Online Supplement

Supplementary methods

BAL supernatant processing for LC-MS/MS analysis

BAL supernatants for proteomic analysis were processed using an S-Trap-based method (protifi.com). Samples were visually inspected for hemolysis and specimens that appeared pink were omitted from the study. Pilot analysis determined protein content per volume BAL to be consistent across healthy and COPD donors.Fifty microliters of BAL from healthy donors (including never-smokers and ex-smokers) and COPD subjects were treated with S-trap buffer (5% sodium dodecyl sulfate, 50 mM triethylammonium bicarbonate (TEABC) buffer, 0.76% phosphoric acid, pH 7.55) and sonicated for 15 min to completely denature proteins. Subsequently samples were reduced in 10 mM tris(2-caroxyethyl)phosphine hydrochloride (TCEP, Sigma), pH 7.8 for 30 min at 65°C followed by alkylation using 40 mM iodoacetamide (IAA, Sigma) in the dark for 30 min at room temperature. Proteins were digested using sequence grade trypsin/lysC (Promega, Madison, WI) at a 15:1 ratio at 37°C for 12 hrs on micro S-Trap cartridges. The resulting peptides were resuspended in 0.1% trifluoracetic acid (TFA, Sigma), desalted using Oasis HLB 96-well plate (2 mg sorbent, 30µm, Waters) and used for tandem mass tag (TMT) (cat. No. A34808, Thermo Fisher Scientific) labelling according to manufacturer's instructions. Digested peptides derived from 25µl equivalent of 110 BAL supernatants from healthy and COPD donors, were randomized across 11 batches and labelled with 145 µg of 11-plex TMT reagents. Each TMT set contained a similar distribution of healthy non-smoker, ex-smoker and COPD samples and TMT 131C was dedicated to a pooled sample comprised of all study specimens. 11plex-TMT labelled samples were then combined, concentrated in a SpeedVac and fractionated on an Oasis plate (Waters # 186001828BA) under basic conditions. Initially 12 different elutions were collected by using a step gradient of acetonitrile containing 10mM TEABC. Distant fractions were then pooled to generate 3 final samples from each TMT batch for mass spectrometry analysis.

Nanoflow LC-MS/MS analysis

LC-MS/MS analysis of TMT labelled peptides was carried out on a Q Exactive HF-X (Thermo Fisher Scientific) mass spectrometer interfaced with a Dionex 3000 RSLCnano system. Peptides were captured on a 2 cm x 75 µm C18 trap column (ReproSil-Pur 120 C18-AQ 7um) and samples were separated on a monolithic column (50 cm, cut from a 2 m long column, 100 µm ID, GL Sciences Inc. USA) using a gradient of solvent A (0.2% formic acid) and solvent B (0.2% formic acid in 90% acetonitrile). Peptides were separated using a 90 min gradient of solvent B as follows: 4% to 16.5%B in 2.5 - 52.5 min; 33.5% B in 73 min followed by a stay at 98% B for 3 min and re-equilibration at 2% B. A flowrate of 0.7 µL/min was used. Peptides were sprayed in an electrospray ionization (ESI) source using a stainless steel emitter with 2kV at a capillary temperature of 275°C. A full-scan MS spectrum was collected at 60,000 resolution at m/z of 200 and scanned at 350-1200 m/z with automatic gain control (AGC) of 3E6. The top 12 precursors were selected, and an MS/MS scan was obtained at 7,500 resolution with 50 ms injection time, isolation window of 0.9 m/z with offset 0.1 m/z, normalized collision energy (NCE) of 29. For MS2, minimum AGC target was set to 1.7E4. Dynamic exclusion duration was set to 15 sec. The fixed first mass was set to 100 m/z. Charge state exclusion was set to ignore unassigned, 1, and 7 and greater charges. For internal mass calibration, lock mass of 371.10124 m/z was used.

Data analysis

Mass spectrometry data was analysed using Proteome Discoverer 2.3 (Thermo Fisher Scientific) software with search engine Mascot (version 2.6.0). Data was searched using latest UniProt Human protein database. Unfragmented precursor and TMT reporter ions were removed using a non-fragment filter in the PD 2.3 workflow. Search parameters included 3 missed cleavages for trypsin, oxidation (M) and deamidation (N, Q) as variable modifications. Tandem label (229.163Da) at N-terminus and lysine residues and carbamidomethylation on cysteine residues were set as fixed modifications. The mass tolerances on precursor and fragment masses were set at 20 ppm and 0.05 Da, respectively for MS2 analysis. Consensus step in PD2.3 included several nodes for spectrum, peptide and protein grouping and FDR calculation. Reporter ions for TMT labelled peptides were quantified using the PD quantitation node and peak integration tolerance was set at 20 ppm by considering most

confident centroid peaks. Signal to noise values were calculated in addition to measurement of intensities of the TMT reporter ion for peptide and protein quantitation. The intensities were normalized by total peptide amount in PD 2.3. To account for protein input, the global quantitative proteome data was reviewed before normalization and no samples showed an unexpected pattern of distribution. Albumin and hemoglobin abundances were not significantly different between sub-cohorts. Further normalization of the data across all samples was carried out using Reporter Ion Quantitation in Proteome Discoverer, which calculates the total sum of the abundance values for each TMT channel over all peptides identified within a file. The channel with the highest total abundances serves as a reference for correcting abundances across the remaining channels by a constant factor.

