMP2, PRCP, LILRB2, FCAR
GOTERM_CC_DIRECT	GO:0035579~specific granule membrane	7	2.68E-03	2.64E-02	CEACAM1, PLAU, PLAUR, TNFRSF1B, CKAP4, HMOX2, FCAR
GOTERM_CC_DIRECT	GO:0030669~clathrin-coated endocytic vesicle membrane	6	4.55E-03	4.33E-02	SCARB2, CD74, CD4, HLA-DRA, AREG, IGF2R
GOTERM_CC_DIRECT	GO:0005794~Golgi apparatus	29	5.58E-03	4.97E-02	CANT1, CPQ, DPY30, GALNT16, FTCD, DPP7, MAN1A2, QSOX1, ENPP7, MAMDC4, VCAM1, GOLM2, GDF15, ENTPD6, MTUS1, TNFRSF10A, GFRA1, IGF2R, BST2, ATRN, GLB1, TPP1, SCLY, LTBR, ITGA5, FAM20A, GLA, VAMP5, FGFR2
GOTERM_CC_DIRECT	GO:0016327~apicolateral plasma membrane	4	5.58E-03	4.97E-02	OCLN, CXADR, CDH2, KRT8
GOTERM_CC_DIRECT	GO:0061617~MICOS complex	3	9.59E-03	8.04E-02	CHCHD6, CHCHD10, IMMT
GOTERM_CC_DIRECT	GO:0005911~cell-cell junction	9	9.62E-03	8.04E-02	CEACAM1, BCAM, OCLN, CXADR, CDH2, HEG1, KRT8, TEK, ITGA5
GOTERM_CC_DIRECT	GO:1904724~tertiary granule lumen	5	1.04E-02	8.30E-02	CANT1, GGH, QSOX1, CTSD, NIT2
GOTERM_CC_DIRECT	GO:0016324~apical plasma membrane	14	1.05E-02	8.30E-02	ACY3, HIP1R, PIZK1, PTPRH, DPP4, BST2, ACE2, CEACAM1, OCLN, CDH2, CDHR2, ERBB2, MUC13, TEK
GOTERM_CC_DIRECT	GO:1905370~serine-type endopeptidase complex	3	1.16E-02	8.90E-02	PLAU, PLAUR, HTRA2
GOTERM_CC_DIRECT	GO:0030424~axon	13	1.40E-02	1.05E-01	NRP1, NRP2, TGFBI, MME, GFRA1, IGSF9, ROBO1, NELL2, NFASC, ALCAM, BSG, ALDH1A1, CNTN3
GOTERM_CC_DIRECT	GO:0031528~microvillus membrane	4	1.48E-02	1.07E-01	CEACAM1, CDHR2, PDZK1, PTPRH
GOTERM_CC_DIRECT	GO:0098978~glutamatergic synapse	14	1.56E-02	1.10E-01	RTN4R, NRP1, NRP2, CLSTN2, CLSTN3, HIP1R, PLAT, IL1RAP, SEMA3F, BAIAP2, PCDH17, CDH6, NELL2, ITGA5
GOTERM_CC_DIRECT	GO:0044853~plasma membrane raft	4	1.60E-02	1.10E-01	CR1, CD82, TREM2, PRTN3
GOTERM_CC_DIRECT	GO:0005581~collagen trimer	6	1.85E-02	1.24E-01	MSR1, MARCO, C1QTNF1, COL5A1, COL4A1, TIMP1
GOTERM_CC_DIRECT	GO:0030667~secretory granule membrane	6	1.99E-02	1.29E-01	CR1, ADGRE5, MME, ANPEP, IQGAP2, IGF2R
GOTERM_CC_DIRECT	GO:0031093~platelet alpha granule lumen	5	2.00E-02	1.29E-01	TGFBI, HGF, QSOX1, TIMP1, GAS6
GOTERM_CC_DIRECT	GO:0034362~low-density lipoprotein particle	3	2.13E-02	1.34E-01	MSR1, APOM, APOF
GOTERM_CC_DIRECT	GO:0005769~early endosome	11	2.30E-02	1.41E-01	NRP1, PTPN43, CD4, VCAM1, MME, ERBB2, ENTR1, CD22, IGF2R, TLR3, HAVCR2
GOTERM_CC_DIRECT	GO:0005796~Golgi lumen	6	2.39E-02	1.44E-01	TGFBI, MUC13, SDC1, FURIN, AGRN, GAS6
GOTERM_CC_DIRECT	GO:1990682~CSF1-CSF1R complex	2	3.02E-02	1.77E-01	CSF1R, CSF1
GOTERM_CC_DIRECT	GO:0005771~multivesicular body	4	3.28E-02	1.89E-01	BST2, CRIBP, CD74, GRA1
GOTERM_CC_DIRECT	GO:0030175~filopodium	5	3.52E-02	1.96E-01	KITLG, VCAM1, CXADR, IQGAP2, BAIAP2
GOTERM_CC_DIRECT	GO:0005802~trans-Golgi network	8	3.55E-02	1.96E-01	MME, LAMP2, DPY30, FURIN, LTBP2, TGFBI, LTBP3, IGF2R
GOTERM_CC_DIRECT	GO:0043231~intracellular membrane-bounded organelle	22	4.13E-02	2.23E-01	CSF1R, MVK, CPQ, CTSZ, HIP1R, PRCP, IFI30, TNFSF13B, PLA2G15, BST2, DPP7, GLB1, BSG, LAMP2, QSOX1, PRTN3, HAO1, GUSB, AGXT, GPRC5C, CTSC, CES2
GOTERM_CC_DIRECT	GO:0005782~peroxisomal matrix	4	4.47E-02	2.34E-01	FABP1, HAO1, AGXT, ACAA1
GOTERM_CC_DIRECT	GO:0005896~interleukin-6 receptor complex	2	4.50E-02	2.34E-01	IL6, IL6ST
GOTERM_CC_DIRECT	GO:0005903~brush border	4	5.85E-02	2.93E-01	MME, DCSR, CDHR2, PDZK1
GOTERM_CC_DIRECT	GO:0030141~secretory granule	5	5.91E-02	2.93E-01	CRHBP, TGFBI, OXT, PLAT, BAIAP2
GOTERM_CC_DIRECT	GO:0002947~tumor necrosis factor receptor superfamily complex	2	5.95E-02	2.93E-01	TNFRSF1B, TNFRSF1A
GOTERM_CC_DIRECT	GO:0043025~neuronal cell body	11	6.50E-02	3.15E-01	RTN4R, CALCA, TGFBI, ALCAM, MME, HIP1R, GFRA1, IL6ST, BAIAP2, TNFRSF1B, ROBO1
GOTERM_CC_DIRECT	GO:0030054~cell junction	7	6.65E-02	3.16E-01	CDH6, CEACAM1, OCLN, CXADR, CDH2, IF130, AMOT
GOTERM_CC_DIRECT	GO:0032587~ruffle membrane	3	7.05E-02	3.30E-01	ADGRE2, ERBB2, HIP1R, EPS8L2, ITGA5
GOTERM_CC_DIRECT	GO:0098636~protein complex involved in cell adhesion	2	7.38E-02	3.32E-01	CD80, CD28
GOTERM_CC_DIRECT	GO:0097180~serine protease inhibitor complex	2	7.38E-02	3.32E-01	PLAU, PLAT
GOTERM_CC_DIRECT	GO:0042470~melanosome	5	7.46E-02	3.32E-01	GCHFR, BSG, GGH, TPP1, CTSD
GOTERM_CC_DIRECT	GO:0005912~adherens junction	7	8.44E-02	3.67E-01	CDH6, CEACAM1, KRT18, CXADR, CDH2, BAIAP2, PVR
GOTERM_CC_DIRECT	GO:0030139~endocytic vesicle	4	8.52E-02	3.67E-01	DPP4, OCLN, IGF2R, AMOT