Macrophage expression analysis

The RNA-sequencing was conducted as a total RNA-seq using the Kapa RNA HyperPrep Kit with RiboErase, and a paired-end sequencing approach (2 x 51) on an Illumina NovaSeq 6000 platform. Fastq files were processed, quality checked and estimated read counts as well as variance-stabilized transformed data generated. All as been previously been described (1). The average read depth per macrophage sample were 55.9 million. Statistical analysis of the transcriptomic data set was explored using differential expression testing and Weighted Gene Correlation Network analysis (WGCNA) (2). Differential expression testing was performed using DESeq2 (v1.26.0) using apeglm (3) for fold change shrinkage, all in R (v3.6.1). Estimated counts was used as input for DESeq2 with lowly expressed genes excluded (required at least 10 counts in at least 20 samples). In the models used to assess differential expression between subject groups, effects from gender and a technical batch-effect (library batch effect) were taken into account. The Benjamini-Hochberg multiple testing correction method was applied. Weighted Gene Correlation Network Analysis (WGCNA) was also implemented to explore this transcriptomics dataset. WGCNA was performed using the WGCNA R package(2). Variance-stabilized transformed genes expression data were used as input for this analysis. Construction of the gene network was performed using the WGCNA automatic network construction method, which is a 1-step network construction and module detection function. A soft thresholding power of 7 was chosen based on the scale-free topology fit output of the *pickSoftThreshold* function. Parameters used to cluster genes into modules included *minModuleSize* =50, *mergeCutHeight* = 0.25 and *deepSplit* = 2. Module clustering using

module eigengenes was used to identify relationships between modules. Assessment of module association with clinical trait metadata was performed to determine the presence of modules with high trait significance, which may indicate presence of genes or pathways of biological relevance. Gene list enrichment analysis was performed on gene lists extracted from modules or module clusters of interest using ToppFunn, which is part of the online ToppGene Suite using default parameter settings (FDR multiple correction method and enrichment significance cut off level 0.05) (4).

Serum processing for LC-MS/MS proteomic analysis

Serum total protein has minimal inter-individual variability and is highly consistent across donors. The serum proteome has a broad concentration range spanning ~11 orders of magnitude with albumin accounting for more than half the total protein in circulation. In this study, 10 µl of serum per donor underwent depletion of the top fourteen most abundant blood proteins using High Select Top14 Abundant Protein Depletion Kit (Thermo Fisher Scientific) according to manufacturer's instructions. Depleted serum was subjected to reduction, alkylation and trypsin/lysC digestion via EasyPep 96 MS Sample Prep Kit (Thermo Fisher Scientific) as outlined by the manufacturer. All serum samples were processed in a single 96-well EasyPep plate eliminating batch effects. Resultant peptides were dried and resuspended in 0.1% formic acid aqueous buffer.

Serum proteomic nanoflow LC-MS/MS analysis

Serum LC-MS/MS analysis was carried out on an Exploris 480 (Thermo Fisher Scientific) mass spectrometer interfaced with a Dionex 3000 RSLCnano system. Peptides, 150 ng per sample, were injected on an Acclaim PepMap RSLC 75 µm x15 cm column (Thermo Fisher Scientific) at a flow rate of 350 µl/min and separated over a 45 min gradient of solvent A (0.1% formic acid) and solvent B (0.1% formic acid in acetonitrile). Gradient of solvent B as follows: 4% to 24% in 2.5 - 40 min; 36% B at 48 min; 64% B at 48.5 held for 4.5 min; 98% B at 53.5 min held for 1.5 min followed by re-equilibration at 4% B. Peptides were sprayed in an electrospray ionization (ESI) source using a stainless-steel emitter with 1650V at a temperature of 270°C. A full-scan MS spectrum was collected at 120,000 resolution at m/z of 200 and scanned at 350-1200 m/z with automatic gain control (AGC) of 100% corresponding to 1E6. DIA MS/MS scans were obtained at 30,000 resolution with the isolation window set to 21 m/z and an overlap of 1 m/z over a precursor mass range of 350-1200 m/z. AGC target was set to 2000% (100% = 1E5).

Serum proteomic data analysis

Serum DIA analysis was conducted in Spectronaut v15 (Biognosys) using the latest UniProt Human protein database and a spectral library representative of healthy and COPD serum proteomes. Serum DIA raw files were searched against a spectral library generated from data-dependent acquisition (DDA) raw files from five pooled and fractionated serum samples, comprised of ten donors each (five male and five female) merged with DDA serum data from this cohort (non-fractionated). The final spectral library used for this analysis contained 3075 proteins (1417 protein groups) representative of 50 healthy donors (25 male and 25 female) in addition to this entire study cohort. Analysis was performed without imputation, with an FDR=0.01 (Qvalue cut off). All observations that passed the Qvalue threshold at least once were included. A list of protein groups identified in each sample and their corresponding intensities was exported to Perseus for further statistical and graphical analysis.

Lipidomics sample preparation

Lipid extraction from BAL supernatants were performed using a modified Maytash method (5). Frozen BAL aliquots (50 µL) were thawed at 4 °C and mixed for 30 seconds at 2000 RPM and 4 °C. 225 µL cold (-30 °C) methanol (MeOH) was added to samples on ice and mixed for 1 minute at 2000 RPM. Samples were spiked with 1 µL Splash Lipidomix (Avanti Polar Lipids) comprised of 14 deuterated lipid internal standards and mixed for 1 minute at 2000 RPM and 4 °C. 750 µL of methyl tert-butyl ether (MTBE) was added and samples were mixed at 2000 RPM for 6 minutes at 4°C. 187.5 µL H_2O was added to induce phase separation and samples were mix at 2000 RPM for 6 minutes at 4°C. Centrifugation was performed for 5 minutes at 14,000 x*g* and 20 °C. Aliquots of 650 µL lipid supernatant were transferred into separate tubes. Samples were dried in a SpeedVac (Thermo Scientific). Dried extracts were stored at -80 °C until reconstitution and subsequent LC-MS and LC-MS/MS analysis.