GOTERM_CC_DIRECT	GO:0045211~postsynaptic membrane	7	8.75E-02	3.72E-01	NELL2, NRP1, NRP2, CLSTN2, CLSTN3, ITGA5, PCDH17
GOTERM_CC_DIRECT	GO:0005777~peroxisome	5	8.97E-02	3.75E-01	RIDA, MVK, HAO1, AGXT, ACAA1
GOTERM_CC_DIRECT	GO:0031410~cytoplasmic vesicle	9	9.44E-02	3.89E-01	NRP1, OCLN, CPB1, MME, ERBB2, CTSZ, ITGA5, FGFR2, AMOT
GOTERM_CC_DIRECT	GO:0009925~basal plasma membrane	4	9.71E-02	3.94E-01	CEACAM1, DTNB, ERBB2, TEK
KEGG_PATHWAY	hsa04060~Cytokine-cytokine receptor interaction	34	2.80E-14	6.61E-12	CSF1R, IL1RN, TNFRSF6B, CXCL8, CSF1, TNFRSF11B, IL1RAP, TNFSF13B, IL1RL1, IL10, IL32, TGFB1, IL4R, TNFRSF12A, IL10RB, CCL20, GDF15, IFNGR2, TNFSF12, IL1R2, IL18, TNFRSF10A, TNFRSF1B, INHBC, TNFRSF1A, CXCL10, CD4, IL6, LEP, FAS, TNFSF8, LTBR, IL6ST, IL18R1
KEGG_PATHWAY	hsa05144~Malaria	12	1.22E-08	1.42E-06	IL10, IL6, TGFB1, CR1, VCAM1, CXCL8, HGF, IL1R, SDC1, THBS2, SELE, ICAM1
KEGG_PATHWAY	hsa04061~Viral protein interaction with cytokine and cytokine receptor	15	5.64E-08	4.38E-06	IL10, CSF1R, CXCL8, CSF1, IL10RB, CCL20, IL18, TNFRSF10A, TNFRSF1B, TNFRSF1A, CXCL10, IL6, LTBR, IL6ST, IL18R1
KEGG_PATHWAY	hsa04142~Lysosome	16	3.15E-07	1.83E-05	SCARB2, ARSA, IDUA, CTSZ, NAGPA, IGF2R, PLA2G15, CTSO, GLB1, LAMP2, ACP5, TPP1, GUSB, CTSD, GLA, CTSC
KEGG_PATHWAY	hsa05323~Rheumatoid arthritis	13	1.42E-06	6.63E-05	TGFB1, CXCL8, CSF1, CCL20, CD80, IL18, TNFSF13B, ICAM1, IL6, CD28, HLA-DRA, ACP5, TEK
KEGG_PATHWAY	hsa01100~Metabolic pathways	64	1.87E-06	7.25E-05	ACY1, TREH, CPOX, HNMT, ENO3, GALNT10, FTCD, KHK, MAN1A2, CA5A, ANPEP, KYNU, ENPP2, ACP5, ACAA1, GUSB, GGT1, ENPP7, ARSA, ENTPD2, PHYKPL, DCXR, ENTPD6, UPB1, SDHB, ALDH3A1, ALDH5A1, ALDH1A1, AGXT, FBP1, RBKS, DPC, CANT1, ECHS1, MVK, IDUA, ADH1B, NPL, PTS, ADH4, NT5E, CBS, HMOX1, HAO1, PCBD1, HMOX2, GGT5, RRM2, GOT1, GSR, ADA2, AKR1C4, COQ7, ASS1, QDPR, VNN1, AKR1B10, GLB1, GSTA3, NT5C1A, GSTA1, SCLY, GLA, NIT2
KEGG_PATHWAY	hsa04640~Hematopoietic cell lineage	13	2.49E-06	8.29E-05	CSF1R, CR1, IL4R, MME, CSF1, IL1R2, IL6, CD4, KITLG, ANPEP, HLA-DRA, ITGA5, CD22
KEGG_PATHWAY	hsa04672~Intestinal immune network for IgA production	9	1.35E-05	3.65E-04	IL10, PIGR, IL6, TGFB1, CD80, CD28, HLA-DRA, LTBR, TNFSF13B
KEGG_PATHWAY	hsa04514~Cell adhesion molecules	15	1.41E-05	3.65E-04	CD274, VCAM1, CD80, SELE, PVR, ICAM1, NFASC, CD4, OCLN, ALCAM, CDH2, CD28, SDC1, HLA-DRA, CD22
KEGG_PATHWAY	hsa05143~African trypanosomiasis	8	1.74E-05	4.06E-04	IL10, IL6, VCAM1, IL1R, FAS, SELE, THOP1, ICAM1
KEGG_PATHWAY	hsa04668~TNF signaling pathway	11	3.95E-04	8.36E-03	CXCL10, IL6, VCAM1, CSF1, CCL20, FAS, TNFRSF1B, SELE, IL18R1, ICAM1, TNFRSF1A
KEGG_PATHWAY	hsa05321~Inflammatory bowel disease	8	6.84E-04	1.33E-02	IL10, IL6, TGFB1, IL4R, IFNGR2, IL18, IL1RAP, HAVCR2, IL18R1
KEGG_PATHWAY	hsa05418~Fluid shear stress and atherosclerosis	11	1.48E-03	2.60E-02	VCAM1, GSTA3, IL1R2, GSTA1, HMOX1, SDC1, PLAT, SELE, ASS1, ICAM1, TNFRSF1A
KEGG_PATHWAY	hsa04380~Osteoclast differentiation	11	1.56E-03	2.60E-02	CSF1R, TGFB1, CSF1, IFNGR2, ACP5, TREM2, TNFRSF11B, LILRB1, LILRB2, LILRA2, TNFRSF1A
KEGG_PATHWAY	hsa04614~Renin-angiotensin system	5	1.70E-03	2.64E-02	ACE2, MME, ANPEP, PRCP, THOP1
KEGG_PATHWAY	hsa05164~Influenza A	12	2.00E-03	2.80E-02	CXCL10, IL6, CXCL8, IFNGR2, IL18, HLA-DRA, FAS, TNFRSF10A, PRSS2, TLR3, ICAM1, TNFRSF1A
KEGG_PATHWAY	hsa00480~Glutathione metabolism	7	2.04E-03	2.80E-02	GGT5, RRM2, GSTA3, ANPEP, GSR, GSTA1, GGT1
KEGG_PATHWAY	hsa05152~Tuberculosis	12	2.86E-03	3.70E-02	IL10, CD74, IL6, TGFB1, CR1, IL10RB, IFNGR2, LAMP2, IL18, HLA-DRA, CTSD, TNFRSF1A
KEGG_PATHWAY	hsa00790~Folate biosynthesis	5	3.13E-03	3.84E-02	QDPR, AKR1B10, GGH, PCBD1, PTS
KEGG_PATHWAY	hsa04659~Th17 cell differentiation	9	3.33E-03	3.88E-02	IL6, CD4, TGFB1, IL4R, IFNGR2, NFATC3, HLA-DRA, IL1RAP, IL6ST
KEGG_PATHWAY	hsa04010~MAPK signaling pathway	16	3.83E-03	4.25E-02	CSF1R, TGFB1, CSF1, HGF, NFATC3, IL1RAP, AREG, EFNA4, PGF, TNFRSF1A, KITLG, ERBB2, FAS, TEK, FGFR2, FGF21
KEGG_PATHWAY	hsa04210~Apoptosis	10	4.03E-03	4.27E-02	CTSO, AIFM1, CTSZ, FAS, HTRA2, TNFRSF10A, CTSD, CTSC, LMNB2, TNFRSF1A
KEGG_PATHWAY	hsa00350~Tyrosine metabolism	5	8.95E-03	9.01E-02	ALDH3A1, ADH4, DDC, GOT1, ADH1B
KEGG_PATHWAY	hsa00250~Alanine, aspartate and glutamate metabolism	5	9.86E-03	9.01E-02	ALDH5A1, GOT1, A

REACTOME_PATHWAY	R-HSA-5663084~Diseases of carbohydrate metabolism	5	7.36E-03	1.57E-01	GLB1, IDUA, DCXR, GUSB, KHK
REACTOME_PATHWAY	R-HSA-5676594~TNF receptor superfamily (TNFSF) members mediating non-canonical NF-kB pathway	4	7.59E-03	1.57E-01	TNFRSF12A, TNFSF12, LTBR, TNFSF13B
REACTOME_PATHWAY	R-HSA-9818027~NFE2L2 regulating anti-oxidant/detoxification enzymes	4	8.86E-03	1.71E-01	GSTA3, GSR, GSTA1, HMOX1
REACTOME_PATHWAY	R-HSA-2219530~Constitutive Signaling by Aberrant PI3K in Cancer	7	9.00E-03	1.71E-01	KITLG, HGF, CD80, ERBB2, CD28, AREG, FGFR2
REACTOME_PATHWAY	R-HSA-8956319~Nucleotide catabolism	5	9.02E-03	1.71E-01	NT5E, ENTPD2, NT5C1A, ENTPD6, UPB1
REACTOME_PATHWAY	R-HSA-3000171~Non-integrin membrane-ECM interactions	6	1.13E-02	2.08E-01	DDR1, TGFB1, COL5A1, COL4A1, SDC1, AGRN
REACTOME_PATHWAY	R-HSA-5668914~Diseases of metabolism	13	1.29E-02	2.14E-01	ACY1, IDUA, DCXR, THBS2, KHK, ADAMTS15, GLB1, ADAMTSL2, SDC1, MUC13, AGRN, GUSB, GGT1
REACTOME_PATHWAY	R-HSA-9748784~Drug ADME	8	1.34E-02	2.14E-01	GGT5, PON3, ACY1, BSG, GSTA1, GGT1, CES2, CES1
REACTOME_PATHWAY	R-HSA-216083~Integrin cell surface interactions	7	1.34E-02	2.14E-01	VCAM1, COL5A1, COL4A1, BSG, ITGA5, AGRN, ICAM1
REACTOME_PATHWAY	R-HSA-9012546~Interleukin-18 signaling	3	1.35E-02	2.14E-01	IL18, IL18R1, IL18BP
REACTOME_PATHWAY	R-HSA-9824443~Parasitic Infection Pathways	10	1.35E-02	2.14E-01	IL10, GGT5, IL6, CD163, NT5E, IL18, HMOX1, FURIN, GGT1, BAIAP2
REACTOME_PATHWAY	R-HSA-9658195~Leishmania infection	10	1.35E-02	2.14E-01	IL10, GGT5, IL6, CD163, NT5E, IL18, HMOX1, FURIN, GGT1, BAIAP2
REACTOME_PATHWAY	R-HSA-1474228~Degradation of the extracellular matrix	9	1.55E-02	2.40E-01	MMP7, COL5A1, COL4A1, PHYKPL, BSG, FURIN, TIMP1, CTSD, PRSS2
REACTOME_PATHWAY	R-HSA-2408508~Metabolism of ingested SeMet, Sec, MeSec into H2Se	3	1.70E-02	2.59E-01	CBS, SCLY, HNMT
REACTOME_PATHWAY	R-HSA-975634~Retinoid metabolism and transport	5	1.80E-02	2.68E-01	APOM, AKR1B10, SDC1, AKR1C4, AGRN
REACTOME_PATHWAY	R-HSA-71291~Metabolism of amino acids and derivatives	16	2.24E-02	3.26E-01	DDC, ECHS1, GOT1, PHYKPL, GSR, HNMT, FTCD, ASS1, QDPR, RIDA, CBS, KYNU, PCBD1, HAO1, SCLY, AGXT
REACTOME_PATHWAY	R-HSA-6806667~Metabolism of fat-soluble vitamins	5	2.41E-02	3.43E-01	APOM, AKR1B10, SDC1, AKR1C4, AGRN
REACTOME_PATHWAY	R-HSA-2206281~Mucopolysaccharidoses	3	2.53E-02	3.52E-01	GLB1, IDUA, GUSB
REACTOME_PATHWAY	R-HSA-15869~Metabolism of nucleotides	7	2.65E-02	3.61E-01	NT5E, RRM2, ENTPD2, NT5C1A, GSR, ENTPD6, UPB1
REACTOME_PATHWAY	R-HSA-73621~Pyrimidine catabolism	3	2.99E-02	3.92E-01	NT5E, NT5C1A, UPB1
REACTOME_PATHWAY	R-HSA-71384~Ethanol oxidation	3	2.99E-02	3.92E-01	ADH4, ADH1B, ALDH1A1
REACTOME_PATHWAY	R-HSA-2219528~PI3K/AKT Signaling in Cancer	7	3.26E-02	4.21E-01	KITLG, HGF, CD80, ERBB2, CD28, AREG, FGFR2
REACTOME_PATHWAY	R-HSA-75205~Dissolution of Fibrin Clot	3	3.48E-02	4.29E-01	PLAU, PLAUR, PLAT
REACTOME_PATHWAY	R-HSA-9664433~Leishmania parasite growth and survival	6	3.52E-02	4.29E-01	IL10, GGT5, IL6, CD163, FURIN, GGT1