LC-MS and LC-MS/MS lipidomics analysis

Lipid fractions were reconstituted in 100 µL 90:10 MeOH:toluene and mixed for 1 minute at 1500 RPM. Samples were sonicated for 2 minutes in a water bath, mixed for 1 minute at 1500 RPM, and centrifuged for 5 minutes at 16,000 x*g* and 20°C. 5 µL from each sample was combined to serve as pooled quality control (QC) sample. Samples were transferred to glass HPLC vials and analysed by LC-MS and LC-MS/MS. Lipid samples were analysed in both positive and negative mode ionization. Samples were analysed on a Vanquish UHPLC – Orbitrap ID-X Tribrid MS (Thermo Scientific) using a chromatographic method adopted from Fiehn and coworkers (6). Mobile phase A and B were 0.1% formic acid and 10 mM ammonium

formate in 60:40 ACN:H_2O and 0.1% formic acid and 10 mM ammonium formate in 90:10 IPA:ACN. Chromatographic separation was performed on Acquity UPLC CSH C18 column (1.7 µm, 2.1 x 100mm) (Waters Corporation). Column temperature was maintained at 65°C. LC-MS analysis was performed with a scan range of 120-1200 m/z at Orbitrap resolution of 60,000 on each individual sample. Lipid identification was performed by LC-MS/MS using HCD fragmentation with AcquireX DeepScan data-dependent acquisition workflow (ThermoFisher) performed on iterative injections of a pooled lipid extract from this study.

Lipidomics data analysis

Lipidomics LC-MS and LC-MS/MS data were analyzed using MS-DIAL version 4.60 (7). Peak detection, adduct assignment, identification, alignment, and normalization were performed in MS-DIAL. Lipid annotations were performed using LipidBlast *in silico* fragmentation spectral library provided with MS-DIAL version 4.60 with all lipid classes considered. Lipids were annotated from LC-MS/MS data with identification score cutoff of 70% and MS and MS/MS mass tolerances of 0.005 Da and 0.05 Da, respectively. Lipid acyl chain compositions are reported as the sum composition for species in which fragmentation spectra does not meet score threshold to confidently assign individual acyl chain compositions (e.g., PC 30:0). The concentration of each lipid was quantified by normalizing to the abundance of SPLASH Lipidomix (Avanti Polar Lipids) isotopically labelled internal standard spiked into each sample (described above) for each lipid class and expressed in nmol/ml. Percent composition of individual lipid species is determined by the ratio of individual lipid species concentrations to the sum of all species identified from the same lipid class (e.g, PCs).

References

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Supplementary Tables

	Control			**COPD**	
	HV-NS	HV-ES	P-Value (HV-NS *vs*. HV-ES)		P-Value (HV-ES controls *vs.* COPD)
N of subjects (Total=62)	19	22	-	34	-
M/F	11/8	12/10	0.8294	26/8	0.0863
Age	63.0 (12.0)	66.5 (7.3)	0.0989	70.0 (11.5)	0.5679
Pack-years of smoking	0.0 (1.6)	25.0 (18.1)	**<0.0001**	40.5 (32.6)	0.1272
BMI, kg/m2	28.0 (5.2)	27.7 (4.2)	>0.9999	28.3 (6.6)	>0.9999
FEV1%	102.0 (15.5)	100.0 (10.75)	>0.9999	78.0 (25.0)	**<0.0001**
FEV1/FVC ratio	80.0 (5.0)	87.5 (4.3)	0.5336	55.0 (17.0)*	**<0.0001**
TLCO%	95.5 (15.5)&	89.0 (12.5) &	0.4520	73.0 (23.8) &	**0.0285**
HRCT LAA%	5.32 (4.17)^	5.86 (4.98)^	0.6348	13.16 (8.74)^	**0.0017**
HRCT E/I MLD	0.800 (0.048)^	0.800 (0.060)^	>0.9999	0.875 (0.075)^	**0.0018**
N (%) in ICS	0 (0)	0 (0)	-	14 (44.18)$	**0.00237**
N (%) on bronchodilators	0 (0)	1 (5.00)	**8.33-E05**	20 (70.59)$	**1.26-E06**

Table S1. Demographics of cohort included for proteomic analysis of serum

Data are presented as median and IQR (interquartile range) unless otherwise indicated. Statistical testing performed using Chi-squared test for categorical variables (Sex; Male/Female, ICS use or not and bronchodilator use or not) and Kruskal-Wallis with Dunn's post hoc for continuous variables (all other variables) This table is similar to other research previously reported in the MICAII population [26-29]

[a] *Definition of abbreviations: BMI = body mass index; COPD = chronic obstructive pulmonary disease, FEV 1 = forced expiratory volume in one second, FVC = forced vital capacity, HV-ES = healthy volunteer never-smoker, HV-NS = healthy volunteer ex-smoker, TLCO% = percent of predicted transfer factor for carbon monoxide, %LAA = High-resolution computed tomography determined emphysema measured by % low attenuation areas (%LAA). ICS = inhaled corticosteroids.*

*Notably analysis was undertaken on serum samples from subjects from the final MICAII cohort (table 1), in addition to subjects who were removed from the study prior to bronchoscopy due to numerous reasons, including subject request, not being suitable for bronchoscopy, or not fitting the inclusion criteria as set out in the methodology. Some of these subjects therefore did not undergo *lung function assessment (1 COPD), %TLCO assessment (3 HV-NS; 1 HV-ES; 11 COPD), ^HRCT scan (3 HV-NS; 2 HV-ES; 8 COPD) or $inhaled medications were not recorded (1 COPD). These data for these patients are therefore not included within this table.*

Table S2. Serum proteome summary (table attached at end of document due to size)

UniProt ID and corresponding gene name for serum proteins identified across all donors in this cohort.