REACTOME_PATHWAY	R-HSA-9662851~Anti-inflammatory response favouring Leishmania parasite infection	6	3.52E-02	4.29E-01	IL10, GGT5, IL6, CD163, FURIN, GGT1
REACTOME_PATHWAY	R-HSA-1592389~Activation of Matrix Metalloproteinases	4	3.95E-02	4.73E-01	MMP7, FURIN, TIMP1, PRSS2
REACTOME_PATHWAY	R-HSA-1638091~Heparan sulfate/heparin (HS-GAG) metabolism	5	4.17E-02	4.91E-01	GLB1, IDUA, SDC1, AGRN, GUSB
REACTOME_PATHWAY	R-HSA-186797~Signaling by PDGF	5	4.40E-02	5.10E-01	COL5A1, COL4A1, FURIN, PLAT, THBS2
REACTOME_PATHWAY	R-HSA-2142753~Arachidonic acid metabolism	5	4.64E-02	5.28E-01	GGT5, PON3, PON2, PTGR1, GGT1
REACTOME_PATHWAY	R-HSA-156590~Glutathione conjugation	4	4.91E-02	5.49E-01	GGT5, GSTA3, GSTA1, GGT1
REACTOME_PATHWAY	R-HSA-109582~Hemostasis	22	4.99E-02	5.49E-01	LGALS3BP, CD74, TGFB1, CXADR, HGF, PLAUR, PRCP, PLAT, TNFRSF10A, SELE, FCAMR, CEACAM1, PLAU, BSG, LAMP2, SDC1, QSOX1, PRTN3, TEK, TIMP1, ITGA5, GAS6
REACTOME_PATHWAY	R-HSA-2129379~Molecules associated with elastic fibres	4	5.26E-02	5.70E-01	MFAP4, TGFB1, LTBP2, LTBP3
REACTOME_PATHWAY	R-HSA-9840310~Glycosphingolipid catabolism	4	5.99E-02	6.39E-01	ARSA, GLB1, GLA, ENPP7
REACTOME_PATHWAY	R-HSA-373755~Semaphorin interactions	5	6.22E-02	6.54E-01	NRP1, SEMA7A, CD72, ERBB2, TREM2
REACTOME_PATHWAY	R-HSA-9014843~Interleukin-33 signaling	2	6.74E-02	6.98E-01	IL1RL1, IL1RAP
REACTOME_PATHWAY	R-HSA-416700~Other semaphorin interactions	3	6.97E-02	6.98E-01	SEMA7A, CD72, TREM2
REACTOME_PATHWAY	R-HSA-3000480~Scavenging by Class A Receptors	3	6.97E-02	6.98E-01	MSR1, MARCO, COL4A1
REACTOME_PATHWAY	R-HSA-419037~NCAM1 interactions	4	7.16E-02	6.98E-01	COL5A1, COL4A1, GFRA1, AGRN
REACTOME_PATHWAY	R-HSA-2173782~Binding and Uptake of Ligands by Scavenger Receptors	4	7.16E-02	6.98E-01	MSR1, MARCO, CD163, COL4A1
REACTOME_PATHWAY	R-HSA-71387~Metabolism of carbohydrates	12	7.26E-02	6.98E-01	GLB1, IDUA, MAN2B2, DCXR, ALDH1A1, SDC1, AGRN, GUSB, FBP1, ENO3, RBKS, KHK
REACTOME_PATHWAY	R-HSA-388841~Costimulation by the CD28 family	5	7.41E-02	7.03E-01	CD274, CD4, CD80, CD28, HLA-DRA
REACTOME_PATHWAY	R-HSA-114608~Platelet degranulation	7	7.70E-02	7.21E-01	LGALS3BP, TGFB1, HGF, LAMP2, QSOX1, TIMP1, GAS6
REACTOME_PATHWAY	R-HSA-2142691~Synthesis of Leukotrienes (LT) and Eoxins (EX)	3	8.31E-02	7.67E-01	GGT5, PTGR1, GGT1
REACTOME_PATHWAY	R-HSA-76005~Response to elevated platelet cytosolic Ca2+	7	8.87E-02	7.99E-01	LGALS3BP, TGFB1, HGF, LAMP2, QSOX1, TIMP1, GAS6
REACTOME_PATHWAY	R-HSA-194306~Neurophilin interactions with VEGF and VEGFR	2	8.89E-02	7.99E-01	NRP1, NRP2
REACTOME_PATHWAY	R-HSA-2173789~TGF-beta receptor signaling activates SMADs	4	9.32E-02	8.26E-01	TGFB1, FURIN, LTBP2, LTBP3
REACTOME_PATHWAY	R-HSA-9820960~Respiratory syncytial virus (RSV) attachment and entry	3	9.72E-02	8.30E-01	SDC1, FURIN, AGRN
REACTOME_PATHWAY	R-HSA-389948~PD-1 signaling	3	9.72E-02	8.30E-01	CD274, CD4, HLA-DRA
REACTOME_PATHWAY	R-HSA-211945~Phase I - Functionalization of compounds	6	9.73E-02	8.30E-01	ALDH3A1, ADH4, ADH1B, ALDH1A1, CES2, CES1

The significant proteins after Bonferroni correction derived from Cox-proportional hazard regressions in model 1 or model 2 were fed into the Enrichr website (https://maayanlab.cloud/Enrichr/) for enrichment analysis using the Olink proteins as background gene set. The derived results were shown in the table. P-values were calculated under two-sided tests and statistical significance was defined as a false discovery rate-corrected P<0.05.

Supplementary Table 4: Results of protein importance ranking.

All incident MASLD					
Proteins	AUC mean	AUC Std	LCI	UCI	Delong test (*P* value)
FUOM	0.728	0.010	0.710	0.748	NA
FUOM+ACY1	0.742	0.009	0.724	0.761	0.002
FUOM+ACY1+GGT1	0.750	0.009	0.733	0.769	0.003
FUOM+ACY1+GGT1+CDHR2	0.754	0.009	0.737	0.773	0.145
FUOM+ACY1+GGT1+CDHR2+KRT18	0.756	0.009	0.739	0.775	0.170
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2	0.757	0.009	0.740	0.775	0.102
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY	0.760	0.009	0.743	0.778	0.075
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1	0.760	0.009	0.743	0.777	0.732
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1	0.760	0.009	0.743	0.777	0.189
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT	0.760	0.009	0.744	0.778	0.343
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2	0.763	0.009	0.747	0.781	0.096
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3	0.767	0.009	0.750	0.785	0.049
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3+ACE2	0.766	0.009	0.749	0.785	0.491
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3+ACE2+FTCD	0.766	0.009	0.749	0.785	0.930
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3+ACE2+FTCD+MME	0.766	0.009	0.749	0.785	0.857
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3+ACE2+FTCD+MME+ACAA1	0.767	0.009	0.751	0.786	0.476
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3+ACE2+FTCD+MME+ACAA1+GSTA1	0.767	0.009	0.751	0.785	0.834
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3+ACE2+FTCD+MME+ACAA1+GSTA1+GRPEL1	0.767	0.009	0.751	0.785	0.735
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3+ACE2+FTCD+MME+ACAA1+GSTA1+GRPEL1+KYNU	0.767	0.009	0.750	0.785	0.439
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3+ACE2+FTCD+MME+ACAA1+GSTA1+GRPEL1+KYNU+THBS2	0.768	0.009	0.751	0.787	0.517
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3+ACE2+FTCD+MME+ACAA1+GSTA1+GRPEL1+KYNU+THBS2+CEACAM1	0.768	0.009	0.751	0.787	0.921
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3+ACE2+FTCD+MME+ACAA1+GSTA1+GRPEL1+KYNU+THBS2+CEACAM1+PDZK1	0.768	0.009	0.751	0.787	0.923
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3+ACE2+FTCD+MME+ACAA1+GSTA1+GRPEL1+KYNU+THBS2+CEACAM1+PDZK1+CBS	0.768	0.009	0.751	0.787	0.914
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3+ACE2+FTCD+MME+ACAA1+GSTA1+GRPEL1+KYNU+THBS2+CEACAM1+PDZK1+CBS+UPB1	0.769	0.009	0.752	0.788	0.310
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3+ACE2+FTCD+MME+ACAA1+GSTA1+GRPEL1+KYNU+THBS2+CEACAM1+PDZK1+CBS+UPB1+ADH4	0.770	0.009	0.753	0.788	0.201
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3+ACE2+FTCD+MME+ACAA1+GSTA1+GRPEL1+KYNU+THBS2+CEACAM1+PDZK1+CBS+UPB1+ADH4+PLA2G15	0.774	0.009	0.757	0.792	0.027
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3+ACE2+FTCD+MME+ACAA1+GSTA1+GRPEL1+KYNU+THBS2+CEACAM1+PDZK1+CBS+UPB1+ADH4+PLA2G15+PTS	0.775	0.009	0.757	0.793	0.163
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3+ACE2+FTCD+MME+ACAA1+GSTA1+GRPEL1+KYNU+THBS2+CEACAM1+PDZK1+CBS+UPB1+ADH4+PLA2G15+PTS+ADAMTSL2	0.778	0.009	0.761	0.796	0.017
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3+ACE2+FTCD+MME+ACAA1+GSTA1+GRPEL1+KYNU+THBS2+CEACAM1+PDZK1+CBS+UPB1+ADH4+PLA2G15+PTS+ADAMTSL2+ITGBL1	0.778	0.009	0.761	0.796	0.364
FUOM+ACY1+GGT1+CDHR2+KRT18+BST2+SCLY+PCBD1+HAO1+AGXT+PALM2+IGSF3+ACE2+FTCD+MME+ACAA1+GSTA1+GRPEL1+KYNU+THBS2+CEACAM1+PDZK1+CBS+UPB1+ADH4+PLA2G15+PTS+ADAMTSL2+ITGBL1+GOT1	0.782	0.009	0.765	0.799	0.008
The cumulative AUC values were calculated as 30 proteins are incrementally added in each iteration.					
Abbreviations: MASLD, metabolic dysfunction-associated steatotic liver disease.					

Supplementary Table 5: Results of ROC analyses.