	Control			**COPD**	
	HV-NS	HV-ES	P-Value (HV-NS *vs*. HV-ES)		P-Value (HV-ES controls *vs.* COPD)
N of subjects (Total=62)	15	18	-	14	-
M/F	9/6	9/9	0.5659	11/3	0.0977
Age	64.0 (7.0)	67.5 (6.80)	0.1457	72.5 (10.5)	0.4193
Pack-years of smoking	0.2 (1.8)	25.0 (20.9)	**<0.0001**	45.0 (40.8)	0.5947
BMI, kg/m2	28.0 (5.2)	28.2 (4.0)	0.9882	29.3 (5.3)	>0.9999
FEV1%	103.0 (17.0)	100.5 (8.8)	0.8526	79.5 (12.3)	**0.0002**
FEV1/FVC ratio	79.0 (4.0)	77.0 (4.8)	0.3541	61.0 (11.3)	**<0.0001**
TLCO%	95.0 (16.0)	88.0 (10.0)	0.3331	81.0 (16.0)	0.3331
HRCT LAA%	5.69 (3.99)	5.38 (4.32)	>0.9999	10.8 (8.03)	**0.0362**
HRCT E/I MLD	0.800 (0.045)	0.795 (0.050)	0.8184	0.840 (0.070)	**0.0112**
N (%) in ICS	0 (0)	0 (0)	-	7 (50.00)	**0.00237**
N (%) on bronchodilators	0 (0)	1 (5.00)	**8.33-E05**	12 (85.71)	**1.26-E06**

Table S3. Demographics of cohort included for transcriptomic analysis of purified BAL macrophages

Data are presented as median and IQR (interquartile range) unless otherwise indicated. Statistical testing performed using Chi-squared test for categorical variables (Sex; Male/Female, ICS use or not and bronchodilator use or not) and Kruskal-Wallis with Dunn's post hoc for continuous variables (all other variables) This table is similar to other research previously reported in the MICAII population [26-29]

[a] *Definition of abbreviations: BMI = body mass index; COPD = chronic obstructive pulmonary disease, FEV 1 = forced expiratory volume in one second, FVC = forced vital capacity, HV-ES = healthy volunteer never-smoker, HV-NS = healthy volunteer ex-smoker, TLCO% = percent of predicted transfer factor for carbon monoxide, %LAA = High-resolution computed tomography determined emphysema measured by % low attenuation areas (%LAA). ICS = inhaled corticosteroids.*

Supplementary figure legends

Figure S1. Gender differences were not significant across omics datasets.
(A) Lipid distribution between male and female donors was not significantly different. **(B)** Proteome profiles of male and female donors were not significantly different, all had a -log10 adjusted p-value <1.3. SFTPA and SFTPB showed minimal differential expression and abundance differences between genders, SFTPA was slightly more abundant in females and SFTPB was slightly more abundant in males.

Figure S2. Correlation analysis of SFTPB, SFTPA and SFTPD with NAPSA, CTSH and neutrophil elastase in BAL.
Spearman's rank correlation of (**A**) SFTPB correlation with napsin A aspartic peptidase (NAPSA), (**B**) SFTPB correlation with Cathepsin H (CTSH), (C) SFTPA correlation with neutrophil elastase (ELANE), (D) SFTPD correlation with ELANE.

Figure S3. Construction of macrophage gene network and detection of modules.
Construction of dendrogram was performed using an automatic one step network construction and module detection method. **(A)** A soft thresholding power of 7 was chosen based on scale-free topology fit indicating the lowest power which intersected the high value red line (R^2 = 0.9) on the scale independence plot, whilst maintaining a mean connectivity score above 0. **(B)** Clustering dendrogram of genes, with dissimilarity based on topological overlap and colours below indicating module assignment. Performed using the *WGCNA* package in R and the additional parameters: *minModuleSize* =50, *mergeCutHeight* = 0.25 and *deepSplit* = 2.

Table S2. Serum proteome summary

UniProt ID	Genes
A0A024R6I7	SERPINA1
A0A075B6I9; P04211	IGLV7-46;IGLV7-43
A0A075B6K0; P01717; P01718	IGLV3-16;IGLV3-25;IGLV3-27
A0A075B7C5; A0A494C1Q1; P13501	CCL5
A0A087WTK0; A0A087WVC6; Q12913; Q12913-2	PTPRJ
A0A087WTY6; A3KFI1; A3KFI2; A3KFI3; A3KFI4; A3KFI5; E5RFZ1; P41271; P41271-2	NBL1
A0A087WV50; A0A087WYT4; A0A0B4J215; C9J2P9; H3BTT7; J3KNA0; S4R3N7	SENP3;STK4;NIN;CBLL1;HERPUD1;OXA1L;C10orf90
A0A087WWU8; P06753-2; P06753-3; P06753-6	TPM3
A0A087WX77; P13591	NCAM1
A0A087WY68; A0A087WZR0; H0Y3Q0; P29122; P29122-2; P29122-7; P29122-8	PCSK6
A0A087WYI3; P41439	FOLR3
A0A087WYS1	UGP2
A0A087WZM2; D6REQ6; D6RHI9; H0YAE9; O00584	RNASET2;RNASET2;RNASET2;;RNASET2
A0A087WZR4; A0A3B3ISU3; H0Y4U3; M9MML6; O75015	FCGR3B
A0A087X054; A0A494C039; Q9Y4L1	HYOU1

A0A087X0D5; P09668	CTSH
A0A087X0M8	CHL1
A0A087X0Q4	IGKV2-40
A0A087X0S5; P12109	COL6A1
A0A087X0T8; A0A087X1W8; A0A0A0MTJ8; Q9BY67; Q9BY67-2; Q9BY67-3; Q9BY67-4; Q9BY67-5; X5DQS5	CADM1
A0A087X1J7; P22352	GPX3
A0A096LPE2	SAA2-SAA4
A0A0A0MRJ7; P12259	F5
A0A0A0MRN7; Q6YP21; Q6YP21-2	KYAT3
A0A0A0MRZ8; P04433	IGKV3D-11;IGKV3-11
A0A0A0MS08; P01857	IGHG1
A0A0A0MS09; P01880; P01880-2	IGHD
A0A0A0MS15	IGHV3-49
A0A0A0MT69	IGKJ4
A0A0A0MTH3; Q13418; Q13418-2; Q13418-3	ILK
A0A0B4J1R4; P32754; P32754-2	HPD
A0A0B4J1R6; P29401; P29401-2	TKT
A0A0B4J1U7	IGHV6-1
A0A0B4J1X5	IGHV3-74
A0A0B4J231; B9A064	IGLL5
A0A0C4DFP6; Q9NQ79; Q9NQ79-2	CRTAC1
A0A0C4DG49; P15151; P15151-2; P15151-3; P15151-4	PVR