train set: test set = 70%: 30%

All incident MASLD					
Variables	AUC (mean across 1000 boostrap samples of the validation set)	95% CI lower bound (AU	95% CI upper bound (AU	AUC Std (standard deviation across 1000 boostrap samples of the validation set)	AUC (test set)
FUOM	0.732	0.711	0.754	0.011	0.715
ACY1	0.731	0.710	0.753	0.011	0.739
GGT1	0.709	0.688	0.732	0.011	0.703
CDHR2	0.715	0.692	0.736	0.011	0.724
KRT18	0.726	0.703	0.748	0.012	0.723
FUOM + all	0.815	0.797	0.833	0.009	0.789
ACY1 + all	0.813	0.794	0.831	0.009	0.804
GGT1 + all	0.807	0.787	0.823	0.009	0.793
CDHR2 + all	0.806	0.787	0.825	0.009	0.797
KRT18 + all	0.810	0.791	0.828	0.009	0.795
5 protein	0.756	0.735	0.777	0.011	0.753
5 protein + all	0.822	0.803	0.839	0.009	0.808
30 protein	0.789	0.771	0.808	0.010	0.747
30 protein + all	0.829	0.811	0.846	0.009	0.798
PRS	0.540	0.515	0.565	0.014	0.487
5-year incident MASLD					
Variables	AUC (mean across 1000 boostrap samples of the validation set)	95% CI lower bound (AUC)	95% CI upper bound (AUC)	AUC Std (standard deviation across 1000 boostrap samples of the validation set)	AUC (test set)
FUOM	0.791	0.734	0.840	0.027	0.786
ACY1	0.777	0.720	0.831	0.028	0.790
GGT1	0.797	0.747	0.846	0.025	0.747
CDHR2	0.812	0.763	0.861	0.025	0.750
KRT18	0.789	0.739	0.836	0.024	0.763
FUOM + all	0.890	0.856	0.924	0.017	0.825
ACY1 + all	0.888	0.852	0.920	0.018	0.824
GGT1 + all	0.893	0.860	0.926	0.017	0.813
CDHR2 + all	0.893	0.860	0.926	0.017	0.804
KRT18 + all	0.882	0.847	0.914	0.018	0.812
5 protein	0.838	0.793	0.880	0.022	0.787
5 protein + all	0.904	0.872	0.935	0.016	0.821
30 protein	0.889	0.859	0.918	0.015	0.777
30 protein + all	0.917	0.889	0.945	0.015	0.819
PRS	0.591	0.527	0.651	0.031	0.546
10-year incident MASLD					
Variables	AUC (mean across 1000 boostrap samples of the validation set)	95% CI lower bound (AUC)	95% CI upper bound (AUC)	AUC Std (standard deviation across 1000 boostrap samples of the validation set)	AUC (test set)
FUOM	0.739	0.709	0.769	0.015	0.749
ACY1	0.729	0.698	0.762	0.016	0.778
GGT1	0.726	0.693	0.758	0.016	0.751
CDHR2	0.742	0.711	0.772	0.016	0.755
KRT18	0.739	0.709	0.769	0.016	0.755
FUOM + all	0.839	0.819	0.860	0.011	0.798
ACY1 + all	0.836	0.814	0.859	0.011	0.815
GGT1 + all	0.835	0.814	0.857	0.011	0.811
CDHR2 + all	0.837	0.815	0.858	0.011	0.805
KRT18 + all	0.836	0.815	0.859	0.011	0.806
5 protein	0.772	0.744	0.800	0.014	0.788
5 protein + all	0.848	0.828	0.869	0.011	0.820
30 protein	0.823	0.799	0.847	0.012	0.769
30 protein + all	0.860	0.840	0.879	0.010	0.805
PRS	0.547	0.514	0.578	0.017	0.512
over 10-year incident MASLD					
Variables	AUC (mean across 1000 boostrap samples of the validation set)	95% CI lower bound (AUC)	95% CI upper bound (AUC)	AUC Std (standard deviation across 1000 boostrap samples of the validation set)	AUC (test set)
FUOM	0.721	0.690	0.753	0.016	0.679
ACY1	0.730	0.701	0.760	0.016	0.698
GGT1	0.687	0.658	0.716	0.015	0.653
CDHR2	0.681	0.650	0.714	0.016	0.692
KRT18	0.708	0.673	0.742	0.017	0.689
FUOM + all	0.793	0.763	0.818	0.014	0.765
ACY1 + all	0.795	0.769	0.821	0.013	0.776
GGT1 + all	0.782	0.757	0.806	0.012	0.762
CDHR2 + all	0.776	0.748	0.804	0.014	0.776
KRT18 + all	0.786	0.757	0.813	0.014	0.769
5 protein	0.742	0.711	0.771	0.015	0.710
5 protein + all	0.799	0.772	0.825	0.013	0.779
30 protein	0.769	0.742	0.796	0.014	0.698
30 protein + all	0.811	0.786	0.835	0.012	0.764
PRS	0.529	0.476	0.570	0.024	0.486

train set: test set = 75%: 25%

All incident MASLD					
Variables	AUC (mean across 1000 boostrap samples of the validation set)	95% CI lower bound (AUC)	95% CI upper bound (AUC)	AUC Std (standard deviation across 1000 boostrap samples of the validation set)	AUC (test set)
FUOM	0.728	0.705	0.748	0.011	0.728
ACY1	0.734	0.711	0.756	0.011	0.732
GGT1	0.707	0.685	0.730	0.011	0.706
CDHR2	0.710	0.687	0.731	0.011	0.740
KRT18	0.724	0.702	0.745	0.011	0.730
FUOM + all	0.810	0.793	0.826	0.009	0.806
ACY1 + all	0.812	0.796	0.829	0.008	0.812
GGT1 + all	0.806	0.788	0.822	0.009	0.801
CDHR2 + all	0.803	0.786	0.819	0.009	0.813
KRT18 + all	0.809	0.792	0.825	0.008	0.805
5 protein	0.755	0.734	0.774	0.010	0.759
5 protein + all	0.819	0.802	0.834	0.008	0.823
30 protein	0.781	0.761	0.799	0.010	0.781
30 protein + all	0.825	0.809	0.840	0.008	0.820
5-year incident MASLD					
Variables	AUC (mean across 1000 boostrap samples of the validation set)	95% CI lower bound (AUC)	95% CI upper bound (AUC)	AUC Std (standard deviation across 1000 boostrap samples of the validation set)	AUC (test set)
FUOM	0.802	0.753	0.847	0.024	0.748
ACY1	0.791	0.743	0.838	0.024	0.754
GGT1	0.794	0.745	0.839	0.024	0.745
CDHR2	0.812	0.764	0.855	0.023	0.734
KRT18	0.794	0.751	0.839	0.023	0.743
FUOM + all	0.877	0.843	0.912	0.018	0.853
ACY1 + all	0.877	0.843	0.909	0.017	0.855
GGT1 + all	0.877	0.842	0.911	0.018	0.855
CDHR2 + all	0.880	0.846	0.913	0.017	0.825
KRT18 + all	0.870	0.839	0.902	0.017	0.842
5 protein	0.842	0.803	0.879	0.019	0.764
5 protein + all	0.892	0.863	0.922	0.016	0.848
30 protein	0.879	0.851	0.905	0.014	0.790
30 protein + all	0.908	0.880	0.934	0.013	0.840
10-year incident MASLD					
Variables	AUC (mean across 1000 boostrap samples of the validation set)	95% CI lower bound (AUC)	95% CI upper bound (AUC)	AUC Std (standard deviation across 1000 boostrap samples of the validation set)	AUC (test set)
FUOM	0.730	0.701	0.760	0.015	0.775
ACY1	0.742	0.712	0.771	0.015	0.741
GGT1	0.725	0.696	0.753	0.015	0.752
CDHR2	0.741	0.712	0.769	0.014	0.757
KRT18	0.738	0.707	0.768	0.015	0.757
FUOM + all	0.821	0.798	0.843	0.011	0.862
ACY1 + all	0.824	0.801	0.846	0.011	0.855
GGT1 + all	0.821	0.799	0.842	0.011	0.865
CDHR2 + all	0.822	0.801	0.842	0.011	0.854
KRT18 + all	0.823	0.800	0.846	0.011	0.858
5 protein	0.771	0.743	0.796	0.013	0.793
5 protein + all	0.836	0.815	0.855	0.010	0.867
30 protein	0.811	0.786	0.834	0.012	0.822
30 protein + all	0.845	0.824	0.864	0.010	0.863
over 10-year incident MASLD					
Variables	AUC (mean across 1000 boostrap samples of the validation set)	95% CI lower bound (AUC)	95% CI upper bound (AUC)	AUC Std (standard deviation across 1000 boostrap samples of the validation set)	AUC (test set)
FUOM	0.705	0.674	0.737	0.016	0.723
ACY1	0.732	0.702	0.761	0.015	0.692
GGT1	0.676	0.644	0.708	0.016	0.679
CDHR2	0.683	0.649	0.713	0.016	0.688
KRT18	0.697	0.661	0.730	0.017	0.722
FUOM + all	0.787	0.760	0.813	0.013	0.788
ACY1 + all	0.798	0.772	0.823	0.013	0.775
GGT1 + all	0.782	0.755	0.806	0.013	0.768
CDHR2 + all	0.781	0.752	0.808	0.014	0.773
KRT18 + all	0.783	0.755	0.811	0.014	0.789
5 protein	0.737	0.706	0.767	0.015	0.722
5 protein + all	0.800	0.774	0.825	0.013	0.784
30 protein	0.761	0.732	0.788	0.014	0.724
30 protein + all	0.811	0.788	0.835	0.012	0.771

train set: test set = 80%: 20%

All incident MASLD					
Variables	AUC (mean across 1000 boostrap samples of the validation set)	95% CI lower bound (AUC)	95% CI upper bound (AUC)	AUC Std (standard deviation across 1000 boostrap samples of the validation set)	AUC (test set)
FUOM	0.729	0.708	0.748	0.010	0.725
ACY1	0.734	0.714	0.752	0.010	0.736
GGT1	0.710	0.690	0.730	0.010	0.696
CDHR2	0.711	0.691	0.731	0.010	0.743
KRT18	0.724	0.703	0.743	0.010	0.732
FUOM + all	0.811	0.796	0.826	0.008	0.802
ACY1 + all	0.813	0.798	0.828	0.008	0.809
GGT1 + all	0.807	0.791	0.822	0.008	0.797
CDHR2 + all	0.803	0.787	0.818	0.008	0.813
KRT18 + all	0.810	0.793	0.825	0.008	0.803
5 protein	0.756	0.737	0.773	0.009	0.758
5 protein + all	0.820	0.805	0.834	0.007	0.819
30 protein	0.782	0.765	0.800	0.009	0.779
30 protein + all	0.826	0.811	0.840	0.007	0.817
5-year incident MASLD					
Variables	AUC (mean across 1000 boostrap samples of the validation set)	95% CI lower bound (AUC)	95% CI upper bound (AUC)	AUC_Std (standard deviation across 1000 boostrap samples of the validation set)	AUC (test set)
FUOM	0.787	0.740	0.834	0.024	0.802
ACY1	0.776	0.726	0.823	0.025	0.804
GGT1	0.785	0.740	0.832	0.024	0.770
CDHR2	0.796	0.752	0.844	0.024	0.782
KRT18	0.781	0.739	0.824	0.022	0.782
FUOM + all	0.873	0.837	0.906	0.018	0.871
ACY1 + all	0.872	0.837	0.904	0.017	0.875
GGT1 + all	0.874	0.839	0.906	0.017	0.868
CDHR2 + all	0.873	0.838	0.906	0.017	0.854
KRT18 + all	0.866	0.830	0.898	0.017	0.857
5 protein	0.826	0.785	0.865	0.020	0.819
5 protein + all	0.885	0.852	0.915	0.016	0.876
30 protein	0.865	0.833	0.895	0.016	0.844
30 protein + all	0.900	0.870	0.928	0.014	0.865
10-year incident MASLD					
Variables	AUC (mean across 1000 boostrap samples of the validation set)	95% CI lower bound (AUC)	95% CI upper bound (AUC)	AUC_Std (standard deviation across 1000 boostrap samples of the validation set)	AUC (test set)
FUOM	0.726	0.697	0.755	0.015	0.804
ACY1	0.736	0.705	0.765	0.015	0.769
GGT1	0.726	0.697	0.754	0.015	0.759
CDHR2	0.740	0.712	0.767	0.014	0.766
KRT18	0.734	0.705	0.762	0.014	0.776
FUOM + all	0.821	0.797	0.844	0.012	0.875
ACY1 + all	0.823	0.800	0.845	0.012	0.872
GGT1 + all	0.822	0.800	0.845	0.011	0.874
CDHR2 + all	0.823	0.801	0.844	0.011	0.862
KRT18 + all	0.822	0.798	0.845	0.012	0.871
5 protein	0.768	0.743	0.795	0.013	0.809
5 protein + all	0.836	0.815	0.857	0.011	0.878
30 protein	0.807	0.782	0.831	0.012	0.843
30 protein + all	0.844	0.824	0.865	0.010	0.874
over 10-year incident MASLD					
Variables	AUC (mean across 1000 boostrap samples of the validation set)	95% CI lower bound (AUC)	95% CI upper bound (AUC)	AUC Std (standard deviation across 1000 boostrap samples of the validation set)	AUC (test set)
FUOM	0.710	0.680	0.738	0.016	0.709
ACY1	0.732	0.704	0.759	0.014	0.677
GGT1	0.680	0.649	0.708	0.015	0.667
CDHR2	0.685	0.656	0.714	0.015	0.686
KRT18	0.699	0.670	0.729	0.015	0.719
FUOM + all	0.792	0.768	0.816	0.012	0.770
ACY1 + all	0.802	0.779	0.824	0.012	0.757
GGT1 + all	0.786	0.763	0.809	0.012	0.751
CDHR2 + all	0.784	0.759	0.808	0.013	0.762
KRT18 + all	0.788	0.763	0.812	0.012	0.777
5 protein	0.738	0.709	0.765	0.014	0.715
5 protein + all	0.803	0.780	0.826	0.012	0.772
30 protein	0.763	0.734	0.789	0.014	0.712
30 protein + all	0.814	0.791	0.837	0.011	0.754