A0A0C4DH25	IGKV3D-20
A0A0C4DH34	IGHV4-28
A0A0C4DH67	IGKV1-8
A0A0D9SEN1; Q12884	FAP
A0A0G2JMB2	IGHA2
A0A0G2JMC9; A0A0G2JMW8; A8MZH0; Q8N149; Q8N149-2; Q8N149-3; Q8N149-4	LILRA2
A0A0G2JMW3; A0A0G2JP44; Q9HBB8; Q9HBB8-2; Q9HBB8-4	CDHR5
A0A0G2JMY9; Q8N6C8; Q8N6C8-3	LILRA3
A0A0J9YX35	IGHV3-64D
A0A0J9YXX1	IGHV5-10-1
A0A0J9YY99	
A0A0M3HER1; P48059; P48059-2; P48059-3; P48059-4; P48059-5; Q7Z4I7; Q7Z4I7-2; Q7Z4I7-3; Q7Z4I7-4; Q7Z4I7-5	LIMS1;LIMS1;LIMS1; LIMS1;LIMS1;LIMS1; LIMS2;LIMS2;LIMS2; LIMS2;LIMS2
A0A0S2Z4L3; A0A3B3ISJ1; P07225	PROS1
A0A0U1RQQ4; Q9UNN8	PROCR
A0A140T8Y3; A0A140T902; A0A140TA33; A0A140TA52; A0A3B3ISX9; P22105; P22105-1; P22105-4	TNXB
A0A140TA49	C4A
A0A1B0GV23; A0A1B0GVD5; A0A1B0GWE8; P07339	CTSD

A0A286YES1; A0A4W9A917; P01860	IGHG3
A0A286YEY4; P01859	IGHG2
A0A286YFJ8; P01861	IGHG4
A0A2Q2TTZ9	IGKV1D-33
A0A2R8Y430; P48637	GSS
A0A2R8Y478; A6NNI4; G8JLH6; P21926	CD9
A0A2R8Y524; A0A2R8YEC9; E9PFW2; O00462	MANBA
A0A2R8YEP4; P30043	BLVRB
A0A2U3TZL5; E9PNW4; P13987; P13987-2	CD59;;CD59;CD59
A0A3B3IQ51; P36980; P36980-2	CFHR2
A0A3B3IS66	F13B
A0A3B3IS80; P05062	ALDOB
A0A3B3ISD1; C1KBH7; P11362-19; P11362-21; P11362-7	FGFR1
A0A3B3ISR2; B4DPQ0	C1R
A0A3B3ISS6; Q14956; Q14956-2	GPNMB
A0A3B3ISU0; Q02487; Q02487-2	DSC2
A0A494C0L6; C9JGI3; P19971; P19971-2	TYMP
A0A494C0X7; D3DSM0; P05107	ITGB2
A0A494C165; K7ES25; P12955	PEPD
A0A499FJK2; P01137	TGFB1
A0A4W8ZXM2	IGHV3-72

A0A590UJJ6; B4DEB1; K7EK07; K7EMV3; K7EP01; K7ES00; P68431; P84243; Q16695; Q5TEC6; Q6NXT2; Q71DI3	H3-3A;H3-3A;H3-3B;H3-3B;H3-3B;H3-3B;H3C1;H3-3A;HIST3H3;H3-2;H3F3C;HIST2H3A
A0A590UK92; O14746; O14746-2; O14746-3; O14746-4	TERT
A0A5F9UJX7; A0A5F9UP49; G3V1E2; Q9BRK5; Q9BRK5-3; Q9BRK5-4; Q9BRK5-6	SDF4
A0A5F9UY30; A0A5H1ZRP2; O43493; O43493-3; O43493-5; O43493-7	TGOLN2
A0A5F9ZHM4; P07195	LDHB
A0A5H1ZRQ3	IGKC
A0A5H1ZRQ7; A0M8Q6	IGLC7
A1A5D9-2; Q9UJX6-2	BICDL2;ANAPC2
A1L4H1	SSC5D
A6NC48; Q10588	BST1
A6XND0; A6XND1; P17936; P17936-2	IGFBP3
B0QYF7; B0QYF8; F2Z2F1; P02144; Q8WVH6	MB
B0YIW2; P02656	APOC3
B1ALD9; Q15063; Q15063-3; Q15063-5	POSTN
B1AN99; P35030; P35030-2; P35030-3; P35030-4; P35030-5	PRSS3

B1AP13; H3BLV0; H7BY55; P08174; P08174-2; P08174-3; P08174-4; P08174-5; P08174-6; P08174-7	CD55
B1B0D4; Q86TH1	ADAMTSL2
B4DV12; F5GXK7; F5GYU3; F5H265; F5H2Z3; F5H388; F5H6Q2; F5H747; J3QKN0; J3QS39; J3QTR3; P0CG47; P0CG48; P62979; P62987; Q5PY61; Q96C32	UBB;UBC;UBC;UBC;UBC;UBC;UBC;UBB;UBB;RPS27A;UBB;UBC;RPS27A;UBA52;UBC;UBC
B4E3Q4; Q9NZK5	ADA2
B7Z6Z4; F8W1R7; G3V1V0; G8JLA2; J3KND3; P60660; P60660-2	MYL6
B7ZKJ8	ITIH4
B9A064-2	IGLL5
C9IZP8	C1S
C9J0J0; Q96EE4	CCDC126
C9JF17; P05090	APOD
C9JFR7; P99999	CYCS
C9JL85; P58546	MTPN
C9JZC2	ZNF621
D3YTG3; H0Y897; H7C556; Q7Z7G0; Q7Z7G0-2; Q7Z7G0-3; Q7Z7G0-4	ABI3BP
D6R934; P02746	C1QB
D6RD17; P01591	JCHAIN
D6RE82; P56182	RRP1

D6RE86	CP
D6RF35; P02774; P02774-3	GC
D6RF86; P55285; P55285-2	CDH6
D6RIU5; P00995	SPINK1
D6W5L6; P07988	SFTPB
E5RJD0; H0YBY3; P17900	GM2A
E7END6; P04070; P04070-2	PROC
E7EQB2; E7ER44; P02788; P02788-2	LTF
E7ESB3; Q13508; Q13508-2; Q13508-3	ART3
E7ET86; Q8IVW4; Q8IVW4-2	CDKL3
E7ETH0	CFI
E7EUF1; Q13822; Q13822-2; Q13822-3	ENPP2
E7EUJ1; P11150	LIPC
E7EV71; Q14766; Q14766-2; Q14766-4; Q14766-5	LTBP1
E9PD35; P35916; P35916-1	FLT4
E9PEK4; P07333	CSF1R
E9PEP6; O14786	NRP1
E9PK25; H0Y4A7; P23528	CFL1;BRWD1;CFL1
E9PKY4; Q03167; Q03167-2	TGFBR3
E9PND2; E9PP21; E9PS42; P21291	CSRP1
E9PRU1; H0YET5; O95967	EFEMP2
F5GXJ9; Q13740; Q13740-2	ALCAM
F5GY80; F5H7G1	C8B

F5GZS6; J3KPF3; P08195; P08195-2; P08195-3; P08195-4	SLC3A2
F5GZZ9; Q86VB7; Q86VB7-2; Q86VB7-3	CD163
F5H2B5	PLD4
F5H8B0; P08709; P08709-2	F7
G3V2W1; Q9UK55	SERPINA10
G3V3A0	SERPINA3
G3V4U0; Q9UBX5	FBLN5
G3XAI2; P07942	LAMB1
G3XAK1; P26927	MST1
G5E9Z4	PI4K2B
H0Y2Y8; Q15942; Q15942-2	ZYX
H0Y5E4; H0YCV9; H0YD13; H0YDW7; P16070; P16070-10; P16070-11; P16070-12; P16070-13; P16070-14; P16070-15; P16070-16; P16070-17; P16070-18; P16070-3; P16070-4; P16070-5; P16070-6; P16070-7; P16070-8; P16070-9	CD44
H0Y755; M9MML0; P08637	FCGR3A
H0YAC1; P03952	KLKB1
H0YGX7; P52566	ARHGDIB
H0YJW9	
H0YLC7; P16930; P16930-2	FAH
H3BR24; H3BTD5; M0R1K8	CCPG1;MYZAP;ARHGEF1

H7BY64; Q96NZ9	ZNF511-PRAP1;PRAP1
H7C1K7	KIF15
H7C5R1	CP
H9KV31; O15394	NCAM2
H9N1E7; P07359	FLT1;GP1BA
I3L145; P04278	SHBG
I3L397; I3L504; P63241; P63241-2	EIF5A
J3KNB4; P49913	CAMP
J3KNV4; Q13683; Q13683-10; Q13683-3; Q13683-7; Q13683-9	ITGA7
J3KPA1; P54108; P54108-2; P54108-3	CRISP3
J3QQR8; J3QQX6; J3QRQ1; J3QRT5; P13598	ICAM2
K4DIA0; O75144; O75144-2	ICOSLG
K7ELL7; P14314; P14314-2	PRKCSH
K7ER74; P02655	APOC4-APOC2;APOC2
K7ERG9; P00746	CFD
K7ERI9; P02654	APOC1
M0QY68; Q9BTV5	FSD1
M0QZ43; P23327	HRC
M0R1Q1	C3
M0R3C9; Q9UM47	NOTCH3
O00151	PDLIM1
O00187	MASP2

O00391	QSOX1
O00533	CHL1
O00592; O00592-2	PODXL
O00602	FCN1
O14498	ISLR
O14645-2	DNALI1
O14791; O14791-2	APOL1
O15204; O15204-2	ADAMDEC1
O43157	PLXNB1
O43852; O43852-3	CALU
O43866	CD5L
O60235	TMPRSS11D
O75083	WDR1
O75368	SH3BGRL
O75594	PGLYRP1
O75636	FCN3
O75882-2	ATRN
O76061	STC2
O94985-2	CLSTN1
O95445	APOM
O95479; R4GMU1	H6PD
O95497	VNN1
O95810	CAVIN2
O95980	RECK
P00338; P00338-3	LDHA

P00450	CP
P00488	F13A1
P00491	PNP
P00533; P00533-3; P00533-4	EGFR
P00558; P00558-2	PGK1
P00734	F2
P00738	HP
P00739	HPR
P00740	F9
P00742	F10
P00747	PLG
P00748	F12
P00915	CA1
P00918	CA2
P01008	SERPINC1
P01009	SERPINA1
P01011	SERPINA3
P01019	AGT
P01023	A2M
P01024	C3
P01031	C5
P01033; Q5H9A7	TIMP1
P01034	CST3
P01042	KNG1
P01042-2	KNG1

P01344-3	IGF2
P01624	IGKV3-15
P01700	IGLV1-47
P01714	IGLV3-19
P01766	IGHV3-13
P01780	IGHV3-7
P01833	PIGR
P01834	IGKC
P01871	IGHM
P01876	IGHA1
P02452	COL1A1
P02461; P02461-2	COL3A1
P02647	APOA1
P02649	APOE
P02652; V9GYM3	APOA2
P02671	FGA
P02675	FGB
P02679; P02679-2	FGG
P02730; P02730-2	SLC4A1
P02741	CRP
P02743	APCS
P02745	C1QA
P02747	C1QC
P02748	C9
P02749	APOH

P02750	LRG1
P02751-1; P02751-3	FN1
P02751-10	FN1
P02753; Q5VY30	RBP4
P02760	AMBP
P02763	ORM1
P02765	AHSG
P02766	TTR
P02768	ALB
P02774-2	GC
P02775	PPBP
P02776	PF4
P02787	TF
P02790	HPX
P03950	ANG
P03951	F11
P04003	C4BPA
P04004	VTN
P04066	FUCA1
P04075	ALDOA
P04114	APOB
P04180	LCAT
P04196	HRG
P04217	A1BG
P04275	VWF