In the main analysis, 70% participants in the UK Biobank from the southern areas of the United Kingdom were included in the training cohort, while rest of whole population were from the northern areas. To confirm the robustness of the results, we randomly split the UK Biobank into training set and testing set base on 0.75 and 0.8 ratio. Based on the ascertained important proteins from the training set, here we tested the predictive performance of these proteins. We reported the performance metrics using median AUCs and 95% CIs, which were obtained through the bootstrap strategy performed with 1,000 iterations. To ensure the robustness of the results, we conducted corresponding analyses for those who developed MASLD under different time scenarios: all time incident, within 5 years, 10 years and over 10 years. All refers to indicators included age, sex, ethnicity, education, TD index, family income, BMI, diabetes, hypertension, dietary habits, physical activity, smoking habits, alcohol intake frequency. 5 protein refers to the combination of FUOM, ACY1, GGT1, CDHR2, AND KRT18 and 30 proteins refers to the combination of FUOM, ACY1, GGT1, CDHR2, KRT18, BST2, SCLY, PCBD1, HAO1, AGXT, PALM2, IGSF3, ACE2, FTCD, MME, ACAA1, GSTA1, GRPEL1, KYNU, THBS2, CEACAM1, PDZK1, CBS, UPB1, ADH4, PLA2G15, PTS, ADAMTSL2, ITGBL1, GOT1.

Abbreviations: MASLD, metabolic dysfunction-associated steatotic liver disease; AUC, area under the curve; CI, confidence interval; Std, standard deviation.

Supplementary Table 6: Prognostic performance of baseline plasma proteins on the risk of clinical progression.

Outcome: MASLD					
Protein	HR	LCI	UCI	P value (Bonferroni-corrected)	Factor
FUOM	9.45	6.73	13.27	2.20E-38	Risk
ACY1	8.69	6.48	11.65	2.73E-47	Risk
GGT1	7.05	5.28	9.41	4.50E-40	Risk
CDHR2	9.81	7.11	13.54	8.60E-44	Risk
KRT18	9.02	6.62	12.29	3.25E-44	Risk
BST2	5.20	3.99	6.78	2.87E-34	Risk
SCLY	6.26	4.78	8.21	3.45E-40	Risk
PCBD1	7.21	5.29	9.83	6.86E-36	Risk
HAO1	6.75	5.05	9.01	2.66E-38	Risk
AGXT	5.94	4.51	7.83	1.39E-36	Risk
PALM2	9.64	6.83	13.61	5.99E-38	Risk
IGSF3	6.97	5.30	9.17	8.37E-44	Risk
ACE2	6.27	4.78	8.22	5.55E-40	Risk
FTCD	8.57	6.12	11.99	6.90E-36	Risk
MME	5.13	3.93	6.70	2.66E-33	Risk
ACAA1	5.64	4.26	7.47	1.17E-33	Risk
GSTA1	8.82	6.45	12.05	1.77E-42	Risk
GRPEL1	5.41	4.11	7.12	2.24E-33	Risk
KYNU	6.29	4.77	8.29	4.78E-39	Risk
THBS2	4.01	3.14	5.13	1.09E-28	Risk
CEACAM1	2.99	2.40	3.73	2.33E-22	Risk
PDZK1	6.09	4.55	8.15	5.75E-34	Risk
CBS	4.80	3.62	6.38	2.03E-27	Risk
UPB1	9.24	6.58	12.98	1.17E-37	Risk
ADH4	9.20	6.66	12.70	2.15E-41	Risk
PLA2G15	5.82	4.46	7.60	2.88E-38	Risk
PTS	4.55	3.55	5.83	5.66E-33	Risk
ADAMTSL2	6.65	4.97	8.89	1.97E-37	Risk
ITGBL1	3.98	3.09	5.13	1.71E-26	Risk
GOT1	2.79	2.20	3.55	3.60E-17	Risk

Plasma proteins are classified by quintile. Cox proportional-hazard models estimated the associations between baseline proteins and MASLD risk, where HRs and *P* values (reference group: Q1 group) were calculated . *P* values were calculated under two-sided tests. The "factor" column indicates whether the protein is a risk factor (i.e. the higher the protein level, the greater the risk of a disease event) or a protective factor (i.e. the lower the protein level, the greater the risk of a disease event).

Abbreviations: MASLD, metabolic dysfunction-associated steatotic liver disease.

Supplementary Table 7: Results of trend tests in the total population.

MASLD	
Protein	P value
FUOM	0.0214
ACY1	0.0023
GGT1	1.25E-04
CDHR2	0.0060
KRT18	0.0026

Mann-Kendall trend tests were performed to examine the slope differences of plasma protein levels over time for indivi

Abbreviations: MASLD, metabolic dysfunction-associated steatotic liver disease.

References

47. Blüher, M. Metabolically Healthy Obesity. *Endocr. Rev.* **2020**, *41* 3., bnaa004. https://doi.org/2021121111034558000.

48. Fletcher, B. R.; Hinton, L.; Bray, E. P.; Hayen, A.; Hobbs, F. R.; Mant, J.; Potter, J. F.; McManus, R. J. Self-Monitoring Blood Pressure in Patients with Hypertension: An Internet-Based Survey of UK GPs. *Br. J. Gen. Pract. J. R. Coll. Gen. Pract.* **2016**, *66* 652., e831–e837. https://doi.org/10.3399/bjgp16X687037.

49. Petermann-Rocha, F.; Gray, S. R.; Forrest, E.; Welsh, P.; Sattar, N.; Celis-Morales, C.; Ho, F. K.; Pell, J. P. Associations of Muscle Mass and Grip Strength with Severe NAFLD: A Prospective Study of 333,295 UK Biobank Participants. *J. Hepatol.* **2022**, *76* 5., 1021–1029. https://doi.org/10.1016/j.jhep.2022.01.010.

50. Li, J.; Zheng, L.; Chan, K. H. K.; Zou, X.; Zhang, J.; Liu, J.; Zhong, Q.; Madsen, T. E.; Wu, W.-C.; Manson, J. E.; Yu, X.; Liu, S. Sex Hormone-Binding Globulin and Risk of Coronary Heart Disease in Men and Women. *Clin. Chem.* **2023**, *69* 4., 374–385. https://doi.org/10.1093/clinchem/hvac209.

51. Wang, H.; Zhao, T.; Zeng, J.; Zhang, R.; Pu, L.; Qian, S.; Xu, S.; Jiang, Y.; Pan, L.; Dai, X.; Guo, X.; Han, L. Methods and Clinical Biomarker Discovery for Targeted Proteomics Using Olink Technology. *Proteomics Clin. Appl.* **2024**, e2300233. https://doi.org/10.1002/prca.202300233.

52. K, S. Genetic Associations with Ratios between Protein Levels Detect New pQTLs and Reveal Protein-Protein Interactions. *Cell Genomics* **2024**, *4* 3.. https://doi.org/10.1016/j.xgen.2024.100506.