P04279; P04279-2	SEMG1
P04406	GAPDH
P04745	AMY1A
P05019; P05019-2; P05019-3; P05019-4	IGF1
P05067; P05067-11; P05067-7; P05067-8; P05067-9	APP
P05106	ITGB3
P05109	S100A8
P05121; P05121-2	SERPINE1
P05154	SERPINA5
P05155; P05155-3	SERPING1
P05160	F13B
P05164; P05164-2; P05164-3	MPO
P05362	ICAM1
P05451	REG1A
P05452	CLEC3B
P05543	SERPINA7
P05546	SERPIND1
P05556	ITGB1
P06276	BCHE
P06312	IGKV4-1
P06331	IGHV4-34
P06396	GSN
P06396-2	GSN
P06681	C2

P06702	S100A9
P06703; R4GN98	S100A6
P06727	APOA4
P06732	CKM
P06899; P23527; P33778; Q16778	H2BC11;HIST1H2BO; HIST1H2BB;HIST2H2 BE
P07237	P4HB
P07307; P07307-2; P07307-3	ASGR2
P07357	C8A
P07358	C8B
P07360	C8G
P07384	CAPN1
P07437; Q5JP53	TUBB
P07451	CA3
P07737	PFN1
P07858	CTSB
P07911; P07911-4; P07911-5; X6RBG4	UMOD
P07996	THBS1
P07998	RNASE1
P08185	SERPINA6
P08253	MMP2
P08254	MMP3
P08294	SOD3
P08311	CTSG

P08493; P08493-2	MGP
P08514; P08514-2; P08514-3	ITGA2B
P08519	LPA
P08567	PLEK
P08571	CD14
P08581; P08581-2	MET
P08603	CFH
P08697	SERPINF2
P09172	DBH
P09382	LGALS1
P09486	SPARC
P09619	PDGFRB
P09871	C1S
P0C0L4	C4A
P0C0L5	C4B
P0DJI8	SAA1
P0DJI9	SAA2
P0DOY2; P0DOY3	IGLC2;IGLC3
P10124	SRGN
P10451; P10451-2; P10451-3; P10451-4	SPP1
P10586; P10586-2	PTPRF
P10599	TXN
P10643	C7
P10645	CHGA
P10646	TFPI

P10720	PF4V1
P10721; P10721-2	KIT
P10909; P10909-2; P10909-4; P10909-5; P10909-6	CLU
P11021	HSPA5
P11047	LAMC1
P11142	HSPA8
P11226	MBL2
P11279	LAMP1
P11597	CETP
P11717	IGF2R
P12111	COL6A3
P12318; P12318-2	FCGR2A
P12724	RNASE3
P12814	ACTN1
P12830	CDH1
P13473; P13473-2; P13473-3	LAMP2
P13497	BMP1
P13671	C6
P13727	PRG2
P13796	LCP1
P14151; P14151-2	SELL
P14209	CD99
P14543	NID1
P14618-2	PKM

P14625	HSP90B1
P14780	MMP9
P15144	ANPEP
P15169	CPN1
P16035	TIMP2
P16109; Q5R349	SELP
P16284; P16284-2; P16284-3; P16284-4; P16284-5; P16284-6	PECAM1
P17301	ITGA2
P17813; P17813-2	ENG
P17931	LGALS3
P18065	IGFBP2
P18206; P18206-2	VCL
P18428	LBP
P18615-4	NELFE
P19021; P19021-2; P19021-3; P19021-4; P19021-5; P19021-6	PAM
P19022; P19022-2	CDH2
P19320	VCAM1
P19652	ORM2
P19823	ITIH2
P19827	ITIH1
P19827-2	ITIH1
P20023; P20023-2; P20023-3; P20023-4	CR2
P20742	PZP

P20851; P20851-2	C4BPB
P21333; P21333-2	FLNA
P21709	EPHA1
P22692	IGFBP4
P22792	CPN2
P22891; P22891-2	PROZ
P22897	MRC1
P23141; P23141-2; P23141-3	CES1
P23142	FBLN1
P23142-4	FBLN1
P23284	PPIB
P23470; P23470-2	PTPRG
P24592	IGFBP6
P24593	IGFBP5
P24821	TNC
P25311	AZGP1
P25786; P25786-2	PSMA1
P25815	S100P
P26038	MSN
P26992	CNTFR
P27105	STOM
P27169	PON1
P27348	YWHAQ
P27487	DPP4
P27797	CALR

P27918	CFP
P28799; P28799-3	GRN
P29279	CCN2
P29622	SERPINA4
P30101	PDIA3
P30530; P30530-2	AXL
P31146	CORO1A
P31151	S100A7
P31260-2	HOXA10
P32004; P32004-2; P32004-3	L1CAM
P32119	PRDX2
P32942	ICAM3
P33151	CDH5
P34096	RNASE4
P35247	SFTPD
P35443	THBS4
P35555	FBN1
P35579	MYH9
P35590	TIE1
P35858; P35858-2	IGFALS
P36222	CHI3L1
P36955	SERPINF1
P39060; P39060-1; P39060-2	COL18A1
P40197	GP5
P41222	PTGDS

P42785; P42785-2	PRCP
P43121	MCAM
P43251; P43251-2; P43251-3; P43251-4	BTD
P43652	AFM
P46531	NOTCH1
P48723	HSPA13
P48740	MASP1
P48740-2	MASP1
P49747	COMP
P49908	SELENOP
P51884	LUM
P54289; P54289-2; P54289-5	CACNA2D1
P55056	APOC4
P55058	PLTP
P55103	INHBC
P55268	LAMB2
P55290; P55290-4	CDH13
P55774	CCL18
P58335; P58335-2; P58335-3; P58335-4	ANTXR2
P59665; P59666	DEFA1;DEFA3
P61158	ACTR3
P61224; P61224-3	RAP1B
P61626	LYZ
P61769	B2M
P61981	YWHAG

P62328	TMSB4X
P62937	PPIA
P63104	YWHAZ
P67936	TPM4
P68366; P68366-2	TUBA4A
P68871	HBB
P69905	HBA1
P80108	GPLD1
P80188; X6R8F3	LCN2
P80723; P80723-2	BASP1
P80748	IGLV3-21
P81605; P81605-2	DCD
P98160	HSPG2
Q01459	CTBS
Q01518; Q01518-2	CAP1
Q02985	CFHR3
Q03591	CFHR1
Q04756	HGFAC
Q04917	YWHAH
Q06033; Q06033-2	ITIH3
Q06413-6	MEF2C
Q07954	LRP1
Q08380	LGALS3BP
Q10001	
Q12794; Q12794-2; Q12794-3	HYAL1

Q12805; Q12805-2; Q12805-3; Q12805-4	EFEMP1
Q12805-5	EFEMP1
Q12841	FSTL1
Q12860	CNTN1
Q13093	PLA2G7
Q13103	SPP2
Q13201	MMRN1
Q13332; Q13332-2; Q13332-3; Q13332-4; Q13332-6	PTPRS
Q13790	APOF
Q14112; Q14112-2	NID2
Q14116-2	IL18
Q14118	DAG1
Q14126	DSG2
Q14515	SPARCL1
Q14520; Q14520-2	HABP2
Q14624	ITIH4
Q14624-2	ITIH4
Q15067-3; Q3I5F7	ACOX1;ACOT6
Q15113	PCOLCE
Q15166	PON3
Q15293; Q15293-2	RCN1
Q15404; Q15404-2	RSU1
Q15485	FCN2
Q15582	TGFBI

Q15848	ADIPOQ
Q16270; Q16270-2	IGFBP7
Q16610	ECM1
Q16627	CCL14
Q16706	MAN2A1
Q16853	AOC3
Q5MJ68	SPDYC
Q5SZC9; Q9P1F3	ABRACL
Q5T123; Q9H299	SH3BGRL3
Q5TFM2	CFH
Q5VY43	PEAR1
Q68G74-2	LHX8
Q6E0U4-16; Q6E0U4-2; Q6E0U4-5; Q6E0U4-6	DMKN
Q6EMK4	VASN
Q6GTS8	PM20D1
Q6UWP8	SBSN
Q6UWP8-2	SBSN
Q6UX71	PLXDC2
Q6UXB8	PI16
Q6UY14; Q6UY14-2; Q6UY14-3	ADAMTSL4
Q6YHK3	CD109
Q71F56	MED13L
Q71U36; Q71U36-2	TUBA1A
Q76LX8	ADAMTS13
Q7Z7M0	MEGF8

Q86U17	SERPINA11
Q86UD1	OAF
Q86UX7; Q86UX7-2	FERMT3
Q86VX2-2	COMMD7
Q86YW5; Q86YW5-2	TREML1
Q86YZ3	HRNR
Q8IWV2	CNTN4
Q8IXL6	FAM20C
Q8IYA8-3	CCDC36
Q8IZF2; Q8IZF2-2	ADGRF5
Q8NBP7	PCSK9
Q8NDA2; Q8NDA2-2; Q8NDA2-4	HMCN2
Q8TDL5	BPIFB1
Q8WWZ8	OIT3
Q8WZ75; Q8WZ75-2	ROBO4
Q92496; Q92496-2	CFHR4
Q92520	FAM3C
Q92743	HTRA1
Q92820	GGH
Q92859; Q92859-2; Q92859-3; Q92859-4	NEO1
Q92954-3	PRG4
Q93063; Q93063-2; Q93063-3	EXT2
Q96IY4	CPB2
Q96KN2	CNDP1
Q96PD5	PGLYRP2

Q99453	PHOX2B
Q99650; Q99650-2	OSMR
Q99784; Q99784-3; Q99784-5	OLFM1
Q99969	RARRES2
Q99972	MYOC
Q9BQ51	PDCD1LG2
Q9BTY2	FUCA2
Q9BUN1	MENT
Q9BWP8; Q9BWP8-10; Q9BWP8-2; Q9BWP8-3; Q9BWP8-4; Q9BWP8-5; Q9BWP8-6; Q9BWP8-7; Q9BWP8-8; Q9BWP8-9	COLEC11
Q9BXR6	CFHR5
Q9BYJ0	FGFBP2
Q9H089; Q9H4S2	LSG1;GSX1
Q9H1U4	MEGF9
Q9H4A9	DPEP2
Q9H4B7	TUBB1
Q9H4G4	GLIPR2
Q9H6X2; Q9H6X2-2; Q9H6X2-4; Q9H6X2-5; Q9H6X2-6	ANTXR1
Q9H8L6	MMRN2
Q9HBR0	SLC38A10
Q9HCB6	SPON1
Q9HDC9	APMAP
Q9NPG4	PCDH12

Q9NPH3; Q9NPH3-2; Q9NPH3-5	IL1RAP
Q9NPR2; Q9NPR2-2	SEMA4B
Q9NPY3	CD93
Q9NQM4	PIH1D3
Q9NY15	STAB1
Q9NZ08; Q9NZ08-2	ERAP1
Q9NZP8	C1RL
Q9NZT1	CALML5
Q9P232	CNTN3
Q9UBG0	MRC2
Q9UBR2	CTSZ
Q9UBX1	CTSF
Q9UEW3; Q9UEW3-2	MARCO
Q9UGM5	FETUB
Q9UHG3	PCYOX1
Q9UIB8; Q9UIB8-2; Q9UIB8-3; Q9UIB8-4; Q9UIB8-5; Q9UIB8-6	CD84
Q9UJC5	SH3BGRL2
Q9UJJ9	GNPTG
Q9UKD1	GMEB2
Q9UKX2	MYH2
Q9ULI3	HEG1
Q9UNW1	MINPP1
Q9Y251; Q9Y251-2	HPSE
Q9Y490	TLN1

Q9Y5C1	ANGPTL3
Q9Y5Y7	LYVE1
Q9Y646	CPQ
Q9Y6R7	FCGBP
Q9Y6Z7	COLEC